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Department of Bio Technology
Govt. of india

National Seminar on

CHALLENGES AND INNOVATIVE APPROACHES IN CROP IMPROVEMENT

Agricultural College & Research Institute, Madurai,
Tamil Nadu Agricultural University

December 16 & 17, 2014

Abstract

Organized by
Indian Society of Plant Breeders
Department of Plant Breeding & Genetics, AC&RI, Madurai
Department of Biotechnology, AC&RI, Madurai

National Seminar on

Challenges and Innovative Approaches in Crop Improvement

On the eve of Golden Jubilee Celebrations at

Agricultural College and Research Institute
Tamil Nadu Agricultural University
Madurai

December 16 & 17, 2014

Seminar Abstracts

Organized by

Indian Society of Plant Breeders
Department of Plant Breeding & Genetics
and
Department of Biotechnology
AC & RI, Madurai

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TAMIL NADU AGRICULTURAL UNIVERSITY

Dr. K. Ramasamy, Ph. D.
Vice-Chancellor

Coimbatore - 641 003
Tamil Nadu, India

FOREWORD

Agricultural College and Research Institute, Madurai was started in 1965 and adjudged twice as the best college and is the second biggest, among the constituent colleges of Tamil Nadu Agricultural University to offer Agricultural education and to perform research pertaining to the Southern parts of Tamil Nadu. This institution has grown in leaps and bounds is now in its Golden Jubilee year and in the process of offering specialized courses in Biotechnology such as Tissue Culture, Recombinant DNA technology, Molecular Breeding and Genomics to students through the Department of Plant Breeding and Genetics and the newly created Department of Biotechnology.

I feel great pleasure that the Department of Plant Breeding and Genetics and the Department of Biotechnology supported by ISPB are organising the national seminar on “Challenges and Innovative Approaches in Crop Improvement” during 16th and 17th December 2014 on the eve of the golden jubilee celebrations of Agricultural College and Research Institute, Madurai.

A majority of the population in developing countries depend on agriculture for their livelihood. Green Revolution of the mid 1960s and 1970s was triggered by a yield enhancing breeding strategy. Sustaining and expanding the green revolution is an ecological necessity. If we were to achieve a “Second Green Revolution” or what has been termed by some as “Gene Revolution”, we have to seek the help of new and innovative tools of science. ‘Plant genomics’ is the application of the newly available vast amounts of genomic DNA sequence, using a range of novel high-throughput, parallel and other technologies. Molecular markers is a biotechnology tool for locating genes governing agronomically/horticulturally-important characters. The biotechnology revolution continues to affect nearly every sector of the economy. Today, the importance of Biotechnology to the economy is without doubt. Its practical benefits? Significant already? Continue to unfold will be discussed in this seminar.

The souvenir is a compilation of abstracts of papers and posters presented in the seminar. Thus the content of the souvenir will be a reference guide to the researchers, students and entrepreneurs associated in the field of innovative Plant breeding and Biotechnology.

I place my greetings to the contributors of technical papers, faculty members of various committees, sponsors, organizers towards the successful conduct of this event.

Place : Coimbatore
Date : 25-11-2014

(K. RAMASAMY)

TAMIL NADU AGRICULTURAL UNIVERSITY

Dr. C. R. Anandakumar, Ph.D.,
Director i/c, Centre for Plant Breeding & Genetics and
President, Indian Society of Plant Breeders (ISPB)

Coimbatore - 641 003
Tamil Nadu, India.

FOREWORD

The Indian Society of Plant Breeders is organizing this years' National Seminar at the Agricultural College and Research Institute, Madurai, second largest constituent college of TNAU, located in the temple city of Madurai. Plant Breeders, mostly from southern part of India are gathering in the foot hills of Yanamalai to discuss various challenges and innovative techniques in crop improvement which includes conventional and innovative breeding tools and techniques used in crop improvement programmes. Researchers, state agricultural university professors and post-graduate students are contributing their scientific findings in the form of more than 300 registered conference abstracts. The crop improvement sessions is divided into multiple themes where leading breeders deliver the lead lectures. Additionally, selected abstracts of post-graduate students are given opportunities for oral presentations to enhance their presentation skills in front of bigger audience. The post graduate students of Plant Breeding & Biotechnology are presenting their posters and participating in the best poster competition. The society recognizes their research work by presenting the best poster award for various sessions.

I hope this seminar will give good exposure to the young plant breeders to start their research career with confidence and also with the guidance of the experienced plant breeders who are always the guiding force for the Plant Breeding programme in this country.

Sd/- C. R. Anandakumar

TAMIL NADU AGRICULTURAL UNIVERSITY

Dr. C. Chinnusamy Agricultural College and Research Institute, Madurai
Dean Tamil Nadu, India

FOREWORD

The National seminar on “Challenges and Innovative Approaches in Crop Improvement” is organised at AC & RI, Madurai to mark the Fifty illustrious years (1965-2014) of leadership in agricultural science, education / technology development and innovations. The Institution has gained a place of eminence in the State for spreading technical education to unreachable areas and at the same time bringing thousands of educationists, academicians, researchers, administrators, industrialists and students under its umbrella. Several alumni of this campus are also working as scientists in Indian Council of Agricultural Research (ICAR) and as Professors in State Agricultural Universities and as leading scientists in international laboratories and foreign universities. The national seminar will bring all the scientific man power generated from this great institution back to home institute and share their ideas to plant the novel ideas to young students and researchers of TNAU.

AC & RI, Madurai is always open to develop partnerships among the scientists to develop mutually beneficial relationships between the College and the wide ranging research institutes, international, national and local input industries and hence this seminar will definitely help to achieve the above mandate. The institute was upgraded as Post Graduate Centre in the year 1969 and as Research Institute during the year 1980. The Department of Plant Breeding and Genetics is one of the earliest department established at AC & RI, Madurai when it was upgraded as post graduate centre. It is noteworthy to mention about varieties released in the 50 years of research in Agricultural crops by the Department of Plant Breeding and Genetics that include, five paddy varieties (MDU 1 to 5), one black gram variety (MDU 1), one *Kolingi* variety (MDU 1). Pre-release Rice ACM 01010 is going to be released during the Golden Jubilee Year. The Department of Biotechnology is established during 2014 on the eve of Golden Jubilee celebrations in order to impart the Biotechnological skills to the agriculture graduates and to establish biotechnological research at AC & RI, Madurai.

I am happy to be part of the organization of National seminar on “Challenges and Innovative Approaches in Crop Improvement” during December 16 & 17, 2014. I wish and believe that this seminar venue will be a best platform to exchange the scientific ideas in the foot hills of Yanamalai and the temple city of Madurai where our college is located.

Sd/- C. Chinnusamy

National Seminar on

Challenges and Innovative Approaches in Crop Improvement

On the eve of Golden Jubilee Celebration

Agricultural College and Research Institute, Madurai,
Tamil Nadu Agricultural University

PROGRAMME

16th Dec 2014

12.00 noon-1.00 pm **Session I: Conventional and Marker Assisted Breeding for Crop Improvement**

1. Harnessing Sex Expression and Pollination Mechanism for Commercial Exploitation of Heterosis in Castor

Dr. Amala Joseph Prabhakaran,
Principal Scientist,
All India Co-ordinated Research Project on Castor
Directorate of Oilseeds Research, Hyderabad.

2. Molecular Approaches for the Horticulture Crops Improvement

Dr. Chenna Reddy Aswath,
Principal Scientist & Head, Department of Biotechnology,
Indian Institute of Horticulture Research, Bangalore

2.00 pm – 3.30 pm **Session II & III: Biotic and Abiotic Stress Management**

1. Understanding on the Host Plant Resistance to Herbivore Insects and its exploitation in Crop Improvement

Dr. M. Maheswaran,
Director of Research i/c,
Tamil Nadu Agricultural University, Coimbatore

2. Deployment of Rust Resistance Genes in Wheat Varieties Increased Wheat Production in India

Dr. M. Sivasamy,
Principal Scientist & Head
Indian Agricultural Research Institute, Regional Station, Wellington

3. Challenges and Opportunities in Development of Abiotic Stress Tolerance Rice Varieties

Dr. R. Chandrababu,
Director i/c, Centre for Plant Molecular Biology and Biotechnology,
Tamil Nadu Agricultural University, Coimbatore
Principal Scientist & Head

3.30 pm to 5.00 pm **Concurrent sessions**

5.00 pm to 6.00 pm **Poster session**

17th Dec 2014

09.00 am - 10.30 am **Session IV: Innovative Breeding Methods, Tissue Culture and Genetic transformation**

1. Role of Induced Mutation in Legume Improvement

Dr. J. Souframanian,
Principal Scientist,
Bhabha Atomic Research Centre (BARC), Trombay, Bombay

2. Challenges and Opportunities in Marker Assisted Breeding: A Critical Overview

Dr. H. E. Shashidhar,
Professor and Head, Department of Biotechnology, GKVK, Bangalore

3. Achievements Made Through Conventional Plant Breeding Techniques in Millet Improvement

Dr. M. V. Channabyre Gowda,
Project Co-ordinator (Small millets) ICAR, GKVK, Bangalore

11.00 am – 12.30 pm **Session V: Horticulture and Plantation Crops Improvement**

1. Improvement of Medicinal Plants: Challenges and Innovative Approaches

Dr. P. Manivel,
Principal Scientist (Plant Breeding),
Directorate of Medicinal and Aromatic Plants Research, Boriyavi, Gujarat

2. Current Status of Coconut Genetic Resources, Conservation and Utilization in India

Dr. V. Niral,
Principal Scientist, Division of Crop Improvement,
Central Plantation Crops Research Institute, Kasargod, Kerala

3. Germplasm Conservation in Oil Palm

Dr. P. Murugesan
Principal Scientist & Head,
Directorate of Oil Palm Research, Research Centre, Palode,
Thiruvananthapuram, Kerala

2.00 pm – 3.00 pm **Session VI: Seed Industry & Valedictory function**

1. Emerging Trends in Seed Industry

Dr. S.R. Sree Rangaswamy,
Former Director,
Centre for Plant Molecular Biology and Biotechnology,
Tamil Nadu Agricultural University, Coimbatore

2. Towards Improvement of Oil Content in Safflower (*Carthamustinctorius* L.)

Dr. P. Kadirvel,
Directorate of Oil Seeds Research, Rajendranagar, Hyderabad

Valedictory Function

ORGANIZING COMMITTEES

Chief Patrons	**Prof. Dr. K. Ramasamy,** Vice-Chancellor
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	Dr. S. Lakshminarayanan
	Dr. E. Kokiladevi
	Dr. P. Arunachalam

INDEX

Session I : Conventional and Marker Assisted Breeding for Crop Improvement

1. Harnessing sex expression and pollination mechanism for commercial exploitation of heterosis in castor

Dr. Amala Joseph Prabhakaran
Principal Scientist,
All India Co-ordinated Research Project on Castor
Directorate of Oilseeds Research, Hyderabad.

Castor is an important non-edible oilseed crop and India completely monopolized the global castor market by producing 21.77 lakh tones of castor seed from 13.17 lakh ha of land cultivated with castor in 2012-13. Interestingly, India also ranks first in productivity among castor growing countries and the productivity levels are ever increasing year after year. In 2012-13, the crop has witnessed a steady increase in the productivity level to 1653 kg/ha when compared to the previous year achievement of 1592 kg/ha. Castor crop continued to be preferred by the farmers in traditional castor growing states due to the increasing demand and remunerative market prices. The timely availability of quality seeds of the most popular hybrids like GCH 7 in Gujarat and Rajasthan facilitated by both public and private seed agencies, expansion of the crop to other nontraditional areas of the country under irrigation and adoption of location-specific nutrient and crop management for varied castor growing environment are the major factors for the improved levels of productivity.

Hybrid development

Identification of completely pistillate plants and presence of exploitable levels of heterosis paved the way for hybrid castor development. Subsequently, hybrid vigour was commercially exploited and the first castor hybrid, GCH.3 (TSP 10R x J1.15) was released for replacing the variety under cultivation. The hybrid was shown to possess more efficient root system than the varieties under receding moisture conditions. Thus hybrid technology has successfully been adopted in castor for the first time and several high yielding hybrids were developed in India suitable for both rainfed and irrigated ecosystems (Table 1). Unlike other hybrid crops, public bred hybrids are more popular and in demand in castor. Most of the private seed companies produce and market hybrids released through AICRP on Castor and GCH 7 is the most popular and high in demand.

Sex expression

The commercially viable hybrid seed production has been facilitated by the use of unique environment sensitive pistillate lines as female parents. Castor is a typically monoecious plant but the proportion of male and female flowers is greatly influenced by non-genetic factors. In normal monoecious varieties, the percentage of pistillate flowers on racemes is usually highest on main raceme and decreases gradually on subsequent raceme orders. A proportionate increase in number of male flowers related with proportionate decrease of pistillate flowers is highly influenced by seasons. Female tendency is highest in spring/early summer or winter, while male tendency is maximum in mid and late summer. The effect of temperature on the male/

Table 1. Castor hybrids released for cultivation in India

Hybrid	Year of release	Area of Adaptability	Salient features	Pedigree
GCH-3	1986	Gujarat	For irrigated condition	VP-1 x JI 35
GCH-4	1988	Gujarat	Dry & irrigated conditions	VP-1 x 48-1
GCH-5	1996	All India	Resistant to wilt, jassids	Geetha x SH-72
DCH-32	1998	All India	Resistant to sucking pests & tolerant to wilt	LRES-17 x DCS-5
GCH-6	1999	Gujarat, Rajasthan, Maharashtra	Resistant to root rot and white flies	JP 65 x JI 96
PCH-1	1999	Rainfed areas of AP	Resistant to leaf hoppers	VP-1 x PCS 124
TMVCH-1	1999	Tamil Nadu	Moderately resistant to wilt and gray mold	LRES-17 x TMV-5
DCH-177	2000	Rainfed areas of South India & Maharashtra	Resistant to white fly, Resistant to wilt	DPC-9 X DCS-9
RHC-1	2002	Irrigated & Rainfed Rajasthan	Tolerant to wilt and resistant to jassids	VP-1 x TMV5-1
DCH-519	2006	All India	Resistant to *Fusarium wilt,* leaf hoppers	M574 X DCS-78
GCH-7	2007	Irrigated, Gujarat	Res. to wilt and tol. to white fly, jassids and thrips	SKP 84 x SKII 215
YRCH-1	2008	Rainfed, Tamil Nadu	Resistant to wilt	DPC 9 x TMV 5
PCH-111	2014	Rainfed, Telangana	Resistant to wilt	DPC 9 x CS 1

female flower ratio was studied. Moderate temperature (32°C) promotes female tendency while high temperature promotes male tendency.

Castor though a typically monoecious type is a sexually polymorphic species. The basic sex forms in castor range from monoecious to pistillate and hermaphrodite forms.

- **Monoecious:** A spike with basal 1/3rd to half portion filled with male flowers and the upper portion female flowers

- **Pistillate**: A spike with female flowers completely
- **Interspersed or ISF:** A pistillate spike with male flowers interspersed throughout the spike
- **Revertant:** A pistillate spike that reverts to monoecious in later orders

At DOR, in order to study the genetic control of this trait, crosses between complete male vs pistillate plants and monoecious vs complete male and the F_1 hybrids have shown differential sex expression in each combination varying from complete male, ISF, IPF, pistillate, monoecious, etc. Monecious trait was found to be dominant over complete male expression with an increase in proportion of male flowers. Substitution BCs have been continued and 8 isogenic male and 2 pistillate stocks have been developed. It will be easy to understand the genetic control of this trait using these genetic stocks.

Seed production

Time of planting and specific season has profound influence on sex expression. While summer and *kharif* seasons provide ideal male promoting environment for undertaking seed production of varieties, male and female parents of hybrids, *rabi*-winter is the most ideal season for taking up hybrid/certified seed production as it is most conducive for production of female flowers. In case of varieties and male parents, such an exposure to male promoting environment i.e. *kharif*-summer encourages good expression of less productive plants bearing mostly male spikes which could be easily eliminated through timely roguing. Similarly, the female parents when raised in male promoting environments produce environmentally sensitive staminate flowers which are very essential for self reproduction of the female parents. Based on the differential genotypic response to environment, the following seeding dates are suggested for various categories of seed.

Hybrid Seed Production

It is done in a female promoting environment where the pistillate line does not produce staminate flowers. Certified hybrid seed requires 85% genetic purity. To attain this high percentage of genetic purity, good quality female and male line seed should be ensured**.** Thus, seed should be collected from authentic sources or the institutes themselves. Secondly, contaminations

Stage of seed production	**Areas / regions**	
	Western and Northern	**Southern states**
Varieties and male parents		
Nucleus and breeder	February 1st FN	January 2nd FN
Foundation and certified	July 1st FN	June 2nd FN
Female parent and hybrid		
Nucleus and breeder	February 1st FN	January 2nd FN
Foundation	July 1st FN	
Certified (Hybrid)	August 2nd FN	September 2nd FN

should be avoided by following stipulated isolation distance (1000M) and timely rouging should be done. Sowing should be done by August end to October- depending on the onset of winter season in different locations so that primary and secondary spikes coincide with cool season. If delayed beyond October, flowering period experiences higher temperatures resulting in ISF in female lines.

Pollination mechanism

It is commonly believed that in castor the staminate flowers open first. The stigma was found to be mature and receptive even 12 hours before opening time and continues to be receptive for 72 hours after the opening of flower. Anthesis in castor takes place from 4 A.M to 8 P.M. Besides wind, insects also play a role in pollen dispersal and results in variable levels of out-crossing leading to contamination of varieties and parental lines. Hence, maintaining proper isolation distance is very important in nucleus and breeder seed production to maintain genetic purity.

Castor hybrid seed production is entirely a cross-pollinating process and it is absolutely essential to avoid undesirable pollen in seed production. The extent of cross-pollination mainly depends on the direction and velocity of wind, which is the primary source of pollen dispersal. Earlier studies on vicinism in monoecious varieties indicate that the pollen travels as much as 270 m from the source in the windward direction if the sky is clear and the wind velocity is above 20 km per hour. On rainy days, no pollen movement/ dispersal has been reported. The proportion of female and male flowers on the raceme also determines the extent of cross-pollination. It was thought that in monoecious varieties which produce abundant pollen, cross pollination is very much limited even when contamination source is nearer because of the failure of foreign pollen to compete with native pollen while genotypes which produce mostly female or 100% female racemes easily get contaminated by foreign pollen from sources located as far as 1000 m distance.

However, it was brought to the notice of the Directorate of Oilseeds Research by the Gujarat Seed Producers' Association that presence of interspersed staminate flowers (ISFs) in SKP 84 (pistillate parent of GCH 7) in seed production plots was not affecting the quality of hybrid seed produced as evident from the pass percentage of seed lots by Gujarat Seed certification agency. Initially, both private seed producers and state seed agencies, have suspected the ISF produced in the pistillate parent SKP 84 to be pollen sterile. However, the studies conducted on the IS flower samples collected from the large scale hybrid seed production plots of GCH 7 at Panjmahal and Vadodara districts of Gujarat state revealed that the pollen fertility was intact in ISFs. The quantum of pollen produced by the ISF was also seems to be normal. In order to ascertain the reason behind the above observation, an experiment was planned in summer 2013. The aim of the study was to understand the selective mechanism in the pistillate flower to accept the foreign pollen even in the presence of its own pollen from ISF when both are available, thereby aiding cross pollination. Interestingly, the same pistillate flower accepts its own pollen when the foreign pollen is not available near by. The results indicated that abundant availability of foreign pollen aids in more of cross pollination rather than self pollination in pistillate lines. To understand this phenomenon further, another experiment was conducted with known quantity of pollen from IS flowers and male lines in different proportions like 1:1, 1:2, 1:3 and 1:4 and vice-versa under controlled pollination. The resultant hybrids have been raised in *kharif* 2013-14 and it was found that pollination with higher proportion of pollen from male parents result in high cross pollination while the self pollination was negligible. However, the same trend was not true with higher proportion of pollen from ISF of the pistillate lines. Though there was an increase in self pollination with the increase in addition of ISF pollen, still cross pollination was observed to an extent. In order to ascertain these obseravations under natural pollination, the female parent SKP 84 has been raised with its male counterpart in isolation. The results were confirming the earlier observations that pollen quantity decides the type of pollination and pistillate flowers prefer foreign pollen rather than its own thus aiding high degree of cross pollination in castor.

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2. Molecular Approaches for the Horticulture Crops Improvement with Special Reference to Ornamental Crops

Aswath C, Lakshmana Reddy and Manjunath Rao
Indian Institute of Horticultural Research,
Hesserghatta Lake post, Bangalore

Despite the tremendous economic importance of the floricultural industry worldwide with production values of several billion US dollars per year strategies for breeding new cultivars lag behind those developed for many horticultural crops. Apart from the high diversity of ornamental species under cultivation which limit the input that can be afforded for the individual crop, reasons can be found in complex genetic systems of the major crops as e.g. roses, carnations, chrysanthemums and in the lack of genetic variability in the gene pools available. For a long time simple breeding schemes were sufficient to generate a large number of varieties with novel traits that could be marketed successfully. However, with increasing competition between breeders and producers, rising prices for energy and increasing limitations for the application of pesticides, more sophisticated strategies for breeding new ornamental varieties are necessary to meet the demands imposed by the markers.

Genomic resources like whole genome sequences, expressed sequence tags (ESTs), genomic survey sequences (GSS) and high throughput genome sequences (HTGs), molecular markers like SSRs and SNPs are developed and integrated in main stream horticultural breeding programmaes to maintain the growth of these crops on par with field crops like rice, wheat and maize and to add associated traits like biotic and abiotic stress, quality parameters. Genomics in ornamental crops are still not being exploited except rose. The flowering plant species *Mimulus guttatus* (monkey flowers) has become a leading model system for studying ecological and evolutionary genetics and has been sequenced by Joint Genome Institute (www.jgi.doe.gov). Like all plant genetic model systems, *Mimulus* species have a small genome (about 430Mb), short generation time (6 to 12 weeks), high productiveness (100 to 2000 seeds per pollination), self-compatibility, and easy propagation.

Apart from the use of molecular tools for the identification and verification of varieties two main areas are relevant for ornamental plant breeding. Marker assisted breeding utilises the information of markers linked to genes of interest to develop more efficient selection strategies. This is of particular importance where important traits are difficult to analyse or where simultaneous combinations of several genes are needed (e.g. resistance genes). In addition, the introgression of interesting target genes from wild species genomes may be more efficient with marker assisted selection against the genetic background of the wild donor species. The second area comprises techniques for genetic engineering of ornamental plants. The available gene pool for novel target genes is virtually unlimited in this area . For both areas the target traits are mainly centred around disease resistance, stress tolerances, delayed senescence, post harvest performance, novel colours and changed plant architecture. Of main importance for the future availability of genes both for marker assisted selection and for genetic engineering are the results from the ongoing genome projects in model organisms. These provide valuable information on the genetic architecture of flowering plants. The efforts undertaken in these projects also boosted technological developments (like e.g. microarrays, bioinformatic tools, transformation technologies) that will strongly influence ornamental plant breeding in the near future.

The objectives of this paper was to compile the availability of genomic resources in horticultural crops with special reference to ornamental crops, make sequence information useful for breeders, to identify potential future challenges which one can face while making proper use of genomic resources. The genomic resources can be utilized for both basic and applied research.

Marker development in ornamentals has been lagging behind compared to marker development in large agricultural and horticultural crops. This is partly due to the fact that there are many different ornamental crops. As markers need to be developed for each of these crops separately, the costs related to development and the time needed to develop them were obstacles. In addition, morphological characteristics are important during ornamental breeding of new cultivars, and these can be assessed without the use of markers. This is slowly changing, as it becomes more important to develop cultivars that have growth characteristics suitable for specific environments, and breeding also has to focus on traits that are difficult to assess and/or are controlled by multiple loci (quantitative traits), including stem production, time to flowering, flower size, and disease resistances. In IIHR, linkage map has been developed in Anthurium and other molecular related work in rose, carnation, tuberose, crossandra, gladiolus etc is in progress.

In ornamental plants higher ploidy levels and aneuploïdy are very common and this is a major drawback because measurement of dosage in random sets of varieties is often not possible. One approach is to take the presence or absence of each allele as a dominant marker . In view of this, for most ornamental crops SSR markers are preferable over SNP markers because of their high information content (multi-allelic) as markers for database building. Recently, 454 pyrosequencing was used to sequence the cDNA of *Lilium* and tulip as a first trial in ornamental plants to generate SNP and SSR markers using high throughput technologies (Shahin et al., in prep.) and Illumina sequencing was used for the transcriptome of rose (Boucoiran, Gitonga et al., in prep.). As is common in lily, the cultivars sequenced are hybrids made by crossing parents from different species within a section of the genus. As a consequence, they are very heterozygous, and the genetic distances between the parental species leads to so many genetic differences between alleles that the distinction between homologous and paralogous genes sometimes is not straightforward in all cases.

The important agronomic traits linked to molecular marker assisted improvement in ornametal crops breeding programs are disease resistance, yield and quality, floral characteristics, cold hardiness and dormancy. *Fusarium* resistance in lily is controlled by six putative QTLs (Shahin *et al.,* 2010). Markers for each of these QTLs would make it possible to select progeny plants that have inherited the combination of these six loci. As this can already be done in a seedling stage, this would speed up the breeding process, especially in bulbous ornamentals, which have a long juvenile phase (3 years in lily, 5 years in tulip). In the case of introgression of disease resistances from wild relatives, markers can also be used to assist selection against wild germplasm unlinked to the desired QTLs.

Many ornamental genomes are too large to completely sequence to sufficient depth with the current techniques. Besides, it is not necessary to generate so much sequence information, as 200 to 1000 SNPs will suffice to generate a genetic map of the two parents, and they are also sufficient to be able to find markers that will be associated with traits in a segregating population derived from a cross between two plants (for an association study more markers mat be needed). In the past five years, the emergence of massively parallel sequencing technologies has dramatically reduced time and costs for sequencing. These developments will continue and sequencing will become cheaper while fragment lengths will increase. Importantly, parallel sequencing can be done for many targets, or even on the complete genomic DNA, without prior knowledge of the DNA. Hence it now becomes feasible to generate large amounts of DNA sequence information for species for which little prior sequence information exists, and to mine these sequences for polymorphisms that form the basis of the development of molecular markers. These molecular markers can be applied for marker-assisted breeding (MAB) and identification of cultivars and hybridization events. It offers great opportunities for ornamental crops, for which few molecular markers are currently available.

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Session II & III: Biotic and Abiotic Stress Management

1. Understanding on the Host Plant Resistance to Herbivore Insects and its exploitation in Crop Improvement

Dr. M. Maheswaran
Director of Research i/c,
Tamil Nadu Agricultural University,
Coimbatore - 641 003.

Crop plants are inflicted by many and of various types of insect pests at different levels of crop growth causing severe yield loss. Crop losses due to these harmful insect pests can be circumvented by adopting various strategies which include 1) cultural practices, 2) biological control, 3) insecticide use, 4) integrated pest management and exploitation of Host-Plant Resistance (HPR). The strategy of employing HPR for insect control is being considered to be one of the ideal means of insect pest control when Painter (1951) recognized the role of HPR in insect pests cop plants. Painter (1957) considered HPR as a source which needs thorough understanding on the biology and behavior of insects in relation to their respective host and proposed three components *viz.* antibiosis, antixenosis and tolerance responsible for HPR. In 1960s agricultural scientists started exploring the genetics behind the HPR anticipating to exploit the HPR to evolve resistant crop varieties through their breeding programmes. Thus much of the knowledge on the inheritance of HPR comes from agricultural research and to evolve durable strategies to conserve plant resistance. In all these inheritance studies, simple screening methods were employed and the level of resistance in the segregating progenies is measured based on visual scores based on which the number of genes are decided. In many of the situations, the continuity in the levels of resistance observed in the segregating progenies was categorized to fit a genetic model to decide the number of genes. The scoring system employed to assess the levels of resistance does not identify the cause for resistance is due to antibiosis or antixenosis or tolerance. As far as resistance/susceptibility in a host, a score based on visual damage at plant level ignores stage specific variations in defense patterns and never resolves the multiplicity of factors responsible for plant resistance. The present day tools such as molecular markers to translational genomics facilitated to move from the cognitive level of plant resistance to molecular level so that the component of plant resistance can be better exploited to evolve varieties with durable resistance to mankind. The presentation deals with facts and fallacies associated with inheritance of plant resistance to insect pests and its exploitation in crop improvement.

2. Deployment of rust resistance genes in wheat varieties increased wheat production in India

Dr. M. Sivasamy
Principal Scientist & Head,
Indian Agricultural Research Institute,
Regional Station, Wellington

Introduction

Wheat is one of the most staple cereal food crop produced in the world followed by maize. Global wheat production reached a record high of 690 mt - 4.3 percent up on 2012 (FAO 2013). Over the last 50 years, in India the wheat production and productivity gradually increased to reach all time high of 95.91mt from 31.3 mha area during 2013-14 (*Anon,*2014) and it ranks second in the world wheat production next to China, with an average productivity of 3.12 t/ha, which is higher than the global average of 3.1t/ha (*Anon,*2013). In India 95% of wheat production contributed by *Triticum aestivum*, followed by *T.durum*(4%) and *T.dicoccum* (1%). Over the past, wheat production in India witnessed a moderate growth rate of 2.25% and to meet the growing demand from projected population growth we need to produce over 110 million tons by 2020 AD which is a challenging task for the wheat researchers and planners. There are several biotic and abiotic constraints towards sustaining and realizing the potential yield in wheat. Among biotic stresses, the rust pathogens challenge wheat production globally with diverse race profiles. In India also, wheat crop is severely damaged by all the three rusts viz., black or stem rust (*Puccinia graminis* f. sp. *tritici* Erik. & Henn), brown or leaf rust (*Puccinia triticina* Erik.) and yellow or stripe rust (*Puccinia striiformis tritici* West). By effectively managing the rust diseases through planned deployment of effective rust resistance genes India could gradually increase the wheat production to reach a record harvest of 95.91m.tonnes during 2014-15. An analysis and report of PD wheat 2013-14 high lights that for the decade (2004-05 to 2013-14) indicated that the production has witnessed an increase of 27 million tonnes which is 40 percent change during the period which is attributed to release and replacement of rust resistant wheat varieties.

Wheat Production trend:

India's Wheat Production and Area

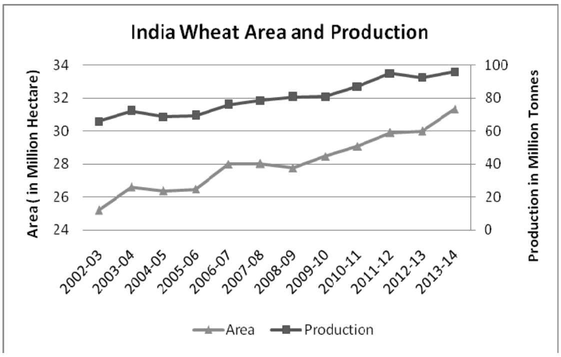

Figure-1

Source: DE&S

- India's wheat production has increased in last 10 years at CAGR of 2.58%
- Area under wheat cultivation has also increased in last 10 years at CAGR of 1.67 %.

- India's share in global production was 13.1% in year 2013-14.

In India three species of wheat namely *Triticum dicoccum, T.durum* and *T.aestivum* are cultivated and major area and production from is *T.asestivum.*

Wheat rusts in India: Occurrence, epidemiology and management

Stem rust pathogen *Puccinia graminis* f.sp. *tritici* survives throughout the year only in the Nilgiri hills of south India and the Himalayas are too cold for pathogen to survive during winter. Therefore, consequent upon cessation of wheat cultivation from Nilgiris the stem rust has drastically disappeared from India owing to debilitated inoculum build up in absence of host. Leaf rust pathogen *Puccinia triticina* needs an intermediate temperature thus survives and spreads both from southern (Nilgiris) and northern (Himalayas) foci and is of countrywide importance (Nagarajan and Joshi, 1985). A second leaf rust pathogen infects both durum and bread wheat. The pathogen is a member of the *P. recondita* complex (*P. triticiduri* V. Bourgin). Subsequently, this rust has ravaged wheat crop several times causing varietal break down of famous post green revolution wheat cultivars WL 711, Arjun, WH147, HD2329, HD2285, PBW 343 etc. Stripe rust pathogen *Puccinia striiformis* that needs low temperature survives the whole year in the Himalayas is an endemic pathogen in cooler parts of the country and its epidemic in early seventies were responsible for withdrawal of a high yielding semi dwarf variety Kalyansona in north India

Table-1. Field dominance of pathotypes of wheat rust pathogens monitored through survey/ surveillance in India over the years

Span	Black rust	Brown rust	Yellow rust
Till 1975	11,11A,14,15,17,21,24,24A,34, 34 –1,40,42	10,11,12,12a,17,20,63, 77,106.107,108, 162	13,14,19,20,31,38
1975 - 80	21-1,40A,21A-2	77A, 104	14A,20A,38A, I
1980 - 85	117A-1	114A,104B,12-2	K
1985 - 90	40-1,117-1	77-1,77-2,77-3,12-1, 12-3,12-4,107-1,108-1	L,N,P
1990 - 95	117-2,117-3,117-4,117-5,117-6	77-4,77-5,104-2,104-3	T,U,CI, CII, CIII
1995 - till date	40-2	77-6,77-7,77-8	*Yr9* virulence (46S119), 78S84

Types of rust resistance in wheat

During the last two decades, identification of resistance genes and development of near isogenic lines has been accomplished in Wheat – *Puccinia* system. In recent compilation McIntosh (2012) has listed >55 of stem rust, > 70 of leaf rust, >48 of stripe rust that accord resistance against pathogenic populations of *P. recondita tritici*, *P. graminis tritici* and *P. striiformis* and some of the linked genes conferring multiple disease resistance which include rusts, powdery mildew, Bydv, eye spot etc.,. Majority of them classified as race specific genes(genes with major effect, vertical resistance) with hypersensitive response to the pathogen and the others being race non-specific(minor genes or APR or horizontal).

Gene Deployment strategies to combat rusts

The cultivation of rust resistant wheat varieties is the most economical, efficient and environmentally advantageous method to reduce yield losses caused by rust diseases. Judicious deployment of rust resistance genes has kept the rust diseases under control. Evolution of new virulent races of rust pathogens is a continuing phenomenon which renders resistance genes ineffective and thus necessitates deployment of newer genes. However, this approach demands a constant effort to identify, characterize and incorporate resistance genes, mainly due to the great capability of rust populations to change (McCallum *et al.,* 2005).

Lagudah (2011) proposed the effective use of specific rust resistance genes, out of which over 150 resistance genes that confer resistance to either leaf rust, stripe rust or stem rust have been catalogued or introgressed into wheat from related species. Few of these genes are highly influenced by environmental factors as well as genetic background of the host plants (McGregor and Manners, 1985) and few of these genes are the slow-rusting adult plant resistance (APR) type that confer partial resistance in race non-specific manner to one or multiple rust diseases. Slow rusting, race non- specific or partial resistance was defined by Parlevliet (1975). Slow rusting is a type of resistance where disease progresses at a retarded rate, resulting in intermediate to low disease levels against all pathotypes of a pathogen. The concept of race non specific, horizontal resistance was widely used by Caldwell (1968) in breeding leaf rust resistant wheat varieties. APR is commonly detected at the post-seedling stage and often as field resistance, although some APR genes are sensitive to varying temperature and light conditions. Developing elite and durable disease resistant wheat cultivars by introgression of effective genes through hybridization and marker assisted selection at IARI, Regional Station, Wellington

Leaf rust resistance maintained and utilised at IARI, RS, Wellington

Sl.No	Leaf rust genes (Out of 67 cataloged genes)	Source
1	*Lr9**	*Aegilops umbellulata*
2	*Lr19*+Sr25*	*Thinopyrum ponticum= Agropyron elongatum*
3	*Lr24+Sr24**	*Thinopyrum ponticum= Agropyron elongatum*
4	*Lr26+Sr31+Yr9+Pm8**	*Secale cereale(Petkus Rye)*
5	*Lr28**	*Aegilops speltoides*
6	*Lr32*	*Aegilops squarossa=Triticum tauschii*
7	*Lr34*+Yr18+Bdv1+Ltn*	*Triticum aestivum*

Sl.No	**Leaf rust genes (Out of 67 cataloged genes)**	**Source**
8	*Lr35(APR Race specific)+Sr39**	*Ae.speltoides*
9	*Lr37+Sr38+Yr17**	*Ae.ventricosum*
10	*Lr39* (Down this all are under current programe)*	*T.tauschii*
11	*Lr41*	*T.tauschii*
12	*Lr42*	*T.tauschii*
13	*Lr44*	*Triticum spelta*
14	*Lr45*	*Secale cereale(Imperial Rye)*
15	*Lr46(APR-Race non-specific) +Yr29**	*T.aestivum*
16	*Lr47**	*Ae.speltoides*
17	*Lr48*	*T.aestivum*
18	*Lr49*	*T.aestivum*
19	*Lr53+Yr35**	*T. dicoccoides*
20	*Lr57*	*Aegilops geniculata*
21	*Lr67+Yr46(APR gene)*	*T.aestivum*

Stem / Yellow Rust Resistance gene Sources maintained and introgressed
*** markers available   # Ug99 specific progrmme under way**

Stem Rust genes (Out of nearly 50 catlouged genes)	**Sources**	**Yellow Rust genes (Out of nearly 50 catlouged genes)**	**Sources**
Sr2 +Lr27+ Yr30+ Pseudo Black Chaff #*	*T.aestivum*	*Yr5**	*T.spelta*
Sr22 (APR) # (Reduced segment available)*	*T.boeoticum*	*Yr9+Sr31+Lr26+ Pm8**	*Secalecereale*
Sr24+Lr24 #*	*Thinopyrumponticum*	*Yr10**	*T.Spelta (moro)*
Sr25 +Lr 19 #*	*Thinopyrumponticum*	*Yr15**	*T.dicocoides*
Sr26 #*	*Thinopyrumponticum*	*Yr16*	*T.Aestivum - Capelle-Desprez*
Sr27 #	*Secalecereale(Imperial)*	*Yr17+Lr37+Sr38**	*T.venticosum*
Sr29 #	*T.aestivum*	*Yr18+Lr34**	*T.aestivum*
Sr30	*T.aestivum*	*Yr24*	*T.aestivum*

Stem Rust genes (Out of nearly 50 catlouged genes)	**Sources**	**Yellow Rust genes (Out of nearly 50 catlouged genes)**	**Sources**
*Sr31+Lr26+Yr9+ Pm8**		*Yr26**	*Hynaldiavillosa*
Sr32 (Yeild penalty)	*Ae.speltoides*	*Yr27+Lr13*	*T.aestivum*
Sr33 #*	*T.tauschii*	*Yr28**	*T.tauschii*
Sr35 #	*T.monococcum*	*Yr29+Lr46**	*T.aestivum*
Sr36+pm6 #*	*T.timophivii*	*Yr30+Sr2+Lr27**	*T.aestivum*
*Sr38+Lr37+Yr17**	*Ae.ventricosa*	*Yr35+Lr53**	*T.dicocoides*
Sr39+Lr35 # (Yeiild penalty)*		*Lr57 + Yr40(APR)*	*Ae.geneculata*
Sr42	*Ae.speltoides(APR)*	Lr67+Yr46	Aestivum
Sr43	*T.aestivum*		
Sr44 #	*T.ponticum*		

List of varieties released carrying known resistance genes

Name of the variety	**Pedigree**	**Year of release/ Genes it carries**	**Zone for which released**
Released Ones 1.HW 2004 (Amar)	C 306//Tr 380-14*7//3 Ag # 14	*1997Lr24+Sr24*	Central zone, Rain fed
2.HW 1085(Bhavani)	HW 2002A//CPAN 3057	*1998Lr24+Sr24, Sr31+Lr26+Yr9+ Pm8*	Southern Hill Zone, Medium Fertility, Timely Sown
3.HW2044 (Kurinji)	PBW 226*5//Sunstar* 6/C 80 -1	*2000Lr19+Sr25*	Southern Hill Zone, Medium Fertility, Timely Sown
4.HW2045 (Kaushambi)	HD2402*5//Sunstar*6/ C80-1	*2003Lr19+Sr25*	North Eastern Plain Zone, Late Sown
5.HS 375 (HIMGIRI)	BB/G11/CJ 71/3/ TAEST//KAL/BB	*2003Lr13+, Sr31+*	Northern Hill Zone, very high altitude, Timely sown
6.HS 420(Shivalik)	RAJ3302//cmh 73a-49*7/3*cno 79	*2003*	Northern Hill zone, Late Sown, RIR

Name of the variety	**Pedigree**	**Year of release/ Genes it carries**	**Zone for which released**
7.HD 2833 Pusa wheat 105	PBW 226/HW 1042 (Tr 380-14*7/3 Ag#14)// HD 2285	*2005/06Lr24+Sr24, Sr31+Lr26+Yr9+ Pm8*	Peninsular Zone, LS
8.MACS 6145 (HW 2034)	C 306*9/CS 2A/2M* 4/2	*2004Lr28*	North Eastern Plain zone, Rain-fed
9.COW(W) 1 (HW 3094)	HD 2646//HW 2002A/ CPAN 3057	*2005Lr24+Sr24, Sr31+Lr26+Yr9+ Pm8*	Areas adjoining Southern hills and hills in Tamil Nadu/ Karnataka (wheat for warmer areas)
10.HD 2888	C 306/*T. spherococcum*/ HW2004	*2008Lr24+Sr24,*	North Eastern Plain Zone, Rain fed
11.COW2 (HW1095)	NP200/20Kr	*2010*A semi-dwarf disease resistant dicoccum	Areas adjoining Southern hills and hills in Tamil Nadu/ Karnataka – Southern Hill zone
12.HD 2967	ALD/COC//URES/HD 216 OM/HD 2278	*2011APR genes for stem and Yellow,*	For the state of Punjab as state release
13.HW 5216	PBW 343//HW 3083	*2012Lr24+Sr24, Sr31+Lr26+Yr9+ Pm8*	Areas adjoining Southern hills and hills in Tamil Nadu/ Karnataka – Southern Hill zone
14.HW 1098	NP 201//200Gray		All diicoccum growing areas in India
15.HD 3059 (Pusa Pachheti)	KAUZ // ALTAR84 / AOS /3 / MILAN / KAUZ / 4/HUITES		NWPZ
16. HD 3086	DBW14/HD 2733// HUW 468		NWPZ

Name of the variety	Pedigree	Year of release/ Genes it carries	Zone for which released
17. HD 3090	SFW/VAISHALI/UP 2425	*Lr24+Sr24, Sr31+Lr26+Yr9+ Pm8*	PZ
18. HW 1098(dic) Nilgiri Khapli	NP 201/200 gray	*Sr2+*	All dic cultivating zones(PZ/CZ/SHZ)
19. HW 5207(COW3)	Hw 3029// V763-2312 (Yr15)	*Sr2, Sr24/Lr24, Yr15*	Non-Traditional areas in TN
Identified ones			
1.HW 3070	HW 3002// HI 1077	*2003Lr24+Sr24, Sr31+Lr26+Yr9+ pm8*	Southern Hill Zone, MF, TS
2. HW 5001	HD 2626// HW 2002A/ CPAN 3057	*2004, Lr24+Sr24, Sr31+Lr26+Yr9+ Pm8*	Southern hills, areas adjoining Southern hills
3.HW 5207	HW 3029//Yr15	*2009-10Lr24+Sr24, Sr2+, Yr15*	Southern hills, areas adjoining Southern hills

Single gene concept

Initially during 1980's the single dominant or major genes were intreogressed into cultivars through conventional back cross menthod which include Lr9, Lr19/Sr25, Lr24/Sr24, Lr26/Sr31/Yr9/Pm8, Lr28, Lr32, Lr37/Sr38/Yr17 etc.,. and subsequently some of the genes had been overcome newly evolved pthotypes and hence adapted to gene pyramiding .

Pyramiding Resistance Genes: several genes accumulated in a single cultivar to bring in the field durability of resistance

When only a single resistance gene is there in a host soon it tends to become susceptible. Subsequently adding one or a few more resistance gene in the background of that cultivar will make it resistant. But if these genes are brought into one background, as gene action is additive, the host will be resistant to a wide spectrum of the pathogen and the resistance base will last long. Since gaining virulence is at the cost of fitness, a pathotype able to infect all the resistance genes in such a variety is likely to be less fit in nature and hence may not induce epidemic. This approach of pyramiding resistance genes, might also prolong the usefulness of the resistance genes.

Current status of gene pyramiding in India

If India had not experienced frequent rust epidemics, it is because of the cultivation of diverse genotypes carrying different resistance genes. The current status of rust resistance breeding involves both conventional and molecular breeding approaches including QTL mapping. Pyramiding of major genes using marker assisted selection in agronomically suitable cultivars is being pursued (Samsampour *et al.,* 2009; Revathi *et al.,* 2010; Kailash *et al.,* 2011; Vinod *et al.,* 2010; Chhuneja *et al.,* 2011) to prevent the breakdown of resistance and the pyramided lines are being tested at multi-locations for their yield potential. Resistance genes have also been incorporated through conventional breeding methods, which have later been confirmed molecularly (Sivasamy *et al.,* 2009) . Leaf rust resistance genes *Lr19/Sr25* and *Lr28* are pyramided in the background of cv. HD2687 carrying 1BL.1RS translocation using marker assisted (back-ground selection) breeding (Kailash *et al.,* 2011). Marker assisted background selection can result in rapid recovery of recurrent parent genotype in a short span of 2-3 backcross generations (Ribaut *et al.,* 2002).

Cook*6/C80-1, an Australian line carries *Lr19/Sr25* plus a DNA segment carrying *Sr36/Pm6* from *Triticum timopheevi* was used as donor for *Lr19*. The pyramided line showed more than 90% genomic similarity with recurrent parent, HD2687. Another popular cultivar HD2932 has been improved for multiple rust resistance by marker assisted transfer of genes *Lr19, Sr26* and *Yr10* (Niharika 2012). Similarly, popular cultivars HD2733 and HD2967 are being improved by transferring multiple rust resistance genes utilizing MAS. Effective gene for stripe rust resistance (*Yr*15) has been introgressed into a popular but rust susceptible cultivar HD2329 (Vinod *et al.,* 2006).

Currently, the cultivar HD2967 is occupying a large area in NWPZ. It exhibits resistance to all the three rusts at adult plant stage. A high degree of APR against most virulent and prevalent races 77-5 and 104-2 is ascribed to minor gene based durable resistance (Malik *et al.,* 2012), although it has been postulated to carry *Lr13*+ which alone is not effective against above mentioned races of leaf rust. Details on genetical markers can be accessed through *maswheat. ucdavis. edu/*

Conclusion

To effectively combat and checkmate the rust epidemics in the country the race specific and non-race specific resistance genes needs to be pyramided with the high yielding varietal background which are expected to confer durable rust resistance by taking advantage of 'hot spot' locations and available markers in the public domain, linked to catalogued genes. Identification and mapping of rust resistance genes is crucial for development of effective and durable resistance in wheat. The intense efforts are currently made worldwide search for APR genes and many of identified ones are from Indian bread wheat genotypes offer much scope to exploit the large pool of Indian old varieties and land races expected to carry additional APR genes. Hence, the search for this type of novel or similar type of resistance in the durum or hexaploid wheat should be intensified.

3. Genomics assisted breeding for resilient rice: Progress and Prospects

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Rice, (*Oryza sativa L.)* is an important food crop for half of the worlds' population. Rice production increased by 180 per cent, from 257 to 718 million tons between 1996 and 2011 and 25 per cent more rice needs to be produced by 2030 (Khush, 2013) and 70% of this increase has to come from shrinking land, water and other resources (Foley et al., 2011). Current productivity growth in rice (Ray et al., 2013) will not be sufficient to meet the predicted demand. In addition, climate change (Thornton and Ceamer, 2012) poses further threat to agriculture by increasing the frequency of occurrence of drought, salinity, submergence, temperature extremes etc.,

Progress in developing resilient rice through conventional breeding is slow due to the quantitative nature of stress tolerance, lack of precise high throughput phenotyping systems, limited understanding of the physiological, genetic and molecular basis of stress tolerance mechanisms and lack of coordinated efforts by multidisciplinary team of scientists. Use of genomics approaches may hasten development of resilient rice. QTLs for tolerance to drought, salinity, submergence, high temperature, nutrients' stress have been mapped in rice and are being applied in molecular breeding. Advances in high throughput whole genome sequencing, transcriptome, proteome, metabolome and ionome profiling methods may help in improved understanding of the mechanisms of rice plant's adaptation to abiotic stresses. Gene expression profiling tools such as microarrays, functional genomics resources including T-DNA mutants etc., provide opportunities to unravel the genetic and molecular basis of abiotic stress tolerance in rice.

Drought Tolerance:

Drought is a serious limitation to rice production and rice is extremely sensitive to drought (Lafitte et al., 2004). Rainfed areas are subjected to drought frequently at any stage of its growth resulting in reduced crop yields (Babu *et al.,* 2004). However, progress in genetic improvement of rice for drought resistance using conventional approaches has been slow. QTLs for drought tolerance in rice have been mapped (Kamoshita et al., 2008, Khowaja et al., 2009, Swamy et al., 2011, Mai et al., 2014, Suji et al., 2012a). Discovery of large effect meta-QTLs for drought tolerance helped development of rice for water-limited environments using marker-assisted breeding (Swamy et al., 2013; Kumar et al., 2014). QTLs for root traits and grain yield under drought are introgressed into IR20 (Suji et al., 2012), IR64 and White Ponni and improved near isogenic and recombinant lines have been developed.

Drought tolerant rice lines by engineering TFs viz., Dehydration Responsive Element Binding Factors (DREB), **N**o Apical Meristem/**A**rabidopsis Transcription Activation factor/**C**up shaped cotyledon (**NAC**), Gibberellin Regulated/ Snakin Factors (GASR), AP2/Ethylene Response factors (ERFs), WRKY and other functional candidate genes viz., Osmotin, *OsCAM* etc., are also being developed in the background of popular rice varieties such as ASD16, ADT 43 etc.,

Salinity tolerance:

Salt stress is a major constraint affecting rice productivity. Recent advances in molecular biology and genomics have led to better understanding of the genes and pathways involved in salt stress response in rice, including those involved in ion transport and homeostasis, osmoregulation, and oxidative stress protection (Munns and Tester, 2008; Singh and Flowers, 2010). QTLs for salinity tolerance were mapped in rice (Singh et al., 2007; Haq et al., 2010), among them the SKC1/*saltol* was found to be best known and most robust QTL (Ahmadi et al., 2011). This QTL "saltol" on rice chromosome 1 has been found to control 70% of phenotypic variation for seedling survival/salt uptake during early stage salinity stress. This QTL is being used to improve salinity tolerance in rice through molecular breeding. Efforts are in progress to improve salinity tolerance of popular rice varieties viz., White Ponni, CR1009 and ADT 37 through marker assisted introgression of *saltol* locus from Pokkali derived FL478. Advanced progenies are tested under MLT. Further, molecular basis of higher level of salinity tolerance in finger millet is studied using RNA-Seq approach (Rahman et al., 2014). Candidate genes have been cloned and are being functionally validated through genetic transformation.

Submergence Tolerance:

Rice production has become more susceptible to submergence since the introduction of semi-dwarf varieties during 1960s. Submergence causes various symptoms of injury, including leaf and stem elongation, leaf degeneration, dry mass loss and a tendency to lodging (Jackson and Ram, 2003). When completely submerged for more than 3 days, most rice cultivars decay and die. Only a few cultivars viz., FR13A, Thavalu, Kurkaruppan and Goda Heenati withstand complete submergence for 10–14 d (Setter et al., 1997). Sub1, a major QTL for submergence tolerance that accounted for 69% of the variation in submergence tolerance was mapped in a donor line, IR40931-26 derived from FR13A (Xu and Mackill, 1996). Xu et al. (2006) fine mapped the Sub 1 locus which contained three ethylene-response-factor (ERF) genes, Sub1A, Sub1B and Sub1C. Sub1A was the major genetic determinant for submergence tolerance. Sub 1 is being introgressed into popular rice varieties from FR13A through MAB and tolerant versions of popular varieties viz., IR64, CR1009 and Samba Mahsuri have been developed and disseminated (Bailey-Serres et al., 2010). CO 43, White Ponni and ADT37 are being improved for submergence tolerance through molecular breeding. Advanced generation progenies are under field testing.

High temperature tolerance:

Heat stress due to high ambient temperatures is a serious threat to crop production worldwide (Hall, 2001). According to a report of the Intergovernmental Panel on Climatic Change (IPCC), global mean temperature will rise 0.3ÚC per decade reaching to approximately 1 and 3ÚC above the present value by years 2025 and 2100, respectively. High temperature stress (HTS) is one of the most important climate factors affecting rice yield and the stability of rice production worldwide (Peng et al., 2004). The period from booting to flowering is the most sensitive stage to HTS in rice (Satake and Yoshida, 1978). Daily temperatures higher than 30ÚC or daily maximum temperatures higher than 35ÚC during the flowering period will result in poor anther dehiscence and lower pollen production, and hence a small number of germinating pollen grains on the stigma and a low rate of fertilization (Prasad et al., 2006). Significant genotypic variation in tolerance to HTS during flowering exists among both indica and japonica ecotypes. QTLs for tolerance to HTS have been mapped (Jagadish et al., 2010; Xiao et al., 2011). Two QTLs (on chromosomes 1 and 4) controlling spikelet fertility under HTS were found to be consistent across different genetic backgrounds. High temperature tolerance can be genetically-engineered by altering HSPs (Burke and Chen, 2006), osmolytes (Gepstein et al., 2005), cell detoxification mechanisms and components that regulate membrane fluidity (Zhang et al., 2005).

Nutrient Stress:

Apart from the above environmental stresses, nutrient deficiency/toxicity ranks next in limiting rice productivity under both irrigated and rainfed ecosystems. Among the various nutrient stresses, deficiency of Phosphorus (P) and Zinc (Zn) and toxicity due to Aluminium (Al) and Iron (Fe) are detrimental to rice growth, development and productivity (Ismail et al., 2007). A major QTL, "Pup 1" controlling phosphorus solubilization and uptake at root level in rice has been identified, characterized and validated across genetic backgrounds for its effect on improving P Use Efficiency (Wissuwa et al., 2002). With regard to tolerance against Zn deficiency in rice, not much progress has been made in detecting large effect QTLs. Similarly not much progress have been made in dissecting out the genetic basis of tolerance against Al/Fe toxicity mainly due to lack of suitable screening procedures. Global gene expression studies may facilitate the identification of genes associated with mapped QTLs as well as genes acting upstream or downstream of those linked to QTLs. Recent advances in genomics research and DNA sequencing techniques hold promise in developing resilient rice.

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Session IV : Innovative Breeding Methods, Tissue Culture and Genetic Transformation

1. Role of induced mutation in legume improvement

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Introduction

Legume crops and oil seeds are important food components as they are major contributors to dietary proteins and oils. Large proportion of Indian population relies on grain legumes as a dietary source of proteins due to economic or cultural reasons. India produces variety of oilseeds and grain legumes, which constitute around 12% and 7% of the total food grain production, respectively (1). Among oilseeds, soybean and groundnut contributes 31.4% and 27.7% to Indian oilseed production, respectively (1, 2). Among the food legumes, chickpea is the major food legume contributing 40.2% to country's total legume production followed by pigeonpea (17.4%), blackgram (10.6%) and mungbean (8.6%) (1). The demand for food and feed is growing with increasing population, while natural resources are limited. The yield potential of crop plants has to be significantly increased to combat the increasing demand. The approach of increasing the productivity by genetically improving the crop plants appears to be viable and eco-friendly in the present scenario. Growing such genetically improved varieties along with appropriate cultural practices can significantly boost the crop productivity. Genetic improvement of crop plants is a continuous process. Success of a crop improvement programme depends on the availability of large genetic variability, which a plant breeder can combine to generate new varieties. This variability is the outcome of naturally occurring mutations. There are a large number of instances in the past where naturally occurring mutations served important role in cultivar improvement. Green revolution genes in wheat (*Norin 10* genes) and rice (*Dee-geo-woo-gen*) are examples of natural spontaneous mutations. In nature, occurrence of natural variability in the form of spontaneous mutations is extremely low (about 10^{-6}), which can be enhanced to several fold (~10^{-3}) by using ionizing radiations or chemical mutagens.

Mutation induction and breeding

Radiation induced genetic variability for target traits and their incorporation in an ideal genotype could be achieved by a well planned and judicious use of induced mutation and hybridization techniques. The prime strategy in mutation-based breeding has been to upgrade the well-adapted plant varieties by altering one or two major traits, which limit their productivity or enhance their quality value. More than 3218 varieties have been released worldwide that have been derived either as direct mutants or from their progenies in 214 plant species. Around 492 and 110 varieties have been released in legumes and oil seed crops, respectively. Induction of mutations with radiation has been the most frequently used method for development of mutant varieties (http://www-mvgs.iaea.org).

Among the induced mutants released as varieties for cultivation, more than 80% were produced using physical mutagens indicating the efficiency and convenience of physical mutagens (http://www-mvgs.iaea.org). More than 60% of the varieties were developed using gamma rays followed by X rays (22%. This high percentage of gamma-rays induced mutants indicates that mutation breeding via gamma-ray irradiation is an effective and highly successful approach for the generation of commercial cultivars.

Development of mutant varieties in oilseeds and grain legumes

Induced mutants are utilized directly for varietal development or in recombination breeding by hybridizing mutant x mutant, mutant x cultivar, mutant derivative x mutant or mutant derivative x cultivar. Sustained induced mutagenesis in oilseeds and grain legumes using gamma-rays, X-rays, beta rays and fast neutrons resulted in wide spectrum of mutants affecting various traits. Traits like large seed size, increased harvest index, assimilate partitioning, semi-dwarf habit, earliness, new plant types, improved seed quality and enhanced disease resistance were incorporated in oilseeds and legumes. The effective blend of mutation and recombination breeding resulted in the release of 50 oilseeds and 60 legume varieties for commercial cultivation in India. Among these, 36 varieties have been released by BARC (www.barc.gov.in). These varieties were evolved by incorporating desirable agronomic features like large seed in TG 1, TKG 19A, Somnath (TGS 1), TPG 41 and TLG 45 (groundnut); TAT 10 and TT 6 (pigeonpea); TAP 7, TM 96-2 and TMB 37 (mungbean); TPU4 (blackgram); semi dwarf habit, high harvest index and better partitioning in TAG 24 (groundnut), TRC 77-4 (cowpea), TAU-1 (blackgram); fresh seed dormancy in TG 22 and TG 26 and drought tolerance in TG 37A (groundnut). Additionally, powdery mildew resistance in TARM 1, TARM 2, TARM 18, TM 96-2; powdery mildew and yellow mosaic resistance in TMB 37 and TJM 3 (mungbean), bacterial pustule resistance in TAMS 38 and multiple pest resistance in TAMS 98-21 (soybean); yellow mosaic virus resistance in TU 94-2 (urdbean) were also introduced in these varieties. Mutant varieties like Pusa 408 (Ajay), Pusa-413 (Atul), Pusa-417 (Girnar) of chickpea, Co-4 of blackgram, MaruMoth-1 of mothbean are among the important varieties of economic significance released in India.

New techniques for mutation induction

In China, spacecraft, recoverable satellites, and high altitude balloons have been used to bring seeds into space for mutation induction. During the past 10 years, more than 60 new mutant varieties were developed through this special programme. The transcriptional activation of transposable elements and their incorporation into various regions of the genome was reported in rice and maize. Since the position of transposable elements could be identified using PCR techniques, the mutation caused by transposition could be precisely positioned, and mutated genes could be easily identified (Shu, 2009).

Electron and ion beam technology for mutation breeding

Electron beam are streams of electrons observed when voltage is applied in a vacuum tube equipped with two electrodes. Modern vacuum tubes use thermionic emission, in which the cathode is made of a thin wire filament which is heated by a separate electric current passing through it. The increased random heat motion of the filament atoms knocks electrons out of the atoms at the surface of the filament, into the evacuated space of the tube. High speed electron beams can also be steered and manipulated by electric and magnetic fields. Particle accelerators such Linear accelerators were used for producing a beam of fast moving electrically charged particles for application in fundamental and applied research.

Apart from the conventional electromagnetic radiations, like X-ray and ã-ray, ion beam is now an alternate source of energy to induce mutation. When charged particles are accelerated under vacuum and finally bombard the target, they deliver their kinetic energy as well as mass and charge (Yu 2006). As they densely deposit their energy to the plant tissue, their high linear energy transfer (LET) has an opportunity to create mutants with new characters compared with the conventional radiations. As ion beams deposit high energy on a local target, it has been suggested that ion beams induce predominantly single- or double-strand DNA breaks with damaged end groups that are unable to be repaired easily (Goodhead, 1995). Therefore, it seems plausible that ion beams frequently produce large DNA alterations, such as inversions, translocations and large deletions, rather than point mutations. The effects of ion beams on plant materials have been investigated using several plant species including *Arabidopsis*, rice, barley, tobacco and *Chrysanthemum*. Several kinds of energies and ions, such as helium (He), carbon (C), neon (Ne) and argon (Ar), were used in these studies, with 220MeV carbon ions being the most common. Biological effects induced by ion beams were greater than those induced by low LET radiation (gamma ray, X-ray). The frequencies of mitotic cells with chromosome aberrations, such as chromosome bridges, acentric fragments and lagging chromosomes, were much higher for ion beams than for gamma rays (Hase *et al*., 1999). Mutation frequency and spectrum induced by ion beams was reported to be higher compared with that induced by low LET radiations (Okamura e*t al*., 2003).

During the last decade, induced mutations have also been gaining increasing importance in plant molecular biology as a tool to identify and isolate genes and to study their structure and function. Knowledge of genes controlling important agronomic and quality traits is critical for plant breeders to develop proper strategies and efficiently implement breeding programmes. Therefore, induced mutations can contribute further to increasing global food production both directly and indirectly by increasing yield potential and stability.

Conclusion

Many mutants have made a transnational impact on increasing yield and quality of several legume crops. Induced mutations will continue to play an increasing role in creating crop varieties with traits such as improved oil quality, protein and starch quality, enhanced uptake of specific metals, deeper rooting system, and resistance to drought, diseases and salinity as a major component of environmentally sustainable agriculture. Electron and ion beams can be utilized as a novel mutagen to generate new mutants for basic research and to create new novel genetic resources. Mutation induction is producing mutation grids for gene discovery and gene function analyses as an invaluable resource for genomics, reverse and forward genetics.

2. Challenges and opportunities in marker assisted breeding: A critical overview

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Plant breeding is art and science of improving crops. Judicious integration of each one of these ensures success. A breeder has to allocate his/ her valuable time and money between the two. It is imperative that due emphasis should be given, during the breeding program, to the prevailing or anticipated changes in the edaphic, climate and biotic conditions for which breeding program is designed. Societal needs/aspirations and culinary preferences are other issues that need to be kept in sight when product quality is a concern. As plant breeding takes considerable time and effort, ideally, plant breeders address anticipated problems of the future. This is in practice called anticipatory plant breeding.

Researching and teaching of the science of plant breeding is relatively easier than the art component. The art of plant breeding is best not taught but inculcated by appropriate examples and practice. Regular field visits, understanding the habit(s) and the corresponding plants' response(s), observing plants /parents/ segregants over days, sessions or variations within a day are required. These efforts would be like establishing an active communication with plants and be empathetic to its plight in a particular environment or across environments/years/ locations.

Plants are living entities and manifest a particular phenotype in response to particular environmental factors. They also show behavioural changes is response to challenges that it faces. As the crops we breed are likely to occupy large and diverse geographical areas over years or decades, where climatic and biotic challenges are variable, plant breeding needs to be able to inculcate the ability to respond to the anticipated changes during the selection program.

Traits follow segregation through generation of selfing or crossing and these can be computed as mathematical ratios by applying appropriate formulae. This is based on the values measured given a particular environment. Response(s) of the plant to the changes in environment are difficult to measure and consequently best 'understood'. This is in the realm of art of plant breeding. The developmental plasticity or wide spread exhibit adaptability that certain genotypes/ varieties due to their ability to adopt to wide geographical area is remarkable. This is exemplified by mega-varieties namely TMV 2 (Groundnut), IR64, IR36, Jaya, Sona Masuri (Rice) Maldandi Local M-35 (Sorghum), Annigiri 1 (Safflower) *etc*. These mega-varieties have wide adaptability across a wide geographical area reflecting their plasticity.

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3. Achievements made through conventional plant breeding techniques in millet improvement

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Session V : Horticulture and Plantation Crops Improvement

1. Improvement of Medicinal Plants: Challenges and Innovative Approaches

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Medicinal plants are integral part of human health care since time immemorial in most part of the world. In India, this group of plants has got greater attention and a separate branch of sciences like Siddha, Ayurveda, Unani and others also called as AYUSH have evolved around them. During the civilization process, these plants got importance for their medicinal properties and used for treatment of common ailments to complex diseases. Apart from curing the ailments of human beings, these plants are also used in the treatment of various veterinary diseases. The medicinal attributes of this section of plants are due to production of secondary metabolites. Medicinal plants are used either in the form of raw drug in the traditional systems of medicine and the crude extracts and the synthetics derived from these plants in the modern medicine. It is estimated that about 80% of the modern medicines in the world are derived from the extracts or synthetics derived from medicinal plants.

Over period of time, the change in the climatic factors, life style of the people, increased population etc. brought many health related problems in the form of diseases. Most of the disease are being handled with help of many medicinal plants either directly or getting active ingredients from them. As a result the demand for medicinal plants has increased many folds. But in contrast, the supply of these plants from natural habitat has shrinking due to the global warming, deforestation, fast growing urbanization, etc. Naturally under such circumstances, many high value medicinal plants have got the status of cultivation in the farmers' field.

India's share (about 1%) in the world trade of medicinal plants is far less than that of China (about 33%). Given, the agro climatic suitability, variability, biodiversity richness, treasure of traditional knowledge and historical pattern of medicinal and aromatic plants in India, the prospects for intensifying and diversifying the country's medicinal and aromatic plants industry are tremendous. Therefore, it is extremely important to conserve the rich medicinal and aromatic plants biodiversity and extend their evaluation for utilization by the industries so as to sustainably meet their domestic and export demands besides maintaining desired quality standards. Shift from collection mode to cultivation will ensure purity, authenticity and availability of medicinal and aromatic plants for user industries.

India is one of the 17 mega bio-diversity rich countries and has 7% of the world's bio-diversity. Almost all the major ecosystem types in the world can be found in India. There are 15 agro-climatic regions, 45,000 different plant species out of which 15,000 are medicinal plants. About 8,000 plants are used in Indian Systems of Medicine and folk medicines (Shiva et al. 1996). Out of these 1,700 medicinal plants, have been documented in Traditional Medicines of which about 500 species are mostly used in the preparation of drugs. At present, about 90% collection of medicinal plants were from the wild, and since 70% of plants collections involve destructive harvesting many medicinal plant species are becoming endangered/vulnerable/threatened. If this situation continues, we will not only loss such valuable plants from the earth, but also face lots of problems in dealing the majority of human disease. Alternatively, the high demanded medicinal plants were brought into the agriculture and being cultivated to meet their increasing demand. The successful examples are ashwagandha, isabgol, senna, aloe, Glariosa, opium poppy and many more.

During the last half century, after globalization, systematic cultivation has got more importance. As a result many public and private organizations have started a systematic research in these crops. The medicinal plants-based industry is growing at the rate of 7–15% annually. At present many medicinal plant species are under cultivation in the country out of which about 32 species are listed in the priority list of the National Medicinal Plant Board (NMPB), Ministry of Health and Family Welfare for commercial cultivation and processing in India. The listed medicinal plants are: Amla (*Emblica officinalis* Gaertn), Ashok (*Saraca asoca* (Roxb.) de wilde), Ashwagandha (*Withania somnifera* (Linn.) Dunal), Atees (*Aconitum heterophyllum* Wall. ex Royle), Bel (*Aegle marmelos* (Linn) Corr.), Bhumi amlaki (*Phyllanthus amarus* schum & Thonn.), Brahmi (*Bacopa monnieri* (L.) Pennell), Chandan (*Santalum album* Linn.), Chirata (*Swertia chirata* Buch-Ham.), Daruhaldi (*Berberis aristata* DC.), Gudmar (*Gymnema sylvestre* R. Br.), Guduchi (*Tinospora cordifolia* Miers.), Guggal (*Commiphora wightii* (Arn.) Bhandari), Isabgol (*Plantago ovata* Forsk.), Jatamansi (*Nardostachys jatamansi* DC.), Kalihari (*Gloriosa superba* Linn.), Kalmegh (*Andrographis paniculata* Wall. Ex Nees), Kesar (*Crocus sativus* Linn.), Kokum (*Garcinia indica* Chois.), Kuth (*Saussurea costus* C. B. Clarke), Kutki (*Picrorhiza kurroa* Benth ex Royle), Makoy (*Solanum nigrum* Linn.), Mulethi (*Glycyrrhiza glabra* linn.), Pathar chur (Coleus) (*Coleus barbatus* Benth.), Pippali (*Piper longum* Linn.), Safed Musli (*Chlorophytum arundinaceum* Baker) (C. *borivillianum*), Sarpgandha (*Rauvolfia serpentina* (L.) BENTH. EX KURZ), Senna (*Cassia angustifolia* Vahl.), Shatavari (*Asparagus racemosus* Willd.), Tulsi (*Ocimum sanctum* Linn.), Vai Vidang (*Embelia ribes* Burm. F.), and Vatsnabh (*Aconitum ferox* wall.). When the crops are given importance and brought under cultivation, it may also invite some inherent problems like, pest and diseases and leads to yield and quality loss. The cultivation of medicinal plants are even in primitive state for most of the plants and yet to receive the attention of plant breeders for their improvements. In this paper, the present status of breeding medicinal plants, strategies and challenges are presented.

Challenges in medicinal plant breeding

Plant breeding depends on a correct combination of specific alleles at the 50, 000-60,000 genetic loci present in a plant genome. The knowledge of where these alleles are best found and the combination and evaluation of these into a single species can be considered the "art" of breeding. Obviously, access to a wide range of genetic diversity is critical to the success of any breeding programme. Promotion of genetic diversity requires introduction of new, unrelated breeding materials into basic and advanced breeding pools. With the advent of possibilities for genetic transformation via molecular techniques, the number of possible uses of gene bank collections and other exotic materials is greatly increased. When genes can be moved across crossability barriers, among genera, families, and even kingdoms, the range of sourcing options is nearly limitless.

Genetic resources of medicinal plants are fundamental to our effort to improve their quality, productivity and adaptation to the changing climatic conditions. These resources, fortunately stored in gene banks, evolved an assortment of alleles needed for resistance and/or tolerance to diseases, pests, and harsh environments found in their natural habitats. Many of these combinations cannot be easily duplicated artificially, even with the help of modern molecular techniques. What is alarming is the fact that many of these valuable genetic resources are essentially "sitting on the shelf" in what have been dismissively termed "gene morgues". The conservation of a resource only becomes important if the resource has acquires recognized value. This clearly requires that the resources be evaluated in a search for critical genetic material.

There is currently a major gap between the operations of medicinal and aromatic plant genetic resources and modern plant breeding that is potentially a major restriction particularly in the use of exotic materials in the development of varieties needed to meet novel agronomic and environmental challenges. This disconnect can be bridged through a process known as genetic enhancement or pre-breeding that is based upon the characterization of genetic resources for traits of interest and then transferring these traits into suitable agronomically adapted genetic backgrounds by combined application of standard plant breeding methods and marker technologies. This is likely to provide a major stimulus to the use of genetic material from vary diverse sources of medicinal and aromatic plants relatives for incorporation into their new cultivars.

Unlike breeding of field crops, medicinal plant breeding needs a special attention as the breeding objectives is mainly for secondary metabolites besides only for biological yield. The present situation is that for most of the medicinal plants, the basic information like flower biology, reproductive biology, basic chromosome number, physiology, genetics of different qualitative and quantitative traits, genetic variability, heritability of traits, genetic advance and other that are needed for successful breeding programme are lacking. Further, the number of breeders working for improvement of medicinal plants in India is also very low and work is being taken up sporadically, except in few crops. Major institutions in India working on breeding of medicinal plants species are:

1. ICAR-Directorate of Medicinal and Aromatic Plants Research, Anand, Gujarat

2. ICAR-National Bureau of Plant Genetic Resources, New Delhi
3. ICAR-Indian Institute of Horticultural Research (IIHR), Bangaluru
4. CSIR-Central Institute for Medicinal and Aromatic Plants (CIMAP), Lacknow, Uttar Pradesh
5. CISR-Indian Institute of Integrative Medicine (IIIM), Jammu, J&K
6. CISR-North East Institute of Science and Technology (NEIST), Jorhat, Assam
7. CISR-National Botanic Garden and Research Institute, Lucknow
8. State Agricultural Universities.

Present status and achievements

Genetic resource management:

Genetic resources are the one of the most important requirement for improvement of any crop. Of late the plant genetic resources (PGR) management of medicinal plants has got importance at national and international level in the last five decades. At the national level, various conservation efforts have been made to cope up with the situation through several *in situ* and *ex situ* measures. Some of the *in situ* measures includes establishment of biosphere reserves, medicinal plants conservation areas, medicinal plants development areas and sacred groves. In general, *in situ* conservation is mainly executed by the Forest Departments where as the *ex situ* is by various research organizations. *Ex situ* conservation includes the establishment of seed gene banks, field gene banks, nurseries, herbal or botanical gardens, medicinal plants conservation parks, *in vitro* repository and cryo-preservation facilities. At national level, ICAR-National bureau of plant genetic resources (NBPGR), New Delhi acts as the nodal agency for the conservation of agricultural biodiversity of medicinal plants and also for the legal exchange of germplasm within and between countries. Presently, there are four national seed gene banks for medicinal plants at Tropical Botanical Garden and Research Institute (TBGRI), Thiruvananthapuram; CSIR-Central Institute of Medicinal and Aromatic Plants (CIMAP), Lucknow; ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi and CSIR-Indian Institute of Integrative Medicine (IIIM), Jammu in India where base collections are conserved. A total of about 6123 accessions of prioritized species are conserved as base collections at NBPGR, New Delhi (Annonymous, 2012).

As a part of national programme, several conservation strategies were taken up by ICAR-DMAPR, Anand, Gujarat and the centres of AICRP-MAP&B on major endangered and rare species like *Chlorophytum borivilianum, Commiphora wightii, Gentiana kurroo, Gloriosa superba, Nardostachys jatamansi* and other. ICAR-DMAPR, Anand is the active germplasm site of ICAR-NBPGR for maintenance of vegetatively propagated medicinal plant germplasm at national level. For maintaining the germplasm specific to particular location or ecology, the AICRP-MAP centres situated in that particular location are engaged.

The systematic collection, maintenance and characterization of the germplasm are being done for some medicinal plant species. To safe guard the intellectual property rights the valuable germplasm identified are being registered with

ICAR-NBPGR, New Delhi. About, 48 trait specific germplasm accessions of 39 MAP species are registered with ICAR-NBPGR (Annonymous, 2012). However, the effective utilization of germplasm is yet to receive the attention. Future programmes on PGR management of medicinal plants must focus on accessioning of large number of germplasm with national identity to safe guard the IPR issues, Input for introduction of more trait specific and elite germplasm from countries conserving through bi-lateral exchange, generate database on feedback on performance of introduced germplasm as well as the performance and utilization of germplasm in improvement, many collaborative collection and evaluation programmes for better and sustainable utilization, supply of more germplasm of medicinal plant species for long term conservation and registration of more unique germplasm.

Breeding

Medicinal plants are belongs to diverse families and different plant types (shrubs, herbs, trees, climbers, etc.) and are having different breeding system like self-pollinating (genetically pure), cross-pollinating (extreme genetic diversity), and asexually propagated (genetically identical) [A very few are sexually sterile, but the majority have some sexual fertility]. As a result there is a need for specific and innovative approaches for their improvement. Some basic information related to major medicinal plants is given in the Table 1.

Table 1: Some basic information relating breeding of important medicinal plants in India

Medicinal plant	Habit	Economic part used	Mode of propagation	Mode of pollination	Ease of breeding
Aloe (*Aloe vera*)	H	Leaf	Vegetative	CP	Difficult
Amlaparni (*Rheum emodi*)	H	Root	Vegetative		Difficult
Asalio (*Lepidium sativum*)	H	Herbage	Seeds	SP	Easy
Asoka (*Saraca asoka*)	T	Bark	Vegetative		Difficult
Ashwagandha (*Withania somnifera*)	H	Whole plant	Seeds	SP	Easy
Datura (*Datura spp.*)	H	Leaf and flower	Seeds		Easy
Foxglove (*Digitalis spp.*)	H		Seeds	CP	
Chirayita (*Swertia chirayita*)	H	Whole plant			
Guggal (*Commiphora wightii*)	S	Gum	Vegetative		Difficult
Isabgol *(Plantago ovata)*	H	Husk and seeds	Seeds	SP	Easy
Jatamansi (*Nardostachys jatamamsi* DC.)	H	Root	Vegetative		difficult
Kalmegh (*Andrographis paniculata*)	H	Whole plant	Seeds	SP	Easy
Kaucha (*Mucuna pruriens*)	H	Root and fruit	Seeds	SP	Easy
Mandukparni (*Centella asiatica*)	H	Leaves	Vegetative		Difficult

Medicinal plant	**Habit**	**Economic part used**	**Mode of propagation**	**Mode of pollination**	**Ease of breeding**
Madhunashini (*Gymnema silvestre*)	H	Leaves	Vegetative and seeds	CP	Difficult
Makoi (*Solanum nigrum*)	H	Seeds	Seeds	SP	easy
Neel (*Indigofera tinctoria*)	S	Fruit, leaves and root	Seeds		difficult
Opium Poppy (*Papaver somniferum*)	H	Latex	seeds		Easy
Palmarosa (*C. martinii* var. motia)	H	Herbage	Vegetative and seeds	CP	difficult
Safed musli (*Chlorophytum borivilianum*)	H	Root	Vegetative and seeds	CP	difficult
Satavari (*Asparagus racemosus*)	H	Root	Vegetative	CP	difficult
Salaparni (*Desmodium gangeticum*)	H	Whole plant	Seeds	SP	easy
Senna (*Cassia angustifolia*)	S	Herbage	Seeds	CP	difficult
Tinospora (*Tinospora cordifolia*)	H	Stem	Vegetative		difficult
Tulsi (*Osmium spp*.)	H	Leaves and seeds	Seeds	SP	Difficult
Brahmi (*Bacopa monnieri*)	H	Leaves	vegetative		Difficult
Dodi (*Leptadenia reticulata*)	H	Whole plant	Vegetative		
Kutki (*Picrorhiza kurroa)*	H	Root	vegetative		
Longpepper (*Piper longam*)	S	Fruit	vegetative		Difficult
Shankhpushpi (*Convolvulus pluricaulis*)	H	Whole plant			
Lal chitrak (*Plumbago rosea*)	H	root	vegetative		
Coleus (*Coleus forskohlii*)	H	Root	vegetative		
Patchouli (*Pogostemon cablin*)	H	Leaf	vegetative		
Kalihari (*Gloriosa superba*)	H	Seed and root	vegetative		
Latakasturi (*Abelmoschus moschatus*)	S	Fruit (seed)			
Kidamari (*Aristolochia indica*)	H	Fruit, seed, stem			
Roselle (*Hibiscus sabdariffa*)	H				
Lemongrass *(Cymbopogon flexuosus)*	H	Herbage	Vegetative		Difficult
Bala (*Sida cordifolia*)	H	Whole plant			
Hypericum (*Hypericum perforatum*)	H	Flower			
Indian valerian (*Valeriana jatamansi*)	H	Whole plant	Vegetative		
Vach (*Acorus calamus*)	H	Root	Vegetative		
Jivanti (*Holostemmaada-kodien*)	H	Root	Seeds	CP	
Periwinkle (*Catharanthus roseus*)	H	Leaf and root	Seeds	SP	Easy
Sarpagandha (*Rauvolfia serpentina*)	S	Root	Vegetative		
Solanum (*Solanum viarum*)	H	Whole plant	Seeds	SP	Easy
Sweat leaf (*Stevia rebaudiana*)	H	Leaves	Vegetative		
Henna (*Lawsonia inermis*)	S	leaves	Vegetative		

H: Herb; S: Shrub; SP: Self pollinated, CP: Cross Pollinated

Factors affecting success of genetic improvement of medicinal plants

- Extent of genetic variability
- Knowledge of reproductive biology
- Information on the genetics of agronomic traits of interest
- Information on the genetics of pathways of secondary metabolism.
- Breeding strategies
- Availability of efficient analytical techniques for quality analysis

Targets for trait manipulation in medicinal plants

- Content of active compounds
- Basic agronomic characters related to uniformity, stability, growth and development, and - resistance/ tolerance to biotic and abiotic stresses.

Traits of importance in medicinal plants breeding

- Male sterility
- Apomixis
- Meiotic restitution
- Sex

At present the breeding of most of the medicinal plants are in primitive stage and a long way to go. In most of the medicinal species, the collection of variability from the natural sources, purification, characterization and evaluation are the major activities in relation to breeding as these are just getting in to the cultivation status. However, crops like opium popy, ashwagandha, isabgol and senna are being cultivated for centuries and systematic breeding works are in progress. In these crops, apart from exploitation of natural variability, creation of variability through artificial hybridization, mutation and polyploidy breeding are also being attempted. In the beginning all the varieties developed and released for commercial cultivations were mostly from introduction from its natural habitats or foreign countries or selection from local land races. The list of varieties developed through AICRP-MAP is given in Table 3. As every species needs some specific environments for its growth and development these varieties were developed for particular areas. Still it can be cultivated in other areas also if suitable growing conditions are available.

Way forward

- Periodic threat assessment medicinal plants are needs to be primary concern and rare species may be banned from exploitation.
- Basic studies like, flower biology, reproductive biology, genetic of different qualitative and quantitative traits are to be under taken.
- Systematic collection, characterization, evaluation and documentation are to be initiated for many of the medicinal plant species.
- Development of high yielding varieties with short duration, resistance to biotic and abiotic stresses with high quality secondary metabolites through conventional breeding as well as using modern biotechnological tools.
- Development of easy, quick and cost effective estimation techniques for rapid screening of germplasm and breeding lines are needed for effective breeding of

medicinal plants with desirable active ingredients.

- Development of DUS guidelines and registration elite germplasm to have IPR. It is also necessary to protect our valuable medicinal plant resources through all means as there are sporadic incidences of patenting our Indian medicinal plants in the foreign counties.

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2. Current Status of Coconut Genetic Resources, Conservation and Utilization in India

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The coconut palm, *Cocos nucifera* L., an important oil yielding palm, is cultivated in an area of 2.07 million hectares in the country. Globally, India is one of the three major coconut producing countries, with an annual production of 23351 million nuts. The palm is referred to as 'Kalpavriksha', since it provides nutritious food and refreshing drink, oil for edible and non-edible uses, fibre of commercial value, shell for fuel and industrial uses, timber and a variety of miscellaneous products for domestic and industrial use. The crop is of greater significance in terms of livelihood sustenance, poverty alleviation and income generation to a sizeable segment of the rural population. About 10 million families depend on coconut for their livelihood and as an important oil crop in the country; it contributes about 6 per cent to the national vegetable oil pool.

The coconut palm, though a monotypic species under the genus *Cocos*, exhibits a lot of variability in forms with several distinct populations and ecotypes, widely differing from each other in morphological characters, particularly with respect to fruit characters and plant habit. ICAR-CPCRI, being the premier national institute undertaking coconut research, maintains the world's largest repository of coconut germplasm and is designated by the National Bureau of Plant Genetic Resources (NBPGR) as the National Active Germplasm Site for coconut in the country. Over the years, ICAR-CPCRI has collected, for conservation and characterization, about 433 coconut accessions, including 132 exotic and 301 indigenous collections. ICAR-CPCRI also hosts the International Coconut Gene Bank for South Asia (ICG-SA) at ICAR-CPCRI Research Centre Kidu in Karnataka.

The field gene bank at CPCRI includes exotic coconut germplasm from 28 major countries, covering the vast majority of the important coconut producing countries of the world and indigenous coconut germplasm from almost all major coconut growing regions within the country. The ICG-SA, presently conserves about 86 coconut accessions, representing indigenous coconut germplasm as well as Indian accessions representing coconut ecotypes of Philippines, Malaysia, Pacific Ocean Islands, Africa and the Caribbean Region and germplasm collected from Sri Lanka, Bangladesh, Indian Ocean Islands of Mauritius, Madagascar, Seychelles, Maldives, Comoros and Reunion. Further the institute is promoting *in situ* conservation in coconut and on-farm diversity studies have been undertaken with respect to coconut ecotypes *viz.* Kuttiadi, Bedakam, Mavinkurva, Devermute, Annur, Mohacho Narel, Komadan, Edava.

Characterization of coconut genetic resources has resulted in the identification of trait specific variability with reference to morphological traits, floral traits and pollen recovery, fruit component traits and tender nut water quality. The quantity and quality of the tender coconut water varies across varieties and regions. The quantity of the tender coconut water is correlated to the size of the coconut fruit and the endosperm cavity. It varies from negligible (Laccadive Mini Micro Tall) to more than 800 ml (San Ramon Tall). The sweetness of the water and mineral content also varies and organoleptically they are graded as very good, good, average or poor. Chowghat Orange Dwarf, Gangabondam Green Dwarf, Cochin China Tall, Philipiness Ordinary Tall, Coco Bleu Tall, Pemba Green Dwarf, Pemba Red Dwarf Mauritius and Comoros Tall are a few of the accessions identified with very good quality of tender nut water. Fruit component analysis indicated wide variability among accessions for most traits studied. Very high copra content (>300 g) was recorded in the accessions, San Ramon Tall, Malayan Tall and Markham Valley Tall. Studies undertaken on >50 accessions to assess the suitability of accessions for ball copra production, indicated highest recovery of ball copra in Laccadive Micro Tall. Accessions, Tiptur Tall, West Coast Tall, Java Tall, East Coast Tall, Sri Lanka Tall, Navasi Tall, Gonthembili Tall, Jamaica Tall, Nigerian Tall, Benaulim Tall, Calangute Tall, Fiji Rotuma Tall, Saint Vincent Tall, Hazari Tall, and Verrikobbari were also found suitable for ball copra production. Variability for fatty acid composition of coconut oil has also been observed among accessions. Further, the conserved coconut germplasm includes unique types such as horned coconut, mini micro coconut, sweet endosperm coconut, soft endosperm coconut, buttery endosperm coconut, edible husk coconut, pink husk coconut, aromatic coconut. Collaborative research in association with CIRCOT, Mumbai, on the physio-chemical and structural characteristics of coconut fibres, with a focus on coconut coir industry, indicated varieties suitable for manufacture of stronger yarns (Gangabondam Green Dwarf), dyeing (Tiptur Tall, East Coast Tall, Benaulim Tall) and production of Q-cellulose (East Coast Tall, Benaulim Tall, Lakshadweep Ordinary Tall, Lakshadweep Micro Tall, Tiptur Tall).

Screening on the basis of accumulation of epicuticular wax on the leaf surface, low stomatal frequency and leaf water potential, the activity of enzymes like glutamate oxaloacetate transaminase and acid phosphatase, has resulted in the identification of drought tolerant aaccessions, *viz.* West Coast Tall, Federated Malay States Tall, Java Tall and Andaman Giant Tall, for utilization in the breeding programme. Breeding for disease resistance, especially root (wilt) disease of coconut has resulted in identification of Chowghat Green Dwarf and Malayan Green Dwarf as disease resistant accessions. Screening of the germplasm for eriophyid mite resistance has been undertaken and fruits of Chowghat Orange Dwarf and Kulasekharam Green Dwarf were found to have low incidence of mite damage while maximum mite damage were recorded in Laccadive Ordinary Tall.

Molecular characterization of coconut germplasm has been undertaken in the country using a range of marker systems *viz.* RAPD, AFLP, DAF, ISTR, IISR and SSR markers. Presently molecular characterization of coconut germplasm is undertaken through SSRs. A database "COCOGEN" has been developed by

CPCRI for microsatellite data of coconut germplasm. Characterization of coconut germplasm based on leaf polyphenols, isozyme analysis and protein polymorphism has also been attempted.

Coconut descriptors have been developed and published for some of the conserved coconut germplasm and CPCRI has also contributed to the development of the World Catalogue of Conserved Coconut Germplasm brought out by the Coconut Genetic Resources Network (COGENT) under Bioversity International. In addition, evaluation and characterization data of the conserved accessions is available in the international Coconut Genetic Resources Database (CGRD) being maintained by COGENT- Bioversity.

Evaluation for yield has been an important component of the coconut improvement programme. The coconut germplasm base has been utilized in the coconut improvement programme both at the institute, coordinating centres under the All India Coordinated Project on Palms and State Agricultural Universities. So far, 42 varieties, including 15 hybrid varieties have been released for cultivation in the various agro-ecological zones of the country. This includes, in addition to varieties for higher copra/nut yield, varieties for tender nut, dual purpose (copra and tender nut) varieties, ball copra varieties, root (wilt) disease tolerant varieties and varieties for ornamental purpose. A few unique accessions have been registered with NBPGR for specific traits such as, dwarf plant habit, tender nut water quality, fruit colour, disease resistance; fruit size, husk content, copra content; cluster bearing habit; fruits with horn like structures; extremely small fruits with very low copra content.

Taking into consideration the challenges to coconut productivity as a result of climate change and other production constraints more focused research is required. Mitigating gene erosion from climate change effects through multi-pronged and multi-site conservation strategies supplemented by *in vitro*/cryogene banks, in addition to augmenting *in situ* conservation efforts through promotion of adapted local ecotypes and inclusive genetic resources management involving various stakeholders are issues requiring urgent action. The major focus, however, is the exploitation of genetic/genomic resources for development of improved varieties with superior agronomical and quality traits, higher nutrient use efficiency, climate resilient adaptability, to address the challenge of producing more with minimal environmental footprints.

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3. Germplasm Conservation in Oil Palm

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Oil palm is propagated by seed and long term conservation by seed is difficult in view of semi recalcitrant storage behaviour of the seed. Long term cryopreservation using kernel, somatic embryo and polyembryos has been reported. Oil palm pollen could be successfully stored after cryopreservation in liquid nitrogen. Desiccation tolerance is significantly correlated with embryo DW and water content and tolerance is acquired at specific stages. Therefore, more extended studies would lead to development of suitable storage protocols especially by cryopreservation.

Introduction

Oil palm has originated from the West Coast of Africa. Genus *Elaeis* of the family Arecaceae contains two tropical species, *Elaeis guineensis* Jacq, and *Elaeis oleifera* (HBK) Cortes. Only *E.guineensis* is of economic interest due to the high oil content in the mesocarp and kernel. It is a pioneer species of African forests traditionally used by locals which exhibited several expansion phases. Oil palm is the most productive oil-bearing crop. Although it is planted in only 5% of the total world vegetable oil acreage, palm oil accounts for 33% of vegetable oil, 45% of edible oil worldwide. As per recent statistics, 12 million hectares have been planted with oil palm in the world with a production of over 45 million tons of palm oil. Oil palm breeding has improved the planting materials. The yield of *duras* has improved from 2.8 to 4.5 t/ha after four cycles of selections. The oil yield of *teneras* from subsequent *dura* selected and introgression with selected *pisiferas* has improved from 6.3 to 11.2 t/ha in the last four decades in Malaysia and other South East Asian countries. This was possible by use of improved and modern material developed from *deli dura* genetic base. But the genetic gain may not long lost as many of the breeding programmes are continuously relay on restricted breeding base. In this context, crop improvement and germplasm conservation have to make major contribution to meet the challenges confronted in oil palm cultivation.

Seed Technology of Oil Palm

It is well known that oil palm seeds take a very long time to germinate under normal conditions and often such germination is not uniform. Pre-heating techniques are being employed universally to break the dormancy of oil palm seeds for accelerating germination. Most palm seeds are thermophilous and hence, optimum temperature is required for germination between 30-40°C (Ehara *et al,* 1998*). Addae-Kagyah et al* (1998) reported that the critical requirement to break dormancy was to maintain seed at 39-40°C up to 80 days. Some reports indicated heating duration of 70-80 days. It was confirmed that soaking fresh oil palm seeds for 5 days and thermal dry heating for 60-70 days followed by 5 days soaking was found optimum for maximum germination (Murugesan *et al,* 2006). Similar finding was reported by Fondom *et al*, (2010) who confirmed suitability of 60 days pre-heating duration under Cameroon condition.

Accelerated aged (AA) treatment at 40°C for 70 days with pre soak is recommended to achieve more uniform and higher germination (Murugesan *et al*, 2005). Reduced dry heat treatment with aseptic de-operculum method of germination technique has been reported for *dura* seeds to obtain maximum germination. The entire germination process could be completed within 30 days after bunch harvest (Murugesan, 2009a). Replacement of conventional polythene bags of about 300-500 gauge thickness with high density plastic containers have been recommended for achieving moisture control during dormancy breaking and germination processes (Mora *et al*, 2007). Nwankwo and Krikorian (1982) successfully stored *pisifera* seeds in aerated sterile distilled water for 6 months and obtained 50% germination. Various studies confirmed that seed germination and seedling quality are influenced by genotypes and their cross combinations. Myint *et al*, (2010) categorized oil palm seeds of different *Dura* × *Pisifera's* into three categories that is light (1.6-3.1g seed^{-1}), medium (3.2 - 4.6 g seed^{-1}) and heavy (4.7-6.1g seed^{-1}) and confirmed that germination was influenced by seed weight and cross combinations. Correlation between physical characteristics of seed and germination was reported by Myint *et al*, (2009). Murugesan and Gopakumar (2010) reported variation in nut, shell and kernel weights of ASD Costa Rican and Indigenous Palode hybrids. Similarly, Martine *et al,* (2009) observed variation in ability of germination in two genotypes developed by Centre National De Recherche Agricole (CNRA) in Cote d' I voire. It was reported that the period during which seeds develop on the parent plant has been found to affect many seed characteristics, including dormancy, through interactions with the environment (Hoyle *et al*., 2008). Hence, seed behavior of oil palm seeds that developed in different environments need to be studied to analyse dormancy, germination and resultant seed quality.

Long term conservation of germplasm

Biotechnological approaches for conservation of all important germplasm of *dura, tenera* and *pisifera* is essential mainly in the form of pollen and embryo to facilitate the breeding programmes. Oil Palm was classified as intermediate seed storage behaviour (Ellis *et al*., 1991). Viability of seeds of oil palm cultivars could be maintained after 12 months of storage at 15$^{æ\%}$ C with 10-12 % moisture content. Zygotic embryos of oil palm are relatively desiccation- tolerant and seeds can be stored for 2-3 years. Dry matter, water content, sugar and ABA contents have been investigated during zygotic embryo development. Embryo dry weight (DW) increases between 3 and 4 months post anthesis (mpa) and then stable until shedding (c.6mpa). Embryos undergo partial desiccation, but water content is high at maturity (c.1.5 g H_2O/g DW). Desiccation tolerance is significantly correlated with embryo DW and water content and tolerance is acquired at approx. 3.5 mpa. More extended studies would lead to development of suitable storage protocols especially by cryopreservation. The efficiency of cryopreservation strategies has been compared in oil palm seed (Engelmann *et al.*, 1995). If extracted from rehydrated kernels, 65% of embryos desiccated to around 0.3 g H_2O/ g DW developed into plantlets after cryopreservation. In contrast, only 25% embryos (at 0.12g H_2O/ g DW) extracted from cryopreserved dry kernels developed into plantlets. However, this value was increased to 63% if kernels were partially rehydrated before freezing until water content of embryos reached 0.3 g H_2O/ g DW. Thus an optimum cryoprotocol can lead to high recovery of cryostored germplasm. Intermediate seeds or kernels are being generally smaller than the recalcitrant seeds, whole seed also been cryopreserved after desiccation to critical moisture content. Grout *et al,* (1983) showed that it was possible to revive and germinate oil palm zygotic embryos (embryo from kernel) after freezing in liquid nitrogen (-196°C). Shiny white, finger-like somatic embryos could be used for cryopreservation. Its efficiency can be markedly improved by completing the 7-day pregrowth period on 0.75 M sucrose by an additional dehydration period carried out either by placing the embryos in the air current of the laminar flow cabinet or in an air tight box containing silica gel (Dumet *et al,* 1993). *In vitro* grown poly emryoids of oil palm were successfully embryo preserved by vitrification with 45% survival. Poly embyoids were subjected to plant vitrification solution-2 (PVS2) 30% (w/v) glycerol plus 15% (w/v) EG plus 15% (w/v) DMSO plus 0.4M sucrose exposure for 5 min at 26± 2° C subsequently plunged into liquid nitrogen. Thawed polyembryoids resumed growth within 8 days of culture and shoot development was recorded 25 days of growth (Suranthran *et al.,* 2011). Cryopreserved stabilized polyembryonic cultures (SPCs) of six elite oil palm clones was monitored for nursery and field growth up to 12 years after transfer in Cote d'Ivoire. Six clones tested showed an average recovery of 34% after freezing in liquid nitrogen. Palm trees originating from control SPCs were found to flower early than preheated, dehydrated and cryopreserved SPCs. This delay in flowering disappeared progressively and all palms had flowered 3 years after planting (Konan *et al,* 2007). Pollen kept in screw-cap polypropylene cryovials (2ml capacity) was directly immersed in liquid nitrogen (at -196°C). After 1 hour, the vials were transferred to vapour phase of liquid nitrogen (-170 to -180°C). After 8 days of storage, cryovials were thawed in a water bath at 38^0 C for 5 min. Pollen sample prehydrated on clean glass micro slide for 1 hour, in 1HC. Pollen inability was retained as high as 54± 1.72% as assessed by FDA with *in vitro* germinability of 49 ± 1.2%. National Bureau of Plant Genetic Resources (NBPGR) has already demonstrated the potential of cryopreservation for successful storage of oil palm pollen after 8 years of storage (Tandon *et al*, 2007).

Summary

Oil palm is propagated by seed and long term conservation by seed is difficult in view of semi recalcitrant storage behaviour of the seed. Long term cryopreservation using kernel, somatic embryo and polyembryos has been reported. Oil palm pollen could be successfully stored after cryopreservation in liquid nitrogen. Desiccation tolerance is significantly correlated with embryo DW and water content and tolerance is acquired at specific stages. Therefore, more extended studies would lead to development of suitable storage protocols especially by cryopreservation.

Session VI : Seed Industry

1. New paradigms in breeder seed production

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Quality assured breeder seed is the key factor in the seed generation cycle of B-FS-CS to sustain higher yield genetic potential in seed and clonal crops. A systematic and well defined maintenance breeding of the valued breeder source material followed by nucleus seed constitution are the essential preceding steps of the Breeder Seed stage. In India, Breeder Seed is mandated with the inception of Seed Acts. Breeder Seed production is a crop specific procedure with inbuilt genetic purity verification and fulfilling minimum standards prescribed. The increasing demand and pressure of the National Food and Nutrition Security is a real time challenge. The breeder seed system needs to vibrate and respond to introduce protocols to fulfill the nutritional quality and the micronutrient contents and their genetic enhancements in each of the stage upto Breeder Seed , concomitant with maintaining high superior yield potential. Advances in the plant genomics applications of MAS now greatly facilitate the breeders to quicken the selection functions precisely in quality and micronutrients contents in food crops, legumes, oil crops, vegetables and fruits. DNA marker application resulted in the development of a rapid protocol namely “Molecular Grow Out Test (Mol. GOT) replacing time consuming Field Grow Out Test. Precise phenotyping techniques at early stages of crop growth by thoroughput Phenomics in the aid of GOT also compliments the Field GOT. Of late, DNA Barcoding innovation enables rapid varietal identification and trueness. Thus, Next Generation Sequencing (NGS) and Phenomics (Next Generation phenotyping) are smart tools in the hands of Breeders to practice the New Paradigms in Breeder Seed Production ensuring genetic trueness, purity and uniformity.

Global agriculture faces growing demand for food due to increasing population and it is accepted that the predicted 70% increased production by 2050 has to come from shrinking land, water and other resources (Foley *et al.*, 2011). This necessitates the implementation of Second Green Revolution by evolving high yielding varieties adapted to marginal and adverse environments, developing crop production technologies to maximize yield under fragile environments and reducing the post harvest losses to achieve the required demand in the food production. Among the various strategies towards second green revolution, supply of pure quality seeds of high yielding varieties is one of the important crop production technologies which need to be given attention. Seed is the most important input component for productive agriculture. As seed quality has much impact on crop yield in most of the annual crops, maintenance of genetic purity and quality is considered to be most important in modern agricultural systems. Seed quality is determined by factors such as, percentage genetic purity, physiological quality and free of seed borne diseases.

During seed multiplication, parental seeds may get contaminated as a result of natural cross pollination; better seed quality control is needed to evaluate the genetic purity of the parents and hybrid seed. In recent decades several methods have been developed for testing variety, parents and hybrid purity which includes tests of morphological characteristics by growing representative samples, restriction fragment length polymorphisms (RFLP) and PCR-based markers (Gupta et al 1999). These techniques are widely used but have various drawbacks including the time required, high cost, complexity of testing, and so forth. There are three major types of genetic markers: (1) morphological markers which themselves are phenotypic traits or characters; (2) biochemical markers, which include allelic variants of enzymes called isozymes and proteins and (3) DNA markers, which reveal sites of variation in DNA sequences (Jones *et al.,* 1997).

The development of improved varieties of major crop plants and availability of seeds of such varieties to Indian Farmers is of crucial importance for a sustained increase in agricultural productivity. Out of various stages of seed multiplication, nucleus seed and breeder seed are produced by the inventor of the variety. Nucleus seed is the seed produced by the breeder who develops the particular variety and this will not be distributed to the agencies. Breeder seed is the seed material directly controlled by the originating or the sponsoring breeder or Institution for the initial and recurring production of foundation seed by various seed production agencies. Hence, high quality Breeder Seed is the critical factor in the seed multiplication chain (BS-FS-CS). Breeder seed production is standardized and practiced by the breeders and it should meet the minimum seed standards. The following phenotyping procedures are followed to maintain genetic purity of seed lots of crop varieties at various stages of multiplication.

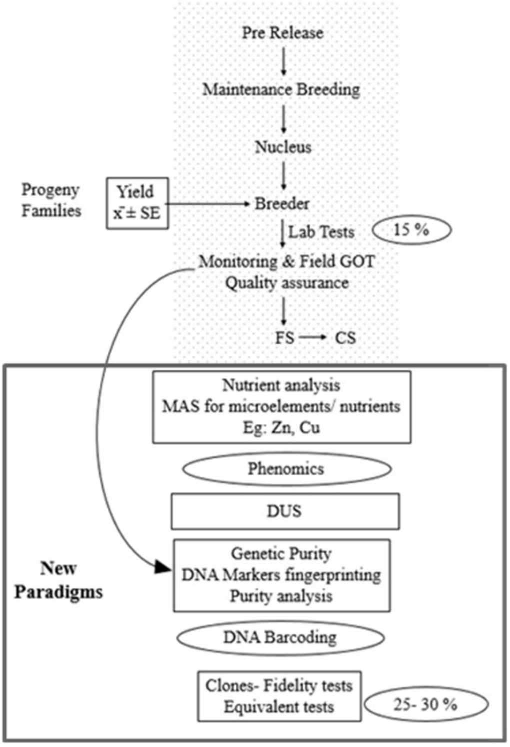

Fig 1. Procedures involved in maintaining and testing of seed genetic purity. New paradigms are shown in boxes.

Distinctness, Uniformity and Stability (DUS) Test:

In DUS growing test, candidate varieties are cultivated in fields or in greenhouses and compared with similar existing varieties (reference varieties) and morphological characteristics (colors, shapes, size, etc.) and physiological characteristics (tolerance to diseases, etc.) are evaluated. Variety specific characters will be identified and used for certification purposes.

Distinctness: New varieties should be clearly distinguishable from any other existing varieties.

Uniformity: Individual plants of new variety should be sufficiently uniform at the same propagation stages.

Stability: Characteristics of new variety should be stable through repeated propagation.

It is essential to develop technical manuals for cultivation, examination of morphological characteristics (color, shape, etc.) and physiological characteristics (tolerance to pests and diseases, particular components etc.) in major crops. It is also essential to collect and conserve reference varieties including standard varieties and development of their database. It is essential to introduce DUS testing at Breeder Seed stage itself for being distinct from other varieties in one or more traits, genetically uniform and stable in expression. Further this will facilitate PVP and variety registration. The PVP & FR Authority, GOI has initiated steps to develop protocols for DUS testing and the Guidelines of Diagnostic Characteristics in the important crops and considerable progress has been made in this direction.

Grow Out Test (GOT):

Grow out Test is conducted in the fields located in ideal growing environment and season to realize favorable G X E interaction and morphological expression of the distinguishing characters. A combination of laboratory and field plot methods may be used to determine the cultivar trueness and genetic purity of the sample. Laboratory methods based on examination of morphological and seed characters, colour reaction to certain chemical treatments, properties of seedlings, response of seedlings to controlled environment and growth stimulants and stable plant characters are used to detect cultivar trueness. The methods for varietal purity are divided in the following groups:

A. Examination of seed in the laboratory.

B. Examination of seedlings grown in a growth chamber or green house.

C. Field plot tests or grow-out test.

It is appropriate to adopt the Phenomics technology to grow the seed samples in controlled and well defined environment green houses that will facilitate ideal plant expression at seedling stage itself for precise phenotypic evaluation. Technological platform in phenomics is being refined and evolved rapidly.

New paradigms in maintaining seed genetic purity

Molecular GOT using DNA markers:

The emerging needs of the food and nutritional security necessitate integration of existing breeder seed production procedures with the advances in the application of DNA mediated marker tools. DNA markers may be broadly divided into three classes based on the method of their detection: (1) hybridization-based; (2) polymerase chain reaction (PCR)-based and (3) DNA sequence-based (Gupta *et al.,* 1999). Essentially, DNA markers may reveal genetic differences that can be visualized by using a technique called gel electrophoresis and staining with chemicals (ethidium bromide or silver) or detection with radioactive or colorimetric probes. DNA markers are particularly useful if they reveal differences between individuals of the same or different species. These markers are called polymorphic markers, whereas markers that do not discriminate between genotypes are called monomorphic markers.

Molecular markers based on DNA amplification using the polymerase chain reaction (PCR) are relatively easy to use (Saiki *et al.,* 1987) in verifying the genetic purity of seeds and various types of PCR-based markers have been developed. RAPD markers are typically obtained using short (10″14 nucleotides) arbitrary primers (Williams *et al.,* 1993). RAPDs have the obvious advantage that they require no prior knowledge of DNA sequences. However, they are typically inherited in a dominant manner that precludes unambiguous classification of genotype (Fig. 2). Moreover, they suffer from a lack of reproducibility because they are sensitive to subtle differences in reaction conditions (Neale and Harry, 1994). Although many RAPD markers can be developed at relatively modest initial cost, no marker system is suitable for detecting the multiple alleles that are common in many out-breeding species.

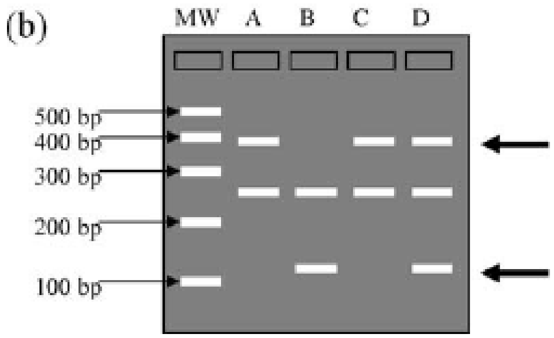

Figure 2. RAPD amplification profile in detecting F1 hybrid between two parents. A, Female parent; B, Male parent; C, selfed line and D, true hybrid.

Recent advancements in the field of molecular markers have led to the invention of Simple Sequence Repeats (SSR) and Amplified Fragment Length Polymorphism (AFLP) markers which are found to be efficient in detecting genetic variation in seeds or plants (Fig 3). SSRs are found to be useful and efficient in crops where sequence information is available (Tamil Kumar *et al.,* 2009). AFLP markers can detect polymorphism at multiple loci and widely used in commercial seed industries (Grzebelus *et al.,* 2001).

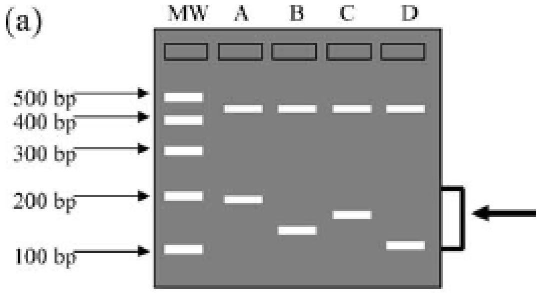

Figure 3. SSR marker finger-printing different genotypes. A,B,C and D represents four different genotypes showing polymorphism for the lower allele.

Other tools *viz.*, ELISA based techniques and microarray based diagnostic chips are also being used commonly to detect genetic contamination in the seed lots. These molecular tools can be used to check pedigrees and also to test for genetic shift and identifying duplicate accessions.

In a pre-release variety, no attention is bestowed to analyze for nutrient quality and micronutrient contents of seed. Directional selection for nutritional qualities combined in the superior performing families in the pre-release stage will ensure the twin objectives of food and nutritional security. Marker Assisted Selection for micronutrients and nutritional quality are now available and applied in corn, soybean, sorghum and other crops. The usage of molecular markers in breeding programs for micronutrient and quality traits enrichment has greatly increased its efficiency (Shankar and Sarla 2010). These markers can be effectively utilized in maintaining the genetic purity of the variety after release. Phenomics in conjunction with Genomics is very reliable for judging trueness, purity and uniformity. Molecular GOT can be conducted in the laboratory itself within a short period of 5 to 10 days thereby avoiding field GOT involving growing the crop for 90 to 120 days time upto flowering and fruiting to assess the genetic purity.

DNA Barcoding:

Apart from DNA based markers, DNA Barcoding for identification of varieties based on the DNA sequence similarity with the standardized short genome region is analogous to the tracking tag Barcoding in commodity business in Super markets. It is yet another handy smart tool since 2009. DNA barcoding aims to assign individuals to given species according to their sequence at a small locus (ex. chlroplastid gene). DNA barcoding is applied for testing genetic purity of given species/varieties like DNA fingerprinting and purity tests (Fig. 4). Breeders are now provided with opportunities of genomics and phenomics innovations to accelerate the fast track approaches in developing quality assured seeds which will contribute for 10-15 % of yield increase.

DNA barcoding in plants with 400-800 bp is a vital new tool comprising two plastid genes, rbcL and matK and a nuclear genic region (ITS). Images of DNA barcoding provide reliable information system, versatility and universality (Hollingworth et al., 2009 and Hollingsworth *et.al.,* 2011). In 2009, Plant DNA barcode Working Group decided in favour of 2 locus combination of rbcL and matK to identify specimens. This technique is being potentially transferred to seed generation system and seed supply chain from lab to field. Further DNA markers with the aid of Multiplex PCR are useful in purity testing and seed health standards.

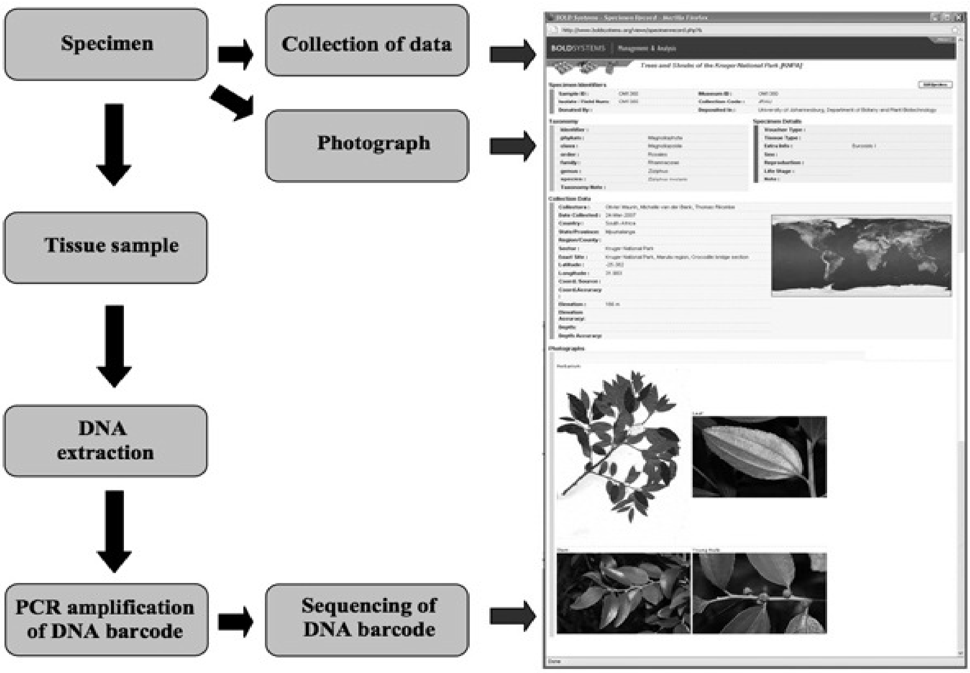

Fig 4. Important steps in Plant DNA Barcoding -

Maintaining genetic purity of clonally propagated crops:

The new paradigms developed for maintaining genetic purity of seed propagated crops are equally applicable to the vegetatively propagated clone crops and micropropagated *in vitro* clone crops as well. The genetic fidelity tests are conducted to confirm the faithful reproduction and thereby trueness, purity and stability. Many forms of the grafted plants including the scion and root stock sources, different kind of layerings and micrografts await the Genetic Fidelity test. The mother clones and organs used for initiating the vegetative cloning should be genetically pure, healthy, vigorous and satisfy phytosanitory norms for inducting them into Breeder Seed process. Vigorous and clean clonal seeds give 25- 30 % yield increase. Testing the source materials for virus, viroid and other pathogenic microbes and accurately index them for disease free condition are the pre requisites and essential steps in each stage of the seed generation. The DBT –NCS –TCP standards and Guidelines and Protocols standardized for more than 10 important crops could be also followed for scaling up of quality assured in vitro plants. **Clean Seed, Clean Field and Clean Crop** is the needs of the hour to the farming community for successfully implementing the Second Green Revolution.

2. Towards improvement of oil content in safflower (*Carthamus tinctorius* L.)

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Safflower (*Carthamus tinctorius* L.) is a multi-purpose oilseed crop grown for vegetable oil, animal feed, natural dyes and medicinal uses globally (Knowles 1989; Li and Mündel 1996). It is a traditional oilseed crop of India, primarily known for its healthy cooking oil containing more than 80% of polyunsaturated fatty acid (PUFA), the highest among edible oils (Kostik *et al.* 2012). Despite economic importance, safflower cultivation is declining in India, from 10 lakh ha. in 1988 to 1.5 lakh ha. in 2013 (FAOSTAT 2013). Seed oil content in the popular cultivars remains low (~28-32%), which is a concern for increasing the profitability of safflower cultivation. Increase of oil content in the cultivar would eventually lead to increase in oil yield, which would make safflower a commercially competitive crop for the farmers and attract the vegetable oil industry to take up safflower promotion in the country. We are exploring various strategies including the introduction of exotic high oil germplasm/ varieties, conventional and molecular breeding to enhance oil content coupled with high seed yield in safflower.

A total of 38 genotypes (30 from Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias-INIFAP, Mexico; 8 from United States Department of Agriculture-USDA) were imported through NBPGR, New Delhi and they were evaluated for oil content along with Indian check varieties at research farm of DOR, Hyderabad. Twenty varieties recorded more than 35% oil content with the maximum of 41% (EC 736516-Centennial, a USDA variety) compared to the checks: A-1 (26%), Bhima (31%) and NARI-57 (37%). High oil content in the Mexican varieties was also confirmed in multi-location trials conducted by AICRP-safflower centres at Indore, Parbhani, Phaltan and DOR. The mean oil content of Mexican varieties ranged from 35.1% to 37.8% whereas the high oil check variety NARI-57 recorded 35.8% at four locations. In order to further establish the potential of the exotic varieties, genetic distance between Indian and Mexican safflower cultivar groups was analyzed by SSR markers. Sixty cultivars (30 from Mexico; 30 from AICRP-safflower centres in India) were genotyped using 48 randomly chosen SSR loci. Cluster analysis based on Neighbour-Joining (NJ) tree method clearly showed that Indian and Mexican safflower cultivars were genetically distinct ($F_{ST\,=}$ 0.396). Overall, the phenotypic and molecular characterization of Mexican safflower varieties suggested that they provide genetically diverse sources of seed yield and high oil traits for Indian breeding programmes.

We have initiated a breeding programme to develop cultivars with high oil yield potential by crossing the exotic high oil germplasm sources with Indian safflower varieties *viz*., A-1, Bhima, PBNS-12 and NARI-57. Currently, the cross between NARI-57 and Centennial has been analyzed for inheritance and selection of desirable breeding progenies. The oil content of F_3 seeds of 248 F_2 progenies of this cross ranged from 19% to 44% with an average of 35% indicating quantitative nature of inheritance. The seed yield per plant of these 248 F_2 progenies ranged from 1.5 g to 82 g while the seed yield per plant of NARI-57 and EC 736516 were 38.3 g and 12.4 g, respectively. A set of F_3 and F_4 families that showed high seed yield coupled with high oil content (~40%) have been identified through pedigree method of selection, which are under field evaluation. Development of multi-parent advanced generation intercross (MAGIC) population (Bandillo *et al.* 2013) is in progress to facilitate genetics research and selection of breeding lines with high oil content coupled with high seed yield.

Historically, combining high oil content with high seed yield has been a challenge in safflower (Ranga Rao *et al.* 1977). Molecular markers offer promise for dissecting genetic basis of complex quantitative traits such as seed yield and oil content and further combining desirable genes/alleles to achieve high oil yield. Nothing is known about genes controlling seed yield components and oil content in safflower except some reports on molecular tagging of genes for oil quality *viz.*, *li* - high linoleic acid content, *tph2* - high tocopherol content and *ol* - high oleic acid content (Hamdan *et al.* 2008; García-Moreno *et al.* 2011; Hamdan *et al.* 2012; Liu *et al.* 2013). We are exploring a combination of traditional QTL mapping and candidate gene based allele mining approaches, using bi-parental/MAGIC populations and germplasm panels, to detect genes and alleles contributing to increased oil content in safflower. Our initial characterization of 148 safflower accessions representing morphological and geographical diversity using 50 SSR loci revealed very weak population structure in the germplasm collection suggesting that genetic diversity is randomly distributed and not constrained by geographical locations/origins. We also observed very low SSR allelic diversity, which is a concern and there is a need to design SNP markers. Currently, lack of reference genome sequence and high density genetic linkage map are the major limitations, which need to be addressed to expedite trait mapping and marker-assisted selection in safflower.

* * *

1. GENETIC IMPROVEMENT OF CROP PLANTS THROUGH CLASSICAL PLANT BREEDING METHODS

PI-1

GENETIC VARIABILITY IN BARNYARD MILLET [*Echinochloa frumentacea* (ROXB.) LINK] GERMPLASM

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A total of 65 barnyard millet indigenous and exotic accessions were evaluated during *rabi* 2012 at Agricultural College and Research Institute, Madurai to determine the genotypic and phenotypic co-efficient of variation (GCV and PCV), heritability and genetic advance. The accessions were planted in Randomized Block Design (RBD) with three replications adopting a spacing of 30 x 10 cm. By using barnyard millet descriptors (IPGRI, 1983) data were recorded on various morphological characters such as days to 50 % flowering, plant height (cm), no. of basal tillers (no.), flag leaf length (cm), flag leaf width (cm), no. of nodes (no.), peduncle length (cm), earhead length (cm), earhead width (cm), lower raceme length (cm), no. of racemes (no.), single earhead weight (g), grain weight per earhead (g), 1000 grain weight (g), straw yield per plant (g) and single plant yield (g). A wide range of variability both at genotypic and phenotypic level was observed for all the characters studied. The difference between PCV and GCV was low for all the traits studied, which indicated little influence of environment over phenotype of the traits. High heritability coupled with high genetic advance observed for the all the characters studied indicates that these traits are under the influence of additive gene action. Selection based on these characters would be effective for future barnyard millet crop improvement programme.

PI-2

CROSSING EFFICIENCY IN INDIAN MUSTARD [*Brassica juncea* (L.) CZERN & COSS]

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Efficient crossing techniques was tried in three crosses (Varuna X RH-819, Ashirwad X RH-819, ACN-9 X Geeta) of Indian mustard [*Brassica juncea* (L.) Czern & Coss] during *rabi* 2011-2012 in randomised complete block design with two replications at the experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. Crossing work was carried out to determine the crossing efficiency under field conditions. Young flower buds of appropriate size of the female

parents supposed to open in the next morning were emasculated and the emasculated buds were pollinated with fresh pollens collected from the male parents during next day morning and were bagged immediately with thin butter paper bags. Pollination timings showed variation in seed setting percentage among the three crosses. Seed setting percentage was more than 90% in all the three crosses when the emasculated flowers were pollinated immediately in the next day morning 7.45 to 9.00 AM and seed setting per cent was less than 32% when pollinated one day after anthesis. Reduction in seed setting was reported in delayed pollination, it was revealed that delayed pollination considerably reduce the pollen viability and stigma receptivity. Among the two time intervals, immediate pollination after emasculation showed significantly high seed set per cent for different cross combinations.

PI-3

STABILITY ANALYSIS FOR YIELD AND YIELD COMPONENTS IN PEARL MILLET (*Pennisetum glaucum*)

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The material consisting 20 hybrids along with two checks viz., RHRBH 9808,AHB 1666 were evaluated during *kharif* 2013-14 at three locations. The material was sown in randomized block design. The observations were recorded on the characters *viz*., days to 50% flowering, days to maturity, plant height (cm), total number of tillers per plant, number of effective tillers per plant, 1000 grain weight (g), ear head girth(cm),ear head length (cm), fodder yield per plant (g), and grain yield per plant (g). Stability and character association were carried out as per model of Eberhart and Russell (1966) and Johnson *et al.* (1955) respectively. Analysis of variance revealed highly significant differences among genotypes for all the characters. The stability analysis as per the Eberhart and Russell model suggested the existence of variability in the experimental material and all the three environments differed significantly among themselves. The pooled deviation was significant for total number of tillers per plant, plant height, number of effective tillers per plant, 1000 grain weight, ear head girth, ear head length, fodder yield per plant and grain yield per plant indicating the predominance of unpredictable portion of G x E interaction for the expression of these characters. Regarding the most important trait grain yield per plant, the hybrids PT 4139 x ICMA 95333 and PT 4801 x ICMA 99222 showed wider adaptability to all environments.

PI-4

GENETIC VARIABILITY STUDIES IN F_1 GENERATION OF INTERSPECIFIC CROSSES IN CHILLI

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Fifteen interspecific (*Capsicum frutescens* x *Capsicum annuum*) hybrids along with their eight parents (five resistant frutescens lines and three susceptible annuum testers) were subjected to genetic variability study in order to ascertain the yield parameters and disease resistance. The parents include five local varieties of *Capsicum frutescens* types and three susceptible popular varieties namely jwalamukhi, jwalasakhi and vellayani athulya. The results indicated that the genetic material in the present investigation possessed high variability. High estimates of PCV and GCV were obtained for green fruit yield per plant, vulnerability index, average fruit weight and number of fruits per plant indicated a good deal of variability for these characters. High heritability (above 80%) assisted with high genetic advance as per cent of mean (above 20%) was observed for green fruit yield per plant, duration of crop, number of seeds per fruit, days to first flowering, duration of flowering, pedicel fruit ratio, number of fruits per plant and average fruit weight. Thus based on phenotypic performance of these characters simple selection would be more effective but medium heritability was recorded for vulnerability index which may require repeated crossing for transfer of resistance. The remaining characters show low variability indicating the presence of non additive gene action which requires heterosis breeding.

PI-5

HETEROSIS IN SEED QUALITY PARAMETERS OF CROSSES IN BARNYARD MILLET [*Echinochloa frumentacea* (ROXB.) LINK]

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Barnyard millet a quick growing crop of all the millets is gaining momentum for its nutritious grains and fodder in dryland areas of the country. The crop which is still needed to be commercialized is taken up for the present study. A total of twenty crosses were raised from five selected parents of barnyard millet crossed in diallel fashion during *kharif* 2014 at Agricultural College and Research Institute, Madurai. The seed quality parameters *viz.,* speed of germination, seedling length, seedling growth rate and vigour index were determined for the crosses and parents by roll towel and top of paper methods. The parents selected were Co (Kv) 2, ACM-10-145, ACM-10-161, ACM-331 and ACM-332. For the seed quality parameters, standard heterosis was calculated by taking Co (Kv) 2 as standard check. All the crosses showed significant amount of heterosis for seed quality parameters

indicating they are true crosses. Speed of germination was significant for 16 crosses with ACM-10-145 x ACM-332 showing the highest heterosis. Seedling length was significant for 11 crosses out of which ACM-10-161 x ACM-331 recorded high heterosis. The cross ACM-10-161 x ACM-331 was highly heterotic for seedling growth rate and 14 crosses were significant for the same. Hybrid vigour was significant for 14 crosses among which Co (Kv) 2 x ACM-332 recorded the highest heterosis. Thus, the study proves the worth of hybrid vigour in barnyard millet for further exploitation.

PI-6

GENETIC ANALYSIS OF GMS BASED HYBRIDS AND THEIR PARENTS IN DESHI COTTON (*Gossypium arboreum* L.)

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The present investigation was undertaken to estimate extent of heterosis. A set of ten parents, two females (GMS lines) *viz.,*GAK-423,GAK-8615 and eight males (testers) *viz.,* AKA-9703, AKA-0110, AKA-9620, AKA-9009-1, AKA-0209, AKA-5, AKA-7, HD-162 and their 16 crosses along with check PKV Suvarna were evaluated in randomized block design with three replication at the field of Cotton Research unit, Dr.PDKV, Akola during *Kharif* 2012-2013.The mean squares due to genotypes were highly significant for all the traits studied expect for numbers of monopodia per plant, ginning percentage and oil content. This indicated the presence of substantial genetic variability among genotypes for all the traits studied. The highest significant useful heterosis for seed cotton yield per plant was recorded in GAK-8615 X AKA-7 (28.26% over check).In case of heterobeltiosis, the cross GAK-8615 X AKA-7 recorded the highest significant heterobeltiosis (51.28%) for seed cotton yield. The cross GAK-8615 x AKA-7 revealed high mean performance (59g), high magnitude of useful heterosis (28.26% over check PKV Suvarna).The cross GAK-423 X AKA-5 depicted high mean performance (253.33g), high magnitude of useful heterosis (15.94% over check PKV Suvarna). So this cross may be employed to exploit non-additive component along with high heterotic response.

PI-7

BREEDING FOR BIOFORTIFICATION OF RICE IN SEGREGATING POPULATION

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Micronutrient malnutrition is recognized as a massive and rapidly growing public health issue especially among the poor people living on an unbalanced diet dominated by a single staple grain such as rice.

Among the major micronutrient deficiencies common in rice consuming countries, iron and zinc deficiency (the so called hidden hunger) affect three billion people worldwide, mostly in developing countries. Biofortification of staple food crops which hold great promise for improving nutritional status and health of poor population in both rural and urban areas of developing world. Besides this approach bridge the field of human nutrition, crop science and public health a set of highly sustainable nutritional intervention in a cost effective manner. A lot of variability does exist for micronutrients (Fe, Zn and vit A *etc.*) content and bioavailability in many crops including rice. The current study was conducted in Agricultural College and Research Institute, Madurai during 2011-2012 to assess the variability for iron and zinc content along with quality traits in dehusked rice grains to identify the mineral rich families. Based on mean, GCV, PCV, heritability and Genetic advance, it was understood that the progenies ADT37 x IR68144-3B-2-2-3 would be more useful for improving grain iron content with the desirable quality traits *viz.*, kernel length, kernel breath after cooking. Similarly TRY(R) 2 x Mapillaisamba segregants could be used for grain zinc content along with breadthwise expansion ratio.

PI-8

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN OKRA (*Abelmoschus esculentus* (L.) MOENCH)

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The present investigation was undertaken in *kharif* season, 2011 on the farm of Chilli and Vegetable Research Unit (CVRU), Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola in Randomized Block Design with three replications on fifty genotypes and observations were recorded on growth parameter, yield parameter and quality parameter. Analysis of variance indicated significant differences among the genotypes for different morphological characters. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The high values of GCV and PCV observed for primary branches per plant, yield per plant, yield per hectare, protein content and number of fruits per plant. High heritability coupled with high genetic advance was observed for yield per plant, yield per hectare and leaf area. On the basis of results obtained from mean value, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance, the studied work might be suggested for further utilization in breeding programme. The genetic analysis of genotypes provides a guideline for the use of superior selection for the enhancement of yield and yield related characters. IC-117011 and IC-117034 are dwarf varieties among all the genotypes.

PI-9

HETEROSIS SCRUTINY FOR YIELD AND GRAIN QUALITY TRAITS IN HIGH YIELDING RICE VARIETIES OF TAMIL NADU

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An investigation in rice was undertaken to study the nature and magnitude of heterosis for yield, yield components and grain quality traits involving ten high yielding lines and three superior grain quality testers and thirty hybrids were developed through line x tester mating design. Significant heterosis for grain yield and quality traits were observed in most of the hybrids. In general, the estimates of heterosis values were low for quality traits when compared to yield and yield contributing traits. Nine hybrids exhibited positive and significant heterosis over standard check but six crosses over better parent for grain yield/plant. Standard heterosis and heterobeltiosis for grain yield ranged from -15.64 to 20.04% and -23.75 to 15.50%, respectively. A total of four hybrids *viz*., ADT 39 x I.W.Ponni, ADT 43 x I.W.Ponni, ADT 49 x I.W.Ponni and CO (R) 50 x I.W.Ponni were recorded higher grain yield over both better parent and standard check and were identified as best hybrids for exploiting hybrid vigor. Most of the heterotic crosses for grain yield/plant were accompanied by heterosis for two or more component traits. The cross combinations ADT 36 x I.W.Ponni and ADT 43 x I.W.Ponni exhibited superior performances for thirteen yield contributing and grain quality traits over both better parent and standard check. The hybrids *viz*., ADT 43 x JGL 3855, CO (R) 50 x BPT 5204 and CO 43 x JGL 3855 were considered as the next best.

PI-10

VARIABLITY STUDIES IN SAFFLOWER (*Carthamus tinctorius* L.) GERMPLASM

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Safflower (*Carthamus tinctorius* L.) is an important oilseed crop that is valued as a source of high quality vegetable oil. Genetic diversity of 40 genotypes of safflower was estimated using D^2 analysis. The genotypes under study were grouped into six clusters. The cluster-I was the largest containing 29 genotypes followed by cluster-II (5 genotypes) and cluster-V (3 genotypes). The average inter cluster distance was maximum between clusters III and VI, followed by clusters II and III, clusters IV and VI, clusters I and VI, clusters I and V. The seed yield per plant contributed maximum towards genetic divergence followed by oil content and days to maturity. The present study projected the importance of GMU-6013, GMU-6083, GMU-6142 as parents for higher heterosis in F_1 and potential transgrants in subsequent generations as they have least means for days to 50% flowering,

days to maturity, whereas high means of GMU-6041, GMU-6894, GMU-6973, GMU-6041, and GMU-PKV-Pink for characters *viz.* number of capitula per plant, number of seeds per capitula, 100 seed weight, seed yield per plant and oil content respectively for their further improvement in yield and oil content.

PI-11

DIVERSITY STUDIES AND DEVELOPMENT OF SINGLE CROSS HYBRIDS FOR GRAIN YIELD AND ITS COMPONENT TRAITS OF MAIZE (*Zea mays* L.)

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The present investigation was carried out to know the genetic diversity among the new inbred lines, identification of good combiners and superior single cross maize hybrids. Experiment material consisted of 30 inbred lines and three testers evaluated during *kharif* 2012 and thirty inbred lines were crossed with each of three testers in a line x tester design to evaluate combining ability and heterosis to identify promising hybrids of maize for various characters. The resulting F_1s along with three checks and the parents were evaluated during summer 2013, in RCBD with three replication at MARS, UAS, Dharwad. Analysis of variance revealed that highly significant difference among all inbred lines. Inbred lines were grouped into six clusters, indicating the presence of genetic diversity among the inbreds. The cluster I is having highest number of genotypes (17). These genetically diverse inbred lines can be further used for developing superior hybrids. Analysis of variance revealed highly significant differences among the genotypes. DMIL767, DMIL318 and DMIL326 among the parental lines and DMIL011 among the testers were identified as the best general combiner for grain yield. Whereas among the hybrids, DMIL765 x DMIL031 and DMIL318 x DMIL011 were identified as a potential cross combination for grain yield while the cross DMIL765 x DMIL031 recorded highest magnitude of economic heterosis of 13.95 percentage over the best standard check. So the crosses DMIL765 x DMIL031, DMIL318 x DMIL011 and DMIL639 x DMIL011 can be utilized for developing high yielding hybrid varieties as well as for exploiting hybrid vigor.

PI-12

ESTIMATION OF HETEROSIS, COMBINING ABILITY AND GENE ACTION STUDIES FOR YIELD TRAITS IN GREENGRAM (*Vigna radiata* (L) WILCZEK)

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Ten lines were crossed with four testers in a line x tester design in green gram. Resultant 40 experimental hybrids were evaluated along with parents and check in randomised block design with three replications. The analysis of variance for combining ability evinced predominance of non-additive gene effects for 11 characters studied indicating relevance of heterosis breeding for improving yield attributes. The *gca* effects of parents revealed that CO7, Pusa 0672, IPM 02-17 and ML 1451 were good general combiners for yield and its direct components. The estimates of *sca* effects revealed that eleven experimental hybrids had significant, desirable and positive *sca* effects for seed yield. The cross combinations ML 1451 x CO 7, Pusa 0672 x CO 6, IPM 02 -19 x CO 6, MH 512 x Local TNY and MH 318 x Local TNY were good specific combiners for number of branches per plant, number of pods per plant, pod length and seed yield per plant. These parental combinations are being used for exploitation of hybrid vigour.

PI-13

CORRELATION AND PATH ANALYSIS IN INTERVARIETAL CROSSES IN RICE (*Oryza sativa* L.)

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An investigation was carried out in rice (*Oryza sativa* L.), at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal during *kharif*, 2008 to genetically analyse the F_3 generations of five crosses *viz*., ADT 43 x Vellaichitraikar, ADT 43 x Arupathamkuruvai, ADT 43 x Varappukudaichan, ADT 43 x IPM Rascadam and ADT 43 x IR 66424. Mean, variability, heritability, genetic advance, correlation and path analysis were worked out for seven quantitative traits *viz.,* plant height, panicles per plant, panicle weight, panicle length, grains per panicle, grain weight and grain yield. The F_3 generations of the five crosses were studied along with the check variety, ADT 43 the common female parent that is a popular ruling variety. Among the five crosses, ADT 43 x IPM Rascadam and ADT 43 x IR 66424 were found to be superior crosses to provide good source populations for exercising an effective selection for high yielding plants, as these crosses registered high mean and greater genetic variability for grain yield and three of its most important component traits *viz.,* panicles per plant, panicle weight and grains per panicle. The possibility of isolating superior

transgressive segregants in the populations of these two crosses was noted based on wider range along with high mean performance for grain yield and the above yield component traits.

PI-14

IDENTIFICATION OF ZINC DEFICIENCY TOLERANT RICE (*Oryza sativa* L.) DONORS *VIA* PHENOTYPING UNDER SUBMERGED CONDITIONS

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Zinc deficiency is a widespread problem in rice grown under flooded conditions, limiting growth, reduce yield and Zn accumulation in grains. Hence, the major emphasis in this study is to identify donors for Zn deficiency tolerance. Ten low land rice genotypes and 40 landraces were grown under Zn deficient condition by adopting augument design. The data on 10 morphological traits *viz*., days to 50 per cent flowering, plant height, panicle length, number of productive tillers per plant, number of filled grains per panicle, spikelet fertility, 1000 grain weight, single plant yield, plot yield, and biomass were recorded. The severe Zn deficiency in the field condition (0.5 mg / kg of soil) facilitated the identification of rice genotypes with true tolerance or susceptibility to low Zn conditions. Moreover, Zn deficiency significantly reduced the grain Zn content compared with Zn sufficient conditions and this response was genotype specific. The scoring was done based on visual observation on browning or yellowing of leaves, height and tillering ability of the plant at three growth stages *viz*., seedling (10 DAP), tillering (25 DAP) and stem elongation (45 DAP), stunting and mortality of plants. Genotypes differed significantly in grain yield and its components. Based on the grain yield and scoring the most Zn efficient genotypes were: Arupadham kuruvai (1.2), Kattanur (1.4), Sorrakuruvai (1.4), Avasara samba (1.5), Mappilai samba (1.7) and these could have been the donor of the genes for tolerance to Zn deficiency.

PI-15

COMBINING ABILITY ANALYSIS FOR YIELD AND ITS CONTRIBUTING CHARACTERS IN CHILLI (*Capsicum annum* var. *annum)*

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Combining ability was studied in six parental line of chilli in a diallel cross including reciprocals for 12 important characters. The mean square for GCA, SCA and RCA were highly significant for all the characters studied. This indicates variation in *gca* of parents and *sca* of hybrids and significant

combination of additive and non additive gene effects in the expression of characters. Among six parental lines, the parent P_2 (K1) expressed highest *gca* for plant height, number branches, fruit length, fruit girth, fresh fruit weight and fresh fruit yield per plant and the parent LCA 625, were identified as good general combiner for number of fruits per plant, dry pod weight, number of seeds per pod, seed weight per pod and dry pod yield. PKM1, LCA 625 and K1 had highest negative *gca* effects for days to 50 per cent flowering. The *sca* effects showed that best specific combination was Pusa Jwala x PKM1, LCA 334 x Arka Lohit, LCA 625 x K1, PKM 1 x LCA 625 and K1 x Arka Lohit for fresh fruit yield per plant and dry fruit yield per plant.

PI-16

COMBINING ABILITY AND HETEROSIS FOR KERNEL CAROTENOIDS IN MAIZE INBREDS POSSESSING FAVOURABLE ALLELE OF ß-CAROTENE HYDROXYLASE (*CRTRB1*) GENE

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Carotenoids are required by humans for the normal growth and development. While, *á* -carotene, ß-carotene and ß-cryptoxanthin are required for vision; lutein and zeaxanthin act as antioxidants. Humans cannot synthesize carotenoids in their body, and are to be provided through dietary means. Yellow maize among cereals possesses sufficient carotenoids, and thus it is important to genetically dissect such traits for effective utilization in breeding programme. In the present investigation, a line x tester (7 x 3) set was generated involving parents having favourable allele of *crtRB1* (ß-*carotene hydroxylase*) gene, that causes higher accumulation of *â*-carotene in maize kernel. The 21 hybrid combinations along with parents and checks were evaluated at two diverse maize growing regions of India viz. Delhi and Almora. Based on GCA effects and mean performance, the lines SE547 and Pant125 were promising for lutein, zeaxanthin and ß-cryptoxanthin, while MGU150-1 was ideal for *â*-carotene. Among the testers, HP467-9 was identified as best combiner for lutein, zeaxanthin and *â*-carotene. The cross, HP233-20 x HP465-20 emerged as promising specific combiner for lutein, zeaxanthin and grain yield, while MGUDM-RIL47 x HP465-20 was identified as the most promising for ß-carotene and grain yield. Preponderance of additive gene action was observed for all the carotenoid components. Majority of experimental hybrids possessed less lutein, zeaxanthin and ß-cryptoxanthin, but had almost double the amount of the ß-carotene as compared to checks. Experimental hybrids showing high standard heterosis for grain yield and ß-carotene (41.9% to 218.7%) have been identified and they hold promise in maize biofortification programme.

PI-17

STUDY ON GENE ACTION AND COMBINING ABILITY IN BITTER GOURD (*Momordica charantia* L.)

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Bitter gourd (*Momordica charantia* L.) is most important vegetable crop extensively grown throughout the country for its nutritive value and therapeutic properties. It is rich source of minerals (iron, calcium and phosphorous) and vitamins (A and C). Combining ability analysis is one of the powerful tools available which estimates combining ability effects and aids in selecting desirable parents and crosses for further exploitation. The present investigation was therefore, undertaken at College of Horticulture, Rajendranagar, Hyderabad using 8 parents and 28 F_1 hybrids to obtain information on gene action and estimates of general and specific combining ability. The results revealed that non-additive gene action played major role than additive gene action in inheritance of yield and yield attributing traits. Among parents, IC-044438, IC-470560, IC-470558 and IC-085622 were found good general combiners for yield attributing characters and earliness hence, these parents can be exploited for hybridization for producing desirable recombinants in the segregating generations. High specific combining ability effects for yield and related characters were exhibited by IC-044438 x IC- 045339 followed by IC-044417 x IC-470558 and IC-045339 x IC-085622. For earliness the crosses *viz.*, IC-044438 x IC-045339, IC-045339 x IC-470550 and IC-045339 x IC-470558 were identified as promising ones. Most superior specific cross combinations involved High x Low and Low x Low general combiners.

PI-18

PHENOTYPING OF ZINC DEFICIENCY TOLERANCE IN RICE BY ZINC RESPONSIVE ANALYSIS UNDER SUBMERGED CONDITIONS

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Zinc is an essential micronutrient and its deficiency causes magnitude of symptoms resulting in severe yield reduction in rice. Phenotypic expression of rice plants in response to different levels of zinc *viz.,* no application (NA), soil application (SA) and soil+foliar application (S+FA) was investigated under submerged and zinc deficient (0.6 mg kg^{-1}) conditions for two rice varieties-PYR-1, ADT-39 and two landraces-Savulu samba, Kotta nel. Zinc sulphate was used as source of zinc for both soil

(25 kg ha^{-1}) and foliar application (@ 0.5% on 10th and 25th day). Phenotyping was done based on the zinc deficiency scoring, yield and yield attributing traits. The results revealed that irrespective of zinc application levels, both the land races recorded score 3 while PYR-1 showed moderate tolerance with score 4 in S+FA and 5 under NA. Extreme sensitivity was noticed in ADT-39 as it scored 7 in S+FA and 8 under NA. The flowering was delayed in PYR-1 (16 days) and ADT-39 (11 days) but it was unaffected in kotta nel and savulu samba. Zinc deficiency tolerance was confirmed in savulu samba and kotta nel which exhibited deficiency symptoms in the initial stages and later recovered, showing no difference among various levels of zinc application. This clearly indicates that the landraces have the capacity to acquire, mobilize and translocate unavailable form of zinc whereas it is inefficient or absent in PYR-1 and ADT-39. This method can be utilized for phenotyping and screening of zinc deficiency tolerant lines.

PI-19

INDUCED VARIABILITY IN M_3 GENERATION OF GREENGRAM (*Vigna radiata* (L.) WILCZEK)

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Greengram (*Vigna radiata* (L.) Wilczek) is a cheap source of dietary protein for the poor, with high levels of folate and iron compared with many other legumes. Variability is less available in mungbean and hence to replace conventional breeding, mutation breeding has gained its momentum. Most of the plant attributes of interest to a plant breeder are quantitative characters which are controlled by a polygenic interaction. Induced mutagenesis thus seems to be an ideal methodology for the induction of desirable genetic variability. In this present investigation, variability induced by gamma rays and Ethyl methane sulphonate (EMS) in two greengram genotypes *viz.,* CO (Gg) 7 and NM 65 for eight quantitative traits *viz.,* plant height, days to 50% flowering, branches/plant, clusters/ plant, pods/ plant, seeds/pod, 100-seed weight (g) and yield/plant (g) was studied in M_3 generation. A wide range of variability existed for different traits coupled with high heritability and high genetic advance for five traits *viz.,* number of clusters per plant, number of seeds per pod, number of pods per plant, hundred seed weight and single plant yield for both the genotypes.

PI-20

EVALUATION OF POPULAR RICE VARIETIES AND IDENTIFICATION OF SELECTION PARAMETERS FOR COLD TOLERANCE DURING PRE BOOTING STAGE

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Low temperature (<18°C) during pre booting stage of rice causes spikelet sterility. It is prevalent in Krishnagiri-Dharmapuri districts of north western zone during late sowing season (Sept-Oct). In order to identify the cold tolerant varieties and fix the selection parameters for breeding for cold tolerance, 21 popular varieties were chosen and evaluated. Date of sowing was adjusted to coincide the pre-booting stage at low temperature months (Nov-Dec). Based on spikelet sterility, three varieties were found to be fertile (75-89%) *viz.,* Anna-4, CO-43 and IR-20. Partly sterile (75-80%) varieties were also identified *viz.,* ADT-38, ADT-39, ADT-43, IR-50, MDU-3, MDU-4 and MDU-5. Highly sterile lines (<50%) included Paiyur-1, White ponni, BPT-5204, bhavani and karuppu nel. Based on pollen fertility and panicle emergence, three groups were identified *viz.,* fertile and complete emergence: Anna-4, CO-43, IR-20 2; partial emergence and fertile: ADT-38, ADT-39, ADT-43, IR-50, MDU-3, MDU-4 3; poor emergence and sterile: White ponni, BPT-5204, Bhavani, Paiyur-1. Anna-4 was found to have high fertility as well as high yield (3.4 t/ha) and it can be recommended for cultivation in Krishnagiri and Dharmapuri districts during late season (Sept-Oct). Based on these selection parameters *viz.,* spikelet fertility, panicle emergence and pollen sterility, breeding programmes for cold tolerance during pre-booting stage can be designed.

PI-21

COMBINING ABILITY ANALYSIS FOR QUALITY TRAITS IN CHILLIES (*Capsicum sp*.) OVER ENVIRONMENTS

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Chilli (*Capsicum* sp) is one of the most valuable solaneceous crop of India. It is also a valuable foreign exchange earner. The quality of chilli is of utmost importance and priced based on its intrinsic characters *viz*., capsaicin (pungency level), oleoresin (good flavour) and capsanthin (bright red colour). The major objective of chilli breeding now aims at upgrading the yield and quality. This can be efficiently achieved by the selection of parents as well as the hybrids that are superior for yield and quality attributes. Combining ability effects are considerably influenced by environments, and for a more valid estimation, a study under different environments is likely to bring out the impact of genotype

x environment interaction on the estimates. In the present investigation fourteen parents and their 45 F_1s of chillies from a line x tester cross were evaluated for four quality assuring characters over three environments. Highly significant variation was observed due to genotype and environment for all the characters studies. The genotypes CO1, NP 46 A, PLR-1, KT-PL-19, G4 and Exotic type-1 were found to be good general combiners. Four cross combinations *viz*., CO1 x Exotic type-1, CO1 x Scotch Bonnet, NP 46 A x PKM-1 and KT-PL-19 x G4 were identified as good specific combiners for quality characters.

PI-22

COMBINING ABILITY AND HETEROSIS FOR YIELD AND FIBRE QUALITY TRAITS IN INTERSPECIFIC CROSSES OF COTTON (*Gossypium spp.*)

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Cotton is a major crop of global importance and popularly known as the “King of fibre crops”. Combining ability studies provide useful information for the selection of parents. Hence, the study of combining ability and heterosis was conducted using 60 interspecific crosses between 15 *G. hirsutum* lines and four *G. barbadense* testers. The line x tester analysis indicated the predominance of dominance gene action in all traits. The knowledge of general combining ability coupled with mean performance of parents would be fruitful in selecting suitable parents for hybridization programme. Based on this, the lines H 34 and H 23 and the tester B 37 and B 26 could be used in breeding programme. The hybrids for heterosis breeding would be selected based on all the three criteria *viz*., high mean, *sca* effects and standard heterosis. Based on this, the hybrids *viz*., H 135 x B 26, H 34 x B 4, H 45 x B 26, H 22 x B 4, H 38 x B 26 and H 139 x B 37 for yield related traits (SCY, NB, NSy, PH, BW), H 139 x B 37, H 34 x B 4 and H 58 x B 3 for fibre related traits (FL, BS) and H 139 x B 37, H 34 x B 4 and H 135 x B 26 for both yield and fibre quality traits (SCY, NB, NSy, BW, FL, BS) could be used for heterosis breeding programme. Hence, these hybrids could be utilized in heterosis breeding programme.

PI-23

STUDIES ON GENETIC DIVERSITY IN SAMAI (*Panicum sumatrense* ROTH. EX.)

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A total of sixty three germplasm accessions maintained at Regional Research Station, Paiyur were evaluated for nine characters.The range of variation for major characters are days to 50% flowering:

45-51, days to maturity: 73-88, plant height (cm): 55-113, Flag leaf width (cm): 0.50-2.20, Flag leaf length (cm): 14-30, Peduncle length (cm): 9-28, Panicle exertion (cm): 0.6-8.2, Length of inflorescence (cm): 13-35, Grain yield per one row of 3m length (g): 60-110.Major donors identified for various traits are Early maturing (>76 days)-IPM 221, Paiyur 2, MS 4779, TNAU 1678, Late maturing (<85days)- TNAU 23, MS 1211, PM 29, IPM 231, TNAU 1/79, IPM 226, RPM 81, Tall accessions (Plant height >100 cm), TNAU 6, TNAU 5, Short accessions (Plant height <60 cm)- TNAU 7/79, IPM 272, MS 1003/1, Broad leaf accessions (Flag leaf width >1cm)- TNAU 7, 9, 12, 22, 23, MS 1826, PM 296/1, IPM272, PM 42, CO 3, MS 4729, Narrow leaf accessions (Flag leaf width <1cm)- PM 3.6, MS 509, IPM 221, MS 4700/1, IMR 762, RPM 81, IPM 226 and IPM 231, High seed yield (>100 g/row)- MS 662, IPM 232, TNAU 1/79, Paiyur 2, TNAU 15,RPM 11.These major donors offer greater scope for utilization in crossing programmes in yield improvement

PI-24

COMBINING ABILITY FOR YIELD AND YIELD ATTRIBUTING TRAITS UNDER MOISTURE STRESS ENVIRONMENTS IN MAIZE (*Zea mays* L.)

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Ninety one cross combinations along with 14 selected drought tolerant tropical parental lines were assessed for their combining ability in maize. The ratio of GCA:SCA variance showed the predominance of non additive gene action for important yield contributing traits *viz.*, cob length,cob girth, number of kernel rows per cob, number of kernels per row, grain yield per plant and protein content and would be improved by heterosis breeding. The traits such as days to 50 % tasseling and silking, ASI, days to maturity, plant height, hundred grain weight, RWC, root volume,root length and starch content had predominantly additive gene action. Based on the *per se* performance and *gca* effects, the parents UMI 285, UMI 1085, UMI 1058 and UMI 233 were found to be superior parents to develop hybrids with enhanced yield through improving yield related characters under moisture stress environments. Considering *per se* performance and *sca* effects, out of six hybrids which were found to be promising, UMI 233 x UMI 1069 and UMI 233 x UMI 1096 possessed desirable *per se* performance and *sca* effects for grain yield per plant, kernel rows per cob, number of kernels per row, 100 grain weight, RWC, protein and starch content.The hybrids with additive X additive type of interaction can be exploited for the development of single cross hybrid under moisture stress environment and also through the population improvement programme in the development of suitable early composite or synthetic.

PI-25

GENETIC VARIABILITY AND DIVERSITY STUDIES IN FOXTAIL MILLET FOR GRAIN YIELD

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The extent of genetic variability**,** heritability and diversity for yield and its attributing traits in the 78 genotypes of foxtail millet were studied. High PCV, GCV, heritability and genetic advances were recorded for grain yield per plant in both the seasons (rainy and post rainy). This indicates the existence of high variability for these traits, which could be exploited for improvement of the traits through selection in advanced generations. Moderate estimates for panicle length, panicle weight and test weight and low estimates for plant height and panicle breadth. Days to flowering, days to maturity, number of tillers per plant, panicle weight, test weight and grain yield in both the seasons exhibited higher heritability coupled with high genetic advance as per cent of mean. This indicates the scope of selection in the population, since there is a wide range of variation and additive gene action. On the basis of Mahalanobis D^2 statistics these genotypes were grouped into seven clusters. The highest intra-cluster distance was recorded for cluster III. The genotypes from cluster V may be crossed with those in cluster VII as they are more diverse. The days to flowering have maximum contribution towards the genetic divergence followed by test weight and grain weight.

PI-26

INFLUENCE OF SEED MORPHOLOGICAL TRAITS ON OIL YIELD AND COMPONENT TRAITS IN SUNFLOWER (*Helianthus annuus* L.)

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Increasing of oil yield is one of the most important goals in sunflower breeding programs and the stripes on seed surface are an undesirable trait and presumed that it linked with low oil content. The field study involved 150 F_3 individual derived from a single cross TNHSF29-68-1-1-1 x 17B. The parent TNHSF239-68-1-1-1 has high oil content with black seed color and absence of stripes on seed surface. Due to this fact, popular hybrids/ varieties with stripes on seed surface fetches low price. The present study was under taken to develop a maintainer inbred with high oil content and no stripes on seed surface. The data recorded for 14 oil yield and yield contributing characters and association between characters were estimated. Based on association analysis the traits *viz*., seed

yield, kernel weight and 100-seed weight are important selection indices for both oil and seed yield improvement because these traits plays a major role and many other traits had high association through these traits. The trait stripes on margin had association with low oil content, light seed color, more hull percentage and more hull weight. The trait stripes between margins had significant and positive correlation with hull percentage and it had a negative significant association with plant height, seed color, 100-seed weight and kernel weight. Both stripes had negative significant association with seed color and oil content. The results clearly indicated linkage between seed stripes and low oil content. Hence, care should be taken during selection that, not have striped seeds.

PI-27

GENETIC IMPROVEMENT OF RICE FALLOW BLACKGRAM VARIETY ADT-3 THROUGH GAMMA IRRADIATION

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ADT 3 is presently cultivated sole variety having all desirable traits for grow well under rice fallow condition in Tamil Nadu, released during 1981, genetic deterioration is observed in this variety as it being cultivated over 25 years, matures in 75 days with low yielding ability and occurrence of narrow genetic base of cultivated varieties in rice fallow blackgram are the major constraints for bringing a major breakthrough in yield improvement. Hence, genetic improvement in this variety ADT 3 is prerequisite. In the present study, new mutants of blackgram were produced and evaluated for the improvement in yield and yield contributing traits. Seeds of blackgram cultivar ADT 3 were irradiated with 200, 300, 400 and 500 Gy Gamma-rays. A large number of mutants with altered morphological characters were identified and characterized during M_2 generation which was raised under rice fallow condition. These mutants were carried forwarded to M_3, M_4 and M_5 generations as plant to row progenies and in each generation selection was made based on improved yield. Finally, 21 desirable mutant lines were fixed in M_5 generation and were evaluated for yield under rice fallow condition. Analysis of variance showed significant variations among mutant lines for yield per plant. Two very promising mutants *viz.*, ADT 3-26 and ADT 3- 38 recorded 113 % and 59 % increased single plant yield respectively over the wild type. The results indicated the possibilities of improving the grain yield of the rice fallow black gram variety, ADT 3 using gamma irradiation.

PI-28

STUDY OF HERITABILITY AND CORRELATIONS IN CROSS DERIVATIVES OF RIDGE GOURD (*Luffa acutangula* (ROXB.) L.) IN F_1 AND F_2 GENERATIONS

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A study of five ridge gourd F_2 progenies involving Jaipur Long x Chitrada, Jaipur Long x Pottibeera, PHS-10 x Chitrada, Jaipur Long x Arka Sujat and Chitrada x Arka Sujat along with corresponding five parents was investigated for the estimates of heritability, character association, inter generation correlations between parents-F_1 and F_1-F_2 and path coefficient analysis High estimates of heritability and genetic advance were recorded in F_2 generations for the characters number of node at which first female flower appeared, number of fruits per plant, fruit shape index, fruit weight, fruit volume, fruit length, TSS and yield per plant whereas high heritability and moderate genetic advance for sex ratio and thickness of skin of fruit. Moderate heritability and moderate genetic advance were recorded for vine length and flesh thickness while moderate heritability with low genetic advance was observed for fruit diameter. Highly significant correlation between parents-F_1 generation for the characters yield per plant, vine length and flesh thickness in the crosses and non significant correlations were observed for the same characters in F_1-F_2 generations. Positive correlation was observed for number of node at which first female flower appeared, fruit shape index, sex ratio and flesh thickness. The path coefficient analysis indicated that fruit length along with number of fruits per plant, fruit shape index, number of node at which first female flower appeared, flesh thickness and sex ratio have direct positive effects on yield per plant.

PI-29

GENETIC VARIABILITY AND CORRELATION COEFFICIENT STUDIES IN AFRICAN MARIGOLD (*Tagetus erecta*)

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Ten genotypes of African marigold were used to study the genetic variability, heritability, genetic advance and correlations among quantitative and qualitative characters. There were highly genotypic differences for all the characters studied except for intermodal length. Considerable variability was observed for the characters like plant height, days to first bud visibility, days to first picking, flower weight and total carotenoid content. Heritability and genetic advance as percent mean were high for plant height, number of primary branches, days to first bud visibility, days to first picking, days to last picking, duration of flowering, flower weight, flower diameter, dry matter production at harvest, germination percentage, total carotenoid content and flower yield per plant in terms of weight and

number. These characters offer scope for their improvement by applying selection pressure in breeding progrmme. The correlation studies revealed that yield had positive significant correlation with plant height, dry matter production at harvest and lower yield per plant in terms of weight. Improvement of these traits will directly improve yield of flowers. Among ten genotypes, Chirala Local Yellow, African Giant Orange and Bapatla Local Orange performed well in terms of flower yield. Pusa Narangi Gainda and African Giant Orange contained more amounts of total carotenoids. These genotypes could be utilized in breeding programme for improvement.

PI-30

EVALUATION OF DOLICHOS BEAN (*Dolichos lablab* L.) FOR YIELD AND QUALITY

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The experiment was laid out in randomized block design with three replications with 20 genotypes over two seasons. High heritability with high genetic advance was observed for green pod yield per hectare, plant height, days to first flowering, days to 50 per cent flowering, days to first harvesting, hundred green pod weight, pod length, number of flower buds per raceme, crude fibre content and pod width in *kharif.* In *rabi,* green pod yield per hectare, green pod yield per plant, plant height, number of pods per plant, ascorbic acid content, number of flower bud per raceme, hundred green pod weight and crude fibre content had high heritability coupled with high genetic advance. The yield attributes number of pods per plant, hundred green pod weight, pod length and pod width were the highest in *kharif* in most of the genotypes due to favorable climate *i.e.*, low temperature and high relative humidity prevailed during flowering period. Among the short duration types, Ankur Gold (13.49 t/ha in *kharif)* and (12.96 t/ha in *rabi)* recorded the highest green pod yield followed by Arya (11.68 t/ha in *kharif*) and (11.26 t/ha in *rabi)* and CO 13 (9.48 t/ha in *kharif*) and (9.11t/ha in *rabi).* Among medium duration types, Sengam local (11.05 t/ha in *kharif)* and (10.31t/ha in *rabi)* recorded the highest green pod yield.

PI-31

EVALUATION OF RICE GERMPLASM FOR HEAT TOLERANCE

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Rising temperatures are global phenomenon although the extent of temperature increment may vary between different regions of rice producing areas. Genetic diversity is the most potent tool in the hands of plant breeder through which one can measure variation and make selection and without this crop improvement could not have taken place in the path of green revolution. An investigation was carried out in rice utilizing the existing 98 breeding materials derived from crosses involving high temperature stress / heat tolerant donors as one of the parents. The aim of the study was to assess the extent of genetic diversity for yield and its related traits in order to identify high temperature tolerant lines that could be utilized either directly or in hybridization programme in the future to keep pace with the global climatic changes. The 98 genotypes were grouped into 13 diverse clusters. Cluster III with three genotypes *viz.,*IR 86970 - 112 - 3, IR 86977 - 122 - 1 and IR 86991 - 103 - 2 involving three heat tolerant donors exhibited the maximum intra cluster distance of 162.33. The inter cluster distance was high between VI and XII (329.80), XIII and VI (265.50) and XII and V (263.45). Hybridization between the genotypes of these clusters and also between I and VI may offer scope for further selection. Total number of tillers per plant (44.03 %) and single plant yield (26.29 %) contributed more towards genetic divergence.

PI-32

POLLEN MORPHOLOGY STUDIES IN FABACEAE FAMILY

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Pulses are important leguminous crop widely cultivated all over the world which is the protein supplier in Indian diet. Pulses are highly self-pollinated crop. In flowering plants the male gamete formed during microsporogenesis are the pollen grains. The appearance and size are the important factors which affect the fertilization in the self-pollinated crops. There are variation in the morphology, size, and shape of the pollen grains in different crops. Pollen grains are important for effecting self fertilization and good seed set. The study of pollen is called palynology and is highly useful in paleoecology, paleontology, archeology, and forensics. Hence, a study was conducted to measure and compare morphological characteristics of pollen grains from pulses. Among the pulses the pollen grains of red gram, black gram, green gram and cowpea were observed and measured in Biowizard software after fixing with Acetocarmine dye. The shape of the pollen grains was globular for redgram, blackgram, greengram, and cowpea. The length ranged from 114 to 181µ and width ranged from 70-138 µ. Highest was observed in cowpea followed by black gram, red gram and green gram. Area of pollen grain in cowpea was higher (44221 μ^2) followed by black gram (24976 μ^2).

PI-33

HETEROSIS FOR GRAIN YIELD AND ITS COMPONENTS IN PEARL MILLET (*Pennisetum glaucum* (L) R. BR.)

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A study was conducted in pearl millet (*Pennisetum glaucum* (L) R. Br.) to assess the extent of heterosis for fourteen quantitative traits including grain yield per plant. Six lines and eleven testers were crossed in a line x tester fashion to develop 66 F_1 hybrids. The analysis of variance for experimental design revealed highly significant differences among the genotypes, parents and hybrids for all the characters, indicating the presence of sufficient amount of genetic diversity in the material for the fourteen traits studied. Heterosis was worked-out over better parent and standard check, GHB-732. The standard heterosis for grain yield per plant ranged from -60.79 to 35.77 %. The crosses ICMA-05333 x J-2527, ICMA-04111 x J-2534, ICMA-05333 x J-2340, ICMA-04111 x J-2454 and ICMA-92777 x J-2340 were the best heterotic combinations for grain yield per plant, which recorded 35.77, 28.90, 21.85, 16.74 and 13.74% standard heterosis, respectively. Whereas the heterobeltiosis for grain yield per plant ranged from -44.86 to 227.18%. The crosses ICMA-05333 x J-2527, ICMA-05333 x J-2454, ICMA-92777 x J-2454, ICMA-04111 x J-2539 and ICMA-92777 x STPT-115 were the best heterotic combinations for grain yield per plant, which recorded 227.18, 170.49, 124.24, 119.23 and 110.67 % heterobeltiosis, respectively. The heterosis for grain yield per plant was associated with the heterosis expressed by its component characters.

PI-34

CORRELATION COEFFICIENTS OF COMPONENT CHARACTERS WITH SEED YIELD AND THEIR DIRECT EFFECTS IN PATH ANALYSIS IN CORIANDER GROWN UNDER THREE ENVIRONMENTS

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Thirty diverse genotypes of coriander were grown in three (D1 to D3) environments during the *rabi* seasons for three consecutive dates in the year 2011 at the Vegetable Research Station, Junagadh. Seed yield per plant showed significant and positive correlation with plant height, number of basal leaves, days to maturity and harvest index in early sowing condition (D1). While longest basal leaf length, umbels per plant, umbellets per plant, 100-seed weight and harvest index was significant and positive correlation in timely sown condition (D2). In late sowing condition (D3) seed yield per plant showed significant and positive correlation with number of basal leaves, longest basal leaf length, number of fruit bearing branches, umbellets per plant, seeds per umbel, 100-seed weight and harvest index. This indicated that importance of these traits as compliment of seed yield. Path coefficient analysis revealed that the days to 50% flowering, 100-seed weight, plant height, number of basal leaves, longest basal leaf length, umbels per plant and umbellets per plant (D1) harvest index, days to 50% flowering, longest basal leaf length, umbels per plant, umbellets per plant, seeds per umbel and 100-seed weight (D2) days to 50% flowering, plant height, number of basal leaves, number of fruit bearing branches and umbellets per plant exhibited high and positive direct effects on seed yield per plant.

PI-35

HETEROSIS AND COMBINING ABILITY FOR EARLINESS AND ITS RELATED TRAITS IN COTTON *(Gossypium hirsutum* L.)

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The present investigation was carried-out to generate information on heterosis and combining ability for three characters in cotton. A line x tester mating design comprises 10 lines and five testers of *Gossypium hirsutum* indicated preponderance of additive and non-additive gene action for days to 50% flowering, days to 50% boll bursting and seed cotton yield per plant. The line MR 786 was the good general combiner for days to 50% flowering and days to 50% boll bursting, while two lines *viz.,* GBHV 170 and GJHV 460 were good general combiner for seed cotton yield per plant. On the other hand, the tester 76 IH 20 was the best general combiners for all the three characters. Crosses G..cot-12 x MR 786 for days to 50% flowering; G.cot-12 x H 1316 and LRA 5166 x H 1316 for days to 50% boll bursting and G.cot-12 x H 1316 and BC 68-2 x GBHV 148 for seed cotton yield plant were the best specific combinations to exploit non-fixable components. Since additive and non-additive components of genetic variances were important for all three traits under study the exploitation of both types of gene action would be imperative and reciprocal recurrent selection for would prove to be most effective for inducing earliness and productivity in cotton.

PI-36

DEVELOPMENT OF SUGARCANE CLONES WITH HIGH CANE YIELD AND SUCROSE CONTENT SUITABLE FOR EARLY AND MIDLATE SEASONS

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Sugarcane is the second most important commercial crop next to cotton in India. Though it is utilized only for the production of sugar in India, it is a potential raw material in the other two most important sectors viz., biofuel and power. Hence the sugarcane production must be increased by evolving high yielding sugarcane varieties with high sugar content. High yielding sugarcane varieties with high sugar content and resistant to red rot disease are evolved by hybridization followed by clonal selection. Some of the promising clones identified for early and midlate season are presented below. The clone C 25006 was selected from C 81129 GC**.** The cane yield, CCS and sugar yield were 138t/ha, 12.92% and 17.82 t/ha, respectively. The clone C 260628 was derived from the cross Co 85002 x HR 83-144. The cane yield, CCS and sugar yield were 135 t/ha, 12.85% and 17.35 t/ha. The clone C 260138 derived from the cross 81V48 x ISH 229, has cane yield, CCS and sugar yield of 139 t/ha, 12.79% and 17.78 t/ha, respectively. The clones C 29064 and C 29090 were selected from the cross Co 85002 x Co 775. The cane yield was 142 t/ha and 152.5 t/ha, respectively. The midlate clones viz., C 260949 (87A298xISH229), C 28169 (Co 775GC) and C 29442 (Co 86032 GC) had cane yield (123.75t/ha, 147 t/ha, 145 t/ha), CCS (12.85%, 12.8%,12.9%) and sugar yield (15.92,18.82,18.71 t/ha).

PI-37

EVOLUTION AND EVALUATION OF GREENGRAM GENOTYPES FOR DEVELOPING MUNGBEAN YELLOW MOSAIC VIRUS RESISTANCE

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With an objective for developing high yielding greengram variety with resistance to yellow mosaic virus and to evaluate introgressed genotypes will be utilized in future crop improvement programmes. The parents were selected based on high yield and resistance of Mungbean Yellow Mosaic Virus. The female parent VGG012 -002 is high yielding nature, short duration with susceptible to Mungbean Yellow Mosaic Virus during *kharif* seasons and male parent VGGru 1 (MYMV donor) which was derived from the wild species *Vigna umbellata* with *Vigna radiata* (female). A total of 3364 flowers were emasculated and 3024 flowers dusted in 29 days. A total of 1216 matured pods were collected. The pod set ranged from 20.74.00 to 72.55.00 per cent were recorded. Seven true F_1 plants were tagged that plants are intermediate. The both parents characters expressed in single plants from which 215 plants were recovered in F_2 generation. Out of 215 plants, 18 plants were affected by Yellow Mosaic Virus. All 215 plants were forwarded to F_3 generation raised in single plant to row basis. In this cross combination some of the modified plant types were also identified for different situation particularly for mechanical harvest apart from MYMV resistant genotypes development.

PI-38

DEVELOPMENT OF NEW BLACKGRAM AND GREENGRAM PLANT TYPES SUITABLE FOR MECHANICAL HARVEST

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With an objective for developing new plant types and to minimize labour intensification in harvesting process, a new plant types development is highly essential for future agriculture. In some crops It is only way to make modification of plant types by conventional introgression of wide gene through breeding method for mechanical harvest. In greengram modification of plant types is conventionally possible from their wild progenitors like *Vigna umbellata* is valuable. The traits like more hypocotyl length and monostem with top podding are achieved in VRM(Gg)1 x *V. umbellata* cross combination. The traits like high hypocotyl length (15 - 25 cm) was achieved and top branching with early duration plant types were selected for further study. In blackgram modification of plant types is possible from blackgram progenitor *Vigna mungo* var *silvestris* . The traits like pods are in above canopy at maturity stage are achieved in the released variety TNAU blackgram VBN6 (*Vigna mungo* VBN1 x *Vigna mungo* var *silvestris*), more no of pods are in top portion of the stem and monostem are also achieved. In ADT3 x *V. silvestris* cross combination, more no of pods are in top portion of the stem, multi pods and monostem are also achieved.

PI-39

BIOCHEMICAL AND MOLECULAR ANALYSIS OF F_2 POPULATION OF RANJIT X KALAJOHA RICE (*Oryza sativa* L.) FOR AROMA TRAITS

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Rice plays a vital role in national food and livelihood security system in India as it is a major producer and exporter of rice with a higher percentage of cultivated area. People's preference chances in choosing wide variety of genotypes. Among these aromatic rice also plays a major role. Aroma is a special trait found both in indica and japonica types of rice. Aromatic rice has three main factors of preference *viz.,* good appearance, aroma and taste. Aromatic rice has natural nutty, popcorn like flavor. It is characterized as a superfine grain, with a pleasant and subtle aroma. The main objective was to introgress the aromatic trait from aromatic genotype Kalajoha to the popular non aromatic variety Ranjith of Assam and to screen the fragrance trait in F_2 generation using biochemical and molecular analysis. Molecular analysis was carried out using BADH2 gene specific primers *viz.,* ESP, IFAP, INSP, EAP using allele specific PCR assay for fragrance. The segregation for aroma

was in conformity with that of the phenotypic expression of 1:2:1 ratio. These gene based markers can be used as an effective tool to identify aroma genotypes in the early stage of development and the influence of environment in the expression of aroma can be overlooked during the selection process.

PI-40

INHERITANCE OF NON-SPINY CHARACTER IN SPINY BRINJAL

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Spiny brinjal (VRM-1Mullukathiri) is a pure line selection from Elavambadi village of Vellore district. Spines are present in the leaf, stem and calyx of the fruit. VRM-1Mullukathiri is high yielding (30-35 t/ha-1) and most suitable for North-Eastern Zone of Tamil Nadu. Spiny is difficult in nature during hand harvest and an objective to develop non-spiny with the quality of spiny brinjal. The crosses were attempted to develop non-spiny brinjal with spiny quality. The both parents are pure for respective spiny and non spiny. The crossing percentage is ranged from 70-80 per cent in spiny and nonspiny cross combination. Two crosses *i.e.,* Spiny x Non-spiny and Non-Spiny x Spiny were made for the inheritance of non-spiny in leaf, stem and fruits in brinjal. The true F_1 of both the crosses were tagged in both crosses combination. In F_1 plant population of Spiny x Non spiny , ninety eight percent of the plants are spiny nature. In F_1 plant population of non spiny x spiny fifteen percent of the spiny plants were observed. From this study in both cases spiny plants are observed in F_1 generation which indicates spiny is expressed as dominant characters. In both cases partial dominance also observed in respective parents are used as female.

PI-41

METROGLYPH ANALYSIS OF MORPHOLOGICAL VARIATIONS IN SUNFLOWER GERMPLASM LINES

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A study was conducted to assess the morphological variations in 46 germplasm lines of sunflower by metroglyph and index score method. In this study, genetic variability was assessed for six characters *viz.,* days to 50% flowering, plant height (cm), head diameter (cm), 100-seed weight (g), volume weight (g) and seed yield per plant (g). Two most variable characters *viz.,* seed yield per plant (g) and plant height (cm) were selected for plotting the genotypes in a graph. All lines were grouped into nine distinct groups which differed among themselves. Scatter diagram indicated that maximum

number of genotypes (11) were found in group IV followed by group V having 9 genotypes. The lines in group V showed moderate seed yield. The group III possessed only one genotype with moderate 100-seed weight and high seed yield/plant. The clusters VI and IX consisting of 3 and 2 genotypes respectively, recorded high 100-seed weight, moderate volume weight and high seed yield. The cluster III possessed two genotypes with moderate head diameter, moderate 100-seed weight, moderate volume weight and moderate seed yield. The genotypes belonging to the groups II,V and VIII showed moderate seed yield and the genotypes in the groups III, VI and IX recorded high seed yield. The genotypes having medium seed yield showed high score. The germplasm lines of groups III, VI and IX could be exploited in future breeding programme for achieving higher grain yield in sunflower.

PI-42

GENETIC ASSOCIATION BETWEEN OIL YIELD CONTRIBUTING CHARACTERS IN SUNFLOWER

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In plant breeding, correlation measures the mutual relationship among various plant characters and determines the component characters on which selection can be relied upon for genetic improvement of yield. Correlation and path coefficient analysis was studied in sunflower for oil yield and its contributing characters *viz.,* days to 50% flowering, plant height, head diameter, 100-seed weight, volume weight, seed yield and oil content in 16 genotypes. Correlation analysis revealed that oil yield per plant had significant positive correlation with 100-seed weight, volume weight, seed yield per plant and oil content. However, days to 50% flowering had significant and negative association with oil yield. Path coefficient analysis for oil yield indicated that the character, volume weight influenced oil yield indirectly through 100 seed weight and oil content. Head diameter showed indirect influence on oil yield through volume weight. Similarly, the traits *viz.,* seed yield and oil content had indirect relationship with oil yield through 100-seed weight. Very high indirect contribution for most of the characters on oil yield was through 100-seed weight. Hence, oil yield contributing characters *viz.,* 100-seed weight, volume weight seed yield per plant and oil content may be used as selection criteria for improvement of oil yield in sunflower.

PI-43

EVALUATION OF MUNGBEAN ADVANCED BREEDING LINES FOR MYMV RESISTANCE UNDER DIVERSE ENVIRONMENTAL CONDITIONS

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Mungbean (*Vigna radiata* (L.) Wilczek) is an important food legume ranking third among pulses after Chickpea and Pigeonpea in area and production. Among several constraints for mungbean production, Mungbean Yellow Mosaic Virus (MYMV) disease is the most serious disease which not only drastically affects the yield but also affects the seed quality parameters. Evolving MYMV resistant varieties is an economical and durable method to alleviate the occurrence of MYMV disease. The present investigation was aimed to screen sixteen advance breeding lines of mungbean under diverse environmental conditions *viz*., at Rice Research Station, Tirur during Rabi, 2013, at Ponboli, Tirunelveli (Hotspot area for MYMV) during Summer, 2013 and at National Pulses Research Centre, Vamban during Kharif, 2014 for identifying stable resistance lines for MYMV. Screening was done under natural environmental condition by raising the susceptible checks SML-1074 and SML-1082 in between the test entries. Percentage Disease Incidence (PDI) was worked out and the genotypes were categorized as Immune, Resistant, Moderately resistant, Moderately susceptible, Susceptible and Highly susceptible using (0-5) arbitrary scale. None of the lines were found to be Immune. A total of ten genotypes at RRS, Tirur, six genotypes at Ponboli, Tirunelveli and nine genotypes at NPRC, Vamban were categorized as resistant lines with less than one percent disease incidence. Eventhough the screened materials exhibited differential response to MYMV disease, the four cultures TM-11-07 (CO-6/ML-99), TM-11-18 (CO-6/UPM-02-18/VBN-2), TM-11-34 (CO-GG-936/CO-6) and TM-11-38 (ML-682/BARIMUNG-5) showed stable resistance reaction in all the three environments and recommended as resistant sources for MYMV disease.

PI-44

SCREENING OF SUNFLOWER GENOTYPES FOR RESISTANCE AGAINST ALTERNARIA LEAFSPOT (*Helianthus annuus* L.)

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Alternaria leaf spot is a potential destructive foliar disease of sunflower in India causing significant yield losses and reduction in oil content. One hundred and twenty genotypes were evaluated under

natural epiphytotic conditions during kharif season. The disease severity was assessed by per cent disease index (PDI) at 80 days after sowing. The result indicated that the PDI ranged from 14.35 percent to 96.14 percent. Among the genotypes, 31 genotypes were recorded moderate resistance against *Alternaria* leaf spot which includes promising maintainer inbreds *viz,* ARM 243B, 17B, COSF 1B, COSF 2B, COSF 7B and TNHSF 239-68-1-1-1. Other lines, which recorded moderate resistance against *Alternaria* leaf spot were CSFI 5019, CSFI 5040, CSFI 5062, CSFI 5083, CSFI 5181, CSFI 5194, CSFI 5205, CSFI 5213, CSFI 5216, CSFI 5232, CSFI 5260, CSFI 5276, CSFI 5292, CSFI 5334, CSFI 5335, CSFI 5336, M 1014-1, M 1014-4, Pop 440-1-2-1, Pop 449-1-2-2, Pop 449-1-2-3, Pop 449-1-2-4, Pop 449-2-1-1, Rpop 24-5-3 and Rpop 26-3-5. These inbreds may be included in resistance breeding programme in sunflower.

PI-45

IDENTIFYING SUITABLE GREENGRAM VARIETY FOR IRRIGATED CONDITIONS OF TIRUVALLUR DISTRICT

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Greengram is cultivated in 8500 ha in Tiruvallur district during *Rabi* season under irrigated conditions. District average yield stands at 570kg/ha still. The low yield is due to the non adoption of high yielding varieties and improved production technologies. Hence a study was made to identify the suitable greengram variety by raising VBN 2, VBN (Gg) 3, Co (Gg) 7 and KM 2 (Check) at 10 locations in three villages *viz*., Puliyurkandigai, Venkatapuram and Cooum of Tiruvallur district during 2011-12, 2012-13 and 2013-14. The varieties were raised in plot size of 40m2 adopting 30 x 10cm spacing. Seed treatment was done with *Rhizobium* and *Phospobacteria* @ 1200g/20kg seeds and *Psuedomonas fluorescens* @ 10g/kg of seeds. Foliar application of 2 per cent DAP was given at flowering and 10 days later. Days to maturity was 68, 74, 68 and 70 days and number of pods per plant was 31, 29, 29 and 28 in VBN 2, VBN (Gg) 3, CO (Gg) 7 and KM 2 respectively. Hundred grain weight was observed to be 3.60g in VBN 2. Highest grain yield of 943.6 kg/ha was recorded by VBN 2 followed by CO (Gg) 7 and VBN (Gg) 3 with 856.3 and 822.0kg/ha respectively. The yield increase was 15.03 and 4.39 per cent in VBN 2 and CO (Gg) 7 than the check KM 2 (820.3 kg/ha). Hence, the variety VBN 2 with consumer preference and high yield was found to be more suitable for Tiruvallur district compared to the other varieties.

PI-46

COMBINING ABILITY AND HETEROSIS FOR YIELD AND ITS CONTRIBUTING TRAITS IN GREENGRAM (*Vigna radiata* (L.) WILCZEK)

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Greengram (*Vigna radiata* (L.) Wilczek) is a third important pulse crop in India after bengalgram and redgram. Genetic information, especially about the nature of gene action, combining ability and heterosis are required for selecting suitable parents and designing appropriate breeding programmes. Genetic potentialities of 14 parents and forty hybrids developed by L x T method were assessed through combining ability and heterosis studies on yield and yield attributing traits. The magnitude of SCA variance was greater than GCA variance for all the characters indicating predominance of non additive gene action to employ heterosis breeding for the improvement of yield traits. Considering the *per se* performance and *gca* effects PUSA 0871 and EC 398897 were adjudged as best parents and crosses involving these will be expected to throw desirable segregants. The cross combinations having non-significant *sca* effects and their corresponding parents showing significant *gca* effects such as VBN 2 x IPM-02-03, ADT 3 x IPM-02-03, ADT 3 x PUSA 0871, VBN 2 x IPM-02-14 and SML 1074 X IPM-02-03 were identified as the best for recombination breeding. The hybrids ADT 3 x IPM-02-03, ADT 3 x IPM-02-14, ADT 3 x PDM 139, ADT 3 x TM-11-34, IPM-409-04 x EC 398897, SML 1074 x PUSA 0871, VBN 2 x EC 398897 and VBN 2 x PUSA 0871 were found to be superior based on high *per se* performance, significant *sca* effects and standard heterosis and these hybrids could be effectively utilized to develop high yielding varieties along with desirable traits in greengram.

PI-47

SELECTION OF SUITABLE RICE VARIETY FOR SAMBA SEASON BY FARMERS PARTICIPATORY VARIETAL SELECTION

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In North Eastern Zone of Tamil Nadu, most of the farmers cultivate BPT 5204 during samba season for its fine grain quality and market preference. However, it is susceptible to major pests and diseases.

Therefore, selecting an alternate variety for samba season with high yield and market preference is need of the hour. To select a suitable variety, Farmers Participatory Varietal Selection (PVS) was employed. PVS was conducted at RRS, Tirur during samba, 2013 involving five rice varieties *viz.,* CO (R) 48, CO (R) 49, CO (R) 50, TNAU Rice ADT 49 and BPT 5204. Scoring method was employed for different traits involving 24 farmers. The most preferred variety was scored with 5 while 1 for least. The results indicated that CO (R) 49 scored high for earliness (130 days) and plant height (90.4 cm) and ADT 49 scored high for productive tillers per hill (18.8). For grain type, ADT 49 and BPT 5204 were the toppers with medium slender fine grain. The varieties CO (R) 50 and ADT 49 scored high for grain yield with 5912 kg/ha and 6174 kg/ha respectively. For pest and disease tolerance, CO (R) 50 scored high values since it has low incidence. The varieties ADT 49, CO (R) 49 and BPT 5204 were found non-lodging. Among the varieties, ADT 49 scored high for most of the traits and also possesses consumer preference and market acceptance. Based on PVS, ADT 49 was identified as a suitable variety for samba season and alternate to BPT 5204.

PI-48

STUDIES ON STANDARD HETEROSIS FOR YIELD AND YIELD ATTRIBUTES IN COTTON (*Gossypium hirsutum* L.)

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Heterosis for seed cotton yield and yield attributing traits in *Gossypium hirsutum* was studied involving twelve hybrids along one check Bunny which were raised during summer 2014 at Cotton Research Station in two replications with spacing of 90 x 60 cm. The row length and rows per entry were 4.5 m and 2 respectively. The standard heterosis for seed cotton yield ranged from -32.76 (Narashima x SCS 267) to 40.74 (Narashima x H 1464) and four hybrid showed the significant positive standard heterosis for seed cotton yield, for numbers of sympodial branches per plant, the standard heterosis ranged from - 25.0 (MCU 5 X GISV 272) to 35.71 (Narashima x H 1464) and only one hybrid showed the significant positive standard heterosis, for number of bolls per plant ranged from -3.62 (SVPR 2 x TSH 0499) to 105.88 (Narashima x H 1464) and four hybrids exhibited significant positive heterosis for this traits. For boll weight, the standard heterosis was ranged from -22.08 (SVPR 4 x GJHV 398) to 6.49 (Narashima x GISV 272). Among the hybrids studied, the hybrid Narashima x H 1464 had significant and positive standard heterosis for all the characters studied except boll weight and hence it would be more desirable to exploit heterosis.

PI-49

STUDIES ON COMBINING ABILITY IN SESAME (*Sesamum indicum* L.)

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An attempt was made to estimates the GCA, SCA, nature of gene action and heterosis in sesame (*Sesamum indicum* L.) through L x T mating design pattern with three lines and seven testers for different ten quantitative and qualitative traits viz; days to 50% flowering, days to maturity, plant height, number of branches/plant, number of capsules/plant, capsule length, number of seed/capsule, 1000 seed weight, oil content (%) and seed yield/plant were studied. The present investigation was conducted at the Departmental Research Farm of Agricultural Botany, College of Agriculture, Latur, Maharashtra during kharif-2012 with two replications in randomized block design. Based on the GCA effects female parent BSG-8 was found to be a good general combiner for seed yield, plant height, number of branches/plant, number of capsules/plant and oil content (%). Similarly, another female parent BSG-15 was found to be a good general combiner for days to 50 % flowering, days to maturity, length of capsule, 1000 seed weight and oil content (%). Among male parents genotype IC-413193 was found to be a good general combiner for seed yield/plant. Five cross combinations viz., BSG-8 x LT-7, BSG-12 x IC-413193, BSG-8 x IC-413214, BSG-8 x IC-413193 and BSG-15 x IC-413193 exhibited significantly maximum positive sca effects. Hence, recommended for yield improvement through heterosis breeding.

PI-50

MARKER VALIDATION IN F_2 POPULATION OF RICE FOR WATER AND NITROGEN USE EFFICIENCY

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Validation of markers helps in determining the reliability and practical applicability of the markers in predicting the phenotype. In the present study, simple sequence repeats (SSR) markers flanking WUE and NUE traits reported to explain high percentage phenotypic variation for their respective traits in RILs population from a cross Swarna x WAB450 were used for validation in F_2 population individuals of BPT5204 x WAB450 and BPT5204 x Mysore Mallige crosses for the same traits for which they are already reported to be associated. Single marker analysis was done with the help of

student's t test and by single factor ANOVA. Among the markers, only few were found to be significantly associated with WUE and NUE traits in F_2 population individuals. This probably may be due to fact that these were detected in other mapping populations with different genetic background, and because the marker intervals may be quite large. The SSR markers RM518 and RM225 are associated with WUE and NUE in F_2 population of BPT5204 x WAB450 and BPT5204 x Mysore Mallige respectively. The per cent contribution of the significantly associated markers to total phenotypic variance were 48.26 and 38.74 percent with a p-value of 0.0135 and 0.0306 located on chromosome number 4 and 6 respectively. Low R2 values indicates large environmental component of variations.

PI-51

GENETIC ANALYSIS OF BIOMETRICAL TRAITS IN PEARL MILLET [*Pennisetum glaucum* (L.) R. BR.] HYBRIDS

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Pearl millet [*Pennisetum glaucum* (L.) R.Br.] is the fifth most important grain crop in India. Pearl millet is primarily grown in areas characterized by low and erratic rainfall (200- 600 mm of annual rainfall), high temperature and poor soil fertility. Variations in Pearl millet can be gainfully utilized for its genetic improvement. Genetic variability parameter studied in twenty three hybrids and one check cumbu hybrid CO 9. Highly significant variation was observed for all the traits studies. Based on the per se performance, the hybrids TNBH 08804 and TNBH 10885 shows superior performance for grain yield and other biometric traits. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The differences between phenotypic and genotypic variance were minimum for all the eleven traits indicating the less influence of environmental factors. High values of GCV and PCV were obtained for the characters *viz.,* grain yield per ha, ear head length and dry fodder yield. High heritability was observed for all the traits. High heritability coupled with high genetic advance as percent of mean was recorded for number of productive tillers, ear head length, dry fodder yield, 1000 grain weight and grain yield per ha. These characters were controlled by additive gene effect. Selection based on these characters would be effective for further pearl millet improvement programme and these hybrids can be effectively utilized in hybridization programme for the commercial exploitation of grain yield.

PI-52

EFFECT OF GAMMA RAYS ON POLYGENIC TRAITS OF SWEET SORGHUM (*Sorghum bicolor* L. MOENCH.)

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Sweet sorghum (*Sorghum bicolor* (L.) Moench.) is the fourth major cereal crop of the world in production and fifth in acreage after wheat, rice, maize and barley. It is well adapted in semi-arid tropics. The dual-purpose nature of sweet sorghum for both grain and sugar-rich stalks gains world attention as a promising bio ethanol crop. Genetic variability is one of the basic factors important for crop improvement. Mutation breeding has become increasingly popular in recent times as to engender genetic variability. Mutations in plants are powerful tools, not only for clarifying physiological mechanisms in plants but also for developing new plant varieties in practical breeding programs. In the present investigation, two popular varieties *viz.,* SSV 84 and VMS 98001 were exposed to varying doses (20, 30, 40, 50 and 60 KR) of gamma rays to study their effect on polygenic characters in M_1 generation. The morphological and yield traits *viz.,* seed germination, survival, shoot and root length, plant height, days to 50% flowering, pollen fertility, single plant yield, seed fertility and 1000 seed weight showed a gradual reduction of mean performance than the control with increasing doses of gamma rays. The maximum reduction was observed at 60Krad for all the characters of both the varieties. The increasing concentration of gamma rays decreased in phenotypic and yield characters have been attributed to the physiological difference or chromosomal anomalies caused to the cells of the plant by the mutagen.

PI-53

MAGNITUDE AND DIRECTION OF ASSOCIATION BETWEEN ß-CAROTENE, YIELD AND ITS COMPONENT TRAITS IN RIL POPULATION OF PEARL MILLET (*Pennisetum glaucum* [L.] R. BR.)

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Pearl Millet [*Pennisetum glaucum* (L.) R.Br.] commonly known as bajra, cat tail millet and bulrush millet in different parts of the world is a highly cross-pollinated crop. ß-carotene is the only carotene that can be converted into vitamin A by the body. A lack of ß-carotene is a major cause of vitamin A deficiency. Vitamin A deficiency is a global health problem affecting 140-250 million children and

accounts for increased childhood mortality and diseases. Response to selection of a character might exert a beneficial or harmful effect on another related character depending on the strength and direction of the association among them. Study on correlation coefficient facilitates simultaneous improvement of two or more characters and is essential for the formulation of breeding programme aimed at achieving the desired combinations of various yield components. Hence, an attempt was made in the present study to understand the direction and extent of association among grain yield and component traits and â-carotene in the 200 RILs of the cross PT 6029 x PT 6129. Number of productive tillers per plant, earhead length, earhead girth, single earhead weight, single earhead grain weight, 1000 grain weight, chlorophyll content and â-carotene recorded highly significant and positive genotypic correlation with grain yield per plant in the present investigation across seasons. This confirmed that these characters were mostly responsible for determining yield in pearl millet. Hence, selection based on these characters will help in improving the grain yield.

PI-54

SCREENING FOR MYMV RESISTANCE AND IDENTIFICATION OF SUPERIOR BATTERING QUALITY GENOTYPES IN BLACKGRAM (*Vigna mungo* (L.) HEPPER)

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An investigation on 47 blackgram genotypes obtained from IIPR, Kanpur, LAM , Guntur, and NPRC, Vamban were raised at Agricultural College and Research institute, Madurai to study the extent of variation between the genotypes for Mungbean Yellow Mosaic Virus disease resistance and its effect on the yield and battering quality. The trial was taken up during June 2014, replicated twice in RBD. The susceptible check Co5 was raised as a infector row at every 5th row. Among the genotypes screened, TK Local, VBG 11 006 and VBN(Bg)4 were found resistant to MYMV and Vamban5, Veppur local, MDU 1, TU40 were moderately resistant to MYMV. Whereas, P1051 and Co5 were highly susceptible to MYMV. There was a wide variation for single plant yield which ranged from 5.13 to 13.95g. Among the genotypes MDU 1 had maximum grain yield (13.95) followed by TK local, VBN(Bg)4, LBG623 with 11.84, 11.77, 11.19g respectively. The genotypes VBG 11 016 (5.17g) and P1051 (5.13g) had registered lowest single plant yield. Considering the battering quality characters like initial and final batter volume, the genotypes MDU 1, KKB05011, Co5, TU40 and LBG623 were found superior. Over all, based on the single plant yield, level of resistance to yellow mosaic virus and battering quality the genotypes viz., MDU 1, TU40, VBN(Bg)4, TK local and LBG623 were adjudged as best. Hence, these genotypes can be used as such or utilized in the breeding as a parental line to develop high yielding MYMV resistant variety coupled with good battering quality.

PI-55

ESTIMATION OF HETEROSIS, COMBINING ABILITY AND GENE ACTION IN CASTOR (*Ricinus communis* L.)

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The estimates of the components of genetic variation were worked out by Kempthorne method from a Line x Tester analysis in castor for eleven plant type related traits. The analysis for combining ability revealed significant mean sum of squares of both general combining ability (GCA) and specific combining ability (SCA) for all the characters which indicated the presence of both additive and non-additive gene actions. The ratio of GCA variance and SCA variance ratio revealed the predominance of non-additive gene action for all the traits except for days to 50 per cent flowering, days to 50 per cent maturity and oil content. VP 1, SKP 84, ANDCM 2, ANDCI 9 and ANDCI 10-4 were good general combiner for most of the characters including seed yield. Cross JP 65 x JC 22 was a good specific combiner for seed yield per plant and for other yield component. In general for yield and other yield attributing traits the promising hybrids with high heterosis were VP 1 x ANDCM 2 and SKP 84 x ANDCM 2 having high mean, high heterosis (over better parent as well as standard hybrid). These cross combinations could be utilized for further use in breeding programme for improvement in yield of castor.

PI-56

GENETIC VARIABILITY AND CORRELATION ANALYSIS OF MAIZE INBRED LINES UNDER WATER LIMITING ENVIRONMENT

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In order to study the variability parameters and correlations among the 62 drought tolerant maize inbred lines, a field trial was conducted under non-stress and water stress condition (flowering stage) at two locations *viz.,* Department of Millets, TNAU, Coimbatore and Maize Research Station, Vagarai during rabi 2013. Totally thirteen biometrical observations were recorded and subjected to variability studies and correlation analysis. Variability studies revealed that, the traits ASI, number of kernels per row, hundred grain weight and yield under irrigated situation, and the traits *viz.,* cob yield, ASI, hundred grain weight and cob placement height under water stress condition recorded high values of GCV and heritability (broad sense) coupled with genetic advance indicating that selection based on these characters may be quite effective and influenced by additive gene action. The

correlation analysis revealed that, the traits *viz.,* hundred grain weight, number of kernel rows per cob, number of kernels per row and plant height recorded positive association with grain yield under both ecosystems (irrigated and moisture stress) these traits can be given importance while selection of promising individuals for grain yield. Days to 50% tasseling and days to 50% silking recorded significant negative association with yield and it can be used for development of early duration lines. Further the significant negative ASI (shorter) could be exploited to develop drought tolerant inbred lines in maize.

PI-57

ESTIMATION OF HETEROSIS FOR FIBRE QUALITY TRAITS IN INTER-SPECIFIC COTTON HYBRIDS

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Cotton (*Gossypium hirstum L.*) is one of the important commercial crops of the world and among the fibre crops it is considered as the ‘King’. The quality of cotton is of utmost importance and priced based on its intrinsic quality characters. One of the method to achieve quantum jump in the yield and quality is heterosis breeding. The estimation of heterosis in five fibre quality traits were investigated in 54 interspecific cotton crosses (*G.hirsutum* x *G.barbadense*) along with their parents during *Rabi 2012*. The hybrid TCHB 213 was used as a standard check. The cross MCU 12 x TNB 10 recorded highest significant standard heterosis percentage for 2.5 per cent span length (9.44), whereas the cross MCU 12 x TNB 1 revealed significant positive heterosis with 24.03 per cent for bundle strength. For the quality characters fibre fineness and uniformity ratio crosses TCH 1744 x TNB 26 and TCH 1716 x SUVIN recorded significant highest standard heterosis per cent of 32.11 and 11.36 respectively. Interestingly all the 54 crosses exhibited significant negative standard heterosis for the trait elongation percentage. These crosses may be used for fibre quality trait improvement through classical cotton breeding programme.

PI-58

QUALITY ANALYSIS ON SINGLE CROSS HYBRIDS IN MAIZE (*Zea mays* L.)

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Twenty three inbred lines and three inbred testers were used for this study. Using 26 inbred parents, 69 hybrid combinations were obtained by crossing them in a Line x Tester design. All the 26 parental lines and 69 cross combinations were evaluated with standard check CoH(M)5. Biochemical analysis such as carotenoid, crude protein, starch and phytate content were estimated along with grain yield per plant in twenty best performing hybrids and their parents. Out of twenty best hybrids eleven hybrids in carotenoid content, nine hybrids in protein content, ten hybrids in starch content were recorded higher mean value and ten hybrids were found to be low phytate content as compared to the overall hybrids mean. Heterosis studies showed that fifteen hybrids in carotenoid, five hybrids in crude protein, nine hybrids in starch content registered significant positive standard heterosis and ten hybrids in phytate content recorded significant negative standard heterosis. Based on association studies grain yield showed significant positive association with carotenoid content and starch content, non significant negative association with protein content and non significant positive association with phytate content. Based on *per se* and heterosis studies the hybrids N09-150 x N148-1 for high carotenoid content (35.64 μg), N09-157 x N171-2 for high protein content (10.38%), N09-150 x N148-1 for starch content (73.03 %) and N10-109 x N148-1 for phytate content (1.35 mg/100gm)were found to be superior over standard hybrid CoH(M)5 for yield and quality parameters.

PI-59

GENETIC STUDY OF YIELD AND ITS COMPONENT TRAITS IN OPIUM POPPY (*Papaver somniferum* L.)

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Twenty diverse genotypes including three checks were evaluated in Randomized block design for the study of variation, heritability and genetic advance among the yield and yield contributing traits at Instructional farm Rajasthan College of Agriculture, Udaipur during rabi season 2012-2013. Data were recorded for days to 50 % flowering, peduncle length, plant height, number of leaves/plant, number of effective capsules/plant, diameter of main capsule, stem diameter, seed yield/plant, husk yield/plant, latex yield/plant, harvest index for seed yield, harvest index for latex yield, morphine content and seed oil content. Statistically significant difference was observed among the genotypes tested for important characters indicating presence of variability. Magnitude of phenotypic coefficient of variability (PCV) is more than genotypic coefficient of variability (GCV) for all the traits under study. The high magnitude of PCV along with GCV was observed for seed yield/plant and latex yield/plant. In addition to above traits, high magnitude of GCV also recorded for harvest index for latex yield/plant and husk yield/plant. Higher magnitude of PCV than GCV, indicated that the apparent variation is not only due to genotypes but also due to the influence of environment. Selection for such traits sometimes may be misleading. Higher estimates of heritability coupled with high genetic advance was observed in plant height, diameter of main capsule and days to 50 per cent flowering indicating that these characters are mainly controlled by additive genes and selection of such traits might be effective for the improvement of yield.

PI-60

CORRELATION AND PATH ANALYSIS IN INTER SUB-SPECIFIC EARLY STAGE DROUGHT TOLERANT GROUNDNUT

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Groundnut is drought tolerant, largely a small holders crop, grown under rainfed conditions in semi arid areas. To develop elite genotypes, knowledge on inter relationship among yield and its component characters and direct and indirect contribution towards yield is important. Hence, the present study was undertaken to asses the nature and magnitude of association between pod yield and its components characters viz., days to 50% flowering, plant height, branches per plant, pods per plant, root length, dry matter production, SPAD chlorophyll meter reading, harvest index, and single plant yield in early season drought tolerant groundnut genotypes and hybrids at Oilseeds Research Station, Tindivanam. Among the characters, the characters viz., plant height, root length, dry matter production and SPAD chlorophyll meter reading had positive significant correlation with pod yield. The path analysis disclosed that the character plant height had the highest positive direct effects on single plant yield followed by root length and branches per plant. The results revealed that the direct selection for the above mentioned traits could improve the pod yield in the early stage drought tolerant groundnut.

PI-61

IDENTIFICATION OF RESTORER LINES FOR AVAILABLE MALE STERILE LINES IN REDGRAM

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Redgram is a legume grain crop with natural out crossing ranges from 20 to 70 *percent*. The natural out crossing in redgram is mainly due to insect pollination. In addition, development of stable male sterile line also offered a scope for exploitation of hybrid vigour in redgram. An experiment was conducted to identify fertility restorers, the available redgram cytoplasmic male sterile lines namely, ICP 67A, CRG 990047A, CRG 990052A, Co(Rg)7A2, UPA 120A, ICP 163A, ICP 84023A, ICPA 2155 and Co(Rg) 7A4 collected from ICRISAT, Hyderabad, IIPR Kanpur and TNAU Coimbatore were used for this study to exploit heterosis. To identify the pollen fertility restorers, 321 redgram inbreds line of 120-130 days duration collected from different co-ordinating centres were used as pollen parents and crosses were made with these nine cytoplasm genic male sterile lines during the period from 2010-13. A total of 532 hybrid combinations were obtained and the entire cross combinations were evaluated during *Kharif* and *summer* seasons 2010 -13 for their pollen fertility. The pollen fertility was observed under microscope. Also the selected F_1 plants were selfed with muslin cloth bags to observe pod setting in the field. The pollen fertility for all the cross combinations

was recorded from 0 to 82.4 percent. Out of the 532 hybrids evaluated during these periods, only the two redgram cross combinations namely, CRG 990052A x CRG 5/6 and ICPA 2155 x AF 284 were recorded the maximum pollen fertility of 82.4 and 80.6 per cent respectively.

PI-62

EVALUATION AND IDENTIFICATION OF SUITABLE BLACKGRAM VARIETIES IN KALAVAI REGION OF VELLORE DISTRICT

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Blackgram (*Vigna mungo* (L) Hepper) is a self-pollinating, widely cultivated grain legume popularly known as Urd or Mash bean. India shares 35.2 percent area and 27.65 percent of global production of pulses, but the productivity has been more or less stagnant, fluctuation between 10 and 12 million tonnes over the last three decades (Chaturvedi and Ali). The present study was carried out at Kalavai region of Vellore district, Tamil Nadu. A total of 5 blackgram varieties were (VBN3, TMV1, VBN4, Early Wonder and T9) collected from different Agricultural Research Stations in Tamil Nadu for evaluation of varietal performance. Biometrical observations were recorded in these varieties for 8 different traits. The variety Early wonder recorded highest mean for germination percentage (39.33), pod length (5.37), grains per pod (7.63), single plant yield (11.45), 100 seed weight (6.51). Among these varieties Early wonder showed high performance and is suitable for cultivation in Kalavai region of Vellore district, Tamil Nadu.

PI-63

SCREENING OF GROUNDNUT GENOTYPES FOR LATE LEAF SPOT AND RUST RESISTANCE

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Field screening was carried out on 147 genotypes of groundnut (*Arachis hypogaea* L.) against late leaf spot (LLS) and rust resistance during June-October 2014. The modified 9 point scale for LLS and rust diseases was used to screen the genotypes. High disease pressure for LLS (2.5-7.6 scale) and rust (1-5.5 scale) diseases were observed in this study. Among the 147 lines, eight lines *viz.,* ICGV 03042, ICGV 06138, ICGV 06139, GPBD 4, ICGV 04093, ICGV 06049, ICGV 00206 and ICGV 05158 recorded resistant reaction (<3) for LLS disease. Whereas the lines ICGV 05193, VRI2, TMV 7,CO Gn 4, Western 44, GG 6 and GG 15 recorded susceptible reaction (>7) for LLS

disease. Resistant reaction (<3) for rust disease was observed in 64 groundnut genotypes whereas eight genotypes recorded susceptible reaction for rust disease. Genotypes *viz.,* ICGV 06138, ICGV 03042, GPBD 4, ICGV 04093, ICGV 06049 and ICGV 00206 recorded resistant reaction for both the diseases. Hence these lines can be used in LLS and rust resistant breeding programme in groundnut.

PI-64

VARIABILITY STUDIES IN F_3 POPULATION OF GROUNDNUT (*Arachis hypogaea* L.)

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Nine crosses involving foliar diseases *viz.,* late leaf spot and rust susceptible (as female) and resistant (as male) parents in F_3 generation were studied for mean and variability parameters. Susceptible female parents *viz.,* CO 7, TMV 2, VRI 2, TMV Gn 13, ICGV 00350 and resistant male parents *viz.,* VRI Gn 6, COG 0437, GPBD 4 were involved in these crosses. Among the crosses, the cross VRI2 x GPBD 4 had higher mean performance for most of the characters *viz.,* pod yield per plant (g), kernel yield per plant (g) and disease score for LLS and rust. It also had high PCV and GCV values coupled with high heritability and GAM for the traits studied. Hence based on mean and variability parameters for pod and kernel yield and foliar disease resistance, the cross VRI 2 x GPBD 4 is adjudged as superior cross. Considering the progeny wise performance, the progenies #1 and #2 of the cross VRI2 x GPBD 4 could be selected due to the superior *per se* performance for most of the traits along with disease resistance. These progenies recorded high or moderate coefficient of variation for all the characters. Hence these progenies need to be advanced further till the attainment of homogeneity to obtain high yielding with resistance to foliar diseases.

PI-65

GENETIC VARIABILITY STUDIES FOR QUANTITATIVE TRAITS IN RESTORER LINES OF PEARL MILLET (*Pennisetum glaucum* [L.] R.BR.)

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Pearl millet is the staple food and fodder crop of millions of poor people living on most marginal agricultural lands of Indian and African subcontinent. In India, it ranks fourth important cereal crop. For developing appropriate breeding and selection strategies, the estimation of genetic parameters plays an important role. The present study was conducted to evaluate twenty five restorer lines to assess the magnitude of variability and to understand the heritable component of variation present in yield and yield contributing characters. A field trial was laid under randomized complete block design (RCBD) with two replications during *kharif* 2014 and observations were recorded for seven morphological characters *viz.,* plant height, days to 50% flowering, number of productive tillers, earhead length, earhead grith,1000- seed weight and single plant yield. In general, phenotypic coefficient of variation (PCV) estimates were higher than genotypic coefficient of variation (GCV) estimates for all the characters in all genotypes displaying the influence of environmental effect. Highest PCV and GCV were observed for single plant yield and lowest PCV and GCV were recorded for days to 50% flowering. High heritability coupled with high genetic advance as per cent of mean was observed for all characters except days to 50% flowering suggesting that these traits are governed by additive gene action which shows the possibility of improving these characters through selection.

PI-66

BIPLOT ANALYSIS IN GERMPLASM CHARACTERIZATION OF INDUSTRIAL LEGUME - CLUSTER BEAN (*Cyamposis tetragonoloba* (L.) TAUB.)

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Clusterbean (*Cyamposis tetragonoloba* (L.) Taub.) is known for its mere vegetable crop now turned into industrial legume crop because of its versatile uses. Germplasm characterization is foremost important to bring the genetic improvement. Principal Component Analysis (PCA) used for identifying major source of variability among agronomical, reproductive and phenological traits in 42 clusterbean genotypes and identified major source of variation as plant architecture *i.e.,* stem type and growth habit contributed more amount of variation. Since the biological explanation of Principal Components (PC) is tricky, the best way to make sense of the PC is to find the degree of influence of each variable weight on each of the components. Primary variability was governed by the traits namely growth habit, leaf surface, stem type, leaf type, flower colour and seed colour as explained by the first four PCs. The genotypes namely PNB, T local, HGS 884, RGC 471, MRSG6 were much diverse as observed in the biplot. These diverse genotypes can be employed as a distinct parent for future breeding programme especially hybridization. There was clear grouping of vegetable genotypes along with fodder type in a single quarter and gum yielding genotypes in separate quarters. These two groups were genetically found diverse and huge variability was exits between these groups. These diverse genotypes are useful to broadening the gene pool of clusterbean.

PI-67

ASSESSMENT OF PERFORMANCE ACROSS SEVERAL LOCATIONS IN BARNYARD MILLET (*Echinochloa frumentacea* (ROXB.) LINK.)

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Barnyardmillet is an important small millet crop, well adapted to low and moderate rainfall areas. The grains of barnyardmillet are low in phytic acid an anti-nutrient factor and rich in iron and calcium. There are indications that diversity in barnyard millet is fast eroding and area under barnyardmillet is gradually decreasing in many states. In southern parts of Tamil Nadu, farmers are eagerly cultivating the barnyardmillet crop in large area. The present investigation was carried out to study stable performance of various traits in five different barnyardmillet genotypes *viz., Sadai kudiraivali*, *Pullu kudiraivali*, CO (KV) 2, VL 29 and VL 172 were evaluated over five different locations (M. Kallupatti, Vandapuli, Vitalapatti, P. Thotipatty and S. Kottaipatty villages) to assess the stability parameters *viz.,* genotype mean, regression coefficient (bi) and mean square deviations (S^2d_i). Variances due to genotype, environment, genotype x environment, environment (linear) and pooled deviation were significant for days to 50 per cent flowering, days to maturity, plant height and grain yield. Based on the stability analysis, the genotype CO (KV) 2 was found to be stable across five different locations for days to maturity, plant height and grain yield. This study finally concluded that, the stable genotypes may be recommended for the commercial cultivation.

PI-68

STUDIES ON GENETIC VARIABILITY AND ASSOCIATION ANALYSIS IN COTTON (*Gossypium hirsutum* L.)

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Studies on genetic variability, character association and path-coefficient analysis were conducted on twenty nine cotton genotypes (*G.hirsutum* L.). Analysis of variance revealed considerable variability among the genotypes for all the characters. A high genotypic (GCV) and phenotypic coefficient of variation (PCV) was observed for Kapas yield (kg/ha) (16.0 and 13.0), number of sympodia per plant (17.0 and 11.0), number of bolls per plant (18.0 and 14.0) and Boll wt (g) (13.0 and 11.0).Characters like Kapas yield (kg/ha) (63), number of bolls per plant (61) and boll wt (g) (68) showed high heritability thus the selection for this characters in the early generation and can be fixed easily. The boll weight showed high heritability (h2) coupled with Genetic Advance (GA) reveling a simple selection procedure can be applied for improvement of this character. Positive association of kapas yield with number of bolls per plant (0.23), boll weight (0.30), seed index (0.15) and lint index

(0.24) results revealed that selection for this character will improve the yield. Significant positive correlation observed between plant height and number of sympodia per plant. Direct and indirect effects showed that maximum positive direct effect of (0.30) and number of bolls per plant (0.23) with kapas yield. Hence genetic improvement of kapas yield in cotton can be achieved by selecting through these characters.

PI-69

IDENTIFICATION AND DEVELOPMENT OF FORAGE SORGHUM LINE FOR HIGH DRY MATTER DIGESTIBILITY

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Sorghum is an important cereal fodder crop in the hot and dry areas and serve as main source of feeding material to cattles, milch animals. It is being fed as green, dry fodder, silage, powdered material and utilized for making concentrated feed blocks. Dry Matter Digestibility (DMD) is the most prominent quality trait in forage crops, expressed as IVDMD (in-vitro DMD). It decides the level of digestibility and value of forage in relation to lignin content and determines the price in market Lignin content present in the stalks and leaves interferes with the digestive process and reduces the digestibility. The IVDMD values of most cultivars ranges from 43-48 %. The promising forage line has been identified for its desirable morphological traits from evaluation of sorghum germplasm maintained at Department of Millets.Since this line performed better than other varietal lines for green fodder production and per day productivity in University trial, this was included in All India coordinated Sorghum Improvement program, Initial single cut Varietal Trial (AICSIP Code SPV 2211) and tested in AICSIP trials for two years, 2012-2014 over 16 locations at National level. It recorded high dry matter digestibility among the other AICSIP entries and recorded the average of 54.6% IVDMD over two years. It also recorded higher green fodder yield of 13% in 2012 and 8 % in 2013 over the other AICSIP entries. It had advantage of early duration of 85-90 days, higher per day productivity for green fodder harvest at 50 % flowering (60 days).

PI-70

HETEROSIS AND COMBINING ABILITY STUDIES INVOLVING DIVERSE HETEROTIC GROUPS OF COTTON (*Gossypium hirsutum* L.)

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At Dharwad, efforts are made constantly to observe most potential crosses and understand the basis

of complementation leading to high heterosis. These efforts have led to the formation of different heterotic groups like stay green, robust, compact and high RGR and their heterotic patterns which in general give potential hybrids. In the present research an attempt was made to assess the heterosis and combining ability using line x tester study. A set consists of eight elite lines (four lines each from robust and stay green heterotic groups) was crossed to set of four elite lines from high RGR group. Thus the Line x tester analysis consisting 32 intra hirsutum crosses along with three popular Bt hybrid checks (Kanaka, Mallika and RCH-2 *Bt*). The results revealed that the stay green/robust lines *viz.*, DSMR-10, DRAC-9565, DSG3-5 and DR-2 recorded highest mean seed cotton yield. Among the high RGR testers, DRGR-32-100 and DRGR-24-100 noticed the highest mean seed cotton yield. The between high RGR - stay green group and high RGR- robust groups crosses *viz.*, DSMR10 x DRGR-24-178, DSG 3-5 x DRGR-32-100, DSMR10 x DRGR-32-100, DSG 3-5 x DRGR-24-178 and DSG 3-5 x DRGR-4 exhibited highest mean seed cotton yield. The robust / stay green x high RGR derived crosses had the desirable features because of higher three dimensional space of robust plant type with high stay green nature and tall vertical fast growing habit coupled with high boll number and less biological mass in RGR types influences final phenotype of resulting hybrids.

PI-71

IDENTIFICATION OF POTENTIAL HETEROTIC BOX INVOLVING DIVERSE HETEROTIC GROUPS FOR INITIATING RECIPROCAL SELECTION FOR IMPROVING COMBINING ABILITY IN COTTON (*G. hirsutum* L.)

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Exploitation of heterosis through hybrids has led to improvement in productivity of both self and cross pollinated crops. In cross pollinated crops, hybrid breeding program is supported by population improvement schemes aimed at improving combining ability. There are very few studies on grouping genotypes based on heterotic pattern and exploiting them in self pollinated crops. At Dharwad, efforts are made constantly to observe most potential crosses and understand the basis of complementation causing high heterosis. These efforts have led to formation of different heterotic groups like stay green, robust, compact and high Relative Growth Rate (RGR) and their heterotic patterns. In the present study, 32 inter group crosses generated from elite lines of Robust, Stay Green Vs high RGR heterotic groups were utilized for predicting the double cross performance to exploit opposite heterotic groups, potential heterotic box involving elite combiners was identified based on predicted choice of most potential heterotic pairs (two each) from the opposite heterotic groups {(A x B) *Vs* (C x D) }. The highest average seed cotton yield was 4020 kg ha-1, indicated that the heterotic box of high RGR Vs Robust /Stay Green (DRGR-24-178 x DRGR-32-100) Vs

(DSMR-10 x DSG3-5) is the best combination of genetically diverse single crosses. After identifying the potential high RGR Vs Robust /Stay green heterotic box. These high RGR and Robust x Stay Green crosses *viz.,* DRGR-24-178 x DRGR-32-100 and DSMR-10 x DSG3-5 respectively were advanced to F_4 generation during succeeding years for initiating reciprocal selection for improving combining ability.

PI-72

INFLUENCE OF ADDITIVE AND NON-ADDITIVE GENES FOR YIELD AND YIELD CONTRIBUTING TRAITS IN HYBRID RICE

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The successful development of rice hybrids by utilizing the CGMS system mainly depends on the availability of stable male sterile lines and economically viable seed production technology. This can be further hastened by choice of suitable elite parents with favourable alleles which on crossing would give heterotic rice hybrids. Three CGMS lines and nine genotypes were crossed and the resultant 27 hybrid combinations were subjected to combining ability analysis for yield and yield contributing traits. The ANOVA for combining ability revealed significant differences among lines, testers and line x testers for all the traits. Significance of mean squares of lines and testers indicated prevalence of additive genetic variance. The *gca: sca* ratio revealed the presence of both additive and non additive gene action. Few characters *viz.,* number of productive tillers, panicle length and grain yield per plant, indicated predominant role of non additive gene action. Two CMS lines IR 68886A and IR 68888A had high *gca* for earliness and for most of the yield traits respectively. With respect to testers four genotypes *viz.,* MTU 7029, MTU 9982, IR 59624-34-2-2 and IR 62030-54-1-2-2 were identified as the best combiners for yield. Based on the per se, *gca* effects, *sca* effects and standard heterosis, 10 hybrid combinations were identified as the best. The hybrids IR 68886A x MTU 7029 and IR 68888A x IR 62030-54-1-2-2 had greater standard heterosis over the check CORH 3 followed by others can be further exploited for hybrid vigour based on their performance by conducting yield trials.

PI-73

TSH 0250 - A HIGH YIELDING SUPERIOR MEDIUM STAPLE COTTON CULTURE IDENTIFIED FOR SOUTH ZONE OF INDIA AND SUMMER IRRIGATED TRACTS OF TAMIL NADU

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In Tamil Nadu cotton is cultivated in different eco systems and the potential yield was obtained in summer irrigated/rice fallow conditions. But the existing cotton varieties under cultivation in above season *viz*., SVPR 2, SVPR 3, SVPR 4, KC 3 are mostly medium staple category and could not match requirements mills which needs 40s. Hence to overcome the above situation, a drought tolerant parent NDLH 1658 was crossed with Surabhi. Pedigree method of selection was followed from F_2 to F_5 generations. A superior segregant with resistance to leaf hopper was isolated in F_2 population and was further evaluated upto F_5 generation as TSH 0250. Based on the consistent performance in station yield trials, TSH 0250 was selected for large scale testing and tested in the AICCIP Southern Zone trial centres under irrigated conditions from 2010 to 2013. The data over three years (2010-2012) revealed that TSH 0250 matured at 150 days and recorded mean seed cotton yield of 1835 kg/ha as against 1635 kg/ha of national check Surabhi and 1680 kg/ha of local check. The increase kapas yield was 12.2 % over Surabhi and 9.2 % over local check. It was Moderately Resistant to leafhopper. The culture TSH 0250 is superior medium staple cotton with a mean ginning outturn 34.9%. It is having a mean 2.5% span length of 29.4mm, mean bundle strength of 22.0g/tex and mean micronaire value of 3.6. This culture has been identified by Central Variety identification Committee for South zone in the year 2013-14.

PI-74

BREEDING FOR HIGH OIL IN SAFFLOWER (*Carthamus tinctorius* L.)

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Safflower (*Carthamus tinctorius* L.) is a multi-purpose crop grown mostly in India for edible oil purpose. Oil content enhancement is a prime objective of Indian safflower breeding programmes. However, the major constraint in developing high oil (>30%) breeding pools was non-availability of high oil sources in Indian safflower germplasm and negative association between oil content and the seed yield contributing hull content. Hence, oil content in the released hybrids and varieties was very

low (25-30%). For enhancing oil content, multiple crosses among parental lines possessing 30% oil content and high seed yield were made initially and then pedigree method was followed with rigid selection for progenies having oil content more than 30% and moderate 100-seed weight (3-5 g). An average of 34% oil content was maintained in advanced generations of many progeny selections. Six of the selections possessed 35-38% oil content while the national check variety, A1 had 25% oil. These high oil selections recorded 5.4 to 141% higher oil yield (308-717 kg/ha) than A1 (292 kg/ha). 100-seed weight ranged from 3.89-4.55 g among these selections while it was 6.98 g in A1, indicting existence of negative association between hull content and oil content. Three selections, DSF2041/SFS2011, SFS824 and SFS841 possessing 37.38%, 35.34% and 35% oil content, respectively, recorded 23% (1415 kg/ha), 61% (1859 kg/ha) and 78% (2050 kg/ha) higher seed yield than A1 (1148 kg/ha), respectively. Stability of these lines for high oil content would be tested in further at multilocations prior to utilizing them as high oil donors.

PI-75

SCREENING FOR DROUGHT TOLERANT SUGARCANE PRE BREEDING CLONES *IN VIVO*

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Drought is acting as a vital environmental stress; limits crop yield significantly. Sugarcane cultivation is experiencing drought in tropical and sub tropical regions. Drought breeding would sustain cane production in the targeted environments. In the present experiment, a total of 16 high yielding sugarcane pre breeding clones with miller preferable traits were tested under *in vivo* situations for their suitability to the targeted environments of North Western zone of Tamil Nadu. The growth characters *viz.*, relative growth rate (RGR), crop growth rate (CGR), stem elongation rate (SER) and leaf area duration (LAD) and other yield and quality attributing traits were analyzed both under normal and droughted conditions to select the ideal clones. Drought affected all physiological process starting from germination to maturity. The clones exhibited variability for the growth traits; the susceptibility and effect vary in relation to growth stage and genetic makeup of the clones. Drought during formative phase significantly reduced RGR, CGR, SER, SER and LAD however SER was more sensitive. The clones *viz.,* G02772 and G02813 possessed better SER of 2.56 and 2.50 respectively. The clone G02772 possessed the highest LAD of 7.25. Early vigour traits *viz.,* tiller number and tiller height were negatively influenced by drought. The least influence of drought on tiller number was observed in G02779 and also it possessed the highest tiller height of 90.64 cm among the test clones. The clones *viz.*, G02772, G02813 and G02779 would be considered for further large scale testing for their suitability under droughted conditions.

PI-76

GENETIC VARIABILITY STUDIES IN SOYBEAN GERMPLASM

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Soybean, the important legume crop of India is a miracle pulse crop that harbors momentous levels of protein and oil. The soybean protein and oil earns momentous foreign reserves. The success of soybean improvement program depends on the variability. TNAU maintains a rich source of soybean germplasm. An investigation was carried out to assess the variability of fifty selected soybean germplasm accessions for the use in hybridization programme. The germplasm lines were raised in augmented design during Kharif, 2014. Six yield and yield contributing traits were analysed to understand the extent of variability for yield and yield attributing traits. The accessions showed wide variability for traits *viz.*, plant height, 100 seed weight, single plant yield, number of seeds per pod, number of clusters per plant and number of primary branches. The qualitative traits *viz.*, growth habit (Erect and semi erect), growth type (determinate, semi determinate and indeterminate) have also showed significant variability. Among the traits studied, plant height and number of primary branches showed higher heritability and genetic advance as per percent mean. The trait association studies showed that the characters *viz.*, plant height, number of pods per plant, number of seeds per pod could be improved and simultaneous selection would offer scope for yield improvement.

PI-77

VARIABILITY AND CORRELATION STUDIES FOR YIELD AND YIELD CONTRIBUTING TRAITS IN GROUNDNUT (*Arachis hypogaea* L.)

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Groundnut is valued as a rich source of energy contributed by protein (25 - 28%), edible oil (48 - 50%) containing essential fatty acids, minerals and anti-oxidants in the kernels. Improvement in kernel yield is the major criteria which can be done through direct and indirect selection for yield contributing traits. The source of variability derived from advanced breeding lines is used most often for improving the yield parameters. The variability, heritability and correlation studies were carried out in the F_4 generation of the cross made between ICGV 05100 x SunOleic 95R. High heritability

was observed for the trait 100-kernel weight (80.49%) whereas medium heritability was observed for the trait number of primary branches (37.96%). High heritability and genetic advance as percentage over mean (GAM) was observed for the traits *viz.,* number of pods per plant, 100-pod weight, 100-kernel weight, pod yield per plant and kernel yield per plant, which indicated the preponderance of additive gene action. Hence, these traits could be further improved through single plant selection. Kernel yield per plant was significant and positively associated with number of pods per plant, 100-pod weight,100-kernel weight and pod yield per plant. Hence, these characters can be considered as selection indices to improve the kernel yield.

PI-78

VARIABILITY, CORRELATION AND DIVERSITY STUDIES IN PIGEONPEA [*Cajanus cajan* (L.) MILLSP] GENOTYPES

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Field experiment was conducted at College of Agriculture, Bheemarayanagudi, University of Agricultural Sciences, Raichur during *kharif* 2012-13 to study the genetic variability, correlation and genetic diversity on various morphological traits of yield and yield related components of pigeonpea. The experiment was laid out with randomized complete block design involved nineteen genotypes of Pigeonpea with 3 replications. The range for plant height, 50 per cent flowering, number of pods per plant, 100 seed weight, seed yield per plant and seed yield per hectare was 165.80 to 211.40cm, 93 to 111.00 days, 177 to 298 pods per plant, 8.60 to 11.60 g, 40.00 to 61.50 g, 1420.60.00 to 2054.60 kg/ha respectively. They were grouped in to two clusters, based on various morphological traits, yield and yield related components, which indicated the presence of amount of genetic diversity. The seed yield per ha was the largest contributor (40.03 per cent) followed by number of pods per plant (32.11 per cent) and number of pods per plant (25.60 per cent) towards the divergence. All the nineteen advanced breeding lines of Pigeonpea show moderate to high heritability and Genetic advance as per cent mean. At the phenotypic level, the correlation seed yield had shown the positive and significant association with the other component traits like number of pods per plant, secondary branches, 100 seed weight, and days to 80 per cent maturity which reveals that selection based on these traits would ultimately improve the seed yield.

PI-79

GENERATION MEAN ANALYSIS FOR DROUGHT TOLERANCE UNDER REPRODUCTIVE STAGE DROUGHT STRESS IN RICE (*Oryza sativa* L.)

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The genetic components of generation means governing yield and drought tolerant traits under reproductive stage drought stress in rice were estimated using six generations of five crosses *viz*., PMK 2/Moroberekkan, MDU 5/Moroberekkan, Norungan/Moroberekkan, Nootripathu/Moroberekan and Kallurundaikar/Moroberekan in the six parameter model of Mather and Jinks, 1971. The scaling tests revealed the presence of epistasis in all the characters except productive tillers/plant in MDU 5/Moroberekkan and Kallurundaikar/Moroberekkan. The drought characters *viz*., days to first flowering, dry root weight and root thickness were controlled by both additive and dominance genetic effects with additive x dominance and dominance x dominance interactions in days to first flowering and root thickness and additive x additive interaction in dry root weight. The characters spikelet fertility, root length and root/shoot ratio were governed by dominance gene action with predominance of additive x additive interaction in all and additive x dominance interaction in spikelet fertility. Among the yield characters, productive tillers/plant, filled grains/panicle, harvest index and grain yield/plant were governed by dominance gene action and one or more interaction effects. Plant height, panicle length and 100 grain weight were controlled by both additive and dominance gene action along with additive x dominance and dominance x dominance interactions in plant height and 100 grain weight and additive x additive interactions in panicle length. Almost all yield and drought characters showed duplicate epistasis. Simple selection for additive gene action, hybridization followed by selection in later generations for dominance gene action and reciprocal recurrent selection for epistatic gene interaction were recommended.

PI-80

PERFORMANCE EVALUATION OF CHILLI (*Capsicum annuum* VAR. *annuum*) GENOTYPES FOR GROWTH AND YIELD UNDER SEMIDRY CONDITIONS OF TAMILNADU (VIRUDHUNAGAR)

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Field evaluation of 89 collections of chilli germplasm was conducted in a farmers field at Virudhunagar district during 2013-2014 in a randomized block design with two replications to identify the appropriate chilli genotype suitable for semi dry conditions. Among the 89 chilli germplasm studied, plant height

was ranged from 102.2cm (CA-31) to 22.8 cm (CA-73) with mean value of 59.29 cm. The mean performance for number of branches was 4.24 and the highest number of branches was recorded by CA-14 (7.4) and lowest was recorded in CA-85 (1.4). The chilli genotype CA-89 recorded the highest root length (19.40cm) and root volume (77cc). Early flowering was found to range from 76.70 days (CA-1) to 101.50 days (CA-87) with mean value of 90.66 days.With regard to yield parameter studied, number of fruits per plant ranged from 11.60 (CA 69) to 242.00 (CA 89) with mean value of 79.15. The individual fresh fruit weight was observed to be the highest (7.47 g) in CA-77 and it was the lowest (1.20 g) in CA-48 with mean value of 3.39. The highest (1.76 g) and lowest (0.23 g) individual dry pod weight were recorded in CA-43 and CA-56 respectively. The fruit characters viz., fruit length and fruit girth showed mean values of 8.85 and 3.67 respectively. The chilli genotype CA-89 produced the highest fresh pod yield (1334.9g per plant) and also dry pod yield (225 g per pant) which was higher than that of local check K1 (667 g and 60.1 g per plant respectively).

PI-81

STUDIES ON CORRELATION AND PATH ANALYSIS IN RICE UNDER FLASH FLOOD

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The present study was carried out to observe the flash flood tolerance of rice genotypes along with the submergence tolerant check variety Swarna Sub 1 during Samba, 2010. The 26 rice genotypes were screened *in vivo* during Samba, 2010. To study the field performance of the genotypes under natural flash flood the field experiments were conducted at two places *viz.,* a low lying field to screen the genotypes for flash flood tolerance (E2) and an elevated field (E1) as irrigated control. Pooled analysis was also carried out.The observations on eleven biometrical and grain quality for 26 rice genotypes were analyzed. The analysis of variance revealed the presence of significant variability among the genotypes for all the 11 characters studied in E1, E2 and pooled analysis.Genotypic and phenotypic correlation studies revealed that grain yield per plant had positive significant correlation with number of tillers and productive tillers per plant at both levels in E1, E2 and pooled analysis. A positive significant association between days to 50 per cent flowering with grain yield in the flash flooded condition E2 indicated the importance of earliness of flowering and hence maturity during flash flood favours higher yield. The cause and effect of relationship among characters studied indicated very high positive direct effect of number of productive tillers per plant and panicle length on grain yield per plant in flash flood condition (E2). Plant height exhibited very high negative direct effect on grain yield emphasizing the importance of low shoot elongation under submergence.

PI-82

SCREENING FOR SHOOT FLY RESISTANCE IN ADVANCED BREEDING LINES OF SORGHUM (*Sorghum bicolor* L. MOENCH)

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An insect pest causes much reduction in yield levels in sorghum, among which shoot fly is a major one. Shoot fly (*Atherigona soccata* Rond.) is an important pest of sorghum in Asia. The experiment was conducted during *kharif* and *rabi* of 2013 at ARS Gulbarga, using 23 advanced breeding lines of sorghum with 2 checks [IS 2312(R), DJ 6514(S)]. To attain uniform shoot fly pressure under field conditions the interlard-fish meal screening technique was followed. Two rows of a susceptible cultivar (DJ 6514) were sown 20 days before sowing the test material all around the experiment in three replications. This was done to allow for multiplication of shoot fly for one generation. Ten days after seedlings emergence, polythene bags containing moistened fish meal were kept in the test material at uniform intervals covering the entire area to attract the emerging shoot flies from infector rows. Glossiness, oviposition, seedling vigour and dead heart percentage was recorded. The shootfly incidence (deadheart percentage) was recorded on 21 days after sowing. The deadheart incident was more in *rabi* as compared to *kharif.* Among the genotypes GS-2, GS-3, GS-5, GS-8, GS-11 and GS-22 recorded less than 30 per cent deadheart indicating moderately tolerant in *kharif.* The genotypes GS-1 showed less than 30 per cent deadheart percentage and showed moderately resistance in *rabi*. The advanced breeding lines were less deadheart per cent, high seedling vigour, less oviposition and high glossiness were recorded significantly associated with resistance to shoot fly.

PI-83

STUDIES ON FLASH FLOOD TOLERANCE IN RICE

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The present study was carried out to observe the flash flood tolerance of rice genotypes along with the submergence tolerant check variety Swarna Sub1 during Samba, 2010. The 26 rice genotypes were screened *in vitro* by three bioassay methods namely test tube method, water lodged soil method and seedling emergence method to evaluate their seedling response under submergence. Pot culture studies were also carried out to study the shoot elongation and lodging score of rice genotypes under submergence. Flood Tolerance Efficiency (FTE) and Flood Susceptibility Index (FSI) were computed to find out the tolerant genotypes of rice. *In vitro* screening for flash flood

tolerance revealed that the genotypes MTU-1010, TN-1 and Swarna Sub 1 registered superior performance in all the three bioassays. Among the three in vitro bioassays used, the test tube method can be adjudged as the most robust and reliable method proposed by Manangkil *et al.*(2008) in mass screening for evaluating seedling vigour of rice under submergence.Submergence screening of seedlings in pots revealed that genotypes IR 55408-01, MTU-1010, NDLR-8, TN-1 and Swarna Sub 1 recorded significantly lower shoot elongation upon submergence. Computation of lodging score revealed the significance of Sub 1 gene in Swarna Sub 1 recorded low shoot elongation upon submergence.Studies revealed that the genotype Swarna sub 1 had the highest FTE (66.00), least FSI (0.52) and minimum percentage of reduction in seed yield (34.00%). The genotype G8 had lowest FTE (9.50), high FSI (9.53) and maximum percentage of reduction in seed yield (90.50%).

PI-84

ASSESSMENT OF MORPHO-MOLECULAR DIVERSITY, VARIABILITY AND CHARACTER ASSOCIATION IN BLACK GRAM (*Vigna mungo* (L.) HEPPER)

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A study on 46 black gram genotypes for 12 morphological characters was conducted during *kharif* 2013. Analysis of variance revealed significant differences among 46 genotypes for all the 12 characters. Plant height had shown highest heritability coupled with genetic advance, followed by seed yield per plant, pod length. Correlation coefficient at phenotypic level revealed that grain yield per plant had a high positive and significant association with number of pods per plant (r=0.712), followed by number of secondary branches per plant (0.552), number of clusters per plant (0.551). The results of path analysis revealed that days to 50 per cent flowering (0.080), days to maturity (0.110), plant height (0.115), number of secondary branches per plant (0.324), branch height(0.136), number of pods per plant (0.604),number of seeds per pod (0.022) and hundred seed weight (0.134) had positive direct effects on grain yield. While the characters *viz*., number of primary branches per plant (-0.156), number of clusters per plant (-0.063) and pod length (-0.088) had negative direct effects on grain yield. Forty six genotypes were grouped into 3 clusters among which, cluster I (44) accommodated maximum number of genotypes. Hundred seed weight has contributed highest for total divergence and genotype M-186 has recorded best mean values. At molecular level genotypes were grouped into seven clusters among which cluster II (14) accommodated highest number of entries. A total of 21 SSR alleles were detected, marker Ccmt1 has sampled highest number of alleles and Maximum PIC was observed.

PI-85

PATH ANALYSIS OF SEED COTTON YIELD IN INTRA SPECIFIC HYBRIDS OF EGYPTIAN COTTON (*Gossypium barbadense* L.)

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Path analysis were studied for yield, yield components and some fibre quality traits in forty eight hybrids of *intra-barbadense* cotton along with check were raised in winter 2011 at Tamil Nadu Agricultural University, Coimbatore in a randomized block design with three replications. In this study, we analysed sixteen biological traits of *intra-barbadense* cotton (plant height, days to fifty percent flowering, number of sympodial branches per plant, number of bolls per plant, boll weight, number of seeds per boll, seed index, lint index, ginning outturn, lint yield, fibre length, fibre strength, micronaire value, uniformity ratio and elongation ratio) which supplied information on direct and indirect effects of the traits on seed cotton yield. The lint yield exhibited the highest direct effect on seed cotton yield. Direct effects of the other traits were low and their high total effects were masked by the indirect effects of the number of bolls per plant, lint index, ginning outturn and number of sympodial branches per plant. The moderate positive direct effect was exhibited by elongation ratio whereas the negative direct effect was shown by ginning outturn and micronaire value on seed cotton yield. The results of this analysis indicate that the lint yield and the components responsible for it through indirect effects was the most important characters to be considered during selection.

PI-86

PATH OF PRODUCTIVITY IN DERIVED F_1S FROM THE CROSSES BETWEEN F_4 LINES OF ROBUST AND COMPACT GROUPS IN COTTON (*Gossypium hirsutum* L.)

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Path of productivity for seed cotton yield and its component traits of the crops have been studied. The cause of superiority of potential genotypes was arrived at by comparing their performances with the mean of all genotypes and expressed as deviation from this group mean. These per cent deviation values help in identifying the important yield contributing traits responsible for high productivity seen in the group as well as in superior genotypes. This per cent deviation of potential genotypes from group mean helps to identify diverse productive genotypes, which differ in the role of yield components and plant type components contributing to productivity. This approach also helps in determining the recombinant of these diverse genotypes for developing segregants accumulating more of the different desirable traits of the ideotype. The top ten performing genotypes had positive value for seed cotton yield, number of bolls per plant, number of sympodia per plant, single boll weight, reproductive points on sympodia, Plant height (cm), inter branch distance (cm), ginning outturn (%). The genotypes showed negative per cent deviation for number of monopodia per plant, sympodial length at 50% height (cm), inter boll distance (cm) and SPAD. This negative deviation for number of monopodia per plant, sympodial length at 50% height (cm) and inter boll distance (cm) are highly desirable because increase in the monopodia per plant, sympodial length at 50% height and inter boll distance makes the plant bushy and robust thus causing a wasteful increase in the space occupied by the plant.

PI-87

EVALUATION OF KODO MILLET (*Paspalum scrobiculatum*) GERMPLASM FOR IMPROVEMENT OF YIELD AND ITS COMPONENT TRAITS

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Forty kodo millet germplasm lines were raised along with check CO3, the high yielding variety in kodo millet, in replicated block design during summer, 2013. Eight biometric traits viz., days to flowering, plant height, inflorescence length, raceme length, number of racemes per inflorescence, days to maturity, grain yield per plant and test weight were analyzed to identify the lines that were significantly different from the CO3. The analysis of mean performance over replications showed that TNPsc 106, TNPsc 170, Aamo 10, Aamo 29, Aamo 36, Aamo 37, Aamo 72 and Aamo 398 showed earliness in flowering (less than 74 days) and TNPsc 155, TNPsc 215, *Peruvaragu*, *Adari*, TNPsc 217 were significantly late in flowering (more than 97 days) when compared with CO3. Among the lines, the land race, *Venganoor* had longer inflorescence and raceme length. *Podivaragu*, *Athipatti*, *Venganoor* and *Peruvaragu,* TNPsc 155, TNPsc 183, TNPsc 231 and TNPsc 232 were taller than CO3. Higher number of racemes was recorded in *Adari,* Aamo 210, Aamo 258, TNPsc 201, TNPsc 215 and RK 50. The higher seed weight was observed in TNPsc 176, TNPsc 215, TNPsc 217, TNPsc 86 and TNPsc 225. Though none had recorded higher yield per plant than the check, the germplasm lines, Aamo 5, Aamo 210, Aamo 258, Sel 21, RK 50, TNPsc 156,TNPsc 176, TNPsc 183, *Pacheri* and *Naraiyur* recorded an average yield on par with the check.

PI-88

MUTAGENIC EFFECTS OF GAMMA RAYS, EMS AND COMBINATION TREATMENTS IN M_1 GENERATION OF BARNYARD MILLET (*Echinochloa frumentacea* L.)

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Hybridization and mutation are possible methods to create variation among genotypes. In barnyard millet, hybridization is tedious method due to small spikelets. Under such circumstances, induced mutagenesis can be profitably employed as a complementary breeding procedure as it offers a single and short alternative to conventional breeding. An investigation was carried out in two genotypes of barnyard millet *viz.* CO(KV) 2 and ACM 296 (local landrace of Paramakudi) using two mutagens, gamma rays and Ethyl Methane Sulphonate (EMS) and combination treatments of gamma rays + EMS to induce earliness and to find out the mutagenic effects in M_1 generation. Lethal dose (LD_{50}) was observed between 800 Gy and 900 Gy, 70 mM and 80 mM in both the genotypes for gamma rays and EMS respectively. Gradual reduction in germination over control was found to be directly proportional to increase in dose levels as indicated by highly significant negative correlation. Observation on the survival of plants on 45th day revealed that dose differences were found to be highly significant. In all the three treatments, pollen fertility percentage showed declining trend with increasing doses of mutagens. These results indicated that both the genotypes were sensitive to both mutagens used. Thus it is inferred that barnyard millet is highly response to physical and chemical mutagens and that both the genotypes used responded differently to gamma rays, EMS and combination treatments of gamma rays + EMS. This study throws limelight towards the development of early duration genotypes in advanced mutant generations of barnyard millet.

PI-89

GENETIC ANALYSIS OF QUANTITATIVE TRAITS INFLUENCING DROUGHT TOLERANCE IN GROUNDNUT (*Arachis hypogea* L.)

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Groundnut is an important food legume in our country. It is being cultivated in about 6.45 m. ha in

India. The productivity of the groundnut in our country is 1341 kg/ha which is very low when comparing the global productivity (1650 kg/ha) whereas the productivity in China is 3390kg/ha. Reasons for low productivity in groundnut are abiotic stresses and biotic stresses. Among the various environmental factors affecting the groundnut productivity, drought is the single most important factor. Studying the genetic parameters for the traits governing drought tolerance in groundnut will give sufficient knowledge to evolve drought tolerant cultures. So, the present study has been formulated to understand the genetic nature of the traits influencing drought tolerance in groundnut. Promising single plants four different cross combinations (VRI 2 X ICGV 86031, VRI (Gn)6 X ICGV 44, VRI 2 X ICGV 76 and VRI(Gn)6 X ICGS 86699) were raised in RBD, with three replications under drought condition at RRS, Vriddhachalam. The drought environment has been created by skipping alternate irrigations. The observations on drought influencing traits were recorded. The GCV estimates revealed that dry matter production on 30 DAS and 65 DAS recorded high variability when comparing the other traits. Heritability and genetic advance studies revealed that plant height on 65 DAS is highly heritable. Hence, selection based on plant height on 65 DAS for drought tolerance will give ample scope to evolve drought tolerant groundnut varieties.

PI-90

INTERROGATION ON TRANSGRESSIVE SEGREGATION FOR DROUGHT RELATED TRAITS AMONG ADVANCED SEGREGATING LINES IN GROUNDNUT

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Interrogation of transgressive segregation gives an early and handy tool for a plant breeder to chalk out a new crop ideotype with desirable traits. During Rabi 2011, BC_1F_2 generations of five crosses developed with background of wild groundnut (*Arachis stenosperma, Arachis kempffmercadoi* and *Arachis cruziana*) were evaluated for drought related traits besides the superior progenies were advanced to BC_1F_3 generation. The calculation for transgressive segregation was taken in favourable direction against those lines having value higher than the parental mean at 5 per cent probability. The dominance x dominance (non fixable genes) and additive x additive (fixable genes) may contribute for arousal of transgressive segregation in BC_1F_2. The cross, VRI 2 x (VRI 2 x *Arachis stenosperma*) had shown higher frequency of transgressive segregation for root dry weight, harvest index, drought tolerant index and pod yield. Also, the cross, CO 3 x (CO 3 x *Arachis cruziana*) had exhibited higher per cent of transgressive segregation for harvest index, pod and kernel yield. These crosses exhibiting higher transgressive segregation for most of the key traits can be utilized for selecting progenies tolerant to drought in future generations.

PI-91

DEVELOPMENT OF EARLY MATURING WHITE GRAINED FINGER MILLET GENOTYPES FOR NORTH WESTERN HILL REGION

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Development of white grained finger millet genotypes has become a thrust area in finger millet breeding due to increased demand of non-glutinous food products in urban areas and least acceptability of brown grained finger millet varieties by the Food Industry. The present study deals with the development of 16 white grained finger millet breeding lines and its evaluation in the North Western Himalayan region .These 16 lines were developed by crossing extra early maturing brown grained finger millet genotypes with late maturing white grained finger millet genotypes. The parental lines of brown and white grained finger millet genotypes exhibited extreme values for grain yield and days to maturity, whereas the developed white grained breeding genotypes showed moderate value for these traits. The PCA revealed that studied traits of majority of developed white breeding lines VL 427, VL 360, VR 485, VR 443, VL 366, VR 425B, VR 425A and VL 356 were similar to adapted variety VL 201 of the region. The cluster analysis indicated that white grained breeding lines from second cluster and brown grained finger millet lines from third cluster can be used as parents for developing another set of early maturing white grained lines for Himalayan ecology. Relationship analysis highlighted selecting plants with more number of fingers per ear rather than finger length. The present work gives a direction to the breeders for the development of high yielding early maturing white grained finger millet varieties for the hill region of the country.

PI-92

ASSESSMENT OF SALINITY EFFECTS ON SEEDLING GROWTH OF FINGER MILLET (*Eleusine coracana* L. GAERTN.)

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The study was conducted at Anbil Dharmalingam Agricultural College and Research Institute, Trichy during October, 2013 to April, 2014. Nine finger millet genotypes comprising of seven varieties (TRY 1, Paiyur 1, CO 9, CO 11, CO 13, CO 14, CO 15) and two advanced cultures (TNAU 1228, TNEC 1256) were evaluated under salinity stress in seedling stage using paper towel method. For paper towel study Yoshida solution was used as the nutrient medium. Saline solutions of different salt concentrations viz., 50mM, 100mM and 150mM were prepared by mixing 2.925g, 5.85g and 8.775g

of NaCl per litre of Yoshida medium. One control is maintained without addition of salt for the experiment. Fifteen days after germination, the samples were collected following Factorial Completely Randomized Design (FCRD) considering three replicates and two factors i.e., genotypes and salinity. Traits viz. root length, shoot length, fresh and dry weights of roots and shoots separately and seedling dry weight was studied. Salinity Intensity Index (SII) and Salinity Susceptibility Index (SSI) were analyzed based on dry seedling weight. In both the experiments data revealed TRY 1 as tolerant (SSI values < 0.8), whereas CO 11 and advanced cultures TNAU 1228 and TNEC 1256 were highly sensitive to salinity stress (SSI values 1.0 - 1.32). SSI values for CO 13, CO 14 and Paiyur 1 were observed between 0.8 - 1.0 thus, these genotypes behaved as moderately tolerant to salt stress.

PI-93

GENETIC DIVERSITY ANALYSIS UNDER HIGH DENSITY PLANTING SYSTEM IN COTTON (*Gossypium hirsutum* L.)

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A study was conducted with 93 germplasm of cotton (*Gossypium hirsutum* L.) accessions to identify genotypes suitable for high density planting and machine picking. The genotypes are studied for their genetic variability, heritability and genetic diversity. Based on this study, none of the genotypes possessed the all ideal characters for machine picking. The genotypes namely Lassani-11, IA-Banda TCH 1705 and DSC 21 had many characters ideal for HDP and machine picking. Based on the *per se* performance, the genotypes namely S3F, NDLH 1938, GSHV 01/ 1338, GJHV 496 were identified as the potential donors for single plant yield, plant height, number of sympodia, number of bolls per plant and boll weight. The traits namely internode length, number of sympodia, length of sympodia, number of bolls, boll weight and kapas yield showed high heritability and high genetic advance and hence these traits were controlled by additive genes and can be improved through selection. Based on genotypic correlation coefficient the characters *viz.,* plant height, number of sympodia, number of bolls per plant, boll weight showed positive significant correlation with seed cotton yield. The 93 cotton genotypes are grouped into 5 clusters when D2 technique was applied. Cluster V (TCH 1705) is genetically diverse from other genotypes. From the study it is concluded that genotypes have narrow genetic base. From the study it is concluded that, the genotype having the few or more ideal character can be improved further by recombination breeding to suit the HDP and machine picking.

PI-94

PRINCIPAL COMPONENT ANALYSIS AND CLUSTER ANALYSIS IN FINGER MILLET (*Eleusine coracana* (L.) GAERTN)

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An experimental material consists of 55 finger millet genotypes, was grown in RBD with three replications at Agricultural college farm, Naira (A.P). Each entry was grown in two rows of three meter length with a spacing of 30×10 cm. The data was recorded on 10 randomly selected plants for 16 quantitative traits.Principal component analysis on correlation matrix, the standardization of columns (here characters) created 16 new variables for 55 genotypes without changing their relative positions. Principal component scores for genotypes were used as an input for clustering using Ward's minimum variance method.Principal component analysis identified five principal components (PCs), which contributed 82.69 per cent of cumulative variance. The significant factors loaded in PC_1 (46.19) towards maximum genetic divergence were number of fingers ear^{-1}, inflorescence width, days to 50% flowering, inflorescence exertion, peduncle length, number of basal tillers and inflorescence length. 2D and 3D graphs showed wide divergence between the genotypes IE 2790, IE 501, IE 196, IE 2323, IE 3543, IE 2322 and IE 4110 signifying their usefulness in finger millet breeding to develop high heterotic hybrids. Agglomerative cluster analysis revealed that wide genetic distance between the genotypes of clusters IV (IE 501, IE 196, IE 2093, IE 3543, IE 2293, IE 2323) and VIII (IE 2790) indicating their usefulness in the breeding programme for finger millet yield improvement.

PI-95

DEVELOPMENT OF COMPOSITE VARIETY WITH EARLY GENERATION PROGENIES IN FODDER MAIZE

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Improvement in fodder maize was a long felt need in forage breeding with the available inbred lines. To achieve this, an attempt was made to develop superior composite variety better than African tall variety. A total of 28 hybrid progenies involving dent corn, sweet corn and baby corn types were synthesized and evaluated at Department of Forage Crops, TNAU, Coimbatore during 2011-12 and segregating progenies were forwarded to F_4 subsequently. Among them, five progenies with low inbreeding depression were selected to assess the heterotic potential and the phenotypically superior and uniform single plants selected from F_4 cross combinations *viz.*, FDM 3514-42, FDM 2514-46, FDM 1436-27, FDM 1422-39 and FDM 3414-61 were allowed to random mate each other in isolation.

The resultant half sib progenies in FDM 3414-61 and FDM 3514-42 were found to perform exceedingly well than the average performance of F_3 generation for green fodder yield which ranged from 417g/plant to 523g/plant and crude protein recorded 8.78 to 11.47% with 8-10 days earliness in the progenies and showed significant improvement from the parental progeny. The result indicated that hybrid vigour could have been fixed in the progenies due to buffering capacity of random mating process by avoiding inbreeding depression in the population. Further selection in the progenies would unambiguously yield a high yielding composite variety with earliness in fodder maize.

PI-96

POLY CROSS BREEDING - A MEAN TO CREATE VARIABILITY IN LUCERNE

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A poly cross breeding in Lucerne was conducted at Department of Forage Crops, TNAU, Coimbatore from 2003 to 2013 with the objective of creating variability for fodder yield and quality in Lucerne involving five popular varieties *viz*., CO 1, Anand 2, LLC 3, RLS 88 and T 9 as parents. As a result, 25 promising lines better for fodder yield and quality were identified of which, six cultures *viz*., ACP 1-2, ACP 3-2, CAP 3-2, RRP 5-4, ALP 1-1 and ACP 3-1 were selected. They were evaluated further for yield and quality against the check CO 1 during *rabi* 2009. ACP 1-2 which had performed better was isolated and renamed as TNLC 12 and subjected to continuous evaluation for three years from 2009-10 to 2011-12 for fodder yield, quality and seed yield. Simultaneously, On Farm Trials were conducted in Coimbatore, Tirupur, Erode and Krishnagiri districts during 2010-11 and 2011-12. In station trials, TNLC 12 accomplished a mean green fodder yield of 134 t/ha /yr as compared to check CO 1 (108 t/ha /yr) while in OFTs it executed 126 t/ha /yr as against 99 t/ha /yr in CO 1. It had recorded highest crude protein percentage of 23.5 as against 20.5 in CO 1. Its profuse flowering nature helps in getting higher seed yield to the tune of 18.2 % over CO 1. Considering the supremacy of TNLC 12, it was released as Lucerne CO 2 during 2013 for general cultivation in Tamil Nadu.

PI-97

GENETIC VARIABILITY IN *Cenchrus spp.*

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A total of 36 genotypes of *Cenchrus* spp. including *C.ciliaris*, *C. setigerus* and *C. glaucus* were evaluated for genetic variability. Various quantitative traits like plant height, leaf length, leaf width, panicle length, internode length, green fodder yield/plant and the qualitative characters like panicle colour, anthocyanin colouration on node, internode and base of the plant, leaf blade attitude and seed fuzz were recorded. Wide variation was observed on both qualitative and quantitative characters. The colour of panicle ranges from white, brown, purple, dark purple and black. Anthocyanin colourations was noticed on nodes in lines VTCC8, VTCC5 and VTCC7 of *C. ciliaris* and in all the lines except CLC288, CLC13, CLC58, CLC82 and CLC265 of *C. setigerus* and no lines in *C. glaucus*. Discernible variation was observed for green fodder yield/plant (46.75-363.25 g) and 100 seed weight (141-552 mg). The GCV was higher than ECV for all the characters except for panicle length indicating low environmental influence on these characters. High PCV and GCV for green fodder yield/plant and 100 seed weight indicates existence of enormous variability for these characters. Heritability and GA as % of mean were almost high for all the characters insisting that there is a predominance of additive gene action and selection could be followed for improvement. The germplasm lines *viz*., VTCC8, VTCC4 and VTCC7 were found to be high yielding accessions with associated yield traits which could be used for future selection.

PI-98

STAY GREEN TRAIT IN SORGHUM (*Sorghum bicolor* (L.) MOENCH) FOR EXPLOITING DROUGHT TOLERANCE - A REVIEW

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Sorghum is an important source of food, feed, and biofuel, especially in the semi-arid tropics. Drought is the major constraint to sorghum production worldwide. Stay-green is one form of drought resistance mechanism. The important sources for stay green traits are observed in the cultures BTx642, E36-1 ,SC56, KS19 and QL41. In the 1980s the germplasm line B35 identified by Darrel Rosenow at Texas A&M University exhibited high levels of stay-green and lodging resistance. The most common source of stay green has historically been the sorghum line, B35 a member in the durra race. The four major Stay green QTL were identified in a variety B35 and it is designated as Stg1, Stg2, Stg3 and Stg4 as well as many additional minor QTL. Stg1 and Stg2 were mapped to sorghum chromosome 3.Stg3 is located on chromosome 2 and Stg4 on 5. In Ethiopia, four high yielding sorghum varieties (Meko, Gambella, Teshale and 76T1#23) have been identified as being susceptible to post- flowering moisture stress and breeding for the SG trait from B35 donor parent into the four varieties was initiated in 2006. The successful introgression of up to two SG-QTLs in the foreground individuals was noted. The individuals advanced will play a role in enhancing farmer's income through improved grain yield especially in the semi-arid regions. Thus the study provided useful evidence that the transfer of stay green QTLs from B35 into a senescent variety has the potential to enhance tolerance of post-flowering drought stress in sorghum.

PI-99

EXPLOITATION OF HETEROSIS AND COMBINING ABILITY IN TGMS BASED HYBRIDS (*Oryza sativa* L.)

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An investigation was carried out with the objective of evaluating the twoline hybrids for heterosis and combining ability using four TGMS lines namely TS09 12, TS09 22, TS09 28 and TS09 410 and thirteen testers by line x tester method. The checks used were Improved white ponni and CORH 3. The lines TS09 22, TS09 410 and the testers namely CO 43, WGL 14 and Improved white ponni were found to be good general combiner for most of the yield contributing traits. The magnitude of SCA variance was higher than the GCA variance in all yield contributing characters, which indicated the presence of non-additive gene action governing the traits and heterosis can be exploited for further improvement. Per se performance and general combining ability studies revealed that the exact potentiality of TGMS lines and testers. The hybrids TS09 12 X CO 43, TS09 22 X CO(R) 49, TS09 22 X CO(R) 50, TS09 22 X T1408.10, TS09 22 X G 14, TS09 28 X CO43 and TS09 410 X T 360 were found to be promising for heterosis breeding programme. Based on the SCA effects and heterosis, TS09 22 X T1408.10, TS09 28 X CO 43, TS09 12 X CO 43, TS09 22 X WGL 14 and TS09 22 X CO(R) 50 were identified as potential hybrids and these two line hybrid combinations could be utilized for commercial exploitation. The present investigation revealed that the TGMS system could be utilized for developing twoline rice hybrids.

PI-100

GRIFFING'S AND HAYMAN'S DIALLEL ANALYSIS FOR DEVELOPING BLAST RESISTANCE LINES IN RICE CULTIVARS (*Oryza sativa* L.)

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Rice is the most important staple food crop of more than half of the world's population. Blast disease caused by a fungal pathogen *Magnoportha grisea* Sacc. is one of the most important rice diseases affecting the yield. Study on the combining ability, gene action, heterosis and graphical analysis to suggest suitable breeding strategies was conducted. Nine parents were subjected to diallel crosses using the model I, method II. It was observed that the ratio of GCA to SCA variance was less than unity for the characters viz., number of productive tillers per plant, number of filled grains per panicle, thousand grain weight, grain yield per plant and harvest index indicating the predominance of non-additive gene action in the control of these traits which could be exploited through heterosis breeding.

Based on per se performance and gca effect, LFR 293 and BL 6 were identified as good parents and hence suggested for further recombinant breeding programme. Two hybrids namely BL 6 x CO 18 and BL 4 x CO 18 were found to be superior for grain yield and other components based on per se performance, sca effect and standard heterosis. Hence, advancing these hybrids and effecting selection in segregating generation would be helpful to develop high yielding varieties. Graphical analysis based on the position of the regression line showed that over dominance type of gene action for all the characters studied except number of productive tillers per plant.

PI-101

EFFECTIVENESS AND EFFICIENCY OF PHYSICAL AND CHEMICAL MUTAGENS INDUCING CHLOROPHYLL MUTANTS IN RICE

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Improvement in rice (*Oryza sativa* L.) needs broad genetic variability and the variability available to the breeder comes from spontaneous or artificially induced mutations. Physical and chemical mutagenesis has been used to raise the genetic variation in most of the crop plant species. An experiment was conducted to study the effect of gamma rays and Ethyl Methyl Sulfonate (EMS) in two quality rice genotypes of White ponni and BPT 5204. In this, frequency and spectrum of chlorophyll mutations, Mutagenic effectiveness and Efficiency, mutation rate of mutagens were estimated to study the nature and effect of both mutagens in two mega varieties of rice in India. The result from the study indicated that, *albino* was the predominant chlorophyll mutants occur in M_2 generations of White ponni and BPT 5204 at lower doses. The mutagenic effectiveness and efficiency were found to be higher 100 Gy of gamma radiation in both the varieties. The mutation rate of gamma rays (0.71) was recorded high in White Ponni in terms of effectiveness whereas mutation rate of EMS (0.67) was found to be higher in BPT 5204. In terms of efficiency, the mutation rate of gamma rays was registered higher based on injury (6.66) and sterility (13.88).

PI-102

BEST COMBINERS FOR DROUGHT TOLERANCE USING LANDRACES IN RICE (*Oryza sativa* L.)

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Among the osmotic stress drought is one of the important constraint to rice production. Present investigation was carried out in rice to select promising parents and their hybrids having potential tolerance to drought. A set of 10 parents comprising of six drought tolerant landraces *viz.*, Kallurundaikar, Kuliadichan, Kuruvaikalangiam, Mattaikar, Nootripathu, and Vellaichithiraikar and four high yielding rice varieties *viz.,* PMK 3, MDU 5, ASD 16 and ADT 36 were studied in L X T design to investigate the combining ability of parents and hybrids based on the genetic behaviour of various physio-morphological traits associated with drought tolerance. Variance due to general as well as specific combining ability, the additive and dominance genetic variances and their relative proportions for all the 13 characters under moisture stress condition revealed that dominance variance (s2 D) was of high magnitude for all the traits. Among the parents, Nootripathu, Kallurundaikar , and Vellaichithiraikar and PMK 3 were found to be the best general combiners, since they exhibited high *gca* effects for majority of drought tolerant and yield contributing characters. Two crosses *viz.*, Nootripathu x MDU 5 and Mattaikar x ADT 36 were found to be the best specific combiners for most of the drought tolerant and yield contributing traits including grain yield per plant.

PI-103

RICE GRAIN QUALITY FOR BETTER CONSUMER PREFERENCE

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Rice is the most important cereal of the globe, being the main source of energy and income for the majority of the world's population. Grain quality in rice is an important component determining domestic consumption and international trade. Major determinants of grain quality are grain size, shape, uniformity, milling percentage, head rice recovery, kernel chalkiness, translucency, colour and cooking properties. In Tamil Nadu medium slender fine grain rice varieties are preferred by consumers, farmers and traders. The proportions and structures of the two types of starch *viz*., amylose and amylopectin are the main factors that affect the cooking and pasting properties of rice. Rice samples differing in amylose content exhibited various pasting temperatures, time and viscosity changes. Grain quality characters are interrelated among themselves which in turn decides the final cooking and eating characteristics. Grain quality interrelationship study conducted using 35 genotypes of rice revealed that grain quality characters *viz*., kernel length, alkali spreading value, elongation ration manifested positive correlation with kernel length after cooking, while head rice recovery exhibited negative association. Kernel length was positively and significantly correlated with L/B ratio and in contrast kernel breadth negatively correlated with L/B ratio. Specific combinations of correlated characters and its inheritance will decide upon preferred/expected qualities of rice genotypes. Intermediate amylose content, intermediate gelatinization temperature, soft gel consistency and taste are the special traits for consumer preference. Therefore in rice breeding program for evolving quality rice, parents with best grain quality characteristics is important.

PI-104

GENETIC VARIABILITY STUDIES IN ELITE GREEN GRAM (*Vigna radiata* (L.) WILCZEK) GERMPLASM

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Greengram, an important grain legume of the arid and semiarid regions has enough genetic diversity both for quantitative and qualitative characters. A total of 40 Green gram germplasm were evaluated during *rabi*2012 at Agricultural College and Research Institute, Madurai to determine the genotypic and phenotypic co-efficient of variation (GCV and PCV), heritability and genetic advance. The accessions were planted in Randomized Block Design (RBD) with two replication adopting a spacing of 30 x 10 cm. Data were recorded on various morphological characters such as days to 50 % flowering, plant height (cm), Number of branches per plant, Number of clusters per plant, Pod length (cm), Number of pods per plant, Number of seeds per pod, Hundred Seed weight (g), Seed yield per plant (g). A wide range of variability both at genotypic and phenotypic level was observed for all the characters studied. The difference between PCV and GCV was low for all the traits studied, which indicated little influence of environment over phenotype of the traits. High heritability coupled with high genetic advance observed for the all the characters studied indicates that these traits are under the influence of additive gene action. Selection based on these characters would be effective for future crop improvement programme.

PI-105

PER SE PERFORMANCE OF PARENTS AND HYBRIDS IN BLACK GRAM (*Vigna mungo* (L.) HEPPER)

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Among pulses, black gram [*Vigna mungo* (L.) Hepper] is one of the important legumes of India, grown under diverse conditions. It is essential to develop varieties with high yield potential. The *per se* performance of parents may not necessarily reveal to be a good general combiners for breeding programme. Combing ability analysis is an important and powerful tool for selecting the parents. A study was carried out in Black Gram at Agricultural College and Research Institute, Killikulam, to identify the potential parents, superior cross combinations and to formulate breeding strategies for yield improvement. The experimental materials comprised of ten lines and five testers. These parents were crossed in line x tester mating design to synthesize fifty hybrids, the hybrids along with their

fifteen parents were evaluated for eleven traits namely, days to 50% flowering, plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant, total dry matter production and harvest index were evaluated. The *per se* performance of parents revealed the superiority of IPU.2006-01 and WBG 26 among lines and VBN 5 among testers. Considering both *per se* performance and *gca* effects crosses involving the parents IPU.2006-01 and IPU-02-33 would result in improving the component traits besides seed yield. The study was undertaken with the aim of gathering information on this aspects and to select suitable parents for further breeding programme.

PI-106

MALE STERILITY IN SESAME (*Sesamum indicum* L.) - PRESENT STATUS, CHALLENGES AND FUTURE PROSPECTS

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Sesame (*Sesamum indicum* L.) is one of the ancient oilseed crops grown in several countries of Asia and Africa. Being an often-cross pollinated crop with very high level of heterosis, it would be feasible to exploit hybrid vigour for higher productivity. For successful and commercial exploitation of heterosis, male sterility is very much essential. Attempts were made earlier to develop both genic male sterility and CGMS systems, but were unsuccessful. With this background, a research work was initiated at Regional Research Station (TNAU), Vridhachalam with the objective of developing stable male sterile lines through wide hybridization. Crosses were effected between the wild species *Sesamum malabaricum* as female parent and two popular varieties *viz*., VRI (Sv.) 1 and VRI (Sv.) 2 as male parents. About 9 and 17 interspecific hybrid plants were successfully recovered from two crosses viz., *S. malabaricum* x *S. indicum* cv. VRI (Sv.) 1 and *S. malabaricum* x *S. indicum* cv. VRI (Sv.) 2, respectively. The mean pollen sterility was observed as 80.5 and 84.1 per cent in respective crosses. At present, a total of 44 lines of *S. malabaricum* x *S. indicum* VRI (Sv.) 1 and 25 lines of *S. malabaricum* x *S. indicum* VRI (Sv.) 2 representing BC_4F_1 generation exhibiting more than 93% sterility were generated. In spite the present study moves towards the expected outcome of developing stable male sterile lines, it also poses serious challenges. Modern and innovative approaches that would be of potential alternative to the existing methods in future are discussed.

PI-107

COMPARATIVE EFFECTS OF MUTAGENS GAMMA RAYS AND EMS ON MUTAGENESIS OF ADT (R) 47 RICE VARIETY

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A study was taken up to resolve the comparative effectiveness of gamma ray and EMS to generate desirable mutants in indica rice cultivar. The rice variety ADT (R) 47 were irradiated at 200,250 and 300Gy of gamma rays and with EMS treatment in 100, 120, and 140mM concentrations. 100 selected panicles based on panicle weight in each of the treatments of gamma and EMS in M_1 were forwarded to M_2 generation and selected the mutants. In M_1 generation, germination percentage, seedlings survival percentage, pollen fertility, plant height, seed fertility showed a dose dependent reduction for both the mutagen. The injury of the plant is pronounced in 300 Gy of gamma ray and 140mM of EMS. A total of 365 and 182 mutants were selected from Gamma and EMS treatments respectively. The notable features of mutants from gamma ray are earliness (flowering - 82 to 111 days), well exerted panicle (-3.1 to 2.3 cm), grain shape difference and dwarfness (59 to 95 cm) More viable mutants for earliness and panicle emergence was obtained in 200 Gy dose and 250 Gy for plant height rather than 300 Gy.The rice genotype ADT 47 is sensitive to gamma ray than EMS. LD 50 dose is 250 Gy for gamma ray and 120mM concentration for EMS in seed mutagenesis. Seedling survival and pollen fertility is greatly affected by higher doses of gamma ray (300 Gy) than EMS(140 mM). More viable mutants were obtained only in 200Gy of gamma ray than EMS treatments.

PI-108

STUDIES ON COMBINING ABILITY ANALYSIS IN SESAME (*Sesamum indicum* L.)

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Sesame (*Sesamum indicum* L.) is one of the most important and conventional oil seed crops of india next to groundnut. Combining ability studies are useful in classifying parental lines in terms of their hybrid performance. The present investigation was carried out through L x T design with 7 lines and five testers for yield and yield contributing characters *viz*., Days to 50 per cent flowering, Plant height, number of branches per plant, number of capsules on main stem, number of capsules on main branches, number of capsules per plant, number of seeds per capsule, 1000 seed weight, oil content and single plant yield. The analysis of variance showed significant differences among the genotypes, for all ten traits The parents NIC 7937, NIC 7907, NIC8010 and TMV 3 were considered as better parents based on gca effect for most of the characters studied. The hybrids NIC 7936 x VRI 1,

NIC7907 x TMV 3, NIC 7936 x TMV 3, NIC 7907 x SVPR 1, NIC7933 x TMV 3, NIC 7908 x CO 1 and NIC 7936 x CO 1 had significant sca effects for majority of the traits. So these hybrids can be considered as suitable for recombination breeding for deriving superior segregants for the traits studied.

PI-109

MOLECULAR MARKER ANALYSIS FOR SEED YIELD AND COMPONENT TRAITS IN SUNFLOWER

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Sunflower is a major oilseed crop gaining paramount importance in the world and ranks next only to soybean and groundnut in the total world production of oil seeds. Molecular markers in applied breeding programs facilitate the appropriate choice of parents for crosses to map or tag the gene blocks associated with economically important traits often termed as Quantitative Trait Loci (QTLs). Single-marker analysis (also 'single-point analysis') is the simplest method for detecting QTLs associated with single markers. Among the 141 F_5 individuals, only 94 individuals were subjected to determine the association of marker to the respective phenotype. Among the 50 SSR markers, a total of 29 SSR markers were found to be linked to various traits. The number of associated marker varies from six SSRS (head diameter and seed color) to one SSRS (stripe on margin and stripes between margins). The adjusted R^2 for the regression equation varies from 3.2 % to 29.8 %. Two traits namely days to flowering (ORS509) and seed colour (ORS533) recorded above 20 per cent R2 value. Hull weight (ORS785) recorded 11.5 per cent R^2 value. The quick discovery and transfer of these QTL from non-adapted to adapted germplasm ultimately opens the door for the expansion of the genetic base of sunflower.

PI-110

STUDIES ON INFLUENCE OF *Triticum timopheevi* CYTOPLASM IN WIDE HYBRIDS

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Wheat is the major cereal of the world and exceeds any other grain crops in acreage and production. The different species of genus *Triticum* are diverse in their phenotypes adapted to a wide range of environments and hold rich pools of genetic variation which could be utilized to improve the common wheat. The present study was under taken to investigate the crossability behaviour of *T. timopheevi* with all the cultivated wheats. This type of study, besides providing recombinants, would also provide

information on genomic relationship and to investigate the usefulness of wild species in improving the *T. dicoccum, T. durum, and T. aestivum* wheats. The crosses attempted using *T. timopheevi* with durum resulted in hybrids which showed normal cytological behavior during meiosis. However, with the other two groups, it showed some abnormalities in diakinesis, anaphase I and in tetrad formation owing to irregular chromosome alignment and separation. All the three hybrids obtained using *T. timopheevi* with cultivated species were completely sterile. The meiotic behaviour of the F_1s from the crosses of *T. timopheevi* with *T. dicoccum* and *T.aestivum* as parent was abnormal when compared to the F_1s from the cross between *T. timopheevi* and *T.durum* which had a normal meiotic behaviour. In spite of all these differences, all the plants were fully sterile. This shows that the cytoplasm of *T. timopheevi* since being used as female has certain influence on the fertility status of the resultant hybrids irrespective of their ploidy status and pairing behavior.

PI-111

POPULATION STRUCTURE ANALYSIS OF RICE (*Oryza sativa*) GERMPLASM USING MICROSATELLITES

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The abundant variation of the rice germplasms provides an important reservoir of genetic diversity and potential sources of beneficial alleles for rice breeding. Advances in DNA research and the greater flexibility of DNA markers facilitated to use them in evaluation of genetic variability and genetic relationships. Microsatellites replaced all the other marker systems because of their abundance, locus specificity, polyallelism, wider genome coverage and co-dominant nature. A set of 60 rice accessions were used as materials for SSR marker analysis. The marker data thus generated were subjected to cluster analysis. Sequential Agglomerative Hierarchial Non-overlapping clustering was performed on similarity matrix using Dice co-efficient for binary data, utilizing the Unweighted Pair Group Method with Arithmetic Averages method. Data analysis was done using NTSYSpc version 2.02 to group the 60 accessions. Cluster analysis was used to group the varieties and to construct a dendrogram. All 60 rice accessions were classified using 45 microsatellites. A total of three distinct groups resulted out of the analysis. The clusters formed were very distinct and with a clear pattern. Among the three clusters, Cluster I possessed PTB33, PTB41 and Rathu Heenati, BG360-2 along with Pusa Basmati, IR50, ADT37 and ADT43. Cluster II was found to be the largest having 41 accessions. Cluster III was found to possess 10 accessions which included Karanellu, Kathanellu, Rascadam and Gandakasala. The aromatic rice accessions *viz.* Pusa Basmati and Basmati370 were found to be in extreme in Cluster I and Cluster III.

PI-112

STUDIES OF CHLOROPHYLL AND MACRO MUTANTS IN GAMMA IRRADIATED AND ETHYL METHANE SULPHONATE TREATED M_2 GENERATION OF BLACKGRAM (*Vigna mungo* (L) HEPPER)

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The genetically pure seeds of blackgram (*Vigna mungo* (L) Hepper) cv. MDU (Bg) 1 and VBN (Bg) 4 were subjected to gamma irradiation (200, 250, 300 and 350 Gy) and EMS (20, 30 and 40 mM). The M_2 population was cautiously scrutinized for various viable macromutations from the date of emergence until the attainment of crop maturity. A range of mutants were recognized and tagged for separate harvesting. The mutagens inducing chlorophyll mutants in M_2 generation were scored which is an index for assessment for genetic effect of mutagenic treatments. Wide spectrum of chlorophyll and viable macro mutants affecting almost all the plant parts and were isolated. The chlorophyll mutants consisting of albino, xantha, chlorina, viridis and xanthaviridis. The increased cholorophyll mutation frequency was noticed at higher doses which may be attributed to the chromosomal aberrations or saturation in the mutational events which may result in the elimination of mutant cells during growth. The Viable macro mutants including Tall mutant, Dwarf mutant, Determinate type, Trailing type mutant, Bushy type, Spreading type, Early type, Late type, Narrow leaf mutant, Broad leaf mutant, lenghty pod mutant, Profuse pods in cluster, Bold seeded mutant, Top poding mutant, High yield mutant, Top Branching, Tetra leaves mutant, Penta leaves mutant, Synchronized maturity and Sterile mutants. Higher frequency of chlorophyll were observed in gamma irradiated treatments in both cultivars than EMS treated populations.

PI-113

IDENTIFICATION OF RICE GENOTYPES FOR DRY DIRECT SEEDED AEROBIC CONDITION

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Thirty six early duration rice genotypes including hybrid check (US 323) and local check (ADT 36) were evaluated under dry direct seeded aerobic condition during Kharif, 2013 at Agricultural Research Station, Pattukkottai. Observations on early vigour score, per cent emergence, Plant height and tillers/plant 30, 45 DAS and at the time of harvest, leaf length, width of 3rd leaf from the top, 50% flowering, panicles/m2, panicle length, panicle weight, spikelet fertility, 100 grain weight and grain yield/plot were recorded. The genotypes, ADV 1312, SVH 026, Rasi and NPH 150 recorded highest

fertility percent of 83.0 to 79.0 per cent spikelet fertility. The entry, IET 22075 which possess fine grains recorded the lowest 100 grain weight of 1.73 g. Twenty six entries out yielded both the hybrid check, US 323 and the varietal check, ADT 36 (2786 kg/ha) and the grain yield/plot ranged from no grain yield (NP 9138) to 3.350 kg (INH 10008). From this study two genotypes INH 10008 and RXEL 15 which recorded 5234 kg/ha and 5130 kg/ha in 105 and 100 days were found to be highly promising. Also the genotypes *viz.,* Bio 648, ADV 1312, ADV 1314, RXEL 16, NPH 909, KPH 63, SVH 026, Arize 61298 and Rasi performed better than the hybrid and varietal checks.

PI-114

GENETICS OF SALT TOLERANCE IN RICE (*Oryza sativa* L.)

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Salinity is a major abiotic stress affecting agriculture production worldwide. Since rice is a major cereals crop, an experiment was conducted in 116 genotypes of released rice varieties, advanced breeding lines and landraces, to study the performance of genotypes for seedling stage salt tolerance under hydroponics. The genotypes were raised in both normal and salinity stress condition in Yoshida nutrient solution culture and the pH of the solution is adjusted daily to 5.0 to 5.1. Salinization was imposed on 14th day after sowing and EC was adjusted to 12 dSm^{-1} having the tolerant check as Pokkali and susceptible check as IR 29. Salinity score was recorded from 8 to 16 days days after salinization and the tolerant, moderately tolerant and susceptible genotypes were identified. Salinity score was subjected to normality test by using STAR package and distribution pattern was found to be normal which indicates the quantitative nature of the trait. Based on the salinity score evaluation system two genotypes from each class of tolerance were selected such as for tolerance FL478 and VTL 1, moderately tolerant IR 64 and ADT 36, susceptible ADT 45 and improved white ponni. These selected varieties were used as a parents and mated in half-diallel mating design to study the genetics of salt tolerance for further analysis.

PI-115

INTROGRESSION OF *SUB1* LOCUS INTO DROUGHT RESISTANT LANDRACES OF RICE (*Oryza sativa* L.) TO IMPROVE CLIMATE RESILIENCE

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The frequent occurrence of abiotic stresses such as drought and submergence has been identified as the key to the low productivity of rainfed ecosystems. Rain-fed fields are prone to flooding and drought due to inadequate water management (Bailey-Serres *et al.,* 2011). The coastal districts of

Tamil Nadu namely Nagapattinam, Trivarur districts are prone to flash floods and Ramanathapuram and Sivagangai districts are drought prone, which do not have any specific rice varieties. Opportunities to combine such adaptive traits have recently become feasible with the progress made in developing molecular tools in breeding. Improvement of combined tolerance to submergence and drought would substantially increase rice productivity while sustaining water resources and soil quality (Bailey-Serres *et al*., 2011). Hence the present study was undertaken in which the rice variety, Swarna-S*ub1* was crossed with two land races Norungan and Kallurundaikar, which are drought tolerant (Robin *et al* 2004). BC_1F_2 progenies were developed during 2012 by backcrossing with land races as recurrent parents with corresponding F_1s to generate BC_1F_1. MAS resulted in 41 plants with heterozygous in Kallurudaikar cross and 22 in Norungan cross forwarded to BC_1F_2 respectively. The marker RM219, when used for genotyping, 25 plants observed with *Sub1* allele in homozygosity, 42 heterozygotes and 83 with land race allele. Introgression of *Sub1* allele in the BC_1F_2 progenies was evident from phenotypic screening under submergence.

PI-116

IDENTIFICATION OF MAINTAINERS AND RESTORERS USING WA SOURCE CMS LINES IN RICE

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A study was undertaken for the development of new non aromatic CMS lines and to identify the fertility restoration ability of different CMS lines of wild abortive cytoplasm for hybrid rice breeding. The materials for the present study consists of 4 CMS lines viz., TNAU CMS 2 A, COMS 23 A, COMS 24 A, CRMS 31A and 75 male parents. Crosses were effected between CMS lines and male parents and hybrid combinations were successfully synthesized. One hundred and thirty hybrid combinations were raised in test cross nursery along with its parents and checks CORH 3, CORH 4, CO 50 and CO51 . From this study eighty testers were found to be effective restorers and eighteen as effective maintainers and thirty two as partial restorers. The promising maintainers identified were ARB 6, JGL 17189, CB 08702, JGL 17233, JGL 17196, CB 06563, CB 06803, JGL 17190, CR 3636-5-1 for the CMS line TNAU CMS 2A and AU 8010, CB 104/1801, CB 132/1819, CB 150/1526, JGL 17233 for the CMS lines COMS 23 A and COMS 24 A. The tester JGL 17196 behaved as an effective maintainer for the CMS line TNAU CMS 2A and effective restorer for the CMS line COMS 23 A. Among the 18 potential maintainers identified back crossing was done with a recurrent parent and the progenies are under conversion programme for the development of new non aromatic CMS lines and the effective restorers identified can be utilized in developing new hybrid combinations for commercial cultivation.

PI-117

HETEROSIS AND COMBINING ABILITY FOR QUANTITATIVE TRAITS IN BARNYARD MILLET (*Echinochloa frumentaceae* (ROXB.) LINK)

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The use of heterosis for getting high yield with improved quality has been largely used in cross-pollinated crops. In self- pollinated crops, evidences are available to confirm the potential use of heterosis for commercial exploition as reported by Nirmalakumari and Vetriventhan (2009) in barnyard millet and Parashuram *et al.,* (2011) in finger millet. Hence exploiting of local varieties for nutritive value in addition yield is foremost important to the breeder. In Barnyard millet, the heterosis and combining ability for yield and yield attributing characters were studied through Line x Tester mating design using six lines and four testers. Combining ability analysis exhibited high *sca* effects for all the traits studied indicating the predominant role of non-additive gene action. The lines CO 2 and ACM 110 and the testers ACM 12 and PMK 331 had recorded high *per se* performance and *gca* values for yield and most of the yield contributing characters studied. The cross combination CO 2 x ACM 12 exhibited high *per se* performance and *sca* effect for eight traits. Significant *gca* effects and non significant *sca* effects were recorded in ACM 110 x ACM 11, ACM 110 x ACM 12, CO 2 x ACM 11 and CO 2 x PMK 332 and these could be used for recombination breeding. The cross combination, CO 2 x ACM 12 exhibited higher *per se* performance, *sca* effects and standard heterosis for most of the traits over their parents. Hence this cross combination could be further utilized for heterosis breeding.

PI-118

COOKING CHARACTERISTICS OF RICE (*Oryza sativa* L.) GERMPLASM

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Rice (*Oryza sativa* L.) is the most important cereal crop and the staple food of over half of the world's population. Higher grain yield is essential for food security. However, better grain quality in rice determines market value and consumer preference. So apart from increasing yield breeder are also focusing on grain quality traits. In rice quality preference varies among different rice eating people. The quality aspects in rice can be grouped into two major categories viz., milling qualities and cooking qualities. Studies were conducted on 45 rice genotypes to assess the grain quality and cooking quality characters. The genotypes viz., Jaishree, ADT 43, JeevanSamba, Varappu Kudaichan and Gamma 278 were performed better for grain and cooking quality characters. Jaishree performed in three traits viz., Length breadth ratio, linear elongation ratio and gel consistency. ADT 43 performed

in length breadth ratio, linear elongation ratio, volume expansion ratio and gel consistency.Jeevan Samba performed three characters viz., linear elongation ratio, volume expansion ratio and gel consistency. Varappu Kudaichan performed two traits viz., head rice recovery and linear elongation ratio. Gamma 278 performed in head rice recovery. The varieties Jaishree and ADT 43 can be used for varietal improvement programme. The land races Jeevan Samba, Varappu Kudaichan and the mutant Gamma 278 were identified as elevated lines which can be used for the crop improvement programme and varietal development programme.

PI-119

GENETIC EVALUATION OF AEROBIC RICE CULTIVARS FOR YIELD AND YIELD COMPONENTS UNDER DIFFERENT WATER REGIMES

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Fifty seven aerobic rice genotypes were evaluated along with two checks Apo and ARB 6 under aerobic and irrigated conditions in alpha lattice design. Under aerobic conditions the genotypes *viz.,* CB-00-15-23, EC 638078, CR 2597, CB-08-709-2, CB-06-803-2, CB-05-758-3, MAS ARB 25, CR 2632-IR 83614-503-B recorded more number of productive tillers, higher panicle harvest index and ultimately more grain yield/ha. Under irrigated condition, all these genotypes performed better and possessed relative grain yield of above 75 %. Significant variation for plant production traits were observed among the aerobic cultivars. All characters showed low GCV than PCV indicating the influence of environment on these characters both under aerobic and irrigated conditions Heritability estimates ranged from 79 % for plant height to 16.0 % for panicle harvest index under aerobic condition where as in irrigated condition it was from 73 per cent for plant height to 12 % for number of tillers per plant. Range of genetic advance as per cent of mean was from 25.3 for days to fifty percent flowering to 3.0 for panicle harvest index where as in irrigated condition it was from 23.2 for plant height to 5.3 for panicle harvest index. High to moderate values of heritability and genetic advance were observed for days to 50 per cent flowering, panicle length, productive tillers per plant and plant height. In the selection of genotypes, maximum importance should be given to these traits in order to obtain high genetic gain under selection.

PI-120

GENETIC ANALYSIS OF YIELD COMPONENT TRAITS FOR THE IMPROVEMENT OF DROUGHT TOLERANCE IN RICE (*Oryza sativa* L.)

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An investigation in rice (*Oryza sativa* L.) was carried out subjecting eight lines and five testers to

Line x Tester mating. The hybrids exhibited significant variation among themselves for all the 15 characters studied. The Line x Tester analysis revealed the importance of non-additive gene action in controlling all the traits *viz*., days to 50 per cent flowering, plant height, number of productive tillers per plant, number of grains per panicle, hundred grain weight, root length, root dry weight, root : shoot ratio, root volume, leaf rolling, chlorophyll stability index, relative water content, proline content, harvest index and grain yield per plant. The selection based on plant height, number of productive tillers per plant, number of grains per panicle, leaf rolling and harvest index will bring about an increase in yield under drought stress as they expressed significant and positive correlation with grain yield. Partitioning correlation co-efficient into direct and indirect effects by path coefficient analysis revealed that number of productive tillers per plant, number of grains per panicle, hundred grain weight and harvest index were the major yield contributing traits under drought conditions and have to be given importance in selection process for yield improvement under drought stress situations.

PI-121

ANALYSIS OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN WINGED BEAN (*Psophocarpus tetragonolobus* (L.) DC.) FOR VEGETABLE POD YIELD AND ITS COMPONENT CHARACTERS

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Twenty one diverse genotypes of winged bean were evaluated for genetic variability during 2013-14 for 12 traits under Kerala conditions. The analysis of variance showed significant difference among all the genotypes for yield and yield contributing traits. High values of PCV and GCV were observed for quantitative characters like yield per plant, pods per plant, days to first flowering, days to 50 percent flowering and primary branches per plant also the GCV was very near to PCV for most of the characters studied, indicating a highly significant effect of genotypes on phenotypic expression with very little effect of environment indicating ample scope for selection of genotypes from available germplasm for the improvement of these traits. The heritability estimates were high for the traits like days to first flowering, days to 50 percent flowering and days to first harvest which is coupled with high genetic advance over mean indicates the presence of flexible additive gene effects and will be a useful criterion for selection for these characters. Based on genetic parameters and performance studies PT-21, PT-1 and PT-4 were selected as superior genotypes for further crop improvement programme.

PI-122

EARLY GENERATION SELECTION FOR GRAIN QUALITY CHARACTERS IN RICE (*Oryza sativa* L.)

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Grain quality has always been an important consideration in rice variety selection and development. The cooking quality is a complex character which is very much influenced by physical, physico-chemical characteristics of rice grain (Kalaiyarasi *et al.*, 2007). The awareness on the grain quality among the traders and the consumers is increasing day by day and hence research has to be focused on the rice grain quality. Among the many quality traits, linear elongation ratio is considered as very important since the rice value is fixed mainly based on this cooking quality. Samina Asghar *et al.*, (2012) reported that rice elongation ratio has a significant relationship with other cooking characteristics. Hence, an attempt was made to study the genetics of linear elongation ratio in the specific cross, Pusa basmati 1 x CB 08 504. Pusa basmati is known for its aroma and elongation with 1.93mm elongation ratio, 70 % milling and 55% head rice recovery. The rice culture CB 08504 has early duration with fine grain qualities. Sarma *et al.*, (2014) reported significant marker (RM142 on chromosome 4) associations for grain length elongation ratio. Such study helps to isolate useful genotypes at an early generation itself besides physical evaluation of linear elongation ratio.

PI-123

ANALYSIS OF ROOT ASSOCIATED WITH PHOSPHORUS DEFICIENT TOLERANCE IN RICE (*Oryza sativa* L.)

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Hundred heterogeneous F_5 lines were randomly selected from the P-deficient field, derived from hybridization between two selected rice genotypes *viz.,*Gobindabhog and Satabdi, collected from RRSS, Sekhampur, BCKV, West Bengal. Two contrasting bulks, comprising of ten lines in each, were made from these RILs based on the variation in the number of filled grains per panicle. These samples were treated in hydroponic culture using Hogland solution with P-replete and P-deplete condition. Objective of this study was to identify the root associated parameters at the seedling stage linked with phosphorus deficiency tolerance. Average filled spikelet per panicle in two extreme bulks was 38.3 and 131.8 and called them as low and high bulk respectively. Dry mass weight of root and shoot, root length and P-accumulation ability were estimated from each member of the selected lines at the seedling stage. Estimation was made both at P-sufficient as well as P-deficient solution in the laboratory condition. Root length and root dry mass weight among the two bulks did differ significantly neither in P-sufficient nor in deficient solution. On the other hand, shoot dry weight was increased significantly in P-depleted condition in low bulk but remain same in other bulk. So, lower ratio of P-accumulation at P-sufficient by deficient solution at the seedling stage may be considered for selection of high yielding lines for P-deficiency tolerance in rice.

PI-124

PERFORMANCE OF MID EARLY AND MEDIUM DURATION RICE GENOTYPES IN IRRIGATED ECOSYSTEM FOR GRAIN YIELD AND ITS ATTRIBUTING TRAITS

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An experiment was conducted at Tamil Nadu Rice Research Institute, Aduthurai to assess the performance of 28 mid-early and 26 medium duration rice genotypes under CSISA. Observations were recorded for 12 quantitative traits. In Mid early group, Sabour Surhit recorded the maximum productive tillers (20.6 nos.). The differences between unproductive and productive tillers were found to be narrow for the genotypes RYC 213, RYC 221 and RYC 487. Three cultures *viz.*, RYC 248, AD 08138 and UPR 2805-14-1-2 had long panicles of above 26.0 cm. Pant Dhan 22 recorded maximum number of secondary branches (44 nos.) followed by IET 22075 and AD 08132. The genotype NP 9167 recorded the maximum spikelet fertility of 88.3%. Two genotypes *viz.*, PD 22 and RYC 213 had highest 100 grain weight of 2.8g. Regarding grain yield, AD 08132 and Lalat ranked first and second with an increase of 12.7 and 11.2 per cent respectively over the best check ADT 39 (5318 kg/ha). In Medium group, Rajendra Sweta recorded maximum productive tillers (20.1). The local check ADT(R) 46 had long panicles (27.1 cm) followed by RYC 643. The secondary branches per panicle were high in PAU 3791-26-3-3 (39.0) followed by AD 09442 (37.3). The genotype RAU 724 (6865 kg/ha) ranked first and surpassed ADT (R) 46 and NDR 359 by 8.8 and 23.5 per cent respectively. The next best entries were RYC 255 (6706 kg/ha) and Akshayadhan (6627 kg/ha).

PI-125

GENETIC DIVERSITY AND HETEROSIS IN CASTOR

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Castor (*Ricinus communis* L.) is important oilseed crop of India. Castor is monotypic with only one cultivated species (*Ricinus communis*L.) It is highly cross pollinated crop. According to the available literature it is indigenous to eastern Africa most probably Ethiopia and india is important center of diversity. Hence proper utilization of available diversity is important to generate heterotic hybrids. At

Tapioca and Castor Research Station, Yethapur diversity studies using 32 castor genotypes utilizing ten yield components by applying D2 statistics has been done. The lines formed 7 clusters with varying inter cluster distances. Total of 52 heterotic hybrids were generated utilizing the pistillate lines and monoecious lines from diverse groups. Lines from distant clusters yielded more heterotic hybrids. Among them one heterotic hybrid namely YRCH 1214 with strikingly dissimilar parents performed consistently superior for 3 seasons in station trials and promoted to Multi Location Testing for further evaluation and release. The hybrid YRCH1214 is medium tall with spreading type with 16 node and having light red stem color. The hybrid recorded 5o days of 50 % flowering and having of 100 seed weight of 36 g with the seed yield of 1923 kg/ha. The castor test hybrid YRCH 1214 has recorded highest average seed yield of 1923 kg / ha against best check YRCH1 with seed yield of 1119 kg / ha in station trails.

PI-126

GENETICS OF BITTERNESS IN CUCURBITACEOUS VEGETABLE CROPS

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Bitterness has been reported in about 90 of the approximately 825 known species of the Cucurbitaceae. Bitterness is preferred by consumers in case of bitter gourd, but it is not favored in case of cucumber, summer squash etc. Cucurbitaceous vegetables are important because they are good source of carbohydrate and fiber. They have medicinal property like antimicrobial, anti-cancer, anti-diabetic etc. The seeds of most Cucurbitaceae are not bitter, but a few hours after germination, very high concentrations of bitter principles may be encountered in the root tips. Cucurbitane type compounds like cucurbitacin, momordicine are responsible for bitterness in varieties of cucurbits. The cucurbitacin occur in all parts of the plant namely leaves, stems and roots of most cultivated varieties, at varying amounts of these compounds. Bitterness does not accumulate uniformly in the Plant. The compounds are likely to be more concentrated at stem end than at blossom end of the fruit. In cucumber, Bi, bi gene are responsible for foliage bitterness and Bt, bt genes, for fruit bitterness. Bi gene is present on chromosome 6 while Bt gene is present on chromosome 5 in cucumber. Loose linkage is found between bitterness gene Bi and mutant leaf (golden) gene v-1 and bitter free gene and gynoecy gene F in cucumber. "Improved Long Green" is the best variety which can be used for breeding for non-bitter cucumber. In summer squash, Cu gene is responsible for bitterness. In Luffa Cylindrica and Luffa actangula, Bi is responsible for bitterness and s is suppressor gene.

PI-127

GENETICS OF RED KERNEL MUTANT (*Arachis hypogaea* L.)

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A Spanish bunch groundnut *(Arachis hypogaea* L.) cultivar VRI 2 with rose testa was irradiated with 30 kR of gamma rays. The M_1plants were harvested individually and raised as M_2 plant to progeny rows. One single plant in the M_2generation exhibited kernels with red colour testa (Red Kernel Mutant). The selected single plant was raised as M_3progeny rows and found to be true breeding for the testa colour. The mutant was phenotypically similar with the cultivar VRI 2 for all the morphological, pod and kernel characters except the seed coat colour. An investigation was made to understand the inheritance of red seed coat colour of the mutant. Crosses were made between red kernel mutant (RKM) and the cultivar VRI 2 at the Regional Research Station, Vridhachalam during *kharif* 2012. In the F_1 generation all the plants possessed red colour testa indicated that red colour is dominant over rose. The F_1plants were harvested individually and raised as plant to progeny rows in the next generation. In the F_2generation, the plants were segregated as 83 red and 28 rose colour testa types fitted in 3:1 ratio, indicating the role of single dominant gene control in the expression of seed coat colour in the mutant.

PI-128

DIFFERENTIAL ELIMINATION OF CHROMOSOMES IN INTERSPECIFIC HYBRIDS OF SUGARCANE DERIVED WITH DIFFERENT CYTOTYPES OF *Saccharum spontaneum* L.

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Saccharum spontaneum, L.(a wild relative of sugarcane) attained revolutionary credit in plant breeding history as it has been the first wild species involved in the successful development of commercial variety (Co 205) in 1912. It exists with about 41 cytotypes from 40 - 128. The cytotype 2n=64 is predominantly distributed and utilized. In order to understand the dominance of the cytotype 64 over other cytotypes, cytological analyses of 52 hybrids of 7 crosses involving commercial varieties of sugarcane and different cytotypes of *S. spontaneum* viz., Co 1148 (2n=114) x *S. spontaneum* (2n=60, 64, and 80) and CoH 114 (2n=108) x *S. spontaneum* (2n=64 and 72) were made. It revealed n+n transmission with aneuploidy in all hybrids. The progenies derived with the cytotype 2n=64 were stable with the expected chromosome number or with elimination of few chromosomes (1.6), while the other cytotypes involved hybrids had elimination of chromosomes from 2-15 (10.8). In CoH 114

x SES 375 (2n= 64), two clones had 2n= 86 as the expected number. The hybrid 04-643 derived with 2n=72 had elimination of 10 chromosomes. Two hybrids (04-1247 and 04-1257) of Co 1148 x SES 404 (2n=64) exhibited with 2n=89 without loss. Elimination of 4-15 chromosomes was noticed with the cytotype 2n=60 and 80. The hybrid 04-1326 obtained with 2n=80 had 2n=82 with deletion of 15 chromosomes.This study indicates stable progenies with the cytotype 2n=64 which imparts its complete genomic complement so as to incorporate all available desired genes.

PI-129

SYNTHESIZING AND EVALUATION OF SINGLE CROSS MAIZE (*Zea mays* L.) HYBRIDS SUITABLE FOR WATER LIMITED ENVIRONMENTS

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Maize (*Zea mays* L.) is the most versatile food crop of global importance. Drought is the most important constraint across the rainfed lowland and upland environments, covering about 70 per cent of the maize production area in India. In this investigation, an attempt was made to develop high yielding single cross maize hybrids suitable for water limited environments. Crossing block was raised with nine promising drought tolerant inbred lines *viz.,* VIM 92, VIM 140, VIM 147, VIM 189, VIM 197, VIM 201, VIM 244, VIM 280 and VIM 321 with the three testers VIM 15, VIM 58A, VIM 371 in line x tester mating design. A total of 27 hybrids were synthesized by manual detasseling and crossing. These hybrids along with three checks *viz.,* CoH(M)5, Monsanto 900M Gold and Hishell were evaluated in RBD with three replications in rainfed situation at Maize Research Station, Vagarai during rabi 2009-2010. Selection was made based on the plant type, ASI, stay green trait and yield. Nine hybrids out yielded than all the three checks in terms of yield. Among them VMH 09020 (4931kg/ha) recorded the best performance followed by VMH 09024 (4517kg/ha) and VMH 09019 (4392kg/ha) over the best check COH(M)5 (3978 kg/ha) and expressed lesser ASI (1-3 days). ASI is the crucial factor in developing drought tolerant hybrids, since maize is highly cross pollinated and possess dicliny and heterogamous (protoandry) nature. These hybrids could be popularized in water limited environments after assessing their stable performance over varying environments in increasing the productivity.

PI-130

HETEROSIS STUDIES IN CHILLI (*Capsicum annuum*)

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The experiment was carried out in a diallel model at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani (2012-14). Thirty crosses were developed by crossing 6 parents in chilli. All the crosses were evaluated along with the parents and check in RBD with three replications. Analysis of variance indicated highly significant differences among the genotypes for all the characters. Heterosis studies revealed that standard heterosis was highly significant and positive in Pusa Sadabahar x Jwalasakhi for plant height and number of fruits per plant. Anugraha x Pusa Sadabahar for number of branches per plant, Jwalasakhi x Pant C 1 for average fruit length, Vellayani Athulya x Jwalasakhi for average fruit girth, Vellayani Athlya x Pusa Sadabahar for fruit weight and yield per plot.Yield parameters like number of fruits per plant and average fruit weight can be exploited through heterosis breeding or recombination breeding. The above mentioned promising hybrids can be directly popularised as hybrids after yield trails or can be carried forward to evolve high yielding varieties. Evaluation of promising hybrids *viz.*, Vellayani Athulya x Pusa Sadabahar, Jwalasakhi x Pusa Sadabahar, Pant C 1 x Vellayani Athulya, Pusa Sadabahar x Ujwala and Pusa Sadabahar x Jwalasakhi would be essential for reliable conclusion towards their commercial exploitation or these can be used for further breeding programme.

PI-131

INTERSPECIFIC AND INTERVARIETAL HYBRIDIZATION FOR STEM WEEVIL (*Hypera postica Gyll.)* TOLERANCE IN LUCERNE (*Medicago sativa* L.)

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Two different approaches were made to hybridize Indian lucerne cultivars for incorporating stem weevil (*Hypera postica* Gyll.) tolerance. *viz.,* i) Wide hybridization of Indian lucerne cultivar [RL 88 and Anand 2 (2n=32)] with *Medicago scutellata* L. (Mill.) (2n=30), a potential source for resistance and embryo rescue. ii) Collection of already released lucerne stem weevil resistant cultivars elsewhere and intervarietal hybridization with Indian lucerne, which are high yielding and susceptible to weevil infestation. EC 697041 was one among such varieties obtained from Margot Forde Forage Germplasm Centre, New Zealand. Out of 1287 florets attempted for interspecific crosses between RL 88 x *M. scutellata* (EC 541685 – Source: NBPGR), only five normal appearing pods developed till maturity and onely two germinated, under in vitro condition. The normal thick stemmed seedling with proper root did not survive during hardening and the second thick stemmed seedling is in root initiation stage. In the second approach, eighty five Anand-2 x Weevlcheck F_1 plants and sixteen RL 88 x Weevlcheck F_1 plants were obtained by in vitro seed germination. Screening of the F_1 plants under in vivo endemic hot spots in Jhansi (U.P) and also under controlled in vitro conditions in the laboratory showed tolerance to lucerne stem weevil. Upon selfing of the tolerant plants, the segregating progenies obtained will be subjected to weevil feeding test and best performing clones will be combined into a synthetic lucerne cultivar in near future.

PI-132

STUDIES ON COOKING AND EATING QUALITY TRAITS OF BEST F_1 INDICA RICE HYBRIDS

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Rice quality is great importance for all people involved in producing, processing and consuming, because it affects the nutritional and commercial value of grains. Eighty F_1 hybrid combinations were developed using eight CMS lines and 10 elite genotypes for the development of rice hybrids with desirable grain qualities. Among the eighty hybrids, 20 top yielding hybrids were identified for the assessment of grain quality characters. Combining all superior quality traits in a single hybrid is very difficult. Higher magnitude of genotypic variability in terms of GCV of more than 20 per cent was recorded for gel consistency, gelatinization temperature and amylose content. Eight hybrids *viz.,* IR 72081 A x MDU 5 R, IR 72081 A x TP 1021 R, IR 75601 A x MDU 5 R, IR 80559 A x MDU 5 R, APMS 6 A x TP 1021 R, IR 72081 A x IR 62037 R, APMS 6 A x IR 62037 R, CRMS 32 A x IR 62037 R and seven parents, IR 72081 A, IR 80559 A, APMS 6 A, CRMS 32 A, MDU5 R, IR 62037 R, TP 1021 R were identified with desirable quality attributes such as milling quality traits, linear elongation ratio, intermediate GC, GT, amylose content with medium slender grain type. For selection of parents and hybrids with quality traits, pooled *per se* performance, *gca*, *sca,* standard heterosis in different environments were also considered. Hence, these materials can be utilized further in heterosis breeding.

PI-133

INDUCTION OF MORPHOLOGICALLY DISTINCT GREENGRAM (*Vigna radiata* (L.) WILCZEK) MUTANTS THROUGH GAMMA IRRADIATION

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Being self pollinated nature of greengram (*Vigna radiata* (L.) Wilczek), available genetic variation is very limited for crop improvement. Hence, genetic variation was created in three greengram varieties *viz.*, CO5, CO(Gg)7 and VBN(Gg)3 through 550 Gray and 600 Gray dose of gamma irradiation at Tamil Nadu Agricultural University, Coimbatore during 2011-12. Five types of chlorophyll deficient mutants *viz.*, albino, xantha, chlorina, viridis and variegated leaves were observed in M_2 generation. A wide range of morphologically distinct greengram mutants with regards to leaf, stem, flower, pod, seed and growth habit were isolated and the heritability of these modifications were

confirmed further in M_3 and M_4 generations. Higher frequencies of both chlorophyll deficient and morphologically distinct mutants were observed in 550 Gray dose of gamma irradiation in greengram. A mutant namely CO7-550Gy-372 was isolated in CO(Gg)7 greengram variety which recorded high yield with synchronized maturity. While screening against Mungbean Yellow Mosaic Virus infection, this mutant showed resistant reaction under natural epidemic conditions over three locations *viz*., National Pulses Research Centre, Vamban, Agricultural Research Station, Vaigai Dam and Agricultural College and Research Institute, Madurai. The further confirmation of MYMV resistance of this mutant is under progress.

PI-134

PHYSICOCHEMICAL, BIOCHEMICAL AND PASTING PROPERTIES OF FORTY ONE CASSAVA LANDRACES

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Cassava (*Manihot esculenta* Crantz.) is a perennial woody shrub of the Euphorbiaceae, native of South America that is extensively cultivated as an annual tuberous root crop. Forty one cassava landraces received from CTCRI, Thiruvanathapuram were evaluated for their physicochemical, biochemical and pasting properties to find their industrial applications. In the present study, amylose content ranged between 15.2-32.4 per cent and starch content between 10.8-38.52 per cent. Among the 41 landraces studied, paste clarity was high for nineteen landraces. Swelling of cassava flours increases with increasing temperature and was measured from 50-80°C. Correlation study revealed that the amylose content was positively correlated to starch content and peak viscosity while it was negatively correlated to paste clarity suggesting its importance in food, textile and paper industries. Peak viscosity showed significant positive correlation with BDV, HPV, CPV and SBV. The identified two landraces *viz., Manjettan* and *Thukkuvella 6* possess low amylase content with high paste clarity. The landraces *Mysore* and *Kavaram Kutty* recorded high swelling power with high amylose and starch content and the landrace *Attukomban* had low final viscosity, pasting time with acceptable amylase and starch content. These genotypes are selected for their suitability to food based industries.

PI-135

GENETIC VARIABILITY IN BARNYARD MILLET [*Echinochloa frumentacea* (ROXB.) LINK] OVER DIFFERENT ENVIRONMENTS

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An investigation in barnyard millet was carried out in three different environments *viz*, Agricultural College and Research Institute, Madurai (E1), Agricultural Research Station, Paramakudi (E2),

Regional Research Station, Arupukkottai (E3) to study and evaluate the extend of variation, character association and stability for seven quantitative characters and five qualitative characters. Out of seven quantitative traits studied inflorescence weight, fodder yield, grain yield per plant recorded high phenotypic and genotypic coefficient of variability in all the three environments indicating wide variability that could be exploited for successful isolation of genotypes. Also most of the traits are less influenced by the environment since the difference between genotypic and phenotypic coefficient of variation are low. The traits grain yield per plant, inflorescence weight, fodder yield, plant height and inflorescence length at all the three locations recorded high heritability with genetic advance as percent of mean indicating this least influence of environment factors on these characters. The genotype ACM- 10-145 exhibited superior mean performance for grain yield, fodder yield and inflorescence weight. Based on AMMI analysis, stable high grain yield per plant, fodder yield, inflorescence weight was recorded by the genotype ACM-10-145 in all the three locations. Based on nutritional characters, ACM-10-145 had high yielding as well as good in carbohydrate, protein and iron content.

PI-136

STUDY OF HETEROSIS AND COMBINING ABILITY IN UPLAND COTTON (*Gossypium hirsutum* L.)

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In India, cotton is an important commercial crop which contributes major share in foreign exchange. To increase cotton production in India, cultivation of hybrids having high productivity will offer viable opportunity for it. Therefore, the present study was carried out to find out the best combination of parents to exploit the hybrid vigour for yield and yield contributing characters. A total of 24 hybrids which were developed from four lines and six testers were evaluated for their performances along with the standard check Bunny. The yield of the hybrids ranges from 1000 to 4250 kg/ha with the highest yield recorded by the cross MR786xMCU13. It was followed by the hybrids MR786xKC2, MR786xTCH 1728, BS279xMCU13 and BS279xGJHV502 with significant positive standard heterosis for yield. The hybrids MR786xKC2 and BS 27xGJHV502 recorded the significant positive standard heterosis for number of sympodia/plant and number of bolls/plant and BS27 x P2150 for lint weight and ginning out turn. Among parents, MR786 and BS 279 recorded as good general combining ability for yield and yield contributing characters like number of bolls and 10 boll weight. The hybrid combination ARBH2002 x KC2 recorded significant Specific Combing Ability for yield and lint index. Based on this study, it was concluded that the hybrids MR786x MCU13 and ARBH2002 x KC2 and MR786 x KC2 could be exploited for heterosis breeding.

PI-137

GENETIC DIVERSITY STUDIES IN EGYPTIAN COTTON (*Gossypium barbadense* L.)

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The Egyptian cotton (*Gossypium barbadense* L.) is known for its superior fibre traits and being cultivated in less 2% of the total area in the world, but the demand for ELS cotton is high in India. After Suvin which is having unbeatable fibre traits, the improvement became very slow due to lack of variability. Study of diversity among the *Gossypium barbadense* germplasm lines helps to identify diverse lines for creation of variability to apply selection pressure for yield and quality traits. With this aim, diversity study was conducted with 50 *G.barbadense* accessions and D2 analysis was carried out. These 50 genotypes grouped into ten clusters. For diversity the traits fibre elongation followed by bundle strength contributed 42.28% and 15.67% respectively. Among the clusters, cluster IV was the largest one having 14 genotypes and clusterX was the smallest having one genotype. The inter cluster distance was the highest between clusterVII and cluster X (22.58) and the shortest between cluster IV and cluster IX (11.39). Cluster VI recorded the maximum intra cluster distance of 15.85 which indicated wider divergence among the genotypes in the cluster. The genotypes *viz.,* NDGB22 for yield, ICB365 for boll weight, NDBG60 for 2.5% span length and NDGB49 for bundle strength can be exploited for trait specific improvement. The genotypes NDGB22 from clusterX and ICB241, ICB365, NDGB76 and NDGB88 from cluster VII may be involved in breeding programmes for creation of more variability in segregating population and application of selection pressure.

PI-138

GENETIC DIVERGENCE OF PROMISING RICE VARIETIES OF TAMIL NADU UNDER AEROBIC CONDITION

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An investigation was carried out in rice (*Oryza sativa* L.) with 49 rice genotypes under aerobic condition in the year 2013 at Anbil Dharmalingam Agricultural College and Research Institute, Trichy. The data recorded on ten biometrical traits namely, days to 50 per cent flowering, plant height, tillers per plant, productive tillers per plant, panicle length, grains per panicle, spikelet fertility, straw yield per plant, grain yield per plant, and Harvest Index. For evaluating rice genotypes, D2 analysis and hierarchical clustering analysis were employed. In D2 analysis, none of the clusters contained genotypes within all the desirable traits which would be directly selected and utilized. However the cluster IV recorded desirable mean value for number of tillers per plant, number of productive tillers per plant and grains per plant. The results showed that between genotypes of different clusters is

necessary for the development of desirable genotypes based on the per se performance of the best genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme. In hierarchical clustering analysis, among the five clusters, cluster II had the highest cluster mean revealed that the rice genotypes under this group may be utilized for pedigree breeding is possible. The variety CO 51 has achieved high yield under aerobic condition, hence this genotype may be used as a parent in aerobic tolerant breeding programme.

PI-139

ALG-06-320: A PROMISING GROUNDNUT CULTURE - HIGH YIELDING WITH FOLIAR DISEASE RESISTANCE

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The cultivated groundnut is a premier oilseed crop of India. Productivity is mainly constrained by late leaf spot and rust diseases among the biotic stresses and drought among abiotic stresses. The Spanish bunch groundnut culture ALG-06-320 developed from an advanced breeding line ICGV 94118, developed at ICRISAT. Orginally, ICGV 94118 supplied to CRS, Aliyarnagar in 2005. It was tested during 2005 to 2009 in various yield trials in TN.The culture ALG-06-320 was entered into AICRP for testing in IVT-I during Rabi/Summer 2008-09. It was out-performed the national and zonal checks in yield pooled over three years of testing from 2008-09 to 2010-11. This promising culture exhibited stable yield performance in Zone IIIb during three years of testing under AICRP (G). It recorded a mean pod yield of 2741 kg/ha with yield average of 33 % over TAG 24 (National Check), 29 % over R 8808 (Zonal check) and 7.1 % over ICGV 00350 (Zonal check). This culture has maturity duration of 110-115 days. It has a shelling turn over of 70 % and 100 seed mass of 36 g. It recorded average kernel yield of 1931 kg/ha and has an oil content of 50 %. It possesses resistance to rust and moderately resistance late leaf spot diseases. The groundnut ALG-06-320 culture has been identified for release for Zone III b comprising the state of AP and TN for cultivation in Rabi/ Summer season by the varietal identification committee during annual castor workshop held at ARS, Mandor, Rajasthan.

PI-140

BIPARENTAL MATING AS A WAY TO CREATE GENETIC VARIABILITY IN MUSTARD

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Biparental mating was attempted in the F_2 of four highly heterotic crosses of mustard namely Kranti x ACN-9, Seeta x Ashirwad, Bio-902 x Ashirwad, Vardhan x Kranti during 2013-14 using NCD-1.

The maximum range was recorded in number of siliqua/plant followed by plant height, days to maturity, days to first flower and seed yield/plant. Upper limit value of BIP progenies for days to first flower, plant height, number of primary branches/plant, number of siliqua /plant and seed yield/plant were found to be higher than best check varieties for respective characters. GCV (%) and PCV (%) were either high or moderate for number of siliqua yield /plant and seed yield/plant which can allow more scope for selecting better segregants. In addition low narrow sense heritability estimate were coupled with high genetic advance as per cent mean for the same two traits. In three crosses Kranti x ACN-9, Seeta x Ashirwad, Vardhan x Kranti relationship between early maturity and seed yield/plant was broken and changed to either significant or non significant negative correlation. Percentage of progenies selected over 32 BIPs of each cross were 34.37% in Kranti x ACN-9, 71.87% in Seeta x Ashirwad, 31.2% in Bio-902 x Ashirwad and 65.62% in Vardhan x Kranti and the percentage of progenies selected over total of 128 BIPs evaluated were 8.59% in Kranti x ACN-9, 17.96% in Seeta x Ashirwad , 7.8% in Bio-902 x Ashirwad and 16.40% in Vardhan x Kranti. The selected BIPs will be forwarded to next generation.

PI-141

SCREENING FOR DROUGHT TOLERANCE IN COWPEA (*Vigna unguiculata* (L) WALP.) UNDER FIELD CONDITION

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Cowpea (*Vigna unguiculata* (L.) Walp) is an important grain legume which is grown in most of the tropical countries. It is a multipurpose crop and can be used as vegetable (young pod), grain (seeds) and fodder (plant). Drought is one of the most common environmental stresses affectingplant growth and productivity in Tamil Nadu. Hence identifying a high yielding cowpea variety with drought tolerance is of much importance, since water is becoming a limiting factor. The present investigation was undertaken to screen the cowpea genotypes through *in vivo* drought screening techniques. Eight high yielding genotypes *viz.,* ACM 27, ACM 37, VCP 09024, CP 27, KBC 4, VBN 1, VBN 2 and COCP 7 were studied under normal irrigation, irrigation was withheld at flowering stage and from 5th day from date of sowing onwards in three different experiments. Among the eight genotypes COCP 7 and KBC 4 were identified to be drought tolerant, since they recorded high proline content of 5.60 and 5.34 mg/g respectively.They also recorded high relative water content, chlorophyll stability index and seed yield/ plant. So these genotypes can be suitable for cultivation in drought prune area or used as parents in hybridization programme for developing drought tolerant varieties.

PI-142

CORRELATION AND PATH COEFFICIENT ANALYSIS FOR THE YIELD COMPONENTS OF SAFFLOWER GERMPLASM (*Carthamus tinctorius* L.)

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Twenty safflower germplasm lines were evaluated during rabi 2013-14 at Agricultural Research station, Tandur to determine the relationship among yield and yield components. The genetic parameters like genotypic and phenotypic variability, genotypic and phenotypic coefficient of variation, heritability and genetic advance were studied. Significant differences existed among the germplasm lines for all the characters studied. Range of variation was highest for seed yield per plant followed by number of capsules per plant and number of seeds per capsule. Genotypes had least range of variation for 100-seed weight. High coefficients of variation were observed for seed yield per plant followed by 100-seed weight. The estimate of broad sense heritability was highest for 100-seed weight. Phenotypic coefficient of variation ranged from 4.12 to 42.34% for the traits studied. Genotypic coefficient of variation ranged from 5.11% to 38.34%. The maximum GCV was observed for seed yield/plant followed by 100-seed weight and number of capsules per plant. Thus these traits further provide an opportunity for genetic improvement. Besides these parameters phenotypic correlation coefficient and path analysis were also studied for seed yield and its component traits of safflower. Seed yield/ plant exhibited positive and significant correlation with number of seeds/capsule and 100-seed weight. Path coefficient analysis indicated that 100-seed weight exhibited maximum direct effect followed by number of seed/capsule.

PI-143

STABILITY ANALYSIS FOR YIELD AND RELATED TRAITS IN THE LAND RACES OF RABI SORGHUM

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Rabi sorghum is highly valued as a food grain crop owing to its excellent grain quality. Indian rabi sorghum landraces are rich repository of genetic variability and are preserved by the farmers traditionally due to local adaptability, good grain quality and adaptation to various stresses. Thus, it becomes more relevant to utilize such typical landraces in crop improvement programs to achieve sustained productivity. Forty five rabi sorghum landraces were evaluated along with three checks M35-1, CSV 22R and Phule Chitra for three years (2011-2013) at ARS, Tandur to identify promising and stable genotypes for various yield related traits using Eberhart and Russels model. Analysis of

variance indicated significant differences among the genotypes and environments for days to 50% flowering, days to maturity, plant height, test weight, grain yield and fodder yield. Significant GXE interaction was observed for all the yield related traits. The study identified two stable landraces Bairadogi and Jamkhed local for breeding early duration types The landraces RSV 1449, RSV 1478, Tillehal local, Halyal local, Mundewadi local, Khatarkhatav local, Kavalagudda mungaru, Honawad, SSRG 170 and SSRG 236 can be used to develop semi dwarf and nonlodging types. RSV 1425, RSV 1449, Khadkhat local and Honawad 2 can be used to breed bold grain types. RSV 1449, RSV 1458, RSV 1460, Halyal local, Gondavale local, Mangalwedha local, Pusegaon local and Honawad 2 were identified as donors to improve the grain yield and Dharampur local, Halyal local, Bidar local, Mangalwedha local and SSRG 204 to improve fodder / forage sorghum.

PI-144

HETEROSIS FOR YIELD AND YIELD ATTRIBUTED TRAITS IN RICE HYBRIDS (*Oryza sativa* L.)

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The present study was conducted to assess the magnitude of heterosis for grain yield and its component over Mid parent(MP), Better parent(BP) and standard heterosis (SH) in rice hybrids(*Oryza sativa*) through line x tester analysis. The study comprised of three cytoplasmic male sterile lines (IR 58025A, IR 62829A, PUSA 3A) and ten testers(ADT 39,CO 43, IR 50,IR 36,IR 28, IR 42,IR 64,ASD 16, ASD 19,TRY 1). The resultant 30 hybrids along with their 13 parents were evaluated during 2013-2014 in randomized block design with three replication .The field study was conducted in the plant breeding farm, Department of Genetics and plant breeding, Annamalai university, Chidambaram. The observation on seven biometrical characters viz., first flowering, plant height, number of productive tillers per plant, panicle length, filled grains per panicle,1000 grain weight, grain yield per plant of 43 rice genotypes were studied. The analysis of variance of different characters indicated that the presence of significant amount of variability among genotypes for all the seven traits. The cross combination IR58025A x ASD 19, IR62829 x ASD 16, PUSA3A X IR42 were found to be promising for seed yield in rice as they had exploit high percentage of standarad heterosis (SH).

PI-145

EVALUATION AND IDENTIFICATION OF PROMISING SUGARCANE CLONES SUITABLE FOR MID-LATE SEASON

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Field experiments were conducted at Sugarcane Research Station, Cuddalore during 2012-13 for the evaluation of promising sugarcane clones suitable for East Coast Zone. The experimental materials consist of the two trials *viz*., Initial Varietal Trial (Mid-late) and Advanced Varietal Trial (Mid-late) Plant crop. In IVT (mid-late) four clones and three standards and AVT (mid-late) three clones and three standards were evaluated for yield and quality traits in Randomized Block Design. In IVT among the seven entries, the clone CoA 11326 recorded significantly higher cane yield (128.30 t/ha) over the standard variety CoV 920102 (110.27 t/ha.) followed by the clone CoA 11324 (116.33 t/ ha.). Clone CoV 92102 recorded higher sucrose content (17.21%). For Commercial Cane Sugar (CCS) yield, CoA 11326 recorded higher value of 14.71 t/ha. In AVT, the clone CoC 10337 expressed higher cane yield (136.28 t/ha.) followed by the clone CoA 11324 (116.33 t/ha.). The CoV 92102 recorded higher sucrose content (17.56%) and CCS per cent (12.47). The clone CoC 10337 recorded higher Commercial Cane Sugar yield (16.73 t/ha). followed by the clone CoA 10321(14.05 t/ha.). Based on the higher cane yield and sugar, yield CoA 11326 was identified as the best clone in IVT (mid-late) and the clone CoC 10337 was superior in AVT (mid-late) compared to the standard variety and both the clones were promoted to the future breeding program.

PI-146

GENETIC ANALYSIS OF OIL QUALITY AND AGRONOMIC TRAITS IN BC_1F_2 AND BC_1F_3 GENERATIONS OF GROUNDNUT

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Oil stability and nutritional quality are both dependent on the relative proportions of the saturated and unsaturated fatty acids that constitute the oil. The trait high oleic to linoleic acid ratio (high O/L) in groundnut is favoured over low O/L as it confers health benefits and oil stability. Backcrossing was attempted to recombine oil quality and agronomic traits. Genetic analysis of backcross ((GPBD 4 x GM 4-3, 38 x GPBD 4) generation (BC_1F_2 and BC_1F_3) revealed high heritability coupled high genetic advance as per cent of mean for linoleic acid, polyunsaturated to saturated fatty acids, palmitic to stearic acid ratio, plant height, primary branches per plant, *spodoptera litura* incidence and pod yield per plant. Oleic acid showed high heritability and moderate genetic advance as per cent of mean in both generations, whereas O/L ratio moderate to high heritability and high genetic advance as per cent of mean. Oleic acid exhibited significant positive association with arachidic acid, eicosenoic acid, lignoceric acid, O/L ratio and significant negative association with palmitic acid, linoleic acid, behenic acid, total saturated fatty acids, iodine value and polyunsaturated to saturated fatty acid ratio and palmitic to stearic acid ratio. Few superior segregants with high oleate trait and foliar disease resistance were recovered from backcross generations.

PI-147

STUDY OF HERITABLE VARIATION AVAILABLE IN THE SEGREGATING GENERATIONS UNDER AEROBIC SITUATION IN RICE (*Oryza sativa* L.)

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Rice is the staple food in Asia but is also the single biggest user of freshwater. It is mostly grown under submerged soil conditions. Moreover, lack of rainfall is a major production constraint in rain-fed areas where many poor rice farmers live. Since rice is a self pollinated crop the variation availability is very low. The present study aims at the estimation of measures of variability, heritability and genetic advance, in segregating generations of rice for sixteen traits. Low genetic variability was observed for almost all the biometrical and physiological traits in both F_2 and F_3 generations. Among the traits, 100 grain weight, leaf rolling, leaf drying, chlorophyll stability index and dry root weight and among the crosses, IR 70369A x IR 79200 in F2 and IR 79128A x KMP 105 in F_3 generation were found to expose more genetic variation in both heterogeneous generations.The estimates on heritability increased from F_2 to F_3 in general. Plant height, number of productive tillers per plant, panicle length, 100 grain weight, leaf rolling, root length, dry root weight, root volume and grain yield per plant recorded high heritability coupled with high genetic advance. The cross IR 79156A x IR 80402 in F_2 generation and cross IR 70369A x BI33 in F_3 generation revealed higher estimates for most of these parameters revealing the influence of predominant additive gene action.

PI-148

SELECTION INDICES IN VIRGINIA GROUNDNUT (*Arachis hypogaea* L.)

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Groundnut (*Arachis hypogaea* L.) is one of the most economic oilseed crops of the world. It is considered as the world's fourth largest source of edible oil and third most important source of vegetable protein.The most desirable approach to improve characteristics such as pod yield is simultaneous selection based on related traits . This can be done using selection index, which is multiple regressions of genotypic values on phenotypic values of several traits. Sixty diverse genotypes of Virginia groundnut were evaluated in a randomized block design with three replications to study of selection indices under rainfed conditions during *kharif* 2013. Sixty-three selection indices involving pod yield per plant (X1) and five yield components *viz.*, 100-kernel weight (X2) shelling out-turn (X3), biological yield per plant (X4), harvest index (X5) and kernel yield per plant (X6) were constructed using the discriminant function technique. Discriminant function analysis indicated that selection efficiency of the function was improved by increasing number of characters in the index. Among the

single character index, 100-kernel weight exhibited higher genetic advance and relative efficiency over straight selection for pod yield per plant. The index based on four characters *viz*., pod yield per plant, 100-kernel weight, shelling out-turn and kernel yield per plant recorded the highest genetic advance as well as relative efficiency and selection efficiency. These characters could be advantageously exploited in the groundnut breeding programmes.

PI-149

CENTRALLY IDENTIFIED SUGARCANE VARIETY COC 08 336

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CoC 08 336 was selected from general collection of C 81129 and clone was proposed as C 25006, evaluated in station trials from 2007-08 to 2009-10. In AYT, it recorded a mean cane yield of 137 tonnes/ha, 13.1%CCS and 17.95 t/ha of sugar yield. Per cent increase over Co 86032 for cane yield and sugar yield were 14.2% and 15.1%. Clone was tested in AICRP(S)- Zonal Trials of East Coast Zone from 2010-11 to 2012-13 in IVT, AVT-I & II plant and Ratoon trials. In the IVT the clone was found best with highest cane yield of 126.29 t/ha, CCS of 11.23% &13.94 t/ha over locations. It recorded maximum cane yield of 182.41t/ha in Nellikuppam. In AVT-I plant, CoC 08 336 was found best across locations with 118.66 t/ha of cane yield and 14.09t/ha of CCS. In AVT-II plant it recorded mean cane yield of 120.47t/ha and CCS of 14.22 t/ha. Pooled mean of all the three trials across locations was found to be the maximum in CoC 08 336 for cane yield (110.4t/ha) and CCS (13.12 t/ha). Sucrose per cent in juice and pol% cane of CoC 08 336 was 17.44 and 13.83. Clone has excellent agronomic characteristics of high tillering, tall, thick and erect canes, non flowering, easy detrashing and leaf sheath is non spiny. Clone is moderately resistant to red rot disease. It has fibre content of 13.16% and amenable for cogeneration.

PI-150

GENETIC VARIABILITY STUDIES IN FOXTAIL MILLET (*Setaria italica* (L.)P. BEAUV.)

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Foxtail millet is one of the oldest cultivated millet crop and requires warm weather and minimal water. It is a major millet crop adapted to arid and dry areas of India, China, and other parts of Asia, North Africa and America. Assessment of variability present in any crop species is the essential pre-requisite for formulating an effective breeding programme. An experiment consists of nine parents selected from the germplasm were raised during summer, 2014 at Department of Millets, TNAU, Coimbatore. The observations recorded were days to 50% flowering, plant height, number of productive tillers, inflorescence length (cm), inflorescence width (cm) and grain yield per plant (g). High PCV and GCV were recorded for number of productive tillers, inflorescence width and grain yield per plant. The traits days to 50% flowering and inflorescence length had moderate PCV and GCV values. The values of phenotypic coefficient of variation were greater than genotypic coefficient of variation for all the traits studied suggesting their vulnerability to environment. High heritability along with high genetic advance as per cent of mean observed for all the traits except plant height indicating involvement of additive gene action for these traits so selection will be effective. The grain yield has positive correlation with productive tillers and plant height has positive direct effects with grain yield. Hence direct selection for these traits would be rewarding for yield improvement in foxtail millet.

PI-151

INTERPRETATIONS ON ASSOCIATION OF CERTAIN QUANTITATIVE TRAITS ON YIELD OF RICE (*Oryza sativa* L.) UNDER SALINE ENVIRONMENT

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A study was initiated in the plant breeding farm, department of genetics and plant breeding, Faculty of Agriculture, Annamalaiuniverity during Januray 2009 to assess the genetic associations among yield components and their direct and indirect influences on the grain yield of rice. The Randomized block design was adopted with three replications. According to the magnitude of the direct effects on grain yield, the order of yield components was the number of productive tillers per square metre (0.954) > number of filled grain per panicle (0.0467) > 1000-grain weight (0.0051). The improvement in grain yield will be efficient, if the selection is based on the biological yield, the number of productive tillers per square metre and the number of filled grains per panicle under tropical conditions. Correlation studies indicated that intensive selection on the positive selection for number of productive tillers, number of filled grains and 1000 grain weight will improve the seed yield in rice. Path coefficient analysis further revealed that the number of productive tillers plays a major role in determining the yield per plant of rice cultivars.

PI-152

MOLECULAR CHARACTERIZATION OF LONG SHELF LIFE CASSAVA CLONE BR-105

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One of the major problems for cassava production is the rapid deterioration after harvesting cassava tuberous roots, which limits the possibilities for production and marketing of cassava in the world. Cassava roots undergo rapid deterioration 24 - 48 hours after harvest, a phenomenon referred to as post-harvest physiological deterioration (PPD). It is characterized by a blue-black discoloration of the xylem vessels known as “vascular streaking”. PPD considerably reduces the palatability and marketability of cassava roots. Consequently, cassava roots need to be consumed soon after harvest or supplied to industries for processing. PPD is one of the main obstacles currently preventing farmers from exporting cassavas abroad and generating income. Thus, longer shelf life varieties would be desirable for farmers. A promising clone BR-105 with delayed PPD was identified earlier in this Institute. It has purple young leaves, medium branching and cylindrical tuber shape with purple rind & white flesh colour tuber. The young leaves and rind of the clone can be used for extraction of anthocyanin. The tuber recorded high drymatter (45-47%) and the cooked tubers were hard & sticky. The number of tubers ranged from 4-6 per plant (3-5 kg/plant). The tubers have high latex content in the rind, even at 30 days after harvesting. Tuber can be stored for more than a month without deterioration and discolouration under room temperature. The clone can be used as a parental line for breeding varieties with longer shelf life. The molecular nature of PPD tolerance in this clone is under progress.

PI-153

STABILITY OF YIELD AND YIELD REALTED TRAITS IN SESAME

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An investigation was carried out with sixteen genotypes of sesame with the objective of testing stability in six environments. The analysis of variance for individual environments as well as pooled analysis revelaed significant differences among the genotypes for all the characters studied. The results indicated differential reaction of genotypes with different environments. Among the sixteen genotypes studied N8, CO1, Pragati, Nirmala and TC 289 showed stability for seed yield per plant. Considering stability parameters H12 exhibited high seed yield per plant. Its regression coefficient was less than unity and stability factor was around unity indicating suitability for both favourable and

unfavourable environments. A simultaneous consideration of all the five parameters like mean,regression coefficient , deviation from regression ,stability factor and coefficient of variation showed that VRI1 and TMV 3 were the most adaptable genotypes for poor environment with non significant regression coefficient and deviation of regression for low grain yield per plant. The genotypes TMV 3 and VRI 1 was found stable for yield related traits like day to fifty percent flowering and number of capules per plant and number of seeds per capsule coupled with moderate to high seed yield per plant indicating their commercial potential.

PI-154

STABILITY PERFORMANCE OF INTER AND INTRA-SPECIFIC HYBRIDS OF AMERICAN COTTON OVER LOCATIONS

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Five female lines, ten testers and their resultant 50 hybrids derived from the line x tester mating design were evaluated in RBD with three replications (Surat, Navsari and Achhalia) and materials were subjected to stability analysis in three locations with respect to seed cotton yield and yield contributing traits. Highly significantly genotype x environment interaction was noticed for days to 50% flowering, plant height, numbers of sympodia, number of bolls, average boll weight, seed cotton yield, seed index and lint index at pooled deviation. Surat was noted to be congenial for plant height, numbers of sympodia, seed cotton yield, seed index and lint index. Navsari was proved to be ideal for days to 50% flowering and average boll weight, while Achhalia appeared to be best for number of bolls. None of the parents and hybrids was found to be average stable for all the studied traits. Parents GSHV 112, 76-IH-20 and BC-68-2WW were average stable for seed cotton yield. While parent G Cot 20 was performing better in unfavourable environment. Hybrids G Cot 20 x GSB 40, GSHV 01/1338 x GSB 41 and GSHV 01/12 x GSB 41 (interspecific) and GSHV 01/1338 x GSHV 112, G Cot 10 x 76-IH-20 and G Cot 20 x GSHV 112 (intraspecific) were found average stable over environments for seed cotton yield Parents and hybrids showing average stability for seed cotton yield is might be due to showing stable performance in one or more yield contributing traits.

PI-155

SUGARCANE VARIETY FOR TANNERY EFFLUENT DEGRADED AREA

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Sugar cane yield is markedly influenced by many factors like soil fertility, variety, biotic and a biotic

stresses. Increasing urbanization, industrialization, recycling of heavy metals and other pollutants in the environment through biotic and abiotic pathways is found to increase with increasing use of metals, pesticides and other chemical based commodities. Leather industry, generates more quantity of waste water and disposing them on agricultural lands is a common practice. Such practice converts the cultivable lands as waste and make them unfit for practicing cultivation. More than two third of the tanneries in India are located in Tamil Nadu particularly in Vellore district. A total of about 5000 hectares of land is reported as degraded by the tannery effluents. In this scenario, it is imperative to cultivate suitable sugarcane variety in the resource limiting environments to feed the population with steep rise in unit price of sugar. The sugarcane variety CO G (Sc) 5 is a hybrid derivative of the cross between Co C 671 xCoT 8201 was specifically tested in tannery effluent polluted areas in 20 locations with 40 trials as on farm trials (OFT). In tannery effluent affected soils, the CO G (Sc) 5 has performed better than the popular standard Co G 93076 and Co G 95076 in terms of cane yield and sugar yield. Therefore, Co G (Sc) 5 is recommended as a location specific variety, particularly for tannery effluent affected areas.

PI-156

VARIABILITY, DIVERGENCE AND ASSOCIATION ANALYSIS IN EXTRA EARLY DURATION PIGEONPEA

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Thirty nine extra early pigeonpea genotypes were evaluated for their variability, estimations of correlation, path coefficient analysis and genetic divergence. There was considerable variability in the redgram genotypes for all the traits studied. The heritability estimates and genetic advance were high for seed yield, number of pods per plant and plant height indicating the predominance of additive gene effects for these characters. Positive significant association with seed yield was observed with number of pods per plant indicating direct selection for this character will improve the yield potential of extra early genotypes of pigeonpea. Seed yield increased with greater pod number due to improved sink capacity. Number of pods per plant had direct positive effect on seed yield and indirect positive effects were also manifested through days to 50% flowering, plant height and number of branches per plant resulting in positive significant association with seed yield. Principal component analysis (PCA) performed to analyze the structure of the genetic diversity revealed that 88.94% of the total diversity was explained on the basis of the first three principal components based on Eigen value-one criterion. On the basis of relative magnitude of D2 values 39 extra early pigeonpea genotypes were grouped into eight clusters. Based on D2 value and PCA scores seed yield, plant height and number of pods per plant were identified as the most important traits contributing towards diversity among the 39 extra early pigeonpea genotypes evaluated.

PI-157

COMBINING ABILITY ANALYSIS FOR LATE LEAF SPOT RESISTANCE, YIELD AND YIELD COMPONENTS IN GROUNDNUT (*Arachis hypogaea* L.)

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Development of high-yielding foliar disease resistant genotypes requires identification of resistant sources with good breeding potential. Information on genetic control of resistance and yield helps to plan appropriate breeding methodologies to isolate resistant lines with high yield potential.

The experimental material comprised of 23 genotypes of which five were lines (TPT-4, TCGS-888, TCGS-913, ICGV-91114 and TG-47), three were testers (GPBD-4, ICG-13919 and ICG-15234) and fifteen F_1s derived out of a line x tester design. The analysis of variance for combining ability revealed highly significant difference among the lines, testers and lines x testers for most the characters studied indicating the presence of wide genetic variability among the lines, testers and their interaction effects. The estimates of GCA: SCA variance revealed the predominance of non-additive gene action for all the characters except for number of primary branches per plant, days to 50 per cent flowering and days to maturity.

TG-47 and TCGS-888 among the lines while, ICG15234 among the testers were the best general combiners for late leafspot resistance, yield and yield contributing trais while the F1 crosses viz., ICGV-91114 x ICG-15234, TG47 x ICG-15234, TCGS-888 x ICG13919 and TCGS-913 x GPBD-4 were the best specific combinations with mean and specific combining ability in desirable direction for late leafspot resistance, yield and yield contributing trais.

PI-158

GENETIC CORRELATION- A MEASURE OF ASSOCIATION BETWEEN TRAITS AT THE LEVEL OF BREEDING VALUE (r_A)

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In sexually reproducing crops only breeding value out of entire phenotypic value is passed on to progeny and hence genetic correlation, a measure of association between traits at the level of breeding value (r_A) becomes important. A procedure is described here to utilize the data generated on half sibs and full sibs generated through NC designs for determining r_A. Different methods of estimating the reliable additive component of genotypic variance and also non reliable component of dominance variance are followed to determine the magnitude of these components of variance. It is necessary to visualize that these components of variance in turn contributing to components of correlation giving rise to correlation measured at phenotypic level (r_p), genotypic level (r_g) and at the level of breeding values (r_A). At the breeding level, seed cotton yield exhibited highest positive genetic correlation with number of bolls per plant (0.45) followed by number of reproductive points (0.44), lint index (0.36), inter branch distance (0.30), sympodial length at 50 % height (0.29), seed index (0.25), plant height (0.23), number of seeds per boll (0.23), boll weight (0.21), also it showed negative genetic correlation with ginning outturn (-0.24), sympodia per plant (0.35) and number of monopodia (-0.12). There was a clear difference in magnitude and direction of association among quantitative characters when measured at the level of breeding value as compared to r_p and r_g suggesting that the inferences on relationships among characters and predicted correlated response can be wrong if phenotypic and genotypic correlations are used.

PI-159

SEERAGASAMBA - A PHOTOSENSITIVE TRADITIONAL RICE CULTIVAR

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Seeragasamba is a traditional rice cultivar which is being cultivated in samba season (August-September sowing) from time immemorial in Tamil Nadu. It comes to maturity in about 150 days duration with having small fine grain. The expected average yield under good agronomic management is about 3.0 t/ha. Seeragasamba can't tolerate high chemical fertilizer applications and lodging at the time of maturity is a problem. However, it fetches premium price for its grain and aroma, since it is regularly used for making mutton briyani dishes. Seeragasamba is raised mostly in the Uppiliyapuram panchayat union of Thuraiyur taluk of Trichi district of Tamil Nadu,India.

Seeragasamba is photosensitive in nature. So the sowing was normally taken during samba season *i.e.*, August to September sowing. An experiment was conducted to ascertain its photosensitivity at Agricultural Research Station, Vaigai dam. Nursery sowing was taken up on 14.02.2014 and transplanted on 15.03.2014 in D1 field. The seed germination, seedling initial growth and development were similar to that of the samba season. Normally (samba season sown crop) the 50% flowering will be observed during 115-120 days after nursery sowing. The plant reaches 155 cm height during its growth phase. However under present study even after 6 months no flowering was observed and all the plants started to dry and wither their leaves showing an ornamental look. Thus the result obtained confirmed its photosensitive nature.

PI-160

GENETIC VARIABILITY IN SUGARCANE (*Saccharum spp*. Complex)

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The experimental material consisted of 30 genotypes of sugarcane obtained from the germplasm maintained at Main Sugarcane Research Station, Navsari Agricultural University, Navsari and grown during for 2010-2011 and 2011 and 2012 in randomized block design (RBD) with three repetition each. These sugarcane genotypes were evaluated for cane yield, sugar yield and related morphological and growth characters. Genotypes significantly differed for all the 16 studied characters indicating sufficient variability existing in the experimental material. In case of variability, characters *via*., germination % at 45 days followed by tillers at 120 days and shoots at 240 days showed high GCV and PCV. The values of both GCV and PCV were lower for juice purity percentage. High estimates of heritability along with high genetic advance (% of mean) were observed for tillers at 120 days (000/ha) followed by germination % at 45 days, internodes/stalk at 360 days, shoots at 240 days (000/ha) and stalk height at 360 days. This indicated that these characters are governed by additive gene action and selection for these characters will be useful in choice of best genotype. While rest of the characters inherited with moderate to low coupled with moderate to low genetic advance over as per mean.

PI-161

DEVELOPMENT OF HYBRID DERIVATIVES IN BRINJAL BY USING LOCAL TYPES

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Brinjal (*Solanum melongena* L.) is an important solanaceous vegetable in many countries of Asia and Africa. It is a good source of minerals and vitamins in the tropical diets. In India, the NBPGR is the nodal institute for management of germplasm resources of crop plants and holds more than 2500 accessions of brinjal in its genebank. In the present study, the development of Hybrid derivatives in brinjal by using local types was undertaken. Fifty genotypes were collected from different agro-climatic zones of Tamil Nadu which includes 15 from Madurai district and 35 from other districts of Tamil Nadu. Out of 50 genotypes, 10 local types of Madurai district were selected as female parent for hybrid development by using high yielding varieties *viz*., Annamalai, KKM1, Pusa Uttam and EP65 in LXT method. Forty hybrids were developed and evaluated for its yield and other economic attributes. In the segregating population of the cross L_9 x T_1 (F_2 to F_5) were studied and a promising line was identified. This promising line is consecutively performed well over generations for plant height, number of branches per plant, number of fruits per plant, yield per plant, shoot and fruit borer infestation and little leaf incidence. This particular segregant is having high local preference due to its colour (purple striped) with an average fruit weight of 45 to 50g.The average yield per plant is 2.02kg. Further studies are in progress to attain the homozygosity of the population for its growth and yield attributes.

PI-162

GENETICS OF FERTILITY RESTORATION AND VALIDATION OF RF_3 AND RF_4 GENES OF 'WILD ABORTIVE' SYSTEM BASED CYTOPLASMIC GENETIC MALE STERILITY (CGMS) IN HYBRID RICE (*Oryza sativa* L.)

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The present investigation was carried out at Tamil Nadu Rice Research Institute (TRRI), Aduthurai with 20 restorers and five 'WA' type CGMS lines to study their inheritance and validation of fertility restoration genes. 36 F_1 hybrids with varied pollen fertility were selected, selfed and their F_2 generations were raised during July 2010 with a plant population of 250 to 400 per cross. Results revealed that restoration was governed by two or three major genes with epistatic interactions that differed from crosses to crosses. The inheritance in CRMS 32A x AD 06084R and ten other combinations revealed a F_2 segregation of 12:3:1 (FF: SF: CS), indicating the involvement of two dominant genes which exhibit dominant epistasis. In COMS 24A x IET 20899R, F_2 segregation fell into the digenic ratio of 9FF: 3SF: 4CS showed the involvement of digenic supplementary or an epistasis with recessive gene action. F_2 ratio of 9:6:1 with two dominant genes exhibiting epistasis with incomplete dominance was observed in fifteen cross combinations suggesting the two dominant genes Rf_3 and Rf_4 seem to control the fertility restoration. Presence of Rf_3 and Rf_4 genes were validated using tightly linked and co-segregating 16 SSR markers. Varied F_2 ratio of 27:30:7, 33:38:8, 27:30:7, 34:52:1, 72:105:15, 39:46:7, 17:86:22, 35:23:1 was observed in other crosses indicating the existence of certain modifiers influencing the penetrance and expressivity of restorer genes. Differential mode of restoration may due to the influence of female genotype or to the variable expression of the weaker gene in different genetic backgrounds.

PI-163

EVALUATION OF SODICITY TOLERANCE AT SEEDLING STAGE IN MUNG BEAN (*Vigna radiata* (L) Wilczek) GENOTYPES

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A laboratory experiment was undertaken to evaluate the sodicity tolerance on seedling stage in mung bean genotypes at the Department of Plant Breeding and Genetics, Anbil Dharmalingam Agricultural College and Research Institute. Seeds of 13 genotypes viz.,VGG 11 ,VGG 04-002 ,VGG 04-013 ,VGG 04-12 ,KM-2-B ,SM-4-136 ,RM 11-614 ,PDM 84-229 ,VBN(Gg)-3 ,VBN(Gg)-2, PDM 84-1464,C0 -9 and ,ADT-3 germinated in roll towel method with lower end immersed in $NaHCO_3$ solution at three different concentrations *viz*., 25 mM, 50 mM and 75 mM. control was maintained by keeping the seeds in a distilled water by using the variety VBN(Gg)-2, The experiment was laid out in a Completely Randomised Design and the ANOVA was formulated to calculate SE and CV. The seedling parameters *viz*., germination percentage, root length, shoot length, vigour index and stress tolerance index were recorded. Among 13 genotypes, PDM 84-164 recorded high germination percentage (94), root length(16.2), shoot length (10.0) vigour index(2462.80) and stress tolerance value(94.71) followed by PDM 84-229, VBN(Gg) 2 and VBN(Gg) 3 and these genotypes were found to be suitable genotypes for sodicity tolerance which can be utilized as parent in the hybridization for development of sodicity tolerant cultivars after field evaluation.VGG 04-012, KM-2-B ADT 3 and Co 9 recorded low values for Stress tolerance index which may not be including as a parent in the hybridization programme to develop salt tolerant cultivar.

PI-164

ETHNOBOTANICAL STUDIES IN TAMIL NADU

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Before civilization, people lived in forest and consumed the fruit and seed from edible plants. Forests are treasures of useful plants which are not only for food and livelihood but also contain valuable chemical compounds of medicinal value, pesticidal effects and other defence activities. Though the scientists are discovering so many things, there is still some hidden precious knowledge on those values which are accumulated among the tribals and being transferred to next generations along with centuries. These ethnic groups are rich in Tamil Nadu where great diversity of 1559 medicinal plants, 533 endemic species, 260 wild relatives and 230 red listed species it has 4 gymnosperm

species and pteridophytes 1022 species are discovered till date. The dominant ethnic groups are *Kannikar, Kattunayakas, Irular, Palliyar, Santals, Todas, Malayali, Kotas, Valayans, Klamala, Kammara, Kochu vela, Kondareddis, Koraga and Malai arasan.* They live in different geographical locations of Tamil Nadu, which are rich in diversity. Though the tribal people migrated to other places they sustained the knowledge with in them. As the generations going by and as civilization of man is becoming prominent, transferring of this hidden knowledge is becoming tough. And also the tribes do not reveal secrets of plants to others. So the particular secret of plants is being lost along with death of knowledge holder because of the absence of documentation. The indigenous knowledge on these ethnobotanical plants is gaining importance worldwide as it is very useful. So the present study is concerned with ethnobotanical studies in Tamil Nadu.

PI-165

EFFECT OF PHYSICAL AND CHEMICAL MUTAGENS ON QUALITATIVE TRAITS OF COWPEA IN M_1 GENERATION

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Cowpea (*Vigna unguiculata* L. walp) forms major food crop of millions of people in most developing countries. Most of the crop improvement programmes attempted through hybridization breeding programs have exploited only the natural variability available in the germplasm. Under such circumstances, induced mutagenesis can be efficiently employed as an alternative to induce the variability in morphological and physiological characters. Two cowpea varieties *viz.,* Co 7 and Tirunelveli Local were exposed to varying doses of physical mutagen (gamma rays - 15, 20, 25, 30 and 35 KR) and chemical mutagen (EMS- 5Mm, 10 Mm, 15Mm, 20 Mm and 25 Mm) and evaluated in Agricultural College and Research Institute, Killikulam during 2014 in order to study their effects on qualitative traits of cowpea. The mutagenic treatment seeds were tested for lethal dose 50 percent for all mutagens and those in which 50 percent seed germinated was considered as LD_{50} value. Then 300 seeds under each treatment along with control were raised as M_1 generation. In the present study, seed germination holds good in tirunelveli local for both physical and chemical mutagenesis when compared to Co7, viz.,(95, 93, 54, 49, 46 % in local - gamma) and (92, 86, 52, 47, 40 % - EMS), anthocyanin pigmentation was reported 15 % in chemical mutagenesis of tirunelveli local and few early flowering mutants of 34 days duration (1 %) was noted in Co7 in 35 KR. Besides, different shape and size mutants were observed in gamma ray treatments.

PI-166

GENETIC VARIABILITY STUDY IN F_2 AND F_3 GENERATION OF RICE (*Oryza sativa* L.)

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The present investigation was carried out at Agricultural College and Research Institute, Killikulam during 2011-13. The experimental material consisted of two generations (F_2 and F_3) obtained from two crosses using four parents laid out in a randomized block design with three replications to study the genetic variability, heritability and genetic advance for eleven characters *viz.,* plant height, number of productive tillers per plant, panicle length, days to 50% flowering, number of grains per panicle, 1000 grain weight, hulling percentage, milling percentage, length breadth ratio, amylose content and single plant yield. Analysis of variance revealed that significant differences among the genotypes for all characters, indicating a high degree of variability in the genetic material. In this study, the estimates of phenotypic coefficients of variation for all the characters were higher than the estimates of genotypic coefficients of variation. The difference between GCV and PCV is narrow for most of the character indicating predominance of genetic components. High values of heritability and genetic advance were observed for the traits number of productive tillers per plant and single plant yield in second and third filial generations of cross1 (ACK 09009 x ADT 43). Whereas in cross 2 (IR 8 x ASD 16) the traits plant height, number of productive tillers per plant, number of grains per panicle and single plant yield showed high heritability and genetic advance as percent of mean. It indicates that these traits are controlled by additive gene action, thus offering the possibility of crop improvement through selection.

PI-167

ASSOCIATION OF GRAIN QUALITY TRAITS IN RICE IN THE F_2 POPULATION OF THE CB 04 110 x KDML 105

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Rice is the staple food for more than one third of the world's population and improving the grain quality is one of the major breeding objectives in rice. In the study, correlation analysis was carried out for grain quality traits in the F_2 population of the CB 04 110 x KDML 105 cross at the Paddy Breeding Station, CPBG, TNAU, Coimbatore from 2006-2009. Hulling percent showed significant positive correlation with milling percent (0.767), HRR% (0.633) and with thousand seed weight

(0.15). Milling percent showed significant positive correlation with HRR% (0.810). HRR% recorded significant negative correlation with thousand seed weight (-0.135), length (-0.346), L/B ratio (-0.319) and LAC (-0.238). This indicated that longer grains tend to break more easily during milling. Thousand seed weight showed significant positive correlation with grain length (0.538), grain breadth (0.382), L/B ratio (0.183) and LAC (0.356). Grain length recorded significant positive correlation with L/B ratio (0.748), LAC (0.567) and significant negative correlation with LER (-0.237). Grain length showed positive correlation with ASV (0.128) and WAW (0.174). Grain breadth showed significant negative correlation with L/B ratio (-0.581) and BER (-0.323). L/B ratio showed significant positive correlation with LAC (0.430), BER (0.184) and ASV (0.170) and LER (-0.164). LAC recorded significant positive correlation with LER (0.665) and WAW (0.304). Thus a selection of genetic material with high LAC would result in simultaneous increase in LER. Thus interdependence of the different quality traits will help in the efforts for selection of elite genetic materials possessing best quality traits.

PI-168

ANTIOXIDANT ACTIVITY IN MEDICINAL LAND RACES OF RICE

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Rice landraces have evolved through generations and these colored rices (black and red) are rich in minerals (iron and zinc) and polyphenols and have antioxidant properties were popular in farmer's fields. Free radical-induced oxidative stress is the root cause for many human diseases, naturally occurring antioxidant supplements from plants are vital to counter the oxidative damage in cells. the antioxidant potential of rice grains obtained from different medicinal landraces of rice: Njavara, chennallu (from Kerala) Kavuni, Veeradhangan, Kathanellu (from different districts of Tamil Nadu) were characterized along with eight cultivated released high yielding varieties of rice *viz.,* MDU 5, ADT 36, ADT 43, ADT 45, TPS 4, ASD 16 and IR 72 and selected hybrids. Methanolic extract of dehusked rice grain-powder were used to study their in vitro antioxidant activities by scavenging of 1,1-Dipheny1-2-picrylhydrazyl (DPPH) radical. Rice grain methanolic extract from Njavara, Chennallu, Kavuni, Veeradhangan, Kathanellu showed the significant antioxidant potential by scavenging of 1,1-Diphenyl-2- picrylhydrazyl (DPPH) radical and IC50 values for scavenging DPPH. So, these landraces of rice could be exploited as one of the potential sources for plant - based pharmaceutical products.

PI-169

PARADIGM SHIFT IN BREEDING FOR SUGARCANE TO ENERGYCANE - AN EXCLUSIVE BIOFUEL CROP

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Self-sufficiency in sugar production has been achieved for the past 15 years and in addition surplus sugar is also produced after meeting out the domestic demand. Unfavourable international sugar price and large carry-over of stocks has economically weakened the sugar industry which is looking for alternate generation of income. A new concept of using sugarcane as an exclusive biofuel crop has been conceived by sugarcane breeders and development of such energycanes would serve as a feed stock for cogeneration and alcohol production. Energycane development aims at improving harvestable biomass (HBM), dry matter production (DMP), fibre content, tillers count, amenable for mechanical harvesting and suitable for cultivation in marginal lands and suboptimal management conditions. Energycane breeders were looking for appropriate related wild species for introgression breeding and identified *S. spontaneum*and *Erianthusarundinaceus* as candidate species. The first and second generation hybrids involving *S. spontaneum* generated more number of type I energycanes (>20% fibre and >15 % juice Brix) notably SBIEC 11002, SBIEC 11103 and SBIEC 11005 recorded the > 70 t/ha of dry matter production. Hybrids involving *E. arundinaceus* resulted in type II energycanes (> 25 % fibre) notably SBIEC 11001 and SBIEC 11004 recorded > 75 t/ha of DMP. These clones were tested under drought, water logging, alkaline, suboptimal management conditions and superior clones were selected which can be planted where food crops cannot be cultivated profitably hence no competition with other food crops. Performance of these clones under different abiotic stress and agroclimatic condition is discussed.

PI-170

NEW CMS LINES OF RICE (*Oryza sativa* L.) WITH GOOD OUT CROSSING TRAITS AND GRAIN QUALITY

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In hybrid rice research, CGMS is the most effective system being used to develop rice hybrids. Hybrid rice based on CMS, increases grain yield by more than 20% relative to improved inbred rice varieties. Four CMS lines *viz.,* COMS 27A/B, COMS 28A/B, COMS 29A/B and COMS 30A/B were developed under the background of JGL 384, ADT 39,ADT 43 and DE 2 with the wild abortive (WA) cytoplasm source of rice (TNAU CMS 2A, IR 80151A and DRR 12A) were evaluated for

various morphological, floral and agronomical traits at PBS, TNAU, Coimbatore. High pollen sterility (99.00%-99.9%) was also observed in all the CMS lines. Maximum out crossing was observed for the CMS lines, COMS 29A and COMS 30A. Panicle exertion varied from 60.00% to 78.04% and more than 65% panicle exertion were observed for the CMS lines COMS 29 and COMS 30A. The CMS line COMS 29A and COMS 30A were early (115 days) in flowering. Dwarfism is a desirable trait in rice. The data revealed that semi dwarf plant height was observed in all CMS lines. Based on quality traits, all the lines recorded intermediate GC and alkali spreading value. From the present study, it is concluded that CMS lines COMS 27A/B, COMS 28A/B, COMS 29A/B and COMS 30A/B are found promising for good phenotypic acceptability which offer better scope for utilizing these CMS lines for the development of high yielding rice hybrids.

PI-171

RECURRENT SELECTION FOR YIELD IMPROVEMENT IN SUGARCANE (*Saccharumspp*)

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With the increasing need for new sugarcane varieties and rapid increase in economic development, requirements for new sugarcane varieties gains utmost importance. Concerns exist that sugarcane yield may soon plateau or has already reached a plateau caused by exhaustion of genetic diversity. This study aims for population improvement through recurrent selection schemes with the aim of pyramiding desirable traits, particularly yield combining quality in required selection cycles. At Sugarcane breeding Institute, Coimbatore, population improvement programme for yield and quality through recurrent selection was initiated in 2007 with 40 diverse parents as base population. The mean cane yield increased with cycles of selection. Considerable phenotypic variation was found in the population as evidenced from the phenotypic standard deviation and the range increased from C_o to C_3. Genetic improvement was observed for both yield and quality traits. There was a substantial improvement for cane weight in four cycles of selection. Cycle 1 and Cycle 2 hybrids showed substantial improvement for cane height .C_3 hybrids showed an improvement of 12.21 %, 13.01%, 20.09% and 9.36 %, C_4 hybrids showed an improvement of 6.13 %, 9.19%, 22.21 % and 11.02% for cane height, cane thickness, cane weight and stalk number respectively in comparison to C_o .This new populations developed for yield traits can be introduced into breeding programs. The study suggest that further cycles of selection would result in additional improvement for yield and also indicate the potential of the recurrent selection which will be a good alternative for improving quantitative traits in sugarcane.

2. INNOVATIVE BREEDING TOOLS AND TECHNIQUES FOR CROP IMPROVEMENT INCLUDING MARKER ASSISTED BREEDING

PII-1

STUDIES ON PHENOTYPING AND GENOTYPING OF BC_2F_1 POPULATION FOR SORGHUM DOWNY MILDEW RESISTANCE IN MAIZE (*Zea mays*. L)

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Maize (*Zea mays* L.) is one of the most versatile emerging crops having wider adaptability under varied agro-climatic conditions. In India, maize is the third most important food crops after rice and wheat. Sorghum downy mildew caused by *Peronosclero sporasorghi* is considered as the top priority biotic constraint limiting maize productivity. The cost concerns and the emerging problem of buildup of chemical resistance in the pathogen point to the use of resistant varieties as a cost-effective and environmentally safe alternative for managing the disease. In the present study, UMI 936(w) was used as a donor parent to transfer downy mildew resistant QTLs into an lite inbred line, UMI 79 (recurrent parent) and further backcross progenies. Screening of the BC_2F_1progenies was done under sick plot conditions and phenotypically resistant individuals were identified which were backcrossed and forwarded to BC_3F_1generation.Forty BC_2F_1progenies were phenotypically screened under sick plot conditions and five progenies were identified as resistant for the Sorghum downy mildew. Using the sequence information obtained from the maize DB and from the reports of Nair *et al.* (2005), four SSR markers *viz*., phi053, bnlg420 which is located on chromosome 3 and bnlg1154, nc013 which is located on chromosome 6 were polymorphic between the parents were used to screen the phenotypically resistant BC_2F_1 progenies.The individuals having heterozygotes for four markers have been identified and forwarded to next generation.

PII-2

BREEDING FOR CROP IMPROVEMENT IN GROUNDNUT THROUGH INTEGRATED CONVENTIONAL-MODERN TECHNIQUE: CHALLENGE AND ASPECTS

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This article highlights timelines and breeding objectives regarding crop improvement in groundnut through combination of classical breeding, marker assisted breeding, molecular approaches, transgenic

breeding and innovative tools. Today it is one of the world's leading sources of oil and protein. The kernels are source of oil, protein, several vitamins, minerals, antioxidants, polyphenols, flavonoids, isoflavones .Quality trait include oil (45-50%), protein (20-25%), sugar, minerals (Zn, Fe), fatty acid, flavour, protein content, blanchability. High oil content and high oleic/linoleic fatty acid ratio are important targeted traits in latest breeding programs. Conventional breeding is significant but no longer sufficient because of time consuming, rapid changes in market demands, burden of undesired genetic material, Environmental factors. Main objectives of plant biotechnology are to produce novel products. Marker assisted breeding will be an ideal option for directed improvement of hundred kernel mass. Marker-assisted backcross breeding is used to minimize linkage drag. Deployment of molecular breeding technique is useful in groundnut improvement programs in India, USA and China. At ICRISAT, MABC technique is underway to develop cultivars with rust resistance. Various innovative tools like QTL mapping, Peanut Genome Project (PGP), Genotyping-by-sequencing (GBS), genomics, proteomics, DNA sequencing, genome-wide association studies (GWAS) (genomic-estimated breeding values, GEBVs), biofortification, and genomic tools are used for crop improvement in groundnut. The goal of breeding in groundnut for crop improvement is to improve yield and quality traits especially oil and protein content.

PII-3

APPLICATION OF TILLING AS A REVERSE GENETIC APPROACH FOR CROP IMPROVEMENT

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Recent advances in large-scale genome sequencing projects have opened up new possibilities for the application of mutation techniques in basic studies and in the improvement of crops. The reverse genetics strategy (from gene sequence to phenotypes) has widely replaced the forward approach in studies involved in detecting gene function. This strategy is based on the alteration of a gene structure or its activity, followed by an analysis of the associated change in plant phenotype. Several reversegenetics technologies, such as insertional mutagenesiswith TDNA,transposon/retrotransposon tagging or gene silencing using RNA interference, have been proposed for plant functional genomics. TILLING (Targeting Induced Local Lesions IN Genomes) was developed a decade ago as an alternative to insertional mutagenesis in *Arabidopsis thaliana* (McCallum *et al.* 2000). Perry et al. (2009) identified a large allelic series for 12 genes known to be essential for nodule development in *L. japonicus*. A total population of 4,904 M2 plants was screened and 97 mutant alleles were detected. All possible types of mutation were identified: silent alleles that caused no change in amino acid, changes in splice sites and missense to nonsense types. This unique data set, which combines genotypic and phenotypic information, is an excellent tool for structure-function studies. Among the mutants identified, 19 alleles did not have an effect on gene function and 78 influenced the phenotype, including lines where nodulation deficiency was observed.

PII-4

EST-SSR MARKERS FLANKED TO FUSARIUM WILT RESISTANCE IN SAFFLOWER

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Safflower (*Carthamus tinctorius* L.) is an important edible oilseed crop grown in winter season in rainfed areas in India. Fusarium wilt incited by *Fusarium oxysporum* f. sp. *carhami* is the major disease in safflower. Repeated cultivation of safflower in the same field has been aggravating wilt in major safflower growing areas in the country. Cultivation of a resistant cultivar is an effective way to surmount this soil-borne disease. Accurate selection of wilt resistant genotypes is crucial in resistance breeding. Molecular markers are of great use in accurately selecting resistant genotypes. Hence, an attempt was made to identify molecular markers flanked to wilt resistance in safflower. A total of 250 EST-SSR markers were used for this purpose. Bulk-segregant analysis was applied in F_2 generation of a cross between wilt susceptible parent, Nira and a resistant parent, 96-508-2-90 in order to identify EST-SSRs flanked to wilt resistance. Four EST-SSRs have co-segregated with wilt resistance. The F_2 generation and parents were also phenotyped in wilt sick plot for wilt resistance. Wilt reaction of F_2 plants and parents was recorded in wilt sick plot at one moth interval from 15 to 120 days after planting. Wilt resistance exhibited monogenic dominant (3:1) inheritance in wilt sick plot. One EST-SSR has confirmed the 3:1 segregation of resistance and susceptible F_2 progenies observed in wilt sick plot, thus validating its reliability in marker-assisted selection for wilt resistance in safflower. Using this marker wilt resistant F_3 progenies were identified which have further confirmed resistance in wilt sick plot.

PII-5

TAGGING OF GENE(S) FOR RESISTANCE TO POST FLOWERING STALK ROT IN MAIZE (*Zea mays*) CAUSED BY *Macrophomina phaseolina*

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Maize is one of the most important economic cereal crops and an ideal forage crop. Maize suffers from about 110 diseases on a global basis. Out of these, post flowering stalk rot(PFSR) caused by *Macrophomina phaseolina* is the important disease of maize in Andhra Pradesh. In order to tag the PFSR resistant gene maize inbred lines BPPTI-34(resistant) X BPPTI-66 (susceptible), were crossed to produce F_1. F_1s were selfed as well as back crossed to the susceptible parent to derive F_2 and BC_1F_1 populations respectively. Parents P_1 and P_2, F_1 and two mapping populations (F_2,BC_1F_1) were artificially inoculated with *Macrophomina phaseolina* culture. F_1s inoculated with culture showed resistant reaction revealing for that resistance for PFSR is governed by dominant gene. F_2 population segregated in 3:1 (87 resistant:27 susceptible) and BC_1F_1 population segregated in the ratio of 1:1(26 resistant:24 susceptible) showing that resistance to PFSR is governed by single dominant gene. A total of 150 microsatellite markers distributed on entire genome were used to screen the parents. Of these, 54 SSR markers from ten chromosomes were found polymorphic in the parents. These 54 markers were used to screen the bulk DNAs prepared from 10 plants each of resistant and susceptible individuals from F_2 and BC_1F_1 populations to find the markers linked to the resistance gene. By bulked segregant analysis (BSA), the EST marker *umc*1269 clearly distinguished resistant, susceptible bulks and individual plants used in bulks indicating that this marker is tightly linked to the gene for resistance to PFSR.

PII-6

DEVELOPMENT OF GENETIC AND GENOMIC RESOURCES FOR ABIOTIC STRESS TOLERANCE IN HORSEGRAM (*Macrotyloma uniflorum* (LAM.) VERDC)

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Horse gram is a drought hardy poor man pulse crop with a huge potential to be converted in to a major legume crop in India. It is known for its medicinal properties and usage as legume fodder. It can grow in a wider range of climatic zones with a huge diversity. The National Gene Bank holds the largest collection of Horsegram accessions in the world and is being continuously augmented. To make use of this effective germplasm we started an effort in developing genetic and genomic resources by rigorous germplasm evaluation to develop a core collection. From this core collection of around 320 accessions twenty moisture stress responsive accessions were identified. Using two of these contrasting accessions a SSH library was constructed which lead to the identification of handful of effective genes elucidating the molecular mechanism of moisture stress tolerance in Horsegram. The comparative proteome of the same was used to confirm the results obtained from SSH library construction. Apart from that miRNAs were identified in regulating the stress response of horsegram. Further to use the core collection and the exotic germplasm sources available in horsegram, we have developed a mapping population using this contrasting accessions and a SSR enrichment library has been developed for effective utilization of germplasm, fingerprinting of accessions and varieties as well as mapping of genes.

PII-7

IDENTIFICATION OF MOLECULAR MARKERS LINKED TO FERTILITY RESTORER GENE IN A2 CYTOPLASM MALE STERILITY OF PIGEON PEA [*Cajanus cajan*]

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In pigeonpea the cytoplasmic-genetic male sterility (CMS) system is considered to be feasible approach to develop hybrids. Identification of CMS lines and their putative restorers using molecular markers in the early stage of growth is an important and economical in long duration pigeonpea. The study was executed for ascertaining molecular markers (SSR and RAPD) for fertility restoration gene in male sterility entailing A2 cytoplasm of *Cajanus scarabaeoides* in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Based on phenotyping, the 120 plants of F_2 designated as fertile and sterile. Both visual and pollen staining phenotyping unequivocally exhibited 85 fertile: 35 sterile plants in F_2 population. The segregation of F_2 for fertility restoration of A2 cytoplasm indicated $3F_1S$ segregation indicating dominant monogenic control of fertility restoration. Bulk segregating analysis revealed that 2 of the 139 polymorphic decamer RAPD markers *viz.*, OPC 7617 and OPK 3860 produced precisely distinct bands subjective to fertility restorer DNA bulk while, none of the SSR was found polymorphic between bulks. Based on linkage analysis in F2 individual plants the markers were found at 0.5 and 1.0 cM respectively They could be exploited as a precise selection tool for seminal but stubborn character like restoration of fertility in male sterile lines that has germane significance in otherwise immensely important heterosis breeding in pigeonpea.

PII-8

GENETIC DIVERSITY STUDIES OF QUALITY PROTEIN MAIZE USING RAPD MARKERS

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Randomly amplified polymorphic DNA markers were used to assess the genetic diversity among thirty three maize inbred lines and seven Quality Protein maize lines of maize. A total of 40 operon decamer primers were screened in duplicate and 14 of these primers were selected for further testing. A total of 112 markers were amplified with 14 primers with an average of 8.0 DNA bands per primer. Among the 112 markers, 94 were found to be polymorphic and the percentage of polymorphism was 83.92 per cent. A total of 12 fragments were amplified with primer OPAW 20

and a minimum number of 3 bands were amplified with primer OPAL-10. The approximate size of the largest fragment amplified was in the range 3.0 to 3.5 kb the smallest easily recognizable fragment amplified was approximately 0.3 kb. Maximum d value of 0.96 was observed between UMI 814 and CML 118, and the least distance was observed between UMI 889 and UMI 57. The nature of relationships among the genotypes as revealed by their genetic distances largely involved similarities with the exception of some pairs, which displayed divergence. The most plausible explanation for the comparatively low genetic distances between the populations is that they might probably have descended from a common ancestral population.

PII-9

STUDY OF MUTAGENIC EFFECTS OF EMS ON FIELD PEA (*Pisum sativum* L. var. *Arvense*)

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A study was conducted to determine the sensitivity of EMS (0.05%, 0.1% and 0.15%) on three varieties of filed pea *viz.*, HFP-554, Prakash and Rachna. In M_1generation the pollen fertility showed a negative dependence on the dose of EMS *i.e.,* it decreased with the increasing concentration of the mutagen in all the three varieties. Lowest value of pollen fertility was recorded in variety HFP-554 (68.57%) at 0.15% EMS. Four types of chlorophyll mutations were screened from M_2population which is*chlorina*, *albina*, *xantha* and *viridis*. *Chlorina* type of chlorophyll mutation was induced with highest frequency at all the concentration regardless of variety. Higher concentrations of EMS was observed to induce wider spectrum of chlorophyll mutation in all the three varieties. The overall spectrum of chlorophyll mutations induced in field pea was in the following order; *chlorina* (52.46%)>*viridis* (24.59%)>*xantha* (18.03%)>*albina* (4.95%). In the present investigation, magnitude of mutagenic effectiveness showed a varied response on the one hand it decreased with the increasing concentration of EMS on varieties HFP-554 and Rachna, while on the other hand an increasing trend of it was observed in the variety Prakash. The efficiency of EMS for most of the treatment decreased with increase in the concentration in HFP-554 and Rachna varieties but for Prakash it increased with the concentration in a decreasing trend. The intermediate dose of EMS *i.e.,* 0.1% was found to be efficient in inducing good amount of chlorophyll mutation with higher efficiency.

PII-10

EFFECT OF DIFFERENT PLANTING DATES ON STALK YIELD, SUGAR CONTENT AND ESTIMATED ETHANOL YIELD OF SWEET SORGHUM FOR INCREASED HARVEST WINDOW

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Sweet sorghum unlike grain sorghum has a potential to accumulate sugars in its fresh stalks similar to sugarcane. Ethanol yield potential of sweet sorghum cultivars was assessed at different dates of sowing in monsoon season in order to determine their economic feasibility for commercial production. This study was conducted to determine suitable time of planting sweet sorghum during Kharif season and the experiment was conducted at the farm of the Nimbkar Agricultural Research Institute to evaluate the effects of different planting dates on fresh stalk yield, juice yield, sugar content and ethanol yield of sweet sorghum in Kharif-2010, 2011 and 2012. Three varieties viz. SSV-84, SSV-74 and CSV-19-SS and one hybrid CSH-22-SS were evaluated at five different planting dates (June 1, June 16, July 1, July 16 and July 31). Plant height, fresh stalk yield, juice yield and ethanol yield were affected due to different planting dates. For all the characteristics, the maximum value was obtained for the first planting date. The performance of cultivars showed that the hybrid CSH-22-SS is the best for all the parameters followed by SSV74. Interaction studies of dates of sowing with cultivars for ethanol yield and Total Sugar Index (TSI) showed significantly highest ethanol yield and TSI being recorded for hybrid CSH-22-SS in all the dates of sowing followed by SSV-74 and SSV-84. The study thus recommends hybrid CSH-22-SS as the most suitable cultivar not only for normal planting time but also for late planting for achieving the highest ethanol yield.

PII-11

COMPARISON OF THE EFFECTS OF PHYSICAL AND CHEMICAL MUTAGENS IN SESAME (*Sesamum indicum* L.)

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The effect of treatment with physical (gamma rays) and chemical (EMS) mutagens on seed germination, seedling survival, pollen fertility in three genotypes of sesame *viz.*, CO 1, Paiyur 1 and TMV 4 was studied. Three doses in each of gamma rays (400 Gy, 500 Gy and 600 Gy) and EMS (0.75%, 1.0% and 1.25%) were applied to each of the three genotypes. Lethality and pollen sterility was observed in M_2 generation to understand the efficiency and effectiveness of the mutagens and mutagenic doses in respective genotypes. There was an gradual decrease in germination, seedling survival and pollen fertility with an increase in dose of mutagen in the genotypes. The efficiency estimates of

each mutagen based on lethality and pollen sterility varied widely indicating differential genotypic response to mutagenic doses. In all the three genotypes, 500Gy of gamma irradiation is found to be more effective in inducing variation. In EMS treatment, 0.75% was effective in CO 1 and Paiyur 1, whereas 1.00% was effective in TMV 4. In respect of efficiency on the basis of lethality, 600Gy of gamma irradiation was found to be efficient in all the three genotypes. In EMS treatment, the efficient doses identified were 1.25% for CO 1 and Paiyur 1; 1.00% for TMV 4. On the basis of sterility, 500Gy was efficient for inducing pollen sterility in three genotypes studied. The dose of 1.25% EMS for CO 1 and Paiyur 1 and 1.00% EMS for TMV 4 were identified as efficient doses in inducing the pollen sterility.

PII-12

INSILICO IDENTIFICATION OF POTENTIAL MARKERS FOR DETERMINACY IN TOMATO

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Tomato is a major vegetable crop that has achieved tremendous popularity over the last century. The Indian market value for tomato highly fluctuates because of the season bound nature of the crop and the use of determinate varieties. Determinate type of tomato is preferred by the farmer for cultivation because of the short duration and easy maintenance and harvest. However indeterminate type of tomato is suitable for greenhouse cultivation and can yield consistently throughout the year. Identification of potential markers for the growth habit (determinate and indeterminate) can be used to improve the tomato cultivars based on the preference of farmers and consumers. This study focuses on identifying the genes that are involved in controlling the growth habit of tomato. Available SNP data of 6 tomato cultivars of both determinate and indeterminate types were compared. All the SNPs which differentiated the determinate nature of the crop were selected from the SNP data. Among them the SNPs within the transcribed region were considered for further analysis. The list of genes containing the selected SNPs were analysed and genes involved in plant growth and flower development alone were selected. Out of 254 SNPs in 117 genes, 38 SNPs in 12 genes were found to be involved in the regulation of growth habit. These potential SNPs can be validated for differentiating Indian cultivars by DNA analysis and be possibly involved in marker assisted breeding programs.

PII-13

GENETIC DIVERGENCE IN GROUNDNUT (*Arachis hypogaea* L.) USING MOLECULAR MARKERS AND COMPARISON WITH CONVENTIONAL D^2 DIVERGENCE ANALYSIS

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Twenty four genotypes of *Arachis hypogaea*(L.), belonging to Virginia and Spanish varieties were

used to study the genetic divergence within its botanical varieties using RAPD and 5 agro-morphological characters. Twenty primers belonging to OPH were used in the study. Out of the 20 primers, 16 primers produced 36 and 37 bands in Virginia and Spanish group, respectively. Out of the total bands produced, 18 and 20 bands were polymorphic for Virginia and Spanish group, respectively. Jaccard similarity coefficient for Virginia group ranged from 0.09 to 0.78 and for Spanish group, it ranged from 0.13 to 0.88. The D2 values ranged from 8.33 to 312.57 and from 5.32 to 452.33 for Virginia and Spanish group, respectively.Comparing both the UPGMA dendrograms of genetic divergence analysis by molecular markers and agro-morphological data, it was found that there was little likeness between them. Considering the weak correlation between molecular and morphological genetic divergence analysis, a combine analysis of both molecular markers and morphological method will be desirable. As the diversity predicted by the morphological analysis could not depict the clear-cut and reliable diversity of the germplasm all the genotypes should be subjected to molecular analysis before using them for further breeding programmes in groundnut improvement.

PII-14

DEVELOPMENT AND GENETIC ANALYSIS OF INTER SUB-SPECIFIC RECOMBINANT INBRED LINE POPULATION IN BLACK GRAM (*Vigna mungo* (L.) HEPPER)

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Blackgram (*Vigna mungo*) is fourth important pulse crop of India. Major constraints in achieving higher yield of blackgram are absence of suitable ideotypes for different cropping systems, poor harvest index and susceptibility to pests and diseases. Genetic maps can be constructed based on mapping population. Among the mapping populations, Recombinant Inbred Lines (RIL) is more advantages than others. In the present study, an inter sub specific RIL population was developed by crossing VBN(Bg) 4 x *Vigna mungo* var. *silvestris*22/2 by single seed decent method. A total of 195 RILs were evaluated for 11 biometrical traits. RIL 113 recorded the highest mean for single plant yield (9.90 g) along with more number of pods plant (42.84). RIL 125 recorded the maximum yield of 8.93g per plant along with more number of clusters per plant (17.50) and RIL 131 had single plant yield of 7.99 g along with more number of pods per plant (34.00). Transgressive segregants were observed for all the traits. Normal frequency distribution was observed days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per cluster, number of pods per plant and 100 seed weight indicated that, genetic nature of mapping population is normal and could be used in the mapping of genes for important traits. RILs with high yield and yield attributing traits can be used to develop high yielding varieties. RILs isolated with specific traits could be used as pre breeding material for the improvement of blackgram.

PII-15

SELECTION CRITERIA IN M_3 AND M_4 POPULATIONS OF SESAME (*Sesamum indicum* L.)

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In the present investigation, M_3 and M_4 generations of two popular *Sesamum* varieties *viz*., SVPR 1 and Cardeboriga obtained from different doses of gamma rays and EMS treatments were studied to work out the importance and significance of the most suitable characters to be exploited at the time of selection to improve seed yield in mutated population of sesame. For this purpose sesame cultivars were irradiated with five doses of gamma rays *viz*. 30, 40, 50, 60 and 70 Krad and EMS *viz*. 0.8, 1.0, 1.2, 1.4 and 1.6 per cent. At maturity, data on morphological traits like days to 50% flowering, plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight, single plant yield and oil content were recorded and analyzed for correlation coefficient and path analysis. Number of capsules per plant, 1000 seed weight and plant height showed significant and positive genotypic correlation with single plant yield in both M_3 and M_4 generations of two varieties. Among the varieties, Cardeboriga exhibited more association between the different characters with yield and also inter correlation among the component traits in both the generations. Positive direct effects were observed for number of capsules per plant and 1000 seed weight on single plant yield. It may be concluded that for direct selection maximum emphasis should be given primarily to number of capsules per plant followed by 1000 seed weight.

PII-16

MARKER ASSISTED BACKCROSS APPROACH FOR ENHANCED OLEIC ACID CONTENT IN SUNFLOWER (*Helianthus annuus* L.)

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Marker assisted backcross is routinely applied for the introgression of desired gene in plant breeding programmes. Highly healthy sunflower oil with high oleic acid content may gain market value for food and industrial purposes where high oxidative stability is required. The phenotypic based methods used to select high oleic genotypes in breeding programmes require additional season for phenotypic evaluation in each backcross generation. It also requires quantification of oleic acid content on sunflower seeds using gas chromatography which is time consuming and environmentally affected. Hence marker assisted backcross was carried out in this study for the effective transfer of the high

oleic gene from potential donor inbred, HO 5-13 to recipient parents, COSF 7B and CSFI 99. In the present investigation, molecular marker tightly linked to the oleatedesaturase high oleic (*OD-HO*) allele and polymorphic markers were used to apply foreground and background selection respectively in backcrosses between a high oleic donor and two low oleic recurrent parents. In BC_4F_1 generation, one high oleic plant in each cross were identified that possessed recurrent parent genome (>97%) with *OD-HO* allele. Phenotypic analysis of oleic and linoleic acid content was conducted using near-infrared reflectance spectroscopy (NIRS) which revealed oleic acid composition of 80.47 to 85.42% in sunflower seeds. Thus marker assisted backcross approach serves the purpose of efficient transfer of high oleic gene into elite sunflower inbreds which infers sustainable saving in time compared to conventional backcross breeding.

PII-17

GENOME WIDE ASSOCIATION MAPPING AND GENOMIC SELECTION FOR LEAF TIP NECROSIS AND PSEUDO BLACK CHAFF IN RELATION TO DURABLE RUST RESISTANCE IN WHEAT

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In this fascinating era of genomics, innovative crop improvement techniques like Genome Wide Association Studies (GWAS) and Genomic Selection (GS) provide an excellent solution to the burgeoning need of increasing the gain from selection. GWAS is a powerful tool for crop genetic improvement due to its potential to genetically dissect complex traits and identify significant correlations between phenotypes and underlying sequence variations. Genomic selection (GS) is a new approach for improving quantitative traits in large breeding populations that uses genome wide markers to develop a training/prediction model. Besides accelerating the selection cycles, GS offers the opportunity to increase the selection gains. The availability of Genotyping by Sequencing(GBS) markers, provide an attractive option for GWAS and GS. Besides considerably increasing the efficiency of selection, GBS is very economical and aids in the *de novo* marker discovery.The partial rust resistance genes *Lr34* and *Sr2* have been used extensively in wheat improvement as they confer exceptional durability. Interestingly, the resistance of *Lr34* is associated with the expression of Leaf Tip Necrosis(LTN) and *Sr2* with Pseudo Black Chaff (PBC). Hence, GWAS was employed for 500 CIMMYT lines to identify GBS markers linked to LTN and PBC. Phenotyping for these traits was done in U.S.A., Kenya and Wellington. Using the Mixed Linear Model (MLM), 21 and 15 GBS markers were identified to be significantly associated with LTN and PBC respectively. Genomic Selection for these traits also gave promising prediction accuracies. Thus, this study shows the successful employment of GWAS, GS and GBS markers in selecting for complex quantitative traits.

PII-18

MARKER ASSISTED SELECTION OF FAVOURABLE *crtRB1* ALLELE FOR DEVELOPMENT OF HIGH â -CAROTENE MAIZE

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Maize is a globally important crop, which has got huge potential for larger utilization as food sources for human and animals and raw materials for industry. Enriching corn with vitamin A (provitamin A biofortification) through breeding efforts will serve and assure the human population feeding on maize with enriched â carotene, which will be one of the solutions for Vitamin A deficiency. The predominant carotenoid compound â-carotene in maize grain has the highest pro-vitamin A activity and is present only in a relatively low concentration in maize kernels. Therefore, identification of superior maize inbreds with high â-carotene content by characterizing maize germplasm and subsequent transfer of the high â carotene traits from the superior lines to the adapted maize cultivar through introgression breeding are indispensible. Due to a mutation called 3-TE polymorphism, the *crtRB1*gene (which encodes â-carotene hydroxylase 1 and plays an important role of â-carotene metabolism in maize kernels) exists in the three allelic forms, *viz.,* 3-TE allele 1 (which favors higher â carotene accumulation in kernels), 3-TE allele 2 and 3TE allele 3 (the last two alleles do not favor â-carotene accumulation). Therefore, in this study, we aimed to biofortify a well adaptedagronomically superior inbred UMI 1200by transferring the favorable allele 1 of *crtRB1* from high â-carotene line HP467-15through marker-assisted backcross breeding (MABB). These lines can be used as parent in future hybridization programs for obtaining high â-carotene, high-yielding maize hybrids.

PII-19

IDENTIFICATION OF QTLs FOR YIELD AND YIELD COMPONENT TRAITS IN SESAME (*Sesamum indicum* L.)

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Sesame is one of the oldest oilseed crop in India valued for its high oil content and quality. Quantitative trait loci (QTL) mapping was carried out in randomly selected 94 progenies of F_2 segregating population

of Paiyur 1 × SVPR 1 for yield and yield component traits in sesame. Seed coat color is an important agronomic trait in sesame as it is associated with seed biochemical properties, antioxidant content and activity. Out of 100 ISSR and 10 SSR primers screened, 18 primers were found to be polymorphic for the parents. Among them, four markers were linked with various phenotypic traits in single marker analysis. ISSR811 and ISSR840 had significant association with number of branches per plant. Primer combination ISSR818_826 with number of capsules per plant, SSR primer GBssr-sa-72 with seed color and ISSR811 with seed yield per plant showed significant association. The phenotypic variation explained (R^2) ranged from 3.8 (ISSR811 for number of branches per plant) to 9.1 (GBssr-sa-72 for seed color). Composite interval mapping performed at LOD 3.00 identified nine QTLs for three traits in two linkage groups. Six QTLs for seed color (LG 1 and LG 2), two for seed yield per plant (LG 1) and one for number of capsules per plant (LG 1) were detected in this study. These QTLs may be further validated and utilized in marker assisted breeding of sesame.

PII-20

MAPPING SALT TOLERANCE QTL IN RICE BY SELECTIVE GENOTYPING

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The study was to confirm QTLs on Chromosome 1 for seedling stage salt tolerance in rice by selective genotyping with the previously identified QTLs. F_2 population ($N = 697$) of a cross between salt-sensitive ADT 45 and a salt-tolerant FL 478 was evaluated for salt tolerance in hydroponics. Salinity was imposed fourteen days after sowing and maintained at EC 12 dS/m for eighteen days in green house. Forty seven highly tolerant (score three) and thirty most susceptible (scored nine) plants were selected for analysis of Na^+, K^+ contents and ratios in shoot and root respectively. Partial linkage map of chromosome 1 was constructed using 13 polymorphic markers and linkage order of all markers was same to that of previous maps. Selective genotyping approach led to the identification of five QTLs for shoot Na^+ concentration, shoot Na^+: K^+ ratio, root Na^+ concentration, root K^+ concentration and root Na^+: K^+ ratio and that were clustered together in the *Saltol*region. All the five QTLs were previously identified for this trait in earlier studies (Gregorio, 1997 and Bonilla *et al.* 2002) and thus were validated. Conformity between the results of the studies indicated the genuine nature of the identified QTLs and their potential usefulness for salt tolerance breeding using marker-assisted selection (MAS). A set of SSR markers comprising RM493 on distal and RM1287 on proximal ends with RM3412 as peak marker flanking *Saltol* region will be very ideal for marker assisted backcrossing for improving salt tolerance.

PII-21

MARKER ASSISTED BACKCROSSING (MABC) FOR INTROGRESSION OF *Sub1* LOCUS IN RICE FOR SUBMERGENCE TOLERANCE

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Short-term submergence regularly affects rice growing areas in South and Southeast Asia. A major QTL (*Sub1*) explaining about 70% of phenotypic variation in submergence tolerance has been identified and fine mapped on chromosome 9 in the submergence tolerant cultivar FR13A. This provided an opportunity to apply marker assisted backcrossing (MAB) to develop submergence tolerant versions of rice cultivars that are widely grown in the region. In the present study, molecular markers that were tightly linked to *Sub 1* QTL (*SUB1BC2*-gene based marker) and flanking *Sub1* (SSR markers namely RM 23805 and RM 23935) were used to apply foreground and recombinant selection, respectively, in backcrosses between a submergence tolerant donor (Swarna*Sub1*) and widely grown mega variety ADT 46 (recurrent parent). 343 BC_1F_1 seeds were produced, of which only four single recombinants were identified. Plant no171 for RM 23805 on the proximal end and plants with No.121, 150 and 152 for RM 23935 on the distal end were the single recombinants and inter crossing between the single recombinants and backcrossing with ADT 46 to produce BC_2F_1 are in progress. It is expected that the mega variety ADT 46 could be efficiently converted to a submergence tolerant variety in few backcross generations, involving a time of two to three years. This approach demonstrates the effective use of marker assisted selection for a major QTL in a molecular breeding program.

PII-22

EXPRESSION ANALYSIS OF CANDIDATE GENES OF STARCH SYNTHESIS PATHWAY AND MICROGRAPH ANALYSIS OF ENDOSPERM IN HIGH RS RICE MUTANT 278 AND WILD TYPE ADT43

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Resistant starch (RS) is one of these components, and is defined as the sum of starch and starch degradation products that are not absorbed in the small intestine of healthy individualsdue to their resistance to enzyme digestion. RS although not a fiber; however can be considered so because it acts like soluble fiber in the gastrointestinal tract, thus providing the health benefits of fiber. Many studies on available related to rice quality trait improvement with transgenic technology. Use of transgenic technology in food grains and acceptance of people in question.Nowadays developing mutant population with gamma and screening of mutants for the specific quality trait can be one of the productive form of crop improvement. The high RS mutant 278 and wild type ADT 43 possessing the RS content of 7.26 % and 3.61% respectively were taken for qPCR analysis and micrographic analysis. The qPCR analysis of the six genes in both wild and mutant revealed the maximum downregulation of *SS IIIa* followed by *SS IIa*, *SBE IIb* and *GBSS I* in mutant compared to ADT 43. The micrograph analysis of endosperm has revealed that the crystallinity of starch granules in the high RS mutant was reduced round-shaped starch granules accumulated in the amyloplasts of endosperm cells, in contrast to the sharp-edged polygonal granules in the wild type.

PII-23

MAPPING SALT TOLERANCE QTL IN RICE (*Oryza sativa* L.) BY SELECTIVE GENOTYPING

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A total of 1156 F_2 population of a cross between salt sensitive ADT45 as female parent and a salt tolerant Nona Bokra as male parent was evaluated for seedling stage tolerance in hydroponics culture at EC 12 dSm^{-1}. The screening resulted in the identification of 131 tolerant and 48 susceptible extremes in F_2. Thirty six of the most tolerant and 24 most susceptible individuals were identified based on the salinity screening evaluation conducted in the F_2 and F_3 progeny populations. The 60 selected F_2 plants, representing the two extreme tails were genotyped for 70 polymorphic markers. A genetic linkage map, spanning 1795 cM was constructed with an average marker interval of 25.64 cM. Two approaches were used for QTL mapping in the study such as Trait based analysis (TBA) and Marker based analysis (MBA).TBA approach led to the identification of four genomic regions with a minimum of two closely placed markers showing significant deviations suggesting the putative location of QTLs for salt tolerance. A total of 16 QTLs were detected by employing MBA.One of the Saltol loci tightly linked to RM 3412 for shoot Na:K ratio showed a LOD score of 5.43 with 34 per cent phenotypic variation and other QTLs were co localized in the Saltol region. QTLs identified based on two methods on chromosomes 1,3,5,6 and 12 were correspond to the previously located regions for salt tolerance. Hence these may be the potential candidate QTLs for Marker assisted selection (MAS).

PII-24

GENETIC DIVERSITY, POPULATION STRUCTURE AND LINKAGE DISEQUILIBRIUM ASSESSMENT FOR ASSOCIATION MAPPING STUDIES IN COCONUT (*Cocos nucifera* L.) GERMPLASM

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The coconut germplasm comprising of 79 accessions were analysed for their genetic diversity, population structure and linkage disequilibrium. These include exotic and indigenous collections representing wider geographical regions. Genetic diversity was assessed using 48 SSR primers. The average number of alleles identified was five per locus and the number of alleles ranged from two to seven. Among 48 SSR primers, CnCirC5 shows the highest gene diversity of 0.81. PIC value ranged between 0.14 to a high of 0.78 with a mean of 0.52.Cluster analysis grouped the 79 coconut accessions into two major clusters with four sub-clusters. The clustering of accessions matched with the region of geographic origin. The first group comprised of tall coconut accessions belonging to Indo Atlantic regions and South Asian Islands. The second group consisted of all dwarf accessions along with talls belonging to Indo Pacific regions and South East Asia.The population structure analysis on 79 coconut accessions showed two distinct populations. Linkage disequilibrium estimation in coconut showed that 27 marker pairs out of 1128 loci combinations were in significant LD. Association analysis identified three SSR markers CnCir73, CnCirE4 on chromosome 1 and CnCir1 on chromosome 3, to be significantly associated with fruit components *viz.,* fruit breadth, fruit weight, nut weight, kernel weight and copra content. CnCirE4 was associated with fruit weight, kernel weight and copra content. CnCir1 was found to be associated with fruit weight. These three markers co-localized/mapped in the vicinity of reported QTL governing fruit component traits in coconut.

PII-25

MUTAGENESIS IN TWO VARIETIES OF SOYBEAN [*Glycine max* (L.) Merrill]

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Mutagenic effectiveness and efficiency of EMS and gamma rays were studied in two varieties of soybean namely Co(Soy)3 and JS 335 in terms of lethality and injury observed in M_2 generation. The parameters taken for analysis were chlorophyll and viable mutation frequency. The frequency of mutation was high at higher concentration/ dose of both the mutagens in both varieties of soybean. With increasing doses/ concentration of mutagen, mutagenic frequency was found to be higher while the efficiency was in decreasing trend. Wide spectrum of chlorophyll mutation comprising four types*viz.,* xantha, chlorina, viridis and albina were observed in M_2 generation. There was a linear relationship between the frequency of chlorophyll mutants and dose of the mutagen. The genotype JS 335 appeared to be more sensitive towards different treatments of gamma rays and EMS followed by Co(Soy)3. But, the spectrum of mutation was high in Co(Soy)3 than in JS 335. A number of viable mutants like, leaf mutants, stature mutants, flower colour mutants, duration mutants, pod and seed mutants, sterile and high yielding mutants were recorded in different mutagenic treatments. More number of viable mutants were recovered from lower doses of both mutagens in both varieties. EMS was found to be the most effective and efficient mutagen compared to gamma rays. Among the two varieties, JS 335 was found to be the most sensitive variety to both physical as well as chemical mutagen.

PII-26

MOLECULAR BREEDING FOR IMPROVING DROUGHT TOLERANCE IN RICE

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Rice is the second most important food crop of the world, feeding more than one half of the world’s population. Over 90% of rice is produced and consumed in Asia. Drought is an increasingly important problem limiting rice production in many areas of Asia. The annual losses due to shortage of water are estimated to be of 9.9 million tonnes of grain annually in Asia alone. Even though we have semi dwarf, high yielding, fertilizer responsive and high intensity agricultural practices responding varieties in rice, they fail to perform under rainfed conditions which faces frequent drought conditions. With the advancements in the field of molecular genetics, DNA markers especially SSR markers have been identified that co-segregate with QTLs for yield under stress by exploiting a drought tolerant genotype Apo (Venuprasad *et al*., 2009). Based on the above evidences, efforts were taken to introgress the major QTLs associated with drought tolerance in APO into an elite variety ‘Improved White Ponni’ through marker assisted selection. F2 population was genotyped using SSR markers linked to grain yield under stress and RILs harboring various combinations of QTLs were selected. Their progenies were tested for their level of drought tolerance under controlled stress conditions. Superior progenies possessing high yield potential and improved drought tolerance were selected and advanced to further generations. Few promising entries are being evaluated under MLT. Further, MABB approach was followed to develop drought tolerant versions of IWP for functional genomics studies. Progress and results obtained on the above subject are discussed.

PII-27

MARKER ASSISTED BACKCROSS BREEDING APPROACH TO IMPROVE SALINITY TOLERANCE IN ELITE RICE VARIETIES OF TAMIL NADU

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Salt stress is a major constraint across most of the rice producing areas. A major QTL namely "saltol" on Chromosome 1 associated with seedling-stage salinity tolerance in rice has been identified by exploiting a salinity tolerant genotype Pokkali which explained 43% of the phenotypic variation for shoot Na/K ratio (Bonilla *et al.,* 2002). In this study, attempts were made to introgress*saltol*region (11-12 Mb) of chromosome 1 from a tolerant rice variety FL 478 (Pokkali derivative) into IWP (Improved White Ponni) through marker-assisted selection (MAS). Hydroponic and pot culture studies revealed that FL 478 was found to tolerate salinity stress better than Improved White Ponni. Improved White Ponni (IWP) and FL 478 plants were raised under field conditions for the generation of true F_1 hybrids between IWP and FL 478. Genotyping was carried with *saltol* linked markers namely RM3412 for foreground selection and the plants harboring FL478 alleles were chosen. Recombinant selection was done by genotyping with the markers namely RM493 and RM8070. Background selection was employed to recover the genome of the recurrent parent. Advanced back cross progenies were produced and advanced upto BC_3F_4. A total of 6 BC_3F_4 progenies were identified based on yield performance and its closeness to recurrent parent for further multiplication and evaluation. Identified lines were further evaluated for their responses against salinity stress under hydroponic conditions. All the lines were found to exhibit improved level of tolerance against salinity stress.

PII-28

DIVERSIFICATION OF TRANSGENIC RESISTANCE FOR RICE TUNGRO DISEASE INTO POPULAR VARIETY ASD16 OF TAMILNADU THROUGH MARKER ASSISTED BACKCROSS BREEDING

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Rice is the primary source of food for more than half of the world's population. Rice Tungro is a viral disease caused by the joint infection of *Rice tungro bacilliform virus* (RTBV) and *Rice tungro spherical virus* (RTSV). In order to obtain transgenic resistance against RTBV, rice cultivar Pusa Basmati-1 was transformed to express the coat protein gene of an Indian isolate of RTBV. The transformed PB-1 showed a reduction of tungro symptoms. Hence, the present study was attempted to diversify this transgenic resistance for tungro from PB-1 into superior but highly susceptible

variety ASD 16 by following marker assisted backcross breeding. The promising variety ASD 16 was crossed with transgenic PB1 and the F_1 plants were repeatedly backcrossed with the recurrent parent ASD 16. The transgenic plants that contain the RTBV resistant transgene were identified in BC_3F_1 and BC_3F_2 population by PCR analysis using functional primer associated with that gene. These foreground selected plants were subjected to background analysis with polymorphic markers to find out the recurrent parent genome contribution. Background analysis of the foreground selected homozygous plants revealed that there is 100 per cent recovery of the recurrent parent genome. Phenotypic screening of the Transformed ASD 16 plants showed reduced Tungro symptoms.

PII-29

SCREENING OF RICE (*Oryza sativa* L.) GENOTYPES TO IDENTIFY GENETIC VARIATION IN ROOT GROWTH RESPONSE TO A WATER STRESS

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Drought stress is a common adverse environmental condition that seriously affects rice productivity worldwide. Root length and root system architecture are key determinants of the ability of a plant to access water and nutrients to support shoot growth in water limiting conditions. In order to look for genetic diversity in root growth within rice cultivars, a burette method was used to identify genetic variation in rates of root elongation in a water gradient similar to that found in field. Seedlings were grown on top of burette by using thread, with a gradient of water stress increasing towards the bottom of the burette which was drained up to root tips every 5 hr interval for 15 days. A root elongation ability of genotypes at decreasing water level was found suitable to identify genetic variation. This corresponds to a level of water stress in the field that reduces root growth by 50% or more. Contrasting genotypes that varied in the ability to reach the water gradients in burette were then evaluated for maximum root depth, root volume, root length density, total number of roots, root thickness, root dry weight and root to shoot ratio in the PVC columns on soil. Variation in root traits of rice lines in burette and soil columns was linked with field performance. Despite the complexity of the water stress and root traits, the results can be potentially used to explore genetic diversity in root traits for development of drought tolerant varieties.

PII-30

MARKER ASSISTED PEDIGREE SELECTION IN RICE (*Oryza sativa* L.) FOR SALT TOLERANCE

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An investigation on pedigree selection using combined MAS approach for improving salt tolerance in rice was carried out. F_2 and F_3 generations of *ADT45/FL478* cross were evaluated for seedling stage tolerance in hydroponics culture at EC 12 dSm-1. A total of 185 salt tolerant F_2 plants out of 1212 were identified. Based on yield 101 F_3 plant families were further screened in hydroponics as in F_2 and 280 plants with score 1 and 3 selected. In both F_2 and F_3 generations the distribution of salinity score, was normal indicating polygenic nature of the trait and low realized heritability of 0.27 was observed indicating the scope of marker assisted selection. Using Combined MAS approach, a total of 35 plants comprising of five homozygous salt tolerant plants (BBB type), 23 salt tolerant plants homozygous for two QTLs and heterozygous for one QTL and seven non *Saltol* tolerant plants (AAA type) were selected. Along with this two top yielders which are of HBA and ABA types, totalling 37 plants were selected and forwarded for further testing in F_4. These 37 plants, on genotyping with RID12 marker were grouped into 20 homozygous and five heterozygous red pericarped ones. Remaining 12 were white pericarped ones. Out of 280 salt tolerant F_3 plants 37 plants belonged to 26 families that yielded more than 45 g/plant were selected and forwarded to F_4 for further testing.

PII-31

ASSESSMENT OF GENETIC DIVERSITY IN GREENGRAM GENOTYPES USING SSR MARKERS

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Greengram (*Vigna radiata* (L.)Wilczek) is also known as mungbean is one of the important food legume crops and is a rich source of easily digestible protein. Assessment of genetic diversity in a crop species is prerequisite for its improvement. In the present study, genetic diversity in 18 genotypes of mungbean was assessed using SSR markers. Seven SSR primers derived from adzukibean were used for molecular analysis. All the seven primer pairs showed amplification. Seven primer pairs generated a total of 17 alleles. The number of alleles produced by different primers ranged from one to five with an average of 2.43 markers per primer. Polymorphism Information Content (PIC) value was calculated for six polymorphic primers. PIC value was highest for the primer CEDG 305 (0.670) followed by primer CEDG 068 (0.395) while, the lowest PIC value recorded by the primer CEDG 002 (0.201). The mean PIC value for polymorphic primers was 0.270. The number of alleles generated for the primers CEDG 305 and CEDG 68 were five and three, respectively. The higher PIC value indicated the informativeness of the primer pairs. Hence, the primer pairs CEDG 305 and CEDG 68 are considered to be worth in future studies in the field of taxonomical and genetic resource management of *Vigna* species. Cluster analysis grouped the 18 mungbean genotypes into three main clusters and two solitary clusters. These results on SSR markers could be useful in the assessment of genetic diversity and identifying diverse genotypes for further improvement of mungbean.

PII-32

CASTOR DATABASE: A PHENOMICS RESOURCES FOR CASTOR GERMPLASM

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Castor is an important oilseed crop and its oil is inedible but has multiple industrial and pharmaceutical applications. Castor germplasm collection is a useful genetic resource for improving seed quality and developing new cultivars. Because of this, the gemplasms of former varieties were now collected through exploration and grown in trial fields for conservation, evaluation and utilization getting genetically superior variety. For accessing about these entire Castor germplasms database was developed. In this database 294 Germplasm accessions were taken with 11 morphological characters *viz.,* Type of Internodes, Type of Inflorescence, Spike shape, Compactness of Inflorescence, Branching Pattern of the stem, lascination of Leaf, Petiole Length, Number of lobes in leaves, Height of the Plant, Length of Primary Spike and number of internodes present in the stem. The information is divided into two categories namely: Quantitative chararacters and Qualitative characters. Database search is categorized into four: i) Quick search ii) Detailed search iii) Descriptor and iv) TNAU Agritech portal. This database gives access to users for gaining knowledge about the different phenotypic characters of different germplasms. The results obtained here will be useful for choosing accessions as parents to make crosses in breeding programs, prioritizing regeneration of accessions for distribution, and establishing a core collection in germplasm managing programs.

PII-33

IN SILICO ANALYSIS FOR IDENTIFICATION OF CANDIDATE GENES ASSOCIATED WITH BPH RESISTANCE IN RICE (*Oryza sativa* L.)

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Brown plant hopper (BPH) remains as one of the major pest limiting rice productivity. Many genes/ QTLs responsible for resistance to BPH have been studied and mapped in rice by several researchers using classical as well as molecular methods. Jasmonic acid (JA) and Salicylic acid (SA) are well known and important global signal molecules for regulating the defense genes. Using these information, an attempt was made through insilico methods to understand the putative candidate genes responsible for BPH resistance. The rice sequence and annotation data (TIGR) and GRAMENE database

were utilized, to know the JA and SA biosynthesis genes underlying in regions where genes/QTL governing to BPH resistance was collocated. 119 markers intervals (43 major QTl and 76 minor QTL) were used, most of the markers were bolongs to RFLP,AFLP, SSR and SST. The genes located in the QTL region was predicted by aligning it with a publicly available JA and SA biosynthetic pathway map of rice, obtained through www.gramene.org (Pathway genes). Out of 119 marker intervals useds, 71 markers got a hit of a BAC clone of rice. From each marker interval, the clone number varied from one to more than ten. Among the markers interval, 16 JA genes and 6 SA genes were determined, which were on chromosomes numbers, 12 (G2140-S2545 and C1069-G2140), 6 (P0537F07), 3 (OSJNBa0057G07 and OSJNBa0079B15), 5(P0683B12 and OJ1111_A10), 11 (OSJNBb0005H02, OSJNBa0093J03 and OSJNBb0026K20) and 2 (P0435E12, B1215B07 and P0042D01) respectively.

PII-34

MARKER ASSISTED PYRAMIDING OF STEM AND LEAF RUST RESISTANCE GENES (*SR2, SR24/LR24, SR36 AND LR19/SR25*) IN WHEAT (*Triticum aestivum* L.)

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Wheat is one of the most important cereal crops for food security and rust diseases continually pose a threat to wheat production at national and international level. Resistant cultivars are the cheapest, most reliable and environmentally safest way to control the rust disease. Pyramiding of stem and leaf rust resistance genes, *Sr2, Sr24/Lr24, Sr36* and *Sr25/Lr19* in step wise and simultaneous manner was attempted with recipient parents viz., Lok1, Sonalika, Raj4083, HSB6 and WTN0164 using donor parents viz., Kingbird (*Sr2*), TR380-14*7/3*Ag*#14 (*Sr24/Lr24*) and Cook*6/C80-1 (*Sr36* and *Lr19/Sr25*). Presence/confirmation of the rust resistance genes were carried out at each generation using molecular markers *gwm533* (*Sr2*), *Sr24#12* (*Sr24*), *stm7*33 (*Sr36*) and *Gb* (*Lr19*) in the backcross derivatives and also in the donor parents (initially). In each generation, genotypes with all the four genes combination were forwarded and the stable lines were selected at BC_1F_4 generation. Seedling reaction of the stable lines to major leaf rust (17, 77-A,77-5, 77-7, 77-8 (except *Lr19*)) and stem rust pathotypes (40A and 40-1(except *Sr24*)) and adult plant reaction in the field showed resistant reaction at Wellington location. The use of gene pyramids/stacks of major genes or minor genes or major and minor gene combination that confer resistance to most/all of the pathotypes of rusts could impart durability to the cultivars than single gene deployment.

PII-35

ROLE OF BIOINFORMATICS IN CROP IMPROVEMENT

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Bioinformatics is a new science that combines the power of computers, mathematical algorithms, and statistics with concepts in the life sciences to solve biological problems. At present, the only effective way to keep abreast of the dramatic increase in sequence and related information is to apply biocomputational approaches. Thus, over recent years, the field of bioinformatics has rapidly developed into an essential aid for genomic data analysis and powerful bioinformatics tools have been developed, many of them publicly available through the World Wide Web. The Bioinformatic tools are three types- tools used for sequence analysis (BLAST, FASTA, MOTIF, ClustalW, MFFT and PRRN), genome analysis (OC Viewer, KAAS, MAPLE, EG Assembler, GINIES, DINIES and GECS) and chemical analysis (SIMCOMP, SUBCOMP, KCaM, PathPred, E-zyme, PathComp and PathSearch). Major public data banks which take care of the DNA and protein sequences are GenBank in USA (http://www.ncbi.nlm.nih.gov), EMBL (European Molecular Biology Laboratory) in Europe (http://www.ebi.ac.uk/embl/) and DDBJ (DNA Data Bank) in Japan (http://www.ddbj.nig.ac.jp). The major applications of bioinformatics are data acquisition, assembly of sequence contigs, predicting functional domains in genomic sequences, sequence alignment, searching structure databases, determination of macromolecular structure and molecular evolution. Even though, there lot more applications, there is need to improvement in the data management and the development of various strategies to surf WWW, and reaching a consensus on coining uniform definitions and adopting uniform platforms and technologies are challenges in the practice of bioinformatics.

PII-36

TRANSPOSON TAGGING AND INSERTIONAL MUTAGENESIS

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Transposon tagging and insertional mutagenesis are important reverse genetic tools in plant functional genomics to identify and isolate specific gene loci in plant genome. In the post genomic era, gene sequence information of plants are progressing. The most direct approach to determine the functions of the sequenced genes in an organism is to disrupt or generate mutations in the genes and analyse the consequences. By insertional mutagenesis, with a known mobile DNA insert can generate mutations that are marked by a molecular tag. When the insertion disrupts a gene, causing a mutant phenotype, the tagged mutant gene can easily be cloned using the DNA insert as a molecular probe. DNA sequences of the cloned mutant gene can then be used to isolate the corresponding wild-type allele facilitating the analysis of both mutant and gene. Either T-DNA or transposons can be used as insertional mutagens in plants. T-DNA approach is extremely useful for plant species where quick and efficient transformation methods are available, it may not be feasible in those plant species where the transformation methods are slow or labour intensive. For this reason, insertional mutagenesis using transposable elements offers some advantages over T-DNA mutagenesis. The successful use of this strategy in *A. thaliana* has made it possible to develop databases for reverse genetics, where screening for the knockout of a gene of interest can be performed by computer searches. The extension of these technologies to other plants, particularly agronomically important crops are now feasible.

PII-37

RELATIVE EFFICIENCY OF CHROMOSOME ELIMINATION TECHNIQUES FOR HAPLOID INDUCTION PARAMETERS IN TRITICALE X WHEAT DERIVED GENERATION THROUGH *Zea mays* AND *Imperatacylindrica* MEDIATED SYSTEMS

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The process of obtaining homozygous populations from the triticale x wheat hybrids, advance generations and their back-crosses can be accelerated by utilizing doubled haploidy breeding (DH) following chromosome elimination approach through *Zea mays* and *Imperatacylindrical* mediated systems. The experimental material used were 5 elite and diverse genotypes of triticale (AABBRR) viz., TL 1210, TL 2908, TL 2920, DT 123 and TW 9335 and 5 of spring wheat (AABBDD) *viz*., HS 295, HPW 155, PBW 343, DH 40 and DH 776. In F_1, plant regeneration frequency of triticale x wheat derived lines through *Zea mays*- mediated system ranged from 11.25% to 42.57 % in F_1, from 0 to 22.50% in F_2, from 0 to 8.18% in F_3 and from 1.15% to 22.90% in F_4. In back crosses, BC_1F_1 plant regeneration was ranged from 0 to 13.50%, BC_1F_2 from 2.97% to 16.15% and *I.cylindrica* mediated system in F_1 ranged from 0 to 57.47%, 11.25% to 30.00% in F_2, 38.57% to 72.00% in F_3 and 5.57% to 45.00% in F_4. In back crosses, BC_1F_1 ranged from 31.10% to 63.25%, BC_1F_2 from 19.36% to 65.96%.The results showed that in all the generations, *Imperatacylindrica* performed far better than the *Zea mays* in respect of pseudoseed formation, embryo formation and haploid plant regeneration except in few cases.

PII-38

THE NEED FOR NUTRIENT EFFICIENT RICE VARIETIES: STATUS AND PROSPECTS

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Best agro-management in rice always required large quantum of agronomic inputs such as fertilizers. Modern rice varieties need high positive nutrient balance in the soil to throw their best yields. Nitrogen and phosphatic fertilizers are required by rice crop plants in large quantities. Overdependence of mineral fertilizers for agricultural production envisions problems such as, (a) soil nutrient deficiency, (b) non-recyclable nutrient loss, (c) loss of nutrients by soil processes, (d) nutrient pollution, (e) atmospheric pollution, (f) depletion of natural resources, (g) geographic resource confinement, (h) booming fertilizer costs, (i) constrained fertilizer affordability to farmers (j) no alternate fertilizer resources.To curb ill-effects of indiscriminate fertilization and sustain rice production reduction in soil nutrient input needed. Ability of plants to withstand nutrient starvation is leveraged by a variety of mechanisms such as root system architecture, root exudations and root microfloral symbiosis, besides uptake and transport. Crop tolerance to nutrient deficiency is called as low nutrient tolerance or nutrient starvation tolerance. Considerable genetic variations are reported for nutrient efficiency (NtE) in rice. Experience shows that the key to this genetic variation does not lie with the genes directly responsible for nutrient uptake, transport and assimilation but on the genes that regulate the processes. Nutrient starvation tolerance genes may be better sourced from older germplasm. Molecular isolation of large effect QTLs for phosphorus starvation tolerance and low nitrogen response have also been mapped in rice. Improved rice varieties with better NtE developed using modern molecular breeding technology would lead the agriculture in future.

PII-39

NEXT GENERATION SEQUENCING- A REVOLUTION IN GENOMIC SCIENCE

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Next Generation Sequencing (or massively parallel sequencing) refers to a group of new DNA sequencing technologies that can rapidly sequence DNA on the gigabase scale. This method is now replacing Sanger sequencing, which was the dominant sequencing technology from the late 1970 to the late 2000 and was used for all of the initial genome sequencing projects (*H. influenzae,* Drosophila, Arabidopsis, human). Using next-generation sequencing technologies it is possible to resequence

entire plant genomes or sample entire transcriptomesmore efficiently and economically and in greater depth than ever before. Rather than sequencing individual genomes, we envision the sequencing of hundreds or even thousands of related genomes to sample genetic diversity within and between germplasm pools. To illustrate how this process works, a single genomic DNA (gDNA) is first fragmented into a library of small segments that can be uniformly sequenced in millions of parallel reactions. The newly identified strings of bases, called reads, are then reassembled using a known reference genome as a scaffold (resequencing), or in the absence of a reference genome (de novosequencing). The full set of aligned reads reveals the entire sequence of each chromosome in the gDNA sample. Identification and tracking of genetic variation are now so efficient and precise that thousands of variants can be tracked within large populations, and also this technology is widely used for large-scale development of molecular markers for linkage mapping. This technology is expected to advance crop breeding, leading to crop improvement.

PII-40

MINING GENIC-SSRS RELATED TO SUCROSE METABOLIC PATHWAY ENZYMES FOR SUGARCANE IMPROVEMENT

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Unlike genomic-SSRs, genic-SSRs specifically target the transcribed region of the genome and have increased potential for linkage to loci that contribute to agronomically superior phenotypes. A study was undertaken to mine the microsatellites in the available sugarcane unigene datasets for understanding their abundance and determining the extent of allelic diversity for sucrose metabolic pathway enzymes in a panel of germplasm lines and commercial hybrids. The objectives of current study were to develop genic SSR markers, analyze marker polymorphism among twenty four different clones categorized as sugar and non-sugar species and to integrate the SSR markers to different genomic regions such as open reading frames (ORFs) and untranslated regions (UTRs). Analysis of molecular variance (AMOVA) showed that two groups (sugar- and non-sugar types) as well as the taxa within the groups were significantly different. Most significant finding in the current research is locating erosion of alleles FK1, PPFK 3a, FBP and SPS 1 among the sugar producing taxa. In contrast, a unique allele at FK2 might be a gain of function mutation in sugar producing taxa, which does not appear in non-sugar producing group. A phylogenetic tree built based on neighbor-joining (NJ) analysis of polymorphic alleles of SSRs from sucrose pathway revealed two robust clusters with taxa from the sugar and non-sugar producing groups. The new transcript SSR markers identified for sucrose would be useful for sugarcane breeders as the selection and combination of parents for crossing rely on an understanding of their genetic structures and molecular diversity.

PII-41

MOLECULAR CHARACTERIZATION AND DNA FINGERPRINTING OF ELITE SUGARCANE CULTIVARS (*Saccharumspp*)

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The success of sugarcane improvement through breeding mainly rests in harnessing genetic variability available in the genepool. In the present study, 44 elite sugarcane cultivars including recent and drought tolerant commercial hybrids were subjected genetic diversity analysis with a set of fifteen sugarcane specific STMS primers. The polymorphism scored in silver stained polyacrylamide gels following PCR amplification of genomic DNA was observed for unique bands. Specific markers of each clone were identified to serve as DNA fingerprints for unambiguous identification each clone to aid in plant varietal protection and DUS characterization. The total bands scored were subjected to combined analysis with GGT 2.0 graphical genotyping software. The graphical genotyping showed distinct pattern for each genotype to serve as the genotype images of the clones. The diversity matrix showed that among the possible 946 combinations, 826 had moderate to high diversity reflecting the existence of high genetic diversity in the studied clones for use in sugarcane improvement. For convenience in choosing parents, a core group of twenty genotypes that represented genetic diversity was identified with an estimated diversity value of 1685.93. Based on this, the genotypes *viz* Co 0118, Co 0209, Co 0218, Co 0237, Co 0238, Co 0239, Co 0241, Co 0314, Co 2001-09, Co 2001-13, Co 2001-15, Co 0403, Co 0409, Co 99004, Co 93023, Co 94012, Co 06027, Co 06030, NS 83/ 247 and Co 06020 represented diversity in the investigated material for effectively used in hybridization to improve sugar productivity under normal and drought conditions.

3. PHYSIOLOGICAL AND MOLECULAR BASIS OF ABIOTIC STRESS MANAGEMENT

PIII-1

INSIGHTS ON REGULATORY ROLES OF miRNAs IN DROUGHT TOLERANCE IN COTTON

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Research on RNAs with regulatory activities, termed as micro-RNAs (miRNAs), shown more prominence in molecular biology of plant growth and development. They are about 22 - 24 nucleotide (nt) in length and act as negative regulators of plant gene expression. Role of miRNAs in response to biotic and abiotic stresses were confirmed in several crops. However, their role in drought tolerance in cotton is yet to be established. In this study, differentially expressed drought responsive miRNAs and their targets were identified under natural field conditions through high-throughput small RNA sequencing by comparing leaf samples of drought tolerant*Gossypium hirsutum* cv. KC3 and drought susceptible *G. barbadense*cv. Suvin. Totally four small RNA libraries were constructed and sequenced by employing ion protonTM technology. Altogether, there were 39,407,089 reads with a mean read length of 22 nt. Comparison of miRNAs expressed under water stressed conditions between KC3 and Suvin, have resulted 7,494 miRNA reads and interestingly majority of them were down regulated with at least two folds. Besides identifying large numbers of novel miRNAs, several abiotic stress responsive conserved miRNAs were also noticed. Further, the identified miRNAs were also targeting different classes of dehydrogenases, protein kinases and transcription factors. Our results revealed for the first time that there were large numbers of water stress related miRNAs that might be sequentially and/or complexly involved in gene regulation that confers drought tolerance in cotton under field conditions and they have enormous potential in elucidating the molecular mechanism of miRNA based gene regulation.

PIII-2

NETWORK OF GENES IN ABIOTIC STRESS TOLERANCE OF SOYBEAN

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Legumes being rich in dietary protein, a rich source of dietary fiber (20-15%) form major constituents of a vegetarian diet (Duranti and Gius, 1997) and is the reason being considered important to confront malnutrition. Except soybean and common bean, legumes were considered orphan crops as there were no genomic resources available (Varshney *et al.,* 2009; Tuberosa *et al.,* 2011). Though a stable food, average global yield for legumes (0.86 t/ha) is much less than the average yield of cereals (3.54 t/ha) (FAO, 2011) due to major stress conditions prevailing in the crop growing regions. Plant hormone abscisic acid (ABA) plays an important role under abiotic stresses. When plants encounter the adverse environment conditions, ABA levels are increased and further improve plant survival and productivity. Most of the genes that respond to drought, high salt and cold stress can also be induced by exogenous ABA (Kang *et al.,* 2002; Cheong *et al.,* 2003). Individual reports are indicating the tolerance genes but their interaction is so far least known. Here we present the predicted interaction of the ABA dependent and independent pathway genes of soybean. The reported genes were collected from the available data resources and published research reports. Using the existing bioinformatics tools, analysis was done to predict the prevailing interaction. Based on their levels of interaction the genes were classified into a new class of interdependent genes and signalling molecules responsible for abiotic stress tolerance.

PIII-3

ROLE OF MYOSINS AND RAB-GTPases IN ABIOTIC STRESS TOLERANCE

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Myosins are the intracellular locomotors on the tracks of cytoskeleton with a specific cargo binding site. They facilitate the movement of organelles, contributing to plant growth regulation. Myosins can interconnect actin filaments leading to sliding of actin filaments along each other which creates myosin dependent protrusions in Arabidopsis thaliana and relocation of cytoplasmic strands. Myosins bind interactor proteins that mediate their interaction with organells and signaling molecules.Anti myosin antibody was designed, synthesized and tested. Transient expression of myosins (~100 to 120 K Da) along with GFP only (35 K Da) construct were done using agroinfiltrationprotocol . The infiltrated leaf discs were removed from the plant, 48h after infiltration and protein samples were prepared using USB buffer. The results suggest specificity of the anti myosin XIK antibody with myosin XIA, XIC and XIE.Images obtained from immuno-florescence indicated the co-localization of myosin XI K with the GFP labeled tonoplast in *Arabidopsis thaliana.* Under stress conditions the plants mutant for one or two myosins were able to grow whereas multiple mutants failed to survive along with the control Col type plants. Movement of cytoplasmic sub vesicle or bulb during cytoplasmic streaming was observed in hypocotyls of At-GFP tonoplast plants. The XI K mutants were found to produce shorter root hairs and impaired cytoplasmic streaming when comparing the wild type control plants.

PIII-4

RESPONSE TO WATER STRESS IN CASTOR (*Ricinus communis* L.) GENOTYPES UNDER PEG INDUCED DROUGHT CONDITION

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A lab experiment was conducted to study the response of 45 castor genotypes to drought stress imposed at germination and seedling growth stages. Five water stress levels of zero (control), -0.2, - 0.3, - 0.4, - 0.5 (MPa) were developed by dissolving 11.9, 15.1, 17.8, 20.2 gram of PEG per 100 ml distilled water. The experiment was laid out by complete randomized design with two replications. Ten seeds of each castor germplasm accessions were sown in germination tray containing sterilized sand medium and the Poly Ethylene Glycol solution was given to medium to induce the drought. On tenth day the observations were recorded. Seedling length, root length and germination percentage were used to evaluate the genotypic response to PEG induced water stress. Genotypes showed significant variation in all the characters studied. The highest tolerance for germination was shown by RG 2474 (68.83 percent) followed by RG 3063 (68.20 percent), RG 3233 (62.26 percent). The shoot length values were higher in the genotype RG 2474 (16.40 cm) followed by RG 2368 (15.80 cm), RG 2980 (15.25 cm). The maximum root length was occurred in RG 2326 and RG 3013 followed by RG 2944 (6.10 cm), RG 2474 (5.79 cm) and it was minimum in RG 157 (1.61 cm) followed by RG 2035 (1.71cm), RG 2266 (2.06 cm).

Keywords: castor, genotypes, water stress.

PIII-5

EFFECT OF GRADED LEVELS OF FLY ASH ON MEAN LEAF OPENNESS IN RICE AND ITS RELATIONSHIP WITH si UPTAKE

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In the tropics, rice growth tends to become excessive and mutual shading among the population is often cause low grain yield. Under such environmental condition, leaf openness may assume greater importance than it does under temperate conditions. The decreased leaf openness is a desirable character for high photosynthetic activity, which was observed in the different sources of Si application. A field experiment was carried out in low Si soil and observations made on leaf erectness at tillering stage and correlated with Si uptake and dry matter production. Application of fly ash @100 t ha-1

with SSB and FYM registered the lowest value (16.7) which was on par with application of 50 t ha^{-1} fly ash +SSB and FYM. This parameter was negatively and significantly correlated with Si content (r = -0.83) and uptake (r = -0.92) in rice plant at tillering. Similarly, significant and negative correlation (r= -0.70) was observed with grain yield in loamy sand soil with low Si status. In sandy loam soil with low to medium Si status the parameter was best correlated with grain yield (r=-0.94) and negatively, significantly correlated with Si content (r =-0.55) and uptake (r=-0.82) in plant at tillering. Among the different treatments, application of SSB + FYM recorded the lowest leaf openness of 14.9 which was on par with SSB (16.4) followed by FYM (17.4) whereas control recorded the highest leaf openness of 20.0.

PIII-6

INFLUENCE OF ABIOTIC STRESSES ON EXPRESSION OF SQUALENE EPOXIDASE GENE FROM *IN VITRO* ROOT CULTURES OF *Withania somnifera* AND ITS IMPACT ON MAJOR WITHANOLIDE ACCUMULATION

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Withania somnifera is one of the most extensively used medicinal plants for adaptogenic purposes in Ayurvedic and Unani medicines. Most of its biological activities have been attributed to the presence of a group of compounds referred as withanolides and are used as drugs. Since the roots contain a number of therapeutically applicable withanolides, mass cultivation of roots *in vitro* will be an effective technique for the large scale production of these secondary metabolites. Withanolide A is *de novo* synthesized within root from primary isoprenogenic precursors. Two possible routes for withanolides biosynthesis namely, 24-methylene cholesterol through mevalonate (MVA) and 2-C-methyl-D-erythritol-4-phosphate (MEP) pathways localized in cytosol and plastids respectively are known. Squaleneepoxidase (*Ws SE*) catalyzes the first oxygenation step in phytosterol and triterpenoidsaponin biosynthesis. Expression pattern of *Ws SE* under different abiotic stresses and its influence on major withanolide accumulation were studied in Indian ginseng adventitious root cultures. Interestingly, *Ws SE*upregulated upon exposure to salicylic acid, UV irradiation and cold stress. Comparatively, accumulation of withanolides were also significantly elevated under these conditions. Expression of *Ws SE* on different stress treatments and positive impact on withanolide accumulation suggest that SE gene is not only tightly regulated to the kind of defense signals applied but also suggested to represent one of the rate-limiting enzymes in withanolide biosynthetic pathway.

PIII-7

VIRGINIA BUNCH GROUNDNUT (*Arachis hypogaea* L.) LINES SUITABLE FOR MOISTURE STRESS CONDITIONS

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Groundnut (*Arachis hypogaea* L.) is an important oilseed crop in India and is mostly cultivated under rain dependent condition, where the moisture stress is a major limiting factor affecting the yield. To indentify high yielding groundnut lines suitable for rainfed conditions, a total of 110 groundnut genotypes were evaluated at Dryland Agricultural Research Station, Chettinad from 2010-2013. The evaluations were done in rainy (*Kharif*) and post-rainy seasons to assess the genotypes performance in no moisture and moisture stress conditions. The genotypes performance was assessed based on pod yield traits and physiological parameters such as number of matured pods per plant, pod yield per plant, SCMR, RWC, SLA and stress tolerance index. The results indicated that, Virginia bunch types namely ICGV 07240, ICGV 07241, ICGV 07245, ICGV 07247 and ICGV 07262 were expressed consistence superiority over VRI (Gn) 6 and VRI (Gn) 7 across seasons for pod yield. Further, the genotypes ICGV 07420, ICGV 07245 and ICGV 07247 recorded high relative leaf water content (RWC) and ICGV 07247 and ICGV 07262 recorded high stress tolerance index (STI) over checks. The elite drought tolerant Virginia bunch entries namely ICGV 07245 and ICGV 07247 were evaluated in TNAU multilocation trial during *Kharif*2013 over six locations. The mean pod yield recorded by ICGV 07245 was 2797 kg ha-1 and ICGV 07247 was 2824 kg ha-1. This performance is 19 percent yield increase over VRI (Gn) 7 and 20 percent over TNAU Groundnut CO 6 varieties for both the cultures.

PIII-8

IN VITRO SCREENING STUDIES ON SALINITY TOLERANCE IN *Clerodendrum inerme*

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The present study was undertaken with an aim of in vitro screening of *Clerodendrum inerme* for understanding morphological, physiological, and biochemical basis of salinity tolerance. The plant samples were collected from area of TNAU. The selected genotypes were screened under *in vitro* condition for salinity tolerance by incorporating NaCl in the growth medium at various concentrations from 50mM to 400mM. The *in vitro* studies revealed that the plants tolerated up to 200mM NaCl. These plants were hardened. Further, the *in vitro* studies also carried out in genotypes collected from mangroves region. The experiments were carried out to analyze the morphological, physiological

and biochemical characteristics of hardened plants. One and half year old tissue cultured plants of *C. inerme* grown under control (without NaCl), 50 mM and 100 mM of NaCl conditions were analyzed for various morphological parameters. Salinity stress was found to have significant effect on the plant height, stem diameter and leaf area in NaCl stressed plants. Leaf thickness and midrib thickness were found to increase in salinity stressed plants. The physiological and Biochemical study reavealed that salinity stress has increased proline content in the stressed plants and decreased chlorophyll content in stressed plant.

PIII-9

DETERMINATION OF JASMONIC ACID IN SESAME DURING VARIOUS ABIOTIC STRESS CONDITIONS

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Omega 3-fatty acids catalysis the conversion of dienoic acid to trienoic acid and thus have profound effects on the fluidity and function of biological membranes in plants. It also plays an additional role of being the precursor of fatty acid-derived signaling molecules, such as Jasmonates in the octadecanoid pathway. The concentration of Jasmonic acid depends on plant developmental stage, physiological conditions and environmental stimuli. Reports regarding the influence of environmental stress over omega 3-desaturase genes are available. Being one of the first known oil seed, India is considered as the world leader in production and export of *Sesamum indicum.* This crop is characterized with high quality premium oil with prolonged shelf-life and has a lot of scope in research and development. Considering the interfering substances, volatile nature and extremely low level of Jasmonic acid, a sensitive and selective method like HPLC is mandatory. Our study focuses on Jasmonic acid quantification in sesame, with respect to various stress conditions like cold, drought, heat, salinity and wound, which could give an insight of fatty acid response in the plant during abiotic stress conditions. As expected, variations in Jasmonic acid levels during different abiotic stress conditions are observed in accordance with the expression of omega 3-desaturase genes.

PIII-10

GERMINATION- AND VEGETATIVE- SALT TOLERANCE IN BARNYARD MILLET (*Echinochloa frumentacea*) IS CONTROLLED BY SEPARATE BUT OVERLAPPING PATHWAY GENES.

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Barnyard millet (*Echinochloa frumentacea*; BYM) is one of the six small millets grown in India and many other parts of the world, and is known for its adaptability to unfavourable soil conditions. Several BYM accessions were collected from the farmers' holdings from the Southern districts of Tamil Nadu. The seeds were tested for germination under high salinity conditions, with the varieties,Co1 and Co2 as check. Two accessions ACM183 and ACM126 were tolerant to the tested level of 300 mMNaCl while the controls were susceptible even at 100 mM. Although the accession ACM062 was as susceptible as the controls when germinated on salt-containing media, but were able to tolerate high salt when germinated normally and transplanted to salt-watered soil. Such type of germination-salt tolerance *vs* vegetative-salt tolerance suggests that germination and vegetative - salinity tolerance to be of separate but overlapping pathways controlled by different genes that can overlap in expression. Till now, no work has been initiated for the molecular characterization of BYM to understand the functioning at cellular level. Bioprospecting such indigenous cereals which has withstood the onslaught of time and indigenous cultural practices, should possess novel genes that can contribute to development of stress tolerant crops for climate resilient agriculture.

PIII-11

EFFECT OF DIFFERENT LEVELS OF Zn APPLICATION ON MAIZE GRAIN QUALITY

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In plants, Zn plays a key role as a structural constituent or regulatory co-factor of a wide range of different enzymes and proteins in many important biochemical pathways. Varying levels of Zn at different locations having initially varied soil Zn status had great impact on quality parameters of grains like crude protein, true protein, starch and amylose content. With increasing levels of Zn application, the content of all the quality parameters in grains showed an increasing trend and thereby the difference was minimal in the treatments having higher Zn levels (7.50 and 10.0 kg Zn ha^{-1}). It is evident from the results that all quality content responded well to added Zn at different locations

having varying soil Zn status but the contents were not uniform in all the locations. Among different levels of Zn applied, the treatment 100% NPK + 10.0 kg Zn ha^{-1} (T6) always recorded the highest quality parameters followed by 100% NPK + 7.50 kg Zn ha^{-1} (T5) which recorded next highest value in almost all the location whereas the control treatment recorded the lowest. Hence, increasing levels of Zn application and also with increasing initial soil Zn status, there was an increase in the content of all the quality parameters.

PIII-12

ARTIFICIAL SCREENING FOR SALINITY TOLERANCE AT PANICLE INITIATION STAGE IN RICE (*Oryza sativa* L.)

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A total of 27 rice genotypes were screened for salinity tolerance at panicle initiation stage with EC level of 6 and 8 Dsm-1 under artificial condition. Single plants from each genotype were transferred into pots at tillering stage in two replications. One was maintained as control and another was used for screening at higher EC level. The YOSHIDA nutrient solution was prepared and added to the plants at pots in weekly intervals. The NaCl was used to create different level of EC artificially. The saline solution with EC of 6 Dsm-1 were added three times/week and each genotype was observed closely from panicle initiation to maturity stage. The number of days of survival days in salt stress and salt damage level were used as an indicator for salinity screening. Among the genotypes evaluated, Nona Bokra performed better than the other genotypes and produced fertile spikelets (80 %) and seeds under EC of 6 Dsm-1. The other genotypes *viz*., AC 660 Tulsi, Pooja, Gayatri, Nua-Kalaseera, TRY 1, CSR 10, CSR 13, CSR 23, CSR 27, CSR 36 produced more number of sterile spikelets (80-90 %). Drying of panicles before flowering was observed in the remaining genotypes *viz*., Moti, Hanseswari, Nua-Dhusura, Padimini, Varshadha, Chandan, Patani, Naveen, TRY 2, CST 7-1, Garuda samba, Kaivara samba, Mappilai samba, Eluppaipoo samba and Kavuni.

PIII-13

STABILITY ANALYSIS FOR GRAIN YIELD IN DROUGHT TOLERANT RICE (*Oryza sativa* L.) GENOTYPES

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Development of varieties with high yield potential coupled with wide adaptability is an important

plant breeding objective. The presence of genotype by environment (GxE) interaction plays a crucial role in determining the performance of genetic materials, tested at different locations and in different years, influencing the selection process. Keeping the above points in view, fourteen drought tolerant rice genotypes were evaluated in three different years at Department of Rice, Tamil Nadu Agricultural University from 2010 to 2012 to identify stable and high yielding genotypes. The experiment was conducted using Randomized Complete Block Design with two replications. Combined analysis of variance showed highly significant differences among genotypes, environments and genotype by environment interactions for the trait grain yield. The mean grain yield was ranging from 588 kg/ha (R 1528-1058-1-110-1) to 1897.56 kg/ha (UPR 3413-8-2-1). The genotype CRR 624-207-B-1-B was exhibited high mean yield (1356.72 kg/ha), regression coefficient (b>1) and non significant Sd2 and would be responded well to favorable environments. The above genotype was also exhibited below average values for ecovalence (w) and stability factor (SF) which indicated that it was high stable one. The genotype NP-124-8 showed high mean yield (1126.81 kg/ha), regression coefficient (b<1) and non significant Sd2 and would be responded well to poor environments. Rests of the genotypes were unstable. The AMMI analysis of variance showed that both main effect components *viz.,* genotypes, location and interaction components were significant.

PIII-14

HYDROPONIC SCREENING OF RICE (*Oryza sativa* L.) CULTIVARS FOR SALINITY STRESS TOLERANCE

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Rice crop productivity is greatly hampered by salinity stress, a major obstacle to increasing crop production worldwide. The present study attempted to screen rice genotypes *viz*., FL 478, ASD 16, TRY 2, BPT 5204, IR 64 and White Ponni supposedly differing in their response to salinity stress tolerance under hydroponics screening system. Physiological analysis like germination percentage, root-shoot length was performed and vigour index arrived. ASD 16 recorded a maximum index of 2961.4 followed by FL 478 (2374.75), TRY 2 (2283.75), BPT 5204 (1977.75), IR 64 (1476.03) and White ponni (1379.25). Salinity scoring was done based on IRRI modified standard evaluation scores, FL 478 was found to be highly tolerant to salinity stress followed by TRY 2, BPT 5204, White ponni while IR 64 and ASD 16 were susceptible. Based on the Na+/K+ uptake estimation, FL 478 was found to be tolerant to salinity stress compared to ASD 16. Biochemical analysis, for free proline content and ascorbate peroxidase activity (APX) was done in the selected varieties/lines. PCR analysis using SSR markers revealed distinct banding of the SALTOL specific alleles in the genotypes suggesting the presence of salinity tolerant QTL in the FL 478, TRY 2, BPT 5204 and ASD 16 to be a salinity stress susceptible genotype as evident from the similar results of physio-biochemical analysis. Thus hydroponic screening technique can be proficiently used as simpler and cost effective tool for salinity screening of rice at seedling stage.

PIII-15

INTERACTION BETWEEN DROUGHT TOLERANT INDICES AND BIOLOGICAL NITROGEN FIXATION ON PEANUT UNDER EARLY DROUGHT

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Peanut (*Arachis hypogea* L.) is an integral part of the cropping systems of semi-arid tropics. The knowledge on the response of nitrogen fixation and its interaction with other traits under early drought is limited. A preliminary investigation was carried out at Agricultural research station, Bhavanisagar to study the responses of 39 groundnut genotypes to early drought under two soil moisture regimes [field capacity (FC) and 1/3 available water (AW)] during summer (2013 and 2014). Early drought was given by maintaining 1/3 available soil water (1/3 AW) from emergence to 40 days after emergence (DAE) followed by adequate water supply. Data were recorded for SPAD Chlorophyll Meter Reading (SCMR) at 20, 40, 50 and 60 DAE, nodule dry weight (NDW), total nitrogen fixed (TNF), biomass production (BM), pod yield, harvest index, sound matured kernel (SMK) at harvest and oil content. The result showed that the mean SCMR for drought tolerant genotypes are higher and was strongly related with TNF under both water regimes. Among the genotypes, BSG 1102 (ICGV 98103) showed higher NDW, TNF, higher pod yield and SMK (%) followed by BSG 1101 (ICGV 99159). Under early drought, positive and significant correlations between SCMR and biological nitrogen fixation (BNF) with BM, pod yield and SMK were found. However they have no much influence on the oil content. Hence in the genotypes studied, it was concluded that the negative influence of early drought on biological nitrogen fixation and yield has no significant effect while comparing with field capacity.

4. GENETIC CONSERVATION AND BIODIVERSITY OF EUKARYOTES & PROKARYOTES

PIV-1

GERMPLASM CONSERVATION IN OIL PALM

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Oil palm breeding has improved the quality planting material production with highest productivity per unit area. But the genetic gain may not long lost as many of the breeding programmes are continuously relay on restricted breeding base. Researchers from various oil palm growing countries have collected germplasm and established field gene banks in Malaysia, Ivory Cost, Costa Rica, Brazil and Colombia etc. The major players involved in germplasm collections are Corporation Research Centre for Oil Palm (CENIPALMA), Indu Palma, Hacienda La Cabana in partnership with Palm Elite, La cabana /CIRAD France, Brazilian Agricultural Research Corporation, Agricultural Services Development (ASD), Malaysian Palm Oil Board (MPOB), NIFOR, Nigeria, Centre National De RechercheAgronomique (CNRA) (Ivory Coast), Institut National des RecherchesAgricoles du Bénin (INRAB, Benin), The Institute of Agricultural Research for Development (IRAD),(Cameroon), Socfindo (Indonesia), Palmeras del Ecuador (Ecuador). India (DOPR) is having narrow genetic base and heavily relies on Thodupuzha*duras* and initiated introgression of new germplasm into existing breeding materials for evaluation and improvement. Oil palm is propagated by seed and long term conservation by seed is difficult in view of semi recalcitrant storage behaviour of the seed. Long term cryopreservation using kernel, somatic embryo and polyembryos has been reported. Oil palm pollen could be successfully stored after cryopreservation in liquid nitrogen. Desiccation tolerance is significantly correlated with embryo DW and water content and tolerance is acquired at specific stages. Therefore, more extended studies would lead to development of suitable storage protocols especially by cryopreservation.

PIV-2

DETERMINATION OF GENETIC DIVERSITY IN PIGEONPEA GERMPLASM USING SSR MARKERS

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Pigeonpea is a nutritionally important crop, but there is no impressive improvement in the production of the crop due to the limited scope for increasing its area under cultivation. Research for genetic improvement of this crop is required to raise yield levels effectively through widening genetic base. Hence, this study was initiated with twenty microsatellite markers for studying the molecular genetic diversity in 90 pigeonpea genotypes. The level of polymorphism was too low and 14 markers were monomorphic. A total of 29 alleles were produced and the number of alleles produced ranged from one to three. The mean PIC value of 20 SSR primers was 0.03735 and the primer CcM1026 produced the highest PIC value of 0.187 followed by CcM2977 (0.184). The UPGMA clustering and Neighbour-joining analyses grouped all the ninety germplasm into six clusters. Cluster III is the largest with eighty two entries. Cluster I has two sub-clusters with one entry each. The entries are ICP245517 and CO (Rg)7. Cluster II had only one genotype ICP245335.Cluster IV had two sub-clusters with one entry each. The entries are IC123325 and AF284/2. Cluster V had only one genotype ICP 245527.Cluster VI had two sub-clusters with one entry each. The entries are IC73353 and DPP-2-52.Hence genotypes from different clusters could be used in hybridization programmes to get high yielding hybrids.

PIV-3

BIODIVERSITY CONSERVATION IN CROP IMPROVEMENT

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Genetic diversity in agriculture enables plants to adapt to new pests and diseases, changing environments and climates. The ability of a certain variety to withstand drought, grow in poor soil, resist an insect or disease, give higher protein yields, or produce a better-tasting food are traits passed on naturally by the variety genes. Biodiversity in agricultural ecosystems provides for our food and the means to produce it. The variety of plants that constitute the food we eat are obvious parts of agricultural biodiversity. It is important to take note that biodiversity in agricultural landscapes has powerful cultural significance, partly because of the interplay with historic landscapes associated with agriculture, and partly because many people come into contact with wild biodiversity in and around the farmland. Further wild species of crop plants and their relatives are the source of many genes imparting resistance against many disease pests and abiotic stresses. They are also source of genes that determine quality and other attributes.Thus, reduction of biodiversity in variety, species as well as ecosystem pose a serious threat to our food security. Thus there is necessity to use eco-friendly techniques in agriculture and to minimize the use of pesticides and other chemicals and resorting to organic cultivation, crop rotation so as to check reduction in biodiversity.

PIV-4

CLONING OF PARTIAL cDNA OF ENDOCHITINASE PRODUCED BY *Pseudomonas fluorescens* ISOLATED FROM SUGARCANE RHIZOSPHERE

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Chitin is a significant component in the cell walls of fungi except members of Oomycetes and large number of bacteria can utilize chitin by producing extracellular enzymes that attack the polymer yielding N-acetyl glucosamines, chitobiose and chitotriose as the products. Thus chitinases have the potential as effective antifungal agents. Chitinase genes have been isolated from many bacteria and we report here that *Pseudomonas fluorescens* strain AFG4 antagonistic to sugarcane red rot pathogen, *Colletotrichum falcatum* Went excreted chitinases, N-acetyl glucosaminidase of 97kDa, chitobiase of 66 kDa and chitotriase of 50 kDa and this was detected in the overlay gel using 4-MU-(GlcNAc), 4-MU-(GlcNAc)2 and 4-MU-(GlcNAc)3 as substrates respectively. Cloning of the endochitinase gene from *P. fluorescens* strain AFG4 was done and in this respect, a partial cDNA of endochitinase obtained through RT-PCR technique showed the sequence length of 230bp (Genbank accession number AY743353). Homology analysis of the deduced amino acid sequence with the existing sequences of UniProt revealed a similarity of 61-92%. Future work is on to use the partial cDNA sequence of chitinase as probe to pick the full-length chitinase gene from the cDNA library and to isolate the coding sequences for N-acetyl glucosaminidase and endochitinase from *Pseudomonas fluorescens*AFG4, for pyramiding these genes in sugarcane that would result in resistance to red rot pathogen.

PIV-5

BIOPROSPECTING OF MORINGA FOR ITS NUTRITIONAL, MEDICINAL AND INDUSTRIAL VALUES

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Moringa, *Moringa oleifera* Lam (synonym: *Moringa pterygosperma* Gaertner) is widely cultivated in India as a monocrop and in home-shed kitchen gardens. Despite Moringa leaves and pods are the main course of Indian dishes; its nutritional and industrial values are yet to be known. In general, Moringa is rich in protein, minerals, and vitamins. The tender leaves of *M. oleifera* are used as a highly nutrient leafy vegetable and as cattle feed since it possess high proteins, low fiber content, significant amount of vitamins, and rich source of major trace elements, *viz*., calcium, phosphorous and zinc. In addition, the seed powder is used in water purification, and the seed oil is acquired for edible, lubrication, and cosmetics. Besides, drumstick leaves also contain anti-nutritional factors, antibiotic, anti-inflammatory and anti-carcinogenic activities and clinical trials showed that it induces sleeping time, restore fertility and lower the body temperature. Moringa has also been used as an alley crop for biomass production and biofuel production. Considering the above importance, a detailed study has been started in this institute on morpho-molecular characterization of Moringa germplasm and exploring the available germplasm entries for their role in nutritional, medicinal and industrial application. The details of the results will be presented during the conference.

5. HOST PLANT INTERACTION IN BIOTIC STRESS MANAGEMENT

PV-1

EFFECT OF CLIMATIC FACTORS OVER THE INCIDENCE OF DOWNY MILDEW CAUSED BY *Peronosclerospora sorghi* IN MAIZE

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Sorghum Downy mildew is caused by the fungal pathogen *Peronosclerspora sorghi*(Waston and Uppal) C. G. Shaw), can cause extensive losses to sorghum and maize in tropical and subtropical areas. *P. sorghi* reproduces by both the means i.e. sexual (oospores) and asexual (spore,conidia). Conducive weather is required for conidia germination, infection, and epidemic to develop. With a view of understanding effect of weather parameter on disease incidence, both were recorded in 25 genotypes of maize during kharif season of 2008 and 2009. As the local infections begin at the seedling stage, the weather parameter for the first month is highly responsible for downy mildew disease development. Minimum temperature for first 3 weeks remained 21- 23C in 2009 cropping period whereas it was higher than 23C in 2008. The reduced conidia infection percent was found in almost all the genotypes in 2008 compared to 2009. Humidity and rainfall was also high almost all the weeks during 2009 cropping period, which showed 100% disease incidence in the highly susceptible genotype (CM500) that was only 94% in 2008 cropping period. Thus, weather variable such as temperature, relative humidity, and rainfall are the utmost importance in disease epidemiology and for better management of the disease.

PV-2

IN-SILICO FUNCTIONAL ANNOTATION AND GENOME WIDE CHARACTERIZATION OF DIFFERENTIALLY REGULATED PROTEINS DURING WHEAT-PUCCINIA INTERACTION

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Proteome analysis of seedling resistance to leaf rust conferred by *Lr*57 gene in wheat (*Triticum aestivum* L.) was studied using 2D PAGE to identify differentially regulated proteins during wheat-*Puccinia* interaction. Virulent leaf rust causing fungal pathogen *Puccinia triticina* race 77-5 was used to inoculate resistant (WL711+*Lr*57) and susceptible (WL711-*Lr*57) near isogenic lines (NILs) of wheat. Upon *in-silico*functional annotation, the identified proteins (seventeen) were grouped into six categories - photosynthesis related, defense related, nucleotide repair related, DNA replication related, protein synthesis related and transposable element related proteins. In this study, spot W7, annotated as MCM6 (GenBank#: XP_003322730.1; e-value: 0.0; sequence identity: 47%), a DNA replication related protein (only protein from *Puccinia*in this study) was present only in susceptible 96 hpi plant which indicates that the pathogen will not be able to replicate in 96 hpi resistant plant. For the first time, the differential regulation of a nucleotide repair related protein, MMS19 (Spot W4; GenBank#: EMS62733.1; e-value: 0.0; sequence identity: 100%) during wheat-*Puccinia* interaction is reported in this study. The identified proteins in this study represent a fair range of basis of seedling resistance conferred by *Lr*57 against *Puccinia triticina*. *In-silico* genome wide study of the identified proteins was performed with the chosen species and it was found that the defense related proteins showed maximum divergence compared to other proteins, which can be correlated with the degree of selection pressure that the plant would have experienced from the ancient times due to biotic stress.

PV-3

EXPRESSION OF GLYCOSYL HYDROLASES IN *ARABIDOPSIS NUD 6* & *NUD 7* MUTANTS AS A RESISTANCE RESPONSE AGAINST *Pseudomonas syringae*

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Endomembrane Chitinases are coming under CAZY (Carbohydrate active enzymes). Arabidopsis contains 730 ORF corresponding to two major classes of CAZY: glycosylhydrolases (GHs) and glycosyltransferases (GTs). Of these 379 represent GHs classed in 29 families. Participating in cell wall dynamics *viz*., degradation and reorganization which present both in rice as well Arabidopsis. GHs (class III) are protective plant proteins are specifically induced in pathological or related situations. These proteins are called pathogenesis-related proteins (PR proteins) and involved in the protection of plants against pathogens. Classes III & V are among the candidate of GHs enzymes that are involved in the protection of plants against pathogens. These enzymes that hydrolyse-1,4-N-acetyl-D-glucosamine (GlcNAc) linkages and been classified according to their primary structures. They can able to show higher lysozyme/chitinase activity on bacterial cell walls peptidoglycan (murein). During inoculation of a virulent strain DC3000 *Pseudomonas syringae* on Arabidopsis mutants (NUDT 7, NUDT6 RNAi lines) expression of GHs 19 (endomembrane chitinase) was noticed as a systemic and local response and those mutants expressed with reduced levels of symptom development. These class of GH-19 have a substrate binding cleft, which is having three stranded"sheet and two helices. They prefer to attack the linkage, between N-acetlyglucosamine (GlcNAc) residues, chitosanases the linkage between glucosamine (GlcN) residues, and lyosozymes the linkage between N-acetylmuramic acid (MurNAc) and N-acetylglucosamine.

PV-4

REACTION OF RICE ACCESSIONS AGAINST RICE GALL MIDGE *Orseolia oryzae* (WOOD-MASON)

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Insects are major constraints to rice production and occur in all rice growing environments and estimated yield loss was upto 31.5 per cent. In Tropical Asia about 20 species are of major importance and regular occurrence. Among these, rice gall midge *Orseolia oryzae* (Wood-Mason) has gained great economic significance in recent years as their infestations very often assume epidemic proportions. Breeding resistant varieties has been a viable, ecologically acceptable approach for managing the pest. In this context, field trial on the reaction of rice accessions for resistance / susceptible to rice gall midge was carried out at Rice Research Station, Tirur, Thiruvallur Dt. during samba, 2009. The rice cultures received from Directorate of Rice Research, Hyderabad were planted in two rows of 20 hills with a spacing of 20 x 15 cm. Gall midge incidence as silver shoot was recorded on 30 and 50 days after transplanting and scoring was done as per the Standard Evaluation System, IRRI. Among 45 cultures screened, the cultures viz., RP 4683-29-2-645, RP 4683-30-1-648, RP 4686-49-1-943, RP 4687-52-2-1197, RP 4688-53-2-1258, RP 4688-53-2-1259, JGL 17025, JGL 17183, JGL 17187, JGL 17189, KAVYA, JGL 17190, JGL 17196, JGL 17198, JGL 17211 and JGL 17221 were recorded nil gall midge damage and found to be resistant in field screening. The accessions viz., SYE 11-15-8-36-18-7-20, ENT-GPP-2, Aganni and RP 2068-18-3-5 found to be moderately susceptible and the remaining entries were highly susceptible to gall midge Check variety TN 1 was found to be highly susceptible.

PV-5

INHERITANCE OF RESISTANCE TO MUNGBEAN YELLOW MOSAIC VIRUS (MYMV) IN BLACKGRAM

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An investigation was conducted to study the inheritance pattern of mungbean yellow mosaic virus (MYMV) in six genetic populations *i.e.* P_1, P_2, F_1, F_2, B_1 and B_2 of five selected cross combinations of blackgram involving three highly resistant cultivars (Pu 31, VBN 4 and VBN 6) and two susceptible cultivars (CO 5 and LBG 623) under field conditions at NPRC, Vamban, a hot spot area for MYMV. The highly susceptible cultivar for MYMV, CO 5 was used as indicator-infector and was also sown all around in the field to increase the MYMV incidence. No insecticide was sprayed inorder to maintain the natural white fly population in experimental field. MYMV incidence was recorded on all the plants based on the visual scores on 50th day. The classification was made into scale 1-9 and were furter categorized into five groups : Resistant (R), Moderately resistant (MR), Moderately susceptible (MS), Susceptible (S) and Highly Susceptible (HS) However the plants in the F_2 and back cross generations were classified as resistant (1-3) and susceptible (5-9). Among the five cross combinations, two crosses were found as resistant while the remaining *i.e.* three crosses recorded susceptibility to MYMV incidence. The resistance was found to be under digenic control and dominant.

PV-6

PRINCIPAL COMPONENT ANALYSIS OF MORPHOLOGICAL TRAITS INFLUENCING BROWN PLANT HOPPER(BPH) (*Nilaparvata lugens*) RESISTANCE IN RICE (*Oryza sativa* L.) GERMPLASM

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Rice is one of the most important cereal crops in the tropics as well as parts of temperate regions in the world. It is a host for a large number of insect pests. BPH is the most damaging insect pest of rice in Southeast Asian countries. Rice accessions were obtained from different parts of the Tamil Nadu which includes land races, traditional varieties, established lines and released varieties of India. The experiment was carried out at Paddy Breeding Station as per Augmented Design I. The same accessions were screened for BPH resistance at Genetics Glass House, Coimbatore as per Modified Seed-box Screen Test (MSST). Morphological parameters namely plant height, Culm thickness and days to fifty per cent flowering were recorded in field condition along with assessment of BPH resistance using screening scores at seedling stage by the MSST in glass house. Principal Component Analysis (PCA) revealed that the traits namely plant height and days to fifty per cent flowering contributed in higher magnitude among other variables. PCA accounted for 61.03% of the total variation at the first principal component (PC). The amount of variation accounted for, cumulatively, by adding PCs 2 through 4 was 24.55%, 9.3% and 5.1%, respectively. From the PCA Biplot, the accessions namely T1904, PMK 1, Veeradangan, CO22, CO9, CO39, Sivappuchitraikar, CO40, CO32 and T235 were highly diverse for the measured traits when compared to all other accessions. Hence, these accessions can be employed for study the genetic inheritance of BPH resistance.

PV-7

INDUCTION OF SYSTEMIC RESISTANCE IN GERBERA BY *Bacillus subtilis* AGAINST *Meloidogyne incognita*

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of sample compared to control 2.698) and total phenol activity (6.397 mg g-1 compared to control 0.893). The PAL enzyme activity and total phenol content increased in the bacterized plants over control. Earlier and higher accumulation of defense enzymes and phenolic compounds in gerbera root treated with *B. subtilis* in response to invasion by *M. incognita* collectively contribute to induced systemic resistance and decrease in nematode infection.

PV-8

IDENTIFICATION OF SINGLE NUCLEOTIDE POLYMORPHISMS FOR BLAST RESISTANCE IN RICE

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Rice is a staple food for majority of world's population. One of the major problems in rice cultivation is Blast, a fungal disease caused by *Pyriculariaoryzae*. It affects upto 50% of rice yield. Blast resistance is a multigenic trait. Many blast resistant genes are identified and mapped based on SSR markers. Only, a few conventionally bred blast resistant varieties like Fedearroz 50 confer durable blast resistance for a longer period exceptionally (since 1998). The reason for such durable resistance could possibly due to complementary effect of several resistance conferring genes. *Pi-b; Pi-z; Pi-2; Pi-33; Pi-sh; Pi-k; Pi-ta2* are some of the genes conferring blast resistance. Besides multiple functional polymorphism in a single resistance gene could also contribute to the durable resistance. Exploring SNPs related to blast resistance can be accomplished by comparing the whole genome NGS data available for resistant and susceptible rice varieties. In this study we have chosen Fedearroz 50 as a resistant variety and IR 22 as susceptible variety. The Rice 3000 Giga DB whole genome NGS data was used for the analysis. The locations of SNPs were identified from Nippon bare reference genome. Further, these genes will be short listed based on their role in stress resistance. These SNP could be used as DNA markers in differentiating rice varieties with durable blast resistance.

PV-9

IDENTIFICATION OF SNP FOR LEAF HOPPER RESISTANCE IN *Oryza sativa* (RICE) VARIETY PARA NELLU

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Rice is a staple food source in most of the tropical countries. Green leaf hopper (*Nephotettix virescens)*, Brown plant hopper (*Nilaparvata lugens)* and white backed plant hopper (*Sogatella furcifera)* are devastating rice pests which reduce the yield up to 60%. Plant hopper resistance is a multigenic trait. Various crop varieties have been developed to confer plant hopper resistance in rice. However, the resistance is broken within a short duration when the hoppers evolve in a faster rate to survive the resistance. According to the manual of genetic evaluation for insect resistance in rice; Para nellu, a traditional rice variety from Kerala is identified to confer resistance to all types of plant hoppers. Many Plant hopper resistance genes have been mapped in rice varieties such as PTB33, PTB18 and Pankahari 203. IR 22 is a plant hopper susceptible variety. Para nellu and IR 22 were compared for their difference in genome using rice 3000 GigaDB. On comparison, SNPs were identified and their locations were plotted using Nipponbare reference genome. The shortlisting of the SNPs based on the relevance to biotic stress will be accomplished. These SNP data are potential source for designing DNA markers for leaf hopper resistance.

6. INNOVATIVE TOOLS AND TECHNIQUES FOR IMPROVEMENT OF HORTICULTURAL CROPS

PVI-1

GENETIC VARIABILITY, CHARACTER ASSOCIATION AND PATH ANALYSIS STUDIES FOR YIELD AND YIELD ATTRIBUTING TRAITS OF JACK BEAN (*Canavalia ensiformis* (L.) DC.) AN UNDER EXPLOITED VEGETABLE

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Jack bean (*Canavalia ensiformis* (L.) DC.) is an important underexploited vegetable crop belongs to the family *leguminaceae*. The Genus *Canavalia* consisting of 48 species of which, four species are reported from India. The exploitation of variability is a pre-requisite for the effective screening of superior genotypes. Hence, it is essential to partition the overall variability into its heritable and non-heritable components with the help of genetic parameters like variability, heritability and genetic advance. Keeping in view the importance of above biometrical approaches, an experiment was conducted to study the genetic variability, heritability, genetic advance, character association and path analysis for yield and fifteen yield contributing characters in fifteen jack bean genotypes at NBPGR Regional station, Rajendranagar during Kharif 2013 (August 2013 to February 2014). Significant variation was observed for all the characters. Among the characters studied, the highest heritability as well as genetic advance as percent of mean were observed for plant height, number of primary branches per plant, days to last pod harvest, pod length, pod weight, number of pods per plant, number of seeds per pod, 100 seed weight and marketable pod yield per plant. Results revealed that pod weight and number of pods per plant had significant positive association with pod yield and also had positive high direct effect on pod yield while days to 50 percent flowering have negative effect on yield.

PVI-2

Genetic divergence in brinjal (*Solanum melongena* L.)

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A study on genetic diversity in brinjal (*Solanum melongena* L.) was conducted in thirty genotypes of brinjal were evaluated in terms of plant height, branches per plant, days to 50%flowering, fruit

length, fruit girth, single fruit weight, shoot borer incidence, fruit borer incidence, yield per plant and market yield. These genotypes were grouped into five distinct clusters based on yield contributing traits suggested by Tochers method cluster I contained maximum number of genotypes (26) followed by cluster II, cluster III, cluster IV and cluster V had one genotype each. The genotypes belonging to distinct clusters are utilized in the hybridization programme to obtain superior lines Maximum intra cluster distance was recorded by cluster I (136.14) which revealed the existence of considerable genetic divergence among the genotypes of the cluster I. The highest inter cluster distance of (305.96) was observed between cluster IV and V, followed by cluster II and V (257.25) and cluster I and IV (248.77), revealing that enormous diversity between genotypes belonging to respective pairs of the clusters.

PVI-3

STUDIES ON SCREENING OF CUCURBITACEOUS SPECIES FOR FUSARIAL WILT (*Fusarium oxysporum* f. sp. *Cucumerinum*) RESISTANCE FOR CUCUMBER GRAFTING

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An experiment was carried out at the Department of Vegetable Crops, HC&RI, TNAU to screen cucurbitaceous species against fusarial wilt (*Fusarium oxysporum*f. sp. *cucumerinum*) resistance under pot culture condition. Successful gene exchange between *C. sativus* and related wild species is difficult using conventional breeding methods such as hybridization techniques, since *C. sativus*has a different chromosome number than other related wild *Cucumis* spp. Hence, screening of cucurbits for fusarial wilt resistance will be a useful tool for selection of rootstocks for cucumber grafting technology. The screening studies were conducted in CRD and replicated thrice with seven cucurbitaceous rootstocks *viz.,* Fig leaf gourd (*Cucurbita ficifolia*), Pumpkin (*Cucurbita moschata*), Winter squash (*Cucurbita maxima*), Bottle gourd (*Lagenaria siceraria*), Sponge gourd (*Luffa cylindrica*), African horned cucumber (*Cucumis metuliferus*) and Colocynth (*Citrullus colocynthis*) and two cucumber scions NS 408 (F_1 hybrid) and Green Long (variety) to identify resistance rootstocks for fusarial wilt. Artificial inocultion done with fungal culture was thoroughly mixed with sterilized uniform pot culture soil. The results after 30, 45 and 60 days after inoculation revealed that, the rootsctoks*C. metuliferus, C. colocynthis*were found to be immune with per cent disease incidence of zero (PDI 0 %) up to 60 days after inoculation. However, *C. maxima* (19.67 %) *L. siceraria* (20.00 %) *C. ficifolia* (20.14 %) and *L. cylindrica*(22.22 %) have also recorded the lesser PDI for fusarium wilt at 60 days after infection. Hence these rootstocks could be used for production of fusarial wilt resistant cucumber grafts.

PVI-4

SCREENING OF WILD AND CULTIVATED CUCURBITACEOUS SPECIES FOR ROOT KNOT NEMATODE (*Meloidogyne incognita*) RESISTANCE

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An experiment was carried out during 2013, at HC&RI, TNAU to screen twelve cucurbitaceous species to use as rootstocks in cucumber grafting studies, against root knot nematode (RKN)-*Meloidogyne incognita* resistance. The rootstocks were grown in pots and artificial inoculation of one J2 juvenile per gram of soil at one to two true leaf stage of plants (5000 J2 /5kg pot) was done, 45 days after inoculation, the roots of the plants were uprooted and observations made for calculation of Root Knot Nematode Index. Root knot nematode screening studies in pot culture revealed that *Cucumis metuliferus, Citrullus colocynthis, Cucurbita moschata and Cucumis callosus* were found to be resistance to root knot nematode with a gall index of two (RKI-2), whereas, *Cucurbita ficifolia, Cucurbita maxima* and *Cucumis melo* sub sp. *agrestis* were found to be moderately resistant to RKN (RKI-3). Biochemical studies of cucurbitaceous species against RKN revealed that, *Cucumis metuliferus* recorded highest total phenols (16.98 mg g-1) and peroxidase activity (3.83 OD min-1g-1) followed by *Citrullus colocynthis* (total phenols 16.08 mg g-1 ; peroxidase activity 3.26 OD min-1g-1) and *Cucurbita moschata*(total phenols 15.37 mg g-1; peroxidase activity 15.37 mg g-1) respectively. From the pot culture studies it could be concluded that, *Cucumis metuliferus, Citrullus colocynthis, Cucurbita moschata* and *Cucumis callosus* were found to be resistance to root knot nematode respectively. These rootstocks could be used as RKN resistant source for grafting studies.

PVI-5

GRAFTING STUDIES IN BITTER GOURD (*Momordica charantia* L.) FOR MANAGEMENT OF ROOT KNOT NEMATODE *Meloidogyne incognita* Kofoid and White

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The management of soil borne pathogens is nowadays complicated by the increasing restrictions in the usage of soil fumigants. A possible alternative to the use of these agrochemicals for soil disinfestations in bitter gourd cultivation is the use of grafted plants. Due to the scarcity of studies

concerning bitter gourd grafting to control root knot nematode *Meloidogyne incognita,* an investigation was carried out with ten wild and cultivated cucurbitaceous rootstocks and two bitter gourd scions (Palee F_1 and CO1) at Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agriculture University, Coimbatore during 2011-2013. Screening of rootstocks against root knot nematode under pot culture condition revealed that the rootstocks *viz.,*kumatikai*(Citrullus colocynthis)*, African horned cucumber (*Cucumis metuliferus)* and pumpkin *(Cucurbita moschata)* had the least count of root knot index of 2, attaining a reaction category of resistant (R), whereas mithipakal(*Momordica charantia* var. *muricata)* and sponge gourd *(Luffa cylindrica)* exhibited minimum number of galls with root knot index of 3 attaining the reaction category of a moderately resistant (MR). The grafting technique followed in this study is side grafting. The results on grafting success revealed that Palee F_1 grafted onto pumpkin rootstock recorded the highest success percentage of 89.05, 78.90 and 71.70 followed by sponge gourd which recorded 85.35, 74.35 and 68.26 at 15, 30 and 45 days intervals respectively. From this study pumpkin and sponge gourd could be identified as best rootstock for grafting with bitter gourd for effective management of root knot nematode.

PVI-6

EFFECT OF POST HARVEST TREATMENTS ON PHYSIOCHEMICAL CHARACTERISTICS AND SHELF LIFE OF TOMATO (*Lycopersicon esculentum* MILL.) FRUITS DURING STORAGE

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The experiment entitled, Physiological Basis of extending shelf life in tomato (*Lycopersicon esculentum* mill.) was conducted in the laboratory of Department of Agricultural Botany, Vasantrao Naik Marathwada KrishiVidyapeeth, Parbhani during 20013-14. The experiment was laid out in completely randomized design with three replications. The treatments consist of LDPE packaging, HDPE packaging, paper packaging, Hot water and treatments of various chemicals *viz.* calcium chloride and salicylic acid. In this experiment treated fruits are kept in ambient storage conditions. Among the different chemical treatments, $CaCl_2$ treated fruits shows lower physiological loss in weight, higher titrable acidity and delay in lycopene biosynthesis. Fruits treated with salicylic acid shows significantly lower TSS, lower rate of respiration and ethylene production and increases ascorbic acid content.Significant differences were observed among the physio-chemical parameters due to various post harvest treatments at storage. The tomato fruits kept in HDPE packaging had a significantly low physiologically loss in weight and lycopene content. The highest Total Soluble Solid was recorded in control while the same treatment recorded lower value of titrable acidity. Treatment of Salisylic acid recorded highest ascorbic acid content and lower ethylene evolution rate and respiration rate thus extended the shelf life of tomato fruits.

PVI-7

PERFORMANCE AND GENETIC VARIABILITY STUDIES IN THE F_2 GENERATION OF PUMPKIN (*Cucurbita moschata* (DUCH) POIR.) FOR DIFFERENT YIELD AND FRUIT QUALITY TRAITS

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In Pumpkin, an F_2 population of Ambilli x TCR 011were sown in the protrays and the seedlings were transplanted in the main field of the College orchard, TNAU, Coimbatore. Parental lines, F_1 generation and 107 F_2 individuals of Ambilli x TCR 011 cross combination were observed for days to 1st female flower opening (days), total vine length (cm), node at first fruit harvest, number of fruits per vine, single fruit weight (kg), fruit yield per vine (kg), fruit flesh thickness (cm) and carotene content. Fruit flesh thickness ranged from 1.4 cm to 6.7 cm and 26 segregants recorded more flesh thickness than the parents and F_1 generation. Carotene content ranged from 1.03 to 4.63 mg / 100g of sample and 22 segregants recorded more carotene content than TCR 011. F_2 population of Ambilli x TCR011 cross combination recorded higher GV, PV, GCV, PCV, heritability and genetic advance as per cent of mean for all the characters except for days to first female flower opening. Days to first female flower opening recorded low genotypic coefficient of variation (8.72 %), phenotypic coefficient of variation (9.94 %), high heritability (76.96%) and moderate genetic advance as per cent of mean (15.76 %). All the characters studied have recorded higher heritability coupled with high genetic advance as percent of mean. Hence, these simple selection techniques may be effective for the isolation of segregants with high flesh thickness, high carotene content coupled with greater yield per vine.

PVI-8

MANAGEMENT OF NEMATODES UNDER DIFFERENT CULTIVATION METHODS IN TURMERIC

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Turmeric (*Curcuma longa* L.) is an important spice as well as medicinal plant and contribute a major share in foreign exchange (Chitwood *et al.,* 1949). The rhizomes of turmeric and its powder have been used in culinary spice, in cosmetic preparation, as food preservative, colouring agent and also in drug industries for its pharmaceutical properties and its colouring principle Curcumin**.** Turmeric was affected by diverse group of nematodes among them root knot nematodes was a major pest and its management with special reference to biocontrol approach revealed with the use of rhizobacterium,

Pseudomonas fluorescens available commercially in talc formulation was effective in managing the nematodes and to enhance the yield in conventional flood irrigated turmeric. The yield loss due to *Meloidogyne incognita* in turmeric was ranged from 8.16 to 26.13 per cent quantitatively and 5.70 to 25.00 per cent qualitatively with different irrigation regions. The yield loss caused due to *M. incognita* was found to be higher under controlled conditions compared to field conditions. Its dosage and time of application was optimized as 2.5 kg/ha in two rounds at 90 and 150 DAP. Similarly, bionemagation with liquid formulated *P. fluorescens* (Pf 1) at 3 lit/ha twice at 90 and 150 DAP was found to be effective for the management of root knot nematode in turmeric grown under drip irrigated conditions which also enhance the yield quantitatively and qualitatively.

PVI-9

COLLECTION AND EVALUATION OF LEAFY CORIANDER GENOTYPES FOR GROWTH AND LEAF YIELD PRODUCTION

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In Tamil Nadu, Coriander is cultivated in Villupuram, Virudhunagar, Madurai, Theni, Chengalpet, Coimbatore, Tiruppur and Erode districts in large areas. In general, leafy coriander cultivation quite difficult during summer months due to prevailing of hot weather conditions. Hence, during summer months considered as off season production. With this backround collection and evaluation of leafy coriander genotypes for growth and leaf yield production was carried out at Horticultural College and Research Institute, Periyakulam to identify the promising leafy coriander genotypes suitable for off season coriander leaf production. Totally twenty two leafy coriander genotypes were evaluated. The experimental trial was laid out in randomized block design (RBD) and replicated thrice. The split seeds of leafy coriander were sown soaked in water for eight hours and were sowed at a spacing of 20 x15 cm. Data on growth and yield parameters were recorded and analysed statistically. Among the twenty two leafy coriander genotypes, Acr-1 recorded the highest values of growth and yield parameters like days taken for germination (9.00 days), plant height at 40 days after sowing (31.77 days), number of leaves per plant (6.40), yield per plot (3.75 kg/10m2) and estimated yield of 3.92 t/ha, followed by LCC-232 recorded the higher values then rest of the treatments. However, CS-38 genotype recorded the lowest values in all the growth and yield characters.

PVI-10

STUDIES ON BIO-EFFICACY OF DIFFERENT BOTANICALS AGAINST PURPLE BLOTCH OF ONION (*Allium cepa* L.)

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A study was undertaken to evaluate the efficacy of eco-friendly botanicals against *A. porri*causing purple blotch of onion (*Allium cepa*L.) under *in vitro* conditions. Totally six treatments were used such as, neem (*Azadirachta indica*), tulasi (*Ocimum santum*), Ballarijali (*Prosopis julifera*), nilgiri (*Eucalyptus* spp.), ginger (*Zingiber officinalis*) and *Bougainvillea.* Of them, neem over all the concentrations evaluated; was found to be the most effective botanical recording the highest inhibition of mycelial growth of the pathogen (66.30%) and was on par with ginger (57.65%) followed by nilgiri (56.30%), that was on par with tulasi. However, *Prosopis juliflera* was found to be least effective in inhibiting the fungal growth (21.98%) and was on par with *Bougainvillea* (32.35%).All the botanicals were found to be most effective at higher concentration of 15% as compared to lower concentrations. Maximum inhibition of mycelial growth (59.63%) was observed at 15% concentration and was significantly superior over 5% concentration (39.44%). *A. indica* @15% concentration gave maximum inhibition of mycelial growth (70.74%) and was significantly superior over all other treatments followed by *A. indica* (58.52%) at 5 per cent. The least inhibition of fungal growth was observed in case of *Bougainvillea* (20.00%) followed by *P. julifera* (12.22%) at 5 per cent concentrations.

PVI-11

GENETIC DIVERGENCE IN CUCUMBER

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Cucumber is the most important cucurbitaceous vegetable and serves as the primary source of dietary fiber, vitamins and minerals. Twenty-seven diverse cucumber genotypes collected from different places of TamilNadu were evaluated at Horticulture College and Research Institute, Periyakulam during 2013 by raising them in RBD replicated thrice. The data on vine length, primary branches/vine, days to first male and female flower opening, node number of first male and female flower production, male and female flowers/vine, sex ratio, tender-fruits/vine, tender-fruit length and

diameter, fruit shape index, tender-fruit weight, number of harvests, crop duration, tender-fruit yield/vine, ascorbic acid content and acidity were subjected to Mahalanobis D^2 analysis to assess the genetic divergence between the genotypes. The genotypes aggregated in six clusters. The inter-cluster distance ranged from 16.12 to 179.47. The highest genetic distance was observed between clusters-V and VI. The cluster consists of 1 to 11 genotypes and their intra-cluster distances were of considerable magnitude, ranging from 23.58 to 97.41, indicating the presence of wide genetic divergence within each cluster. The five OldAyakudi, Palani types were distributed in same cluster indicating the presence of similar genetic architecture of the genotypes from the same region. High productivity in cucumber can be achieved by selecting genetically divergent genotypes from different clusters for breeding programme. Assessment of contribution of different characters to genetic diversity revealed the importance of tender fruit yield/vine (47.58%) and male flowers/vine (25.92%).

PVI-12

VARIABILITY STUDIES IN TOMATO

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Variability studies in tomato was conducted during the year 2007-2008 at Horticulture Section, College of Agriculture, Nagpur using 40 genotypes. Range and mean performance of the yield components and quality traits revealed that, the genotypes TMN-35 was found to be superior for yield and yield contributing characters i.e. yield plant-1, yield plot-1 and ha-1, fruit weight, fruit diameter, and fruit length.. The variety Dhanshrree was found superior for earliness and TMN-25 for quality parameters (seed:pulp ratio and juice per cent). High PCV percentage were recorded for seed: pulp ratio, leaf area, weight of fruit yield plant-1, yield plot-1 and ha-1. Phenotypic correlation coefficient was comparatively lower than the genotypic correlation coefficient except for plant height with primary branches which indicates less influence of environment. The genotypic correlation coefficient of yield plant-1 was significant and positively correlated with diameter of fruit, weight and length of fruit. The path analysis revealed that leaves plant-1 and days to Ist fruit set showed high positive direct effect on yield characters and characters like fruit length, fruit plant-1 and weight of fruit showed positive direct effect on tomato yield. These characters directly influenced the improvement in yield. The genotype TMN-35 (yield), Dhanshree (earliness) and TMN-25 (quality) were identified as superior genotypes for further use.

PVI-13

INFLUENCE OF INTEGRATED NUTRIENT MANAGEMENT PRACTICES ON YIELD ATTRIBUTES IN OKRA (*Abelmoschus esculentus* (L.) MOENCH) CV. ARKA ANAMIKA

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A field experiment was conducted to study the integrated nutrient management in Bhendi (*Abelmoschus esculentus* (L.) Moench) at Department of Horticulture, Agricultural College and Research Institute, Madurai in two seasons. The experiment was laid out in a randomized block design with 19 treatments, each replicated thrice. The treatment involved different organic manures viz., FYM, Vermicompost and Pressmud was applied as basal at 12.5, 5 and 5 kg ha-1 respectively; three levels of nitrogen viz.,100 per cent, 75 per cent and 50 per cent of recommended dose as urea, three levels of phosphorus viz., 100 per cent, 75 per cent and 50 per cent recommended dose as single super phosphate and 100 per cent potash; and two different biofertilizers viz., Azospirillum and Phosphobacteria each at 2 kg ha-1 were tried with all possible combinations along with a control. The results revealed that application of of 75 per cent recommended dose of N and 100 per cent recommended dose of P&K + Pressmud + Azospirillum had a significant effect on the yield attributes viz., fruit length, fruit girth, number of fruits per plant, fruit weight, yield per plot and yield per hectare were noticed. Keywords: Integrated nutrient management, okra, inorganic manures, Pressmud, Azospirillum, yield.

PVI-14

HORTIVAR - AN INNOVATIVE TOOL FOR SEARCHING THE VARIETAL WEALTH OF THE HORTICULTURAL CROPS

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Hortivar is FAO's database on the performances of horticultural cultivars over the world. Hortivar is also a platform for exchange of know-how among scientists and a tool to safeguard, retrieve and exchange information related to horticulture. Information can be retrieved regarding six groups of crops: A fruit, vegetables, root and tuber crops, herbs and condiments, ornamentals and mushrooms. The database has two primary functions which are interdependent: data retrieval and data entry. Access and use of the database is free of charge. Hortivar serves as a standard methodology for data collection and record keeping on the performances of horticulture cultivars. It is a powerful search engine for easy retrieval and comparison of information. It is also a template for educational

purposes and a gateway to horticulture knowledge/statistics. Hortivar addresses the needs of producers, public and private sector, seed companies and horticultural research centres for information management related to horticultural crop cultivars in different agro-climatic environments and allows users to identify cultivars and cropping practices adapted to their specific requirements and environment. While FAO maintains and develops this programme and software, it relies on its members to feed it with information either as individual or as institutional partners. Hortivar is not a static programme but it is continuously being adjusted to meet the requirements of its users besides it is an innovative tool for plant breeders to search the varietal wealth of the horticultural crops in crop improvement programme.

PVI-15

MODIFICATION OF FLOWER COLOUR BY GENETIC ENGINEERING OF COLOUR PIGMENTS

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Flowers are wonderful creation of the nature which plays an important role in every sphere of human life. So, Floriculture is gaining importance day-by-day. As man always thirsts for novelty, floriculture thrives on it. Flower colour is the utmost important aspect in the floriculture market where flowers of novel colour can create high demand. Breeding technologies like extensive hybridization and mutation breeding have been employed by breeders to develop novel colours in flowers. Hybridization has its limits due to genetic constraints within the species and mutation breeding has very low success rate and we cannot have control over the variations that occur. These barriers can only be overcome through genetic engineering. Colour pigments like flavonoids, carotenoids and betalains are mainly responsible for flower colour. Of these colour pigments, flavonoids, especially their colour class compounds, anthocyanins are widespread and important contributors to flower colour. Wide range of colors which do not occur naturally in a particular flower can be developed by genetic engineering of flavonoid pathway. So, this novel finding is gaining importance and has a potential application. In this context, this study presents the role of genetic engineering of flavonoids biosynthetic pathway in flower color modification for improvement of floricultural plants.

PVI-16

STANDARDIZATION OF ROOTSTOCKS FOR GRAFTING IN OKRA (*Abelmoschus esculentus*L.) WITH SPECIAL EMPHASIS TO YVMV AND WHITEFLY RESISTANCE

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The study was undertaken to standardize the rootstocks for grafting of okra (*Abelmoschus esculentus*

L.) by cuttings with an aim to develop resistance types for Bhendi Yellow Vein Mosaic Virus and white fly. The genotypes *viz*., EC-755655, EC-755656, EC-755657 and EC-755658 were collected from AVRDC, Taiwan. The genotypes were assessed for YVMV and whitefly from 2011 to 2014 and observed to be highly resistant for YVMV in different seasons under natural conditions. All the four genotypes were subjected to different cutting methods of propagation *viz*., hard wood, semi-hard wood and soft wood cuttings. All the genotypes responded well to cuttings and sprouting was observed in all the cuttings on 5th day irrespective of the genotypes. Differential plantlet production was observed in all the genotypes and in EC-755655, the regeneration capacity was higher in semi hard wood cuttings (100%) while in EC-755656, the hard wood cuttings produced 100% on 16th day. Among the genotypes, EC-755657 had registered higher percent from both semi hard wood and soft wood cuttings (90% each). All the genotypes were successful in production of plantlets with higher success rate ranging from 87.50 % (EC-755657) to 52.38 % (EC-755656). Among the types of cuttings, both semi hard wood cuttings and hardwood cuttings produced more than 80% successful plantlets. This study pave way for further grafting studies in okra which is an emerging breeding tool to develop abiotic and biotic resistant cultivars.

PVI-17

INNOVATIVE BREEDING TOOL TO MAINTAIN GENETIC PURITY IN ANNUAL MORINGA(MORINGA OLERIFERA) Cv.PKM 1

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Moringaolerifera Lam. is one of the multipurpose plant known to man. Virtually every part of the tree is beneficial to both rural and urban population depending upon their lively hood. Maintenance of genetic purity in annual moringa is being the biggest challenge in since it is a cross pollinated crop. With this objective, air layering was carried out in Cv. PKM-1 to propagate the genotype and to maintain genetic purity as clone. The experiment was carried out in RBD with five replications and four treatments (IBA 500, 1000 and 1500 ppm) and control along with coco-peat as media at the model orchard, Department of Horticulture, AC &RI, Madurai during 2014-15. The root initiation in the layers was observed from 20th day at 1500ppm to 28th day in control. The number of days taken to complete root formation to transfer to secondary nursery significantly differed between treatments. Earlier root development was observed at 30th day in plants treated with 1500ppm of IBA, followed by 1000ppm (34th day) and 40th day in control. The plants were hardened and the percent success of regeneration as clone was higher in the layers treated with IBA at 1500ppm (82%) and least in the control with 54%. From the above study, air layering proves to be an innovative breeding tool to maintain the genetic purity in moringa. The propagules are maintained as clone and also, it is produced from stem which indirectly saves the economic parts like fruits and seeds.

7. INNOVATIVE TOOLS AND TECHNIQUES FOR TREE IMPROVEMENT

PVII-1

EXPERIMENTAL DESIGN FOR EVALUATION OF CLONES OF *CASUARINA* FOR WINDBREAK AGROFORESTRY SYSTEM

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Institute of Forest Genetics and Tree Breeding, Coimbatore took an initiative in ideotype breeding to select superior phenotypes of *Casuarina* which are efficacious for a windbreak agroforestry system. 21 phenotypes of *Casuarina* were selected by adopting point grading methods. Trees having more branches were given additional weighted score. On the basis of rooting ability and within clone variation in growth traits, ten clones were short listed for field trials. While establishing field trials, an innovative experimental design was framed for simultaneous evaluation for i) superiority of clones for growth traits and ii) efficacy of these clones for wind speed reduction. In this innovative design, the total perimeter of the field was divided into two halves. Each half of perimeter was further divided into 20 m long sections. In each section of perimeter, one clone was planted in three rows. Each row is considered as a separate block (Replication) as trees in each row will be experiencing different growing conditions. The spacing between the rows was 1 *m* and the spacing within rows was 2 m in zig-zag configuration. The check clone was a hybrid clone of *Casuarina equisetifolia* x *Casuarina junghuhniana*, a commonly planted clone in Tamil Nadu. Superiority of test clones of *Casuarina* under windbreak agroforestry system was compared over the Check clone for growth and branching traits. As a significant outcome of this experiment, five superior clones have been released for commercial planting by Varity Release Committee of Indian Council of Forestry Research and Education.

PVII-2

DIVERSITY ANALYSIS IN *Terminalia chebula* USING MORPHOLOGICAL AND MOLECULAR MARKERS

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Terminalia chebula is an important medicinal plant, extensively used in Ayurveda, Unani and Homoeopathic medicines. The present study was aimed to reveal its genetic diversity based on

morphological and molecular markers from twelve accessions. Significant differences were observed for Qualitative morphological descriptors *viz*., Tree height, canopy spread (North- South and East - West), tree girth, clear bole height, leaf length, leaf width, leaf area, fruit size, fruit volume, fruit weight, husk weight, endocarp weight, kernel weight and qualitative morphological descriptors include branching habit, leaf shape, fruit shape, fruit colour and endocarp colour. Molecular diversity was studied using RAPD markers. 20 RAPD primers were used to examine the extent of genetic diversity in 12 accessions. Amid the 20 RAPD primers, 8 primers gave polymorphic and reproducible banding pattern were chosen for further study. A total of 8 polymorphic primers produced 314 polymorphic bands and 195 monomorphic bands. UPMGA dendrogram divided the accessions into 2 major clusters at 55% similarity. Accession IIHRTc2 and IIHRTc10 showed maximum genetic diversity. This characterization based on morphological and molecular markers will help in identification of economically useful genotypes for further crop improvement programme.

PVII-3

INFLUENCE OF SEED SIZE GRADING ON PHYSICAL, PHYSIOLOGICAL AND BIOCHEMICAL SEED QUALITY CHARACTERS OF BAEL TREE (*Aeglemarmelos* (L.) CORR.)

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Bael is an endangered medicinal tree with multipurpose utility propagated through seeds. Bulk seeds of Bael exhibit polymorphism in seed characteristics. Hence, a study was undertaken to evaluate the influence of seed size grading on physical, physiological and biochemical seed quality characters. Polymorphic seeds based on size were separated by size grading the seeds using round perforated metal sieves of sizes 6.4, 6.0 and 5.5 mm retained and 5.5 mm passed (hole width), and the recovery of seeds retained on these sieves were 40, 23, 31 and 6% respectively. The physiological seed quality characters measured in terms of germination was higher with 6.4 mm sieve retained seeds (77%) and was followed by seeds retained on 6.0 mm (68%), 5.5 mm (55%) sieve; the seeds passed through 5.5 mm sieve registered only 41% germination while the germination recorded with bulk seeds was 63%. The seedling vigour measured through root length (11.3 cm), shoot length (9.3 cm), dry matter production (366 mg) and (1586), vigor index 2 (870) and vigour index 3 (28182) values were also higher in large seeds retained on 6.4 mm sized sieve. The biochemical characters measured as αamylase activity (5.2 cm) and dehydrogenase (0.193) were higher in larger seeds including seed protein (17.4%) and oil content (38.1%). The study thus expressed a linear relationship between seed size and physical, physiological and biochemical seed quality characters and necessitates homogenizing the seed lot based on size.

8. PLANT TISSUE CULTURE , GENETIC TRANSFORMATION, GENETICALLY MODIFIED ORGANISMS, BIOSAFETY AND BIOETHICS

PVIII-1

FUNCTIONAL CHARACTERIZATION OF TWO GENES INVOLVED IN POLLEN DEVELOPMENT OF RICE BY GENE SILENCING METHODS

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The rice mutant *TC-19* which carries a complex T-DNA integration in the first intron of a hypothetical gene in chromosome 8, which we named as a *MALE STERILE UNOPEN FLOWER1* (*MSUF1*), displayed male sterile phenotype in homozygous condition. Another gene, named as *RICE PANICLE3* (*RP3*) by the UD-SC group encodes an RNA recognition motif containing protein (PAN3-CRP). The *RP3* promoter-*GUS* fusion studies revealed that the *RP3* gene expression is confined to the tapetum of premeiotic and meiotic anther stages. Two different RNA silencing approaches were used to study the importance of *MSUF1* and *RP3* genes in anther development. Binary vectors with a hairpin RNA gene of *MSUF1* (hp-*MSUF1*) and artificial microRNA gene for *RP3* were introduced into *Agrobacterium tumefaciens* LBA4404 (pSB1) and used for rice transformations. Nineteen transgenic rice plants with integrated T-DNA were obtained with the hp-*MSUF1*, whereas nine transgenic plants were obtained with the *RP3* gene. Iodine staining was used to evaluate pollen viability in the control and transgenic plants. In control plants 95% of pollen grains were viable. Six of the 19 transgenic plants carrying hp-*MSUF1* gene showed a strong silencing phenotype with pollen viability ranging from 9% to 26%. Two out of three analysed hp-*MSUF1* transgenic plants accumulated siRNA. Out of the nine transgenic plants with the artificial microRNA gene for *RP3*, three plants displayed strong silencing which resulted in the pollen viability in the range of 21.6% to 30%. Our studies showed that both *MSUF1* and *RP3* genes are important for rice pollen development.

PVIII-2

IMPACT OF TDZ (THIDIAZURON) PULSE TREATMENT IN SINGLE AND MULTIPLE SHOOT FORMATION IN CALLI OF *Jatropha curcas*

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Bio fuels are often regarded as an attractive green alternative to fossil sources of energy due to their potential contribution to lowering carbon dioxide emissions. There is growing interest in *Jatrophacurcas* as biodiesel a miracle tree to help alleviate the energy crisis and generate income in rural areas of developing countries. *Jatropha* is becoming a poster child among some proponents of renewable energy. *Jatropha* biofuel contains more oxygen, with higher cetane value increasing the combustion quality, is clean, non-toxic, eco-friendly and economic due to its low production cost. The superior quality oil can be extracted from the seeds. The oil can be used as a mixed fuel for diesel/gasoline engines. Rather being the widely used green alternative to fossil sources of energy, *Jatropha*have so far been commercially utilized and has medicinal values too. As the remunerative benefits accruing it is now really important to micropropagate *Jatropha* in a large extent. Here in a new protocol being proposed to regenerate shoots from calli earlier in time through TDZ pulse treatment. Thidiazuron being a most active cytokinin like substance induces greater *in vitro* shoot proliferation. *Jatopha curcas* (CJC - 19) calli when given 3-5d TDZ (3mg/L) treatment were capable of giving rise to earlier shoots. Calli obtained from *ex vivo* leaves was used to study this effect. The distinct shoots were isolated and rooted in MS media containing IBA (0.3 mg/L). The rooted plants were finally transferred to soil in pots.

PVIII-3

OVER EXPRESSION OF *ARABIDOPSIS* UDP-GLUCOSYL-TRANSFERASE (UGT) GENE IN RICE TO ENHANCE PLANT TRANSFORMATION

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Rice transformation is very stringent due to its recalcitrant nature. The efficiency of *Agrobacterium*-mediated transformation is less in rice, which results in the development of minimal transgenic plants with desired characteristics. Earlier studies using *hat* mutants of *Arabidopsis* showed that there is an increase in the transformation efficiency due to the activation tagging of *UGT* gene. This enhanced transformation may be due to loosening of the cell wall thickness or involved in metabolism of cell wall synthesis and also minimize the activation of defense response. We expected that the heterologous

expression of the above *ugt* gene might increase the transformation efficiency in rice. Towards that the *ugt* gene from *A. thaliana* was amplified and cloned into *sma*I site of pBluscriptII KS. After confirmation of the clone by sequencing, its subsequently cloned into 35S cassette containing plasmid pRT100. This 35S driven *ugt* gene was cloned into binary vector pCAMBIA1301. This construct was mobilized into *A. tumefaciens* LBA4404 by triparental mating and the transconjugants were confirmed by non radioactive Southern hybridization. Rice scutelum derived embryogenic calli were transformed with the *Agrobacterium* strain LBA4404 harbouring*UGT* gene. The hygromycin resistant calli were confirmed by GUS histochemical assay and transferred to regeneration medium. The regenerated putative transgenics were acclimatized in soil and transferred to greenhouse. The putative transformants are yet to be confirmed by detailed Southern analysis for T-DNA integration and copy number determination.

PVIII-4

TARGETED DISRUPTION OF *OsMADS*1 IN RICE BY USING POSITIVE / NEGATIVE SELECTION BASED GENE TARGETING STRATEGY

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Gene targeting (GT) via homologous recombination is an effective method to precisely modify a gene in its native site. In our study, targeted disruption of the *OsMADS*1 gene was attempted by *Agrobacterium*-mediated transformation involving the ‘positive/negative selection’strategy. Rice *OsMADS*1 is a flower-specific gene, which controls identity of floret meristem and its determinate development. In the GT vector, the positive selectable marker hygromycinphosphotrasferase gene (*hph*) is flanked by a 4.28-kb 5’sequence of *OsMADS*1 and a 4-kb 3’sequence of *OsMADS*1. The diphtheria toxin-A subunit gene (*DT-A*) is placed on both ends of the T-DNA to eliminate the plants with ectopic T-DNA integrations. Rice transformation of 2,643 scutellum-derived calli with the GT vector yielded two independent *hph* resistant, transgenic plants. The T_0 plants were analysed by Southern blotting. The plant DNA was digested with *Hin*dIII or *Sac*I and the blot was probed with the *hph* gene. The expected 11.5-kb (upon *Hin*dIII digestion) and 6.5-kb (upon *Sac*I digestion) fragments hybridized. This result confirmed that the *hph* gene was integrated as a single copy in the *OsMADS*1 locus and no ectopic T-DNA integration had occurred. The T_0 plants, upon selfing and forwarding to the T_1 generation, displayed 3:1 segregation of hygromycin-resistant (Hyg^R) and -sensitive (Hyg^S) plants. The homozygous, knock-out T_1 plants were identified by Southern blotting using the 3’ part of the *OsMADS*1 gene as the probe. The GT frequency in our experiment was 0.1 %.The phenotype of flowers in the gene targeted, homozygous plants will be presented.

PVIII-5

CONVERSION OF SUGARS THROUGH PRETREATMENT TECHNIQUES FOR BIOETHANOL PRODUCTION USING FORAGE SORGHUM

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Energy consumption has increased steadily over the last century as the world population has grown and more countries have become industrialized. Alternatives to consumption of energy derived fuels are being sought in order to reduce the world is dependence on non-renewable resources. The most common renewable fuels today is ethanol derived from corn grain and sugarcane. Forage sorghum has high biomass yields. This biomass crops needs to be pretreated prior to saccharification. During pretreatment, the biomass is subjected to a combination of physical, thermal and chemical conditions that open up the plant cell wall structure and expose the cellulose, hemicellulose and lignin fibers. Subsequently, the pretreated biomass is hydrolyzed to sugars using cellulases, hemicellulases and ligninase. In this study, sorghum biomass samples were pretreated with dilute acid and alkaline and recovered solids washed and hydrolyzed with cellulase to liberate glucose. Glucose yields for the sorghum biomass were improved by 29%, 25%, and 37% (acid), 32%, 31%, and 43% (alkaline) from stem, leaf and grains, respectively. Sorghum biomass was pretreated with dilute acid followed by co treatment *i.e.*, enzymatic hydrolysis with crude cellulase derived from *Saccharomyces* sp. strain CYLL32 registered the maximum glucose yield 45%, 48% and 53% from stem, leaf and grains, respectively.

PVIII-6

STANDARDIZATION OF *IN VITRO* MICRO PROPOGATION OF *Moringa oleifera*

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Moringa oleifera is named the ‘miracle tree’ and ‘the tree of life’ as they possess several health benefits. *Moringao leifera* is nutritious, natural and the leaves are rich source of vitamin A, vitamin B and vitamin C, proteins, calcium, minerals and excellent source of iron compared to other leafy vegetables.The tissue culture conditions for *M. oleifera* were standardized in order to study the iron uptake mechanism in controlled conditions. The standardization of multiple shoot induction medium was done with the MS basal medium containing various concentrations of 6- Benzyl aminopurine (BAP). Among the different conditions, 4.44μM BAP produced 5-6 shoots average from the secondary shoot. The multiple root induction medium was standardized with the MS basal medium and various

concentrations and combinations of Naphthaleneacetic acid (NAA), Indole-3-butyric acid (IBA) and Indole-3-acetic acid (IAA). The combination of IBA (4.92 µM) and IAA (2.85µM) produced average of 9-11 roots/shoot. Of course, the above medium is well suited for micropropogation of *M. oleifera* too. The callus induction medium was done with MS basal medium containing various concentrations of 2,4-Dichlorophenoxyacetic acid (2,4-D) among this MS basal medium with 4.0 µM 2,4-D was standardized and regeneration of plants from callus is in progress.

PVIII-7

IN VITRO ORGANOGENESIS IN ASHOKA [*Saraca asoca* (ROXB.) De Wilde.]

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Ashoka, *Saraca asoca* (Roxb.) de Wilde, a vulnerable medicinal plant is highly regarded as a universal panacea in the ayurvedic medicine. International Union for Conservation of Nature and Natural resources (IUCN) has included *Saraca asoca*(*Roxb*.) de Wilde*,* in the red list of medicinal plants. All parts of the tree such as leaves, bark, fruits and seeds possess manifold medicinal properties. Establishing *in vitro* cultures are a highly complex phenomenon and the success depends on a number of factors *viz.,* genotypes, culture media, explants, and hormonal combinations. Callus induction studies were attempted using eleven explants *viz.,* meristematic shoot tip, nodal segment, internodal segment, leaf bits, axillary bud, cotyledon, embryo, seed, anther, ovary and hypocotyl from five different genotypes in three different media *viz.*, MS medium, B5 medium and WPM medium with 2,4 - D at different concentrations (0.5, to 4.0 mg /l). Among the media, MS with different concentrations of 2, 4 - D 0.5-4.0 mg/l responded well for three genotypes. Genotype 4 collected from Periyakulam, explant ovary and the treatment 4 (MS+2, 4-D 2.0 mg/l) responded best for callus induction. For *in vitro* culture of Ashoka species, indirect organogenesis *i.e.,* through the callus induction was found to be the best.

PVIII-8

RELATION BETWEEN EXPLANT AGE, TOTAL PHENOLS AND CALLUS INDUCTION IN TISSUE CULTURED COTTON (*Gossypium hirsutum* L.)

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Cotton (*Gossypium hirsutum* L.) has proven to be a relatively difficult species for *in vitro* culture. One of the major problems for many tissue culturesystem is browning and subsequent death of the cultured explants that usually depended on the phenolic compounds and the quantity of total phenols.

It therefore an essential pre requisite to find out the least phenol synthesizing germination age for the problematic species like cotton which will increase regeneration response and success in tissue culture studies. Hence, this study was carried out to determine the lowest phenol concentration phase during germination and to find out any relation between the age of explants, total phenols and callus induction in cotton. The results revealed that the total phenols estimated from the cotyledon and hypocotyl explants of 4, 7, 10, 14, 21 and 28 days old seedlings of Coker 310, MCU 12 and KC 3 gradually increased between 4th and 14th day, thereafter it showed a higher rate of increase irrespective of the genotypes. Significantly higher callus induction frequencies (100.0%) were observed for cotyledon and hypocotyls explants collected from 7 days old seedlings irrespective of the genotypes studied. Explants collected from younger (4 days) and older (28 days) seedlings exhibited only low callus induction frequencies. With the increase in total phenol content, the callus induction frequency of both hypocotyl and cotyledon explants of all the three genotypes was found to decrease. This study will therefore help in the establishment of tissue culture and gene transfer systems of problematic species like cotton.

PVIII-9

DEVELOPMENT OF EFFICIENT ADVENTITIOUS ROOT INDUCTION IN *Withania somnifera* AND ITS MASS PRODUCTION USING BIOREACTOR

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Withania somnifera(L.)Dunal, (Solanaceae), commonly called Ashwagandha, is used for over 3000 years in ayurveda and other indigenous medicinal systems. Traditionally, field grown plant material has been used for the commercial production of withanolides. Different environmental conditions, pollutants and fungi, bacteria, viruses and insects affect the quality of these products and can lead to heavy loss in yield and alteration in medicinal content of plant. Owing to the variations exhibited by bioactive components, production of large number of plants of superior chemotypes, without seasonal constraints, is desirable, which can be achieved by the use of *in vitro* technologies. As roots contain a number of therapeutically applicable withanolides, mass cultivation of roots *in vitro* will be an effective technique for large scale production of these withanolides. Hence, the objective of the present study was to explore the possibilities for developing a reproducible protocol for adventitious root induction and its mass cultivation in bioreactors. The influence of combination and concentration of auxin, MS media strength, photoperiod and sucrose concentration on adventitious root induction was studied. Full strength MS media supplemented with 0.25mg/L IAA and 1mg/L IBA, 4.5% sucrose was found to be the best media for *in vitro* adventitious root induction in *W. somnifera*. From the suspension culture studies full strength MS media was found to be suitable for mass cultivation of *Withania* roots in bioreactor. Bioreactor cultivated roots showed an increased mass and bioactive compound accumulation.

PVIII-10

COMPARATIVE EVALUATION OF *IN VITRO* GROWTH CHARACTERISTIC AND SECONDARY METABOLITE ACCUMULATION IN CULTIVARS OF *W. coagulans*

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Medicinal plants are of great interest to the researchers in the field of biotechnology as most of the drug industries depend on plant parts for productio n of pharmaceutical compounds. *Withania coagulans*, also known as Indian cheese maker, plays a major role in indigenous systems of medicine in the treatment of various diseases. The therapeutic activity of this plant is mainly attributed due to the presence of various steroidal alkaloids and lactones under the class of compounds called withanolides. Plant tissue culture is extensively used for mass production of elite plants and can be a potential source for important secondary metabolites. Selected cultivars of *W. coagulans* (AUF Wc 001, 008, 025 and AUL Wc) were *in vitro* germinated and the produced plantlets were micro propagated in media supplemented with optimised growth hormones. Adventitious root induction was achieved after auxin standardization followed by which the induced roots were transferred to suspension cultures. The *in vitro* propagated roots of cultivars of *W. coagulans* were then subjected to phytochemical analysis and HPTLC fingerprinting for withanolides quantification. The analysis revealed that AUL Wc and AUF 008 cultivars responded better under *in vitro* culturing and resulted in more withanolides and phytochemical accumulations comparatively. *In vitro* mass scale multiplication of these cultivars with high accumulation of bioactive compounds helps in fulfilling the needs of growing crude drug industries in an effective manner.

PVIII-11

STANDARDIZATION OF *IN VITRO* CULTURE TECHNIQUES AND COMPARATIVE EVALUATION OF MAJOR SECONDARY METABOLITES IN 5 VARIETIES OF VEGETABLE RENNET: *Withania coagulans*

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In ancient system of medicine, many plants have been reported to cure various health problems and diseases. *Withania coagulans* (*W. coagulans*) Dunal commonly known as Indian cheese makers or vegetable rennets belongs to family *Solanaceae* and is one of the important medicinal plants. In the present study, effect of various factors on *in vitro* germination such as light intensity (light and dark) and also full strength and half strength MS basal medium has been studied. Half strength MS

basal medium supplemented with 2% sucrose incubated in dark at 25°C was found to give maximum rate of germination compared to full strength MS supplemented with 2% sucrose in 5 varieties of *W.coagulans*. Different hormonal concentrations were used to test the efficiency of multiple shoot formation at different time intervals after inoculation for a period of 30 days with regular contamination checking. The maximum number of multiple shoots was observed in MS basal medium supplemented with 4.44 µM BAP and 2.62 µM K in in all varieties of *W. coagulans*. Quantification through high performance thin layer chromatography (HPTLC) showed the increased concentration of withanolide accumulation in *in vitro* roots compared to the field grown varieties of *W. coagulans*. This study would be further useful to enhance secondary metabolte content in *Withania coagulans,* rare medicinally important plant.

PVIII-12

AN INVESTIGATION INTO FACTORS INFLUENCING COTTON SOMATIC EMBRYOGENESIS

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Cotton (*Gossypium spp*) is the chief fibre and important source of oil and high quality protein meal. To apply a successful transformation protocol in cotton, it is necessary to obtain a highly efficient and reproducible regeneration and somatic embryogenesis protocols. One of the main drawbacks is the browning of callus within the short period of culture due to phenolic secretion and oxidation and the long time required from somatic embryos to plantlet formation. In the present study, highly reproducible and simple protocol for cotton somatic embryogenesis is described here by using different concentrations of carbon and vitamin source. Embryogenic calli derived from cotyledon explants were transferred to Somatic Induction medium supplemented with different carbon sources *viz*., sucrose, glucose and maltose (30 g/l each) to test their effect on somatic embryo production, somatic embryo maturation and somatic embryo germination. The efficiency of each carbon source on somatic embryogenesis was assessed in terms of number of somatic embryos produced per gram of embryogenic callus. Supplementation of maltose (30 g/l) in the medium resulted in the production of more number of somatic embryos per gram of embryogenic callus. Besides, somatic embryo maturation and somatic embryo germination were better on maltose than glucose and sucrose. The average number of embryos produced per gram of embryogenic calli, frequencies and germination of somatic embryo maturation were better on medium containing MS vitamins than B5 vitamins. Completely matured somatic embryos were germinated successfully on the medium fortified with MS vitamins.

PVIII-13

ORGANIC MEDIA FOR PLANT MICROPROPAGATION

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Production of cloned plants through aseptic *in vitro* conditions can be termed as plant tissue culture. The growth and regeneration rate of tissue cultured plants majorly depend on the media that has been utilised. Organic salts used in all types of media are either unavailable or costly. Organic substitutes can replace the synthetic compounds chosen in the preperation of media as they are eco-friendly and healthy. It has been reported that Yeast extract, malt extract, coconut milk (at various concentrations), caesinhydrosylate, tomato juice etc., have been used as replacements of growth promoters. Similarly wheat flour, chick pea flour, faba bean flour and barley flour at various concentrations have given successful results as replacement for Murashige and Skoog media macronutrients. Optimization of regeneration procedures and the mechanisms of growth stimulants as supplements of growth regulators have been useful in establishing consistent protocols for several medicinal herbs of economic importance. The use of these growth and macro-nutrient supplements in media have resulted in rapid propagation of the plantlets and hence can fulfill the needs of pharmaceutical, perfumery and flavor products based industries. Organic media can revolutionize plant tissue culture by exploiting their significance in near future in the field of medicinal plants research, such as in enormous production of secondary compounds through cell suspension cultures in bioreactors and genetic transformation studies.

PVIII-14

IN VITRO PROPAGATION OF BANANA (*MUSA* SP -ELAKKI (AB) VARIETY) FOR ITS COMMERCIAL PRODUCTION

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Elakki is diploid cultivar (AB), which is under commercial cultivation on a large scale especially in Karnataka and Tamil Nadu. The present study is to develop an efficient protocol for *in vitro*micropropagation of banana plants using sword suckers as explants. MS medium supplemented with different combinations of 6-BAP and NAA on shoot proliferation were investigated. Shoot proliferation media supplemented with 3 mg.L-1 6-BAP and 1 mg.L-1 NAA was found best and maximum rooting were observed in medium supplemented with ½ MS media, 30 mg.L-1 adenine sulphate and 0.1 % Activated charcoal. After seven subcultures, *in vitro* grown plants were primary hardened in poly trays filled with sterilized coco peat and maintained under polypropylene plastic sheet tunnels with humidity above 80%. In secondary hardening plants were kept in poly bags containing soil, coco peat and sand in 1:1:1 ratio and 2 gm/L of macro and micronutrient fertilizer were given as foliar spray. This protocol can be applied for large scale *in vitro* propagation of banana plantlets.

PVIII-15

T-DNA TAGGING OF PHOSPHOLIPASE A2*a* IN RICE REVEALS ITS ESSENTIAL ROLE IN POLLEN DEVELOPMENT

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The TC6 rice line generated with the *Trichoderma virens* chitinase gene (*cht*42), displayed an unusual segregation pattern of 1:1 (null: hemizygous) in the T_1 generation, and no homozygous plant was recovered. The anomaly may have arisen either due to lethality of male/female gametes or due to embryo lethality. T-DNA integration in the *TC6* mutant was mapped to the *PHOSPHOLIPASE A2a* (*OsPLA2a*) gene by genome walking. The panicles of TC6-hemizygous plant had filled seeds in all floret positions. Thus, female gamete lethality and embryo lethality are ruled out. The viability of pollen was studied by I_2-KI staining. As expected for male gamete lethality, the starch-positive and starch-negative pollen ratio was 39:61 in the TC6 hemizygous plants, indicating that nearly 50 % of pollen were not viable. By Northern blot analysis, *OsPLA2a* was found to express predominantly in the P5 and P6 stages of panicle development. Transgenic rice plants with *TC6* promoter-*GUS* fusion showed high GUS expression in the late panicle developmental stages and in the mature pollen grains. Complementation of the *TC6* mutant by supertransformation with the wild-type *OsPLA2* yielded homozygous TC6 plants. Silencing of *OsPLA2a* with the hairpin RNA gene of *OsPLA2a* showed 50-60 % reduction in pollen viability. These results demonstrate a critical role of the tagged *OsPLA2a* gene in post-meiotic pollen development and maturation.

PVIII-16

IN VITRO STUDIES ON DROUGHT TOLERANCE IN RICE (*Oryza sativa* L.) THROUGH POLY ETHYLENE GLYCOL (PEG) INDUCED OSMOTIC STRESS

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Selection by tissue culture through an osmoticum agent polyethylene glycol is precise for drought assessment compared to actual field condition. Mature seeds of fourteen parental lines (four lines and ten testers) and forty hybrids were used for developing callus on Murahige and Skoog (MS) medium supplemented with two treatments *viz.,* MS + 2, 4-D 2 mg/l and MS + 2, 4-D 2 mg/l + CH 1 mg /and further subculture. 100 mg embryogenic callus was exposed to basal medium supplemented with four different concentration *viz.*, 0, 0.5, 1, 1.5 and 2 percent of polyethylene glycol (peg) - 6000 as chemical drought inducer. Callus induction duration, effect of PEG on callus mass, proline content and plantlet regeneration were studied. Callus volume decrease and total proline content was found to be increased significantly with increased in PEG concentration. No drastic changes observed in callus induction duration. In five parents and twelve hybrids plantlets regeneration was observed up to the highest PEG concentration on over all comparison of three parents namely BR 2655, MAS 26, Vandana and three hybrids namely *viz.,* TNAU CMS 2A x MAS 26, IR 58025 A x BR 2655, and IR 68897 A x MAS 26 exhibited positive response for all the four characters acting as drought governing indices.

PVIII-17

GENETIC ENGINEERING OF COTTON WITH A NOVEL *cry2AX1* GENE TO IMPART INSECT RESISTANCE

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Cotton, the backbone of textile industry is one of the globally valued crops. Cotton and its by-products are also part of the livestock feed, seed-oil, fertilizers, paper and other consumer products. A major limiting factor in cotton production is incidence of bollworms, causing more than 50% yield loss. In order to mitigate this problem an attempt was made to develop insect resistant cotton plants. *Agrobacterium* mediated transformation of cotton (*cv.*coker310) was carried out with a synthetic *cry2AX1* gene to impart resistance against *Helicoverpa armigera*. Embryogenic calli were cocultivated with *Agrobacterium tumefaciens* strain, LBA4404 harbouring *cry2AX1* gene (driven by enhanced CaMV35S promoter) and 48 putative transgenic plants were regenerated through somatic embryogenesis. PCR analyses of these plants revealed the presence of *cry2AX1* gene in 40 plants. The level of *cry2AX1* protein expression of PCR positive plants in quantitative ELISA ranged from 0.005 to 0.188 µg/g of fresh tissue. Screening of transgenic cotton events expressing *cry2AX1* gene showed significant insecticidal activity (of about 56% mortality) against *Helicoverpa armigera* in detached leaf disc bioassay. Generation and screening more number of *cry2AX1* expressing cotton transgenic events could result in plants with desirable level of insect protection.

PVIII-18

GENE TRANSFORMATION IN AROMATIC INDICA RICES MEDIATED BY *Agrobacterium tumefaciens*

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Aromatic rice is profitable farming venture and having high consumer demand. The main concerns about aromatic rice are low yield and susceptibility to pests and diseases. A rapid and reproducible genetic transformation protocol was optimized for three aromatic rice varieties using the established plant regeneration protocol. Mature embryos were inoculated with *Agrobacterium tumefaciens* strain EHA 105 carrying binary vector pCAMBIA 1305.1 with *GUS* (reporter gene) and *hpt* (hygromycin resistance) gene and the transformation experiment was performed by optimizing the parameters infection time and co cultivation periods. Callus induction was obtained when the seeds namely Pusa Basmati 1,(58.6%) PusaSugandh 4(56%) and PusaSugandh 5 (55.6%)were cultured on MS medium supplemented with 2.5 mg l-1 IAA + 0.5 mg l-1 kinetin + 1.0 gl-1 CH + 30 g l-1 maltose + 100 ml-1 coconut milk and gelled with agar under dark condition. Maximum regeneration was obtained with MS supplemented with 2.5 mg l-1 BAP + 0.5 mg l-1 K + 1.0 mg l-1 K + 1.0 gl-1 CH + 30 g l-1 maltose + 100 ml-1 coconut milk and 0.8 % agar. It was found that hygromycinupto 30µgl-1 was effective for selection of transformants. Putative transformants as indicated by hygromycin test were subjected to GUS assay. GUS activities were found in rice calli after co cultivation.

PVIII-19

EFFICIENT TRANSFORMATION OF MAIZE USING IMMATURE EMBRYO

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Agrobacterium mediated transformation may offer a better alternative than the biolistic gun for genetic transformation of maize plants. This gene delivery system results in a greater proportion of stable, low copy number transgenic event than the biolistic gun and is highly efficient. In the transformation experiments, *Agrobacterium tumefaciens* strain, EHA 105 harbouring plant immature embryo explants. Among the explants immature embryos were preferred as the target material for transformation as it produced plantlets with 24-30 per cent transformation frequency in COH(M) 5.

Transformant event obtained when immature embryo collected 10-12 DAP with (0.8 - 1.5 mm) size were inoculated with two days culturing *Agrobacterium tumefaciens* (O.D 1.0 at 600 nm) was found higher in transient GUS expression. Immersion of explants in bacterial suspension was the best method of cocultivation and washing with sterile distilled water containing 150 mgl^{-1}cefotaxime and 250 mgl^{-1}carbenicillin gave best response in transient *GUS* expression with COH(M) 5 compared to other methods. Cefotaximeupto 150 mgl^{-1} and carbenicillinupto 250 mgl^{-1} were found to be optimum in obtaining maximum frequency of regeneration. The selection agent hygromycinup to 30 mgl^{-1} was found to be optimum in producing maximum regeneration and more number of shoots. Polymerase Chain Reaction (PCR) confirmed the presence of the *gus* and *hpt* genes in the genome of regenerated plants.

9. SEED VIABILITY, VIGOR, PURITY TEST, DUS TESTING, SEED DEVELOPMENT, PRE AND POST HARVEST HANDLING OF SEEDS

PIX-1

EFFECT OF DRIP IRRIGATION AND FERTIGATION ON RESULTANT SEED STORAGE POTENTIAL IN BHENDI

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Seed quality is a multiple and complex factor comprising of physical, chemical and biological components. Seed being a biological or living entity, deterioration is inevitable, irreversible and inexorable. On account of the diverse biological activities taking place in seed during storage, the seed deteriorates progressively in quality attributes resulting in impairment of germination and vigour. Viability of seed in storage is determined not only by the period of storage, the type of container used, seed treatment, and storage environment. A storage study was conducted in Department of Seed Science and Technology, TNAU, Coimbatore to predict the storability of resultant seeds of bhendi obtained from different irrigation and fertilizer schedules. The resultant seeds along with control were treated with Bavistin (2g / kg) and Imidachloprid (1 ml / kg) and stored in cloth bag and aluminium foil pouches under ambient conditions. Seeds of drip fertigation with 100 % RDF and treated with imidachloprid stored in aluminium foil pouches recorded early germination and maintained higher germination percentage, root and shoot length and vigour index; drip fertigation with 100% RDF and treated with bavistin maintained higher dry matter production throughout the storage period. Drip fertigation with 100 % RDF and treated with imidachloprid maintained lower EC values and maintained higher enzyme activities like dehydrogenase, á-amylase, throughout the storage period. The seeds obtained from drip irrigation with 100 % RDF treated with imidachloprid and stored in aluminium foil pouches maintained the seed quality attributes as well as biochemical characteristics throughout the period of storage.

PIX-2

EVALUATION OF PIGEON PEA HYBRIDS FOR POD SETTING AND FERTILITY

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The per cent pod setting as well as plant and pollen fertility was studied by using 79 F_1s, 24 male parents along with one standard check using RBD design with two replications. The result revealed that per cent pod setting was ranged from 18.7 to 59.1 per cent with an average value of 38.9 per

cent. The highest pod setting was observed in ICPA 2078 x MAL 13 (59.1 per cent) followed by ICPA 2078 x BWR 133 (53.2 per cent) and ICPA 2078 x HPL 24-63 (52.1 per cent). The plant and pollen fertility was found variable in all genotypes under study. The pollen fertility ranged from 90 to 100 per cent,where as it ranged from 74 to 100 per cent in hybrids. As regards to plant fertility, it ranged from 80 to 100 per cent in parents where as it ranged from 30 to 100 per cent in hybrids. Plant and pollen fertility found higher in case of parents as compared to hybrids.The higher yield per plant was recorded by genotypes ICPA 2078 x MAL 13 (251.85 g) followed by ICPA 2078 x HPL 24-63 (177.45 g) and ICPA 2078 x BWR 133 (169.50 g).

PIX-3

EFFECT OF ORGANO PRIMING ON SEED GERMINATION AND VIGOUR IN CHILLI cv. PKM 1

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A study was undertaken in the Department of Seed Science and Technology, Tamil Nadu Agricultural University, Coimbatore to standardize the seed priming with organics (panchagavya, cows urine and coconut water) on seed germination and seedling vigour in chilli cv. PKM 1. To optimize the concentration, seeds were primed with organics such as soaking in water, panchagavya (1%, 2% and 3%), cows urine (1%, 3% and 5%) and coconut water (25%, 50% and 75%). The seeds were also hydroprimed for 3, 6, 9 and 12h for standardization. The nonprimed seeds formed the control. The results revealed that seeds primed with coconut water 50 per cent expressed high values for all the parameters studied namely speed of germination, germination per cent, root length (cm), shoot length (cm), dry matter production (g/10 seedlings) and seeding vigour. The increases over nonprimed seeds for seed quality parameters were 34, 29, 25, 37, 114 and 64 per cent.

PIX-4

PRIMING OF SEEDS WITH DIFFERENT SEAWEED EXTRACTS TO MITIGATE SALINITY STRESS IN PADDY VAR. ANNA 4.

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Salt stress is a major adverse factor that can lower seed germination and seedlings growth, leading to reduced plant growth and ultimately lower crop productivity in all over the world. Paddy seeds were primed with *Sargassum myricocystum*, *Gracillaria edulis* and *Caulerpa racemosa* at the concentrations of 10, 20 and 30 %. The treated seeds were evaluated for various physiological

quality parameters under salinity level of 0.25, 0.50, 0.75 and 1% along with untreated control. The seeds were primed with *Sargassum myricocystum* (10 %) performed well under salinity level of 0.25 % by recording 4.2, 5.6, 9.6 and 23.0 per cent for higher germination, seedling length, vigour index and dry weight, respectively over untreated control and also under higher salinity level of 1% by recording 6.4, 9.6, 15.5 and 15.6 per cent for higher germination, seedling length, vigour index and dry weight, respectively over untreated control. There was nil germination in seeds primed with *Gracillaria edulis* and *Caulerpa racemosa* at the concentration of 10, 20 and 30 % under different salinity levels of 0.25, 0.50, 0.75 and 1 %. The result revealed that the seeds primed with *Sargassum myricocystum* (10 %) can withstand the salinity stress condition.

PIX-5

DORMANCY DURATION AND METHODS TO OVERCOME SEED DORMANCY IN PROSO MILLET GENOTYPES

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Proso millet (*Panicum miliaceum* L.) is one among the six small millets. Like other millets, it also possesses dormancy which needs to be studied thoroughly. Duration of dormancy usually ranges from 28 to 35 days. Seed coat colour, presence of lemma and palea and abscisic acid are the major dormancy inducing factors. Six genotypes were studied in the present investigation. Various physical and chemical treatments were imposed *viz.*, control, exposure to sun light for 48 hr, exposure to 45°C for 24 hr and 48 hr, water soaking for 12 and 24 hr, soaking in KNO_3 at 0.5 and 1 per cent, soaking in HNO_3 at 0.5 and 1 per cent, soaking in ethrel at 25 and 50 ppm, hot water treatment at 50°C and 60°C for 1 min and soaking in Thiourea at 0.5 and 1 per cent to break the dormancy of freshly harvested seeds. For the chemical treatments, soaking duration was 8 hr. and the standard germination test was conducted thereafter. The KNO_3 treatment at 0.5 % showed significantly the highest mean germination (87.89 %), minimum abnormal seedlings (4.39%), minimum dead seeds (1.78), higher shoot and root length (18.56 cm and 10.42 cm respectively), seedling vigour index (2555) and seedling dry matter (44.39 mg) than the control. The laboratory studies were statistically analysed by complete randomized factorial design.

PIX-6

VIGOUR TEST TO IDENTIFY FIELD EMERGENCE POTENTIAL OF DIFFERENT BLACKGRAM SEED LOTS

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Germination test under controlled condition was used to evaluate the physiological potential of seed lot. However, seed lots with similar laboratory germination often differ in field emergence as field conditions are rarely ideal. Therefore, more efficient vigour tests should be employed to detect differences in potential performance among the seed lots with a similar germination. To standardize suitable seed vigour test, seven lots of blackgram cv. TNAU Blackgram CO 6 were exposed to different vigour tests *viz*., accelerated ageing, controlled deterioration, complex stressing vigour test, electrical conductivity test and mean germination time under different test conditions, and correlated with field emergence. Standard germination test grouped the seed lots only into two categories *viz*., seed lots having high germination of 97 to 99% (L1, L2, L5, L6 and L7) and low germination of 95 to 96% (L3 and L4). However, field emergence grouped the seed lots into three groups *viz*., seed lots with high germination of 95% (L7), medium germination of 90-92% (L1, L2, L5 and L6) and low germination of 86 to 87% (L3 and L4). Among the different vigour tests evaluated, accelerated ageing for 3 days showed significant positive correlation (r = 0.993) while electrical conductivity test with incubation of 6h in 75 ml distilled water at 20°C showed significant negative correlation with field emergence (r = -0.962) and both of these tests grouped seed lots similar to field emergence grouping. Hence, these two vigour tests could be used for discriminating blackgram seed lots based on vigour status.

PIX-7

MODE OF ACTION OF VIGOUR IMPROVEMENT IN *Pseudomonas fluorescens* BIO PRIMED RICE SEEDS

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Bio-priming is newly developed technology in which the seeds are hydrated using biological compounds like beneficial bioagents. Biopriming with *Pseudomonas fluorescens*(*PF*1) had a dual action such as control of disease causing pathogens during germination as well as enhance the germination and vigour. Standardization of a suitable concentration and duration for CORH 4 rice hybrid seeds indicates

that bio-priming with 4% *Pseudomonas fluorescens* for 12h is most suitable method for improvement of seedling vigour along with controlled disease. Biopriming promotes the transport of *P. fluorescens* bacterial cell inside the seed. Based on the observation with the use of the scanning electron microscope (SEM), the *PF*1 bacterial cells were identified on embryo of husk removed paddy seeds with 3000X and 6000X magnification which confirmed the passage of bacterial cell through the seed coat into the seed. Analysis of bioprimed (4 % *Pseudomonas fluorescens* for 12h), hydroprimed (12h) and nonprimed rice seeds of CORH 4 during germination showed quicker weakening of tissue that covers embryo and radicle protrusion in bioprimed seeds than hydroprimed and nonprimed seeds. The reason might be due to the increased hydrolyzing enzymes and faster breakdown of storage reserves in bioprimedseeds than hydro and nonprimed seeds of CORH 4 rice hybrid. It was confirmed with undamaged amyloplast in fresh unprimed seed and envelope degraded amyloplast in 4 % *P. fluorescens* for 12 h bioprimed rice seed.

PIX-8

INVESTIGATION OF APPROPRIATE SEED ENHANCEMENT TECHNIQUE TO IMPROVE THE SEED QUALITY IN DROUGHT TOLERANT RICE CV. CO 43

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Seed invigoration is being utilized as a technique for enhancing the quality of aged seeds. The major cause of low productivity in rice is the use of poor quality seeds. An experiment was conducted to study the effect of suitable seed enhancement technique to improve the seed quality in drought tolerant rice cv. CO 43 was used in the study because of the strong and moderate drought tolerant capacities at Annamalai University, Chidambaram during the year 2010- 11. The experimental results revealed that the seeds hardened with 1% KCl for 12hr + polykote @ 3 g kg^{-1} seed significantly increased the higher germination per cent (97.00%), shoot (15.50 cm) and root length (24.30 cm), root volume (0.442), drymatter production (0.285 g $seedling^{-10}$), vigour index (3980.00) over control and other treatments under laboratory conditions. The seeds hardened with 1% KCl for 12hr with polykote @ 3g kg^{-1} showed supremacy and also emerged earlier than control seed, recorded higher field emergence. It can be concluded that the polymer coated seeds along with KCl which responds well for better germination capacity, good crop establishment and seed quality.

PIX-9

CONSTRAINTS IN PRODUCTION AND SALE OF SEED KAPAS IN COTTON cv. MCU 5 IN TAMIL NADU UNDER CONTRACT FARMING SYSTEM

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Cotton, important fiber crop significantly strengthens the economy of Tamil Nadu. A study was conducted to identify problems associated with production and sale of seed kapas of cotton under contract farming by random sampling method with 40 seed growers in four districts *viz.,* Coimbatore, Erode, Namakkal and Salem selected purposively. Descriptive statistics and Garatte's ranking technique were employed and results showed that 68% seed growers followed recommended spacing and 88% seed growers not tested soil for nutrient content. All the seed firms supplied delinted parental seed of foundation class for certified seed production. Majority (>80%) seed growers did not faced any problem due to temperature, water quality and soil, except scanty and uneven distribution of rainfall. Beside, high cost of parental seeds was the major seed related problem faced by 65% seed growers. High transport cost (Rank I) and presence of weed seeds (Rank II) in farmyard manure; high cost of inorganic fertilizers were the major manures and fertilizers associated problems; high wages, inefficiency and shorter working period were major labour oriented problems, encountered by seed growers. As seed firms purchased the kapas, 65% of seed growers did not faced any problem and only few seed growers felt rejection of poor quality kapas (20%) and less price (22.5%) as major problem while selling seed kapas. The policy suggested was timely and subsidized input supply, higher price for seed kapas, crop insurance and pre-payment for kapas from seed companies should be recommended for further growth.

PIX-10

INFLUENCE OF SEED PELLETING WITH HERBAL POWDERS ON SEED VIGOUR IN BLACKGRAM (*Vigna mungo* L.)

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India is the largest producer and consumer of black gram in the world. It contains about 26% protein, 57% carbohydrates and 1.2% fat. It is a good source of phosphoric acid, calcium and vitamins like thiamine (B1), riboflavin (B2) and niacin (B3). Pelleting is a pre-sowing seed management technique,

in which growth promotive substances with protective, nutritive and invigourative function are applied on the seed to enhance the seed-soil relationship. A study was conducted to evaluate the efficacy of seed pelleting with herbal powders in improving seed germination, vigour and field emergence in blackgram cv. ADT 3. The blackgramseeds was coated with the herbal powders *viz.,* noni (*Morinda citrifolia*), tulasi (*Ocimum sanctum*) and gallnut (*Terminalia chebula*) @ 200 g/kg of seed using Carboxy methyl cellulose as adhesive @ 200 ml/ kg of seed. The pelleted seeds were evaluated for seed germination, vigour, nursery emergence and storability. The results revealed that tulasi leaf powder is effective in improving blackgram seed germination and seedling vigour followed by noni leaf powder. At nursery also, the tulasi leaf powder pelleted seed showed enhanced germination and seedling vigour in terms of seedling length, dry matter production, vigour index, root nodulation, chlorophyll index, etc. All seed quality parameters were maintained high during storage in seeds pelleted with tulasi leaf powder upto six month. However, the study identified gallnut fruit powder was not suitable for seed pelleting.

PIX-11

EFFECT OF COLD STRATIFICATION ON SEED GERMINATION AND SEEDLING VIGOUR OF *ROSA* SPP.

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Roses (*Rosa spp.*) seed germination is a much more important issue for getting brand new, never before seen roses that are produced from seeds after successful crosses. In order to get good percentages of seed germination, it is necessary to break the seed dormancy, which is a complicated process and results in changes in the pericarp, testa, and embryo. To overcome the stalemate this study was initiated to overcome the dormancy and develop methods to increase germination percentage, shorten germination time, provide more synchronous germination, and result in more efficient seed propagation techniques for rose seeds. The seeds were subjected cold stratification at 2.6ºC, 5.6ºC and 7.7ºC for 30, 45 and 60 days and without cold stratification served as control. The stratified and control seeds were placed for germination in sand method at 20ºC temperature and 90% relative humidity in walk-in-germinator of the Central Seed Testing Laboratory, NSRTC, Varanasi. The experiment was laid out in a factorial completely randomized block design. Seventy days after sowing (ISTA, 2007) the results reveled that the highest germination percentage of 32, 36 and 37% were recorded the seeds kept in cold stratification at 2.60ºC for 30, 45 and 60 days respectively, the lowest germination of 5, 7 and 6% were obtained, when the seeds were kept at room temperature for 30, 45 and 60 days. The vigour of the seedlings were enhanced by cold stratification treatment.

PIX-12

HYBRID PURITY ASSESSMENT OF BRINJAL (*Solanum melongena* L.) HYBRIDS USING SSR MARKERS

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Use of morphological differences between true hybrids and off types in grow out test (GOT) for hybrid purity analysis are not always apparent and cannot be recognized easily. Further, morphological traits are costly, tedious to score and environment sensitive. Alternatively, it is suggested that recent breakthrough in molecular markers can be employed in hybrid purity analysis. The hybrid purity of two brinjal hybrids (Arka Anand and Asha) were assessed by GOT and molecular markers. A total of 400 individuals from each one of the two hybrids were raised in the field and morphological traits were recorded. It was found that 10 out of the 400 F_1 individuals were false hybrids. Therefore, the hybrid purity of seed lot used in this study was calculated as 97.5%. Out of 119 amplified markers, twenty one markers was showing polymorphism between the parents. These 21 short listed SSR markers were then tested on the hybrid population to detect the heterozygosity of hybrids. A single marker (eme08D09) was found to be co-dominant. This marker generated both the alleles of the parents establishing the hybrid purity. All the two hybrids were clearly distinguished from their selfed females and off types using one SSR marker. Hence, it is proposed that these SSR markers can be used in efficient analysis of hybrid purity since this technique is simple to use, more accurate and not affected by environment when compared with GOT. The same techniques can be replicated in other crops also to validate the purity.

PIX-13

ASSESSMENT OF HYBRID PURITY IN GUAVA (*Psidium guajava* L) HYBRIDS USING MICROSATELLITE MARKERS

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Maintenance of genetic purity of hybrid is essential to exploit its full potential. Genetic purity is generally assessed by conducting grow out test (GOT) where morphological characters are analyzed, however results may be influenced by environment. Further, it is expensive and time consuming. DNA based markers (RAPD, ISSR, AFLP, SSR) are rapid, reliable and cost effective for hybrid purity assessment. Microsatellite (SSR) markers are preferred over dominant markers as they are Co-dominant in nature and reveal the heterozygous condition of the hybrid accurately. The objective of this study was to assess the hybrid purity of 6 guava hybrids (H104, H817, H1314, H5337, H12-5) with their respective parents using Simple Sequence Repeat (SSR) markers. A set of 50 SSR markers were used to characterise the parental lines out of which 23 markers were polymorphic. Among these 23 markers, 6 SSR markers were found co-dominant across the hybrids and produced unique fingerprints. These SSR markers could support the data that the hybrids were genetically pure and true with respect to their parents. This study showed that SSR markers could provide a practical and efficient tool in assessment of genetic purity of the Guava hybrids which supplement the morphological information with the molecular data for identifying gene donors and in the identification of pedigree of the existing cultivars.

PIX-14

INHERITANCE OF MORPHOLOGICAL CHARACTERS IN SUGARCANE (*Saccharum* spp)

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The directives of the international UPOV agreements, DUS guidelines are generally followed in morphological description of sugarcane clones. Morphologically different variants with distinct phenotypic expression can be utilized in breeding for indirect selection of clones when linked with desirable traits. Introgressed hybrids involving improved *S.officinarum,* improved *S.robustum* and CoC 671 with morphological variants were studied for DUS characters. The segregating populations screened for 30 morphological traits showed polymorphism and grouped in five clusters. Least inter-cluster difference was observed between the cluster I and V followed by the Cluster III and V. Clusters II and IV have minimum BC hybrids & maximum intra cluster distance which reflects the broad genetic distance. BC hybrids had prominent swollen growth ring, strap shaped ligule and bobbin shaped internode grouped in to the cluster II with the highest inter cluster distance. Most of BC hybrids possessed transistional auricles & greenish yellow dewlap as the common character and grouped in cluster V.BC hybrids with ovate bud shape & deltoid auricle were grouped in to the cluster VII. Cylindrical, green color internode, corky patches on rind surface, ovate, medium sized buds, deltoid auricles were dominant in the progenies. Most of the characters are under monogenic control with dominant expression in the parents. Being monogenic, the expression of these visible markers can be incorporated effectively as phenotypic tags in marker assisted selection. Introgressed hybrids identified distinct with the morphological clustering and with specific morphological trait can be further characterized with molecular markers to be utilized in selection.

10. NUTRACEUTICALS, FOOD PREPARATION AND DIETARY COMPONENTS

PX-1

ETHNOBOTANY AND NUTRACEUTICAL PROFILE OF MEDICINAL LANDRACES OF RICE (*Oryza sativa* L.) *IN SITU* CONSERVATION IN TAMILNADU

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Rice (*Oryza sativa* L.) is one of the important food crop and main source of nourishment for more than one half of the world population. Though there is no scientific data on the medicinal properties, they are being used in ayurveda in treating diseases like arthritis, cervical spondylitis, muscle wasting, skin diseases and neurological problems. Medicinal landraces like an investigation was carried out in the Department of Plant Breeding and Genetics at Agricultural College and Research Institute, Madurai during 2012-2014 high yielding released variety of Tamil Nadu used for standard check ADT 43 along with four different medicinal landraces of rice collected from different areas of Kerala and Tamil Nadu *viz.,*Navara, Kavuni, Veeradangan and Kathanellu were used. Among the varieties were analysed for biochemical parameters, the medicinal land races are rich in double and triple the amount of iron, zinc, calcium and magnesium. Biofortification of cultivated high yielding varieties with these medicinal landraces with conventional method decrease the hunger of malnutrition. By improving the strain of these traditional medicinal rice varieties, scientists hope to make it stronger to withstand the onslaught of climate and ensure higher output. With the above reasons medicinal rice will be recommended for future generation to build a healthy society.

PX-2

VARIATION, ASSOCIATION AND PATH ANALYSIS OF GRAIN QUALITY ATTRIBUTES IN BLACK GRAM (*Vigna mungo* L. HEPPER)

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Black gram (*Vigna mungo*L. Hepper (or) urd is one of the important pulse crops in India. India is the largest producer and consumer of black gram in the world. It contains about 26 percent protein which is almost three times that of cereals. It supplies a major share of protein requirement of vegetarian population of the country. Thirty nine blackgram (*Vigna mungo* L. Hepper) genotypes were tested for 10 physical characters which determine seed quality. There were significant differences observed among the genotypes for 100 seed weight and volume before and after soaking, hydration capacity, swelling capacity, hydration index and swelling index. KUG 531, KUG 540, UH07-17 and CBG 757 were found to have good physical characters. Swelling index was positively and significantly correlated with hydration capacity, swelling capacity and hydration index. Hydration capacity, swelling capacity and hydration index were found to be important attributes affecting cooking quality and cooking time to a greater extent. Path analysis, however, showed that hundred seed volume after soaking, dry seed density and hydration index were observed to have high positive direct effect on swelling index while other characters had negative effect on swelling index important for cooking quality. The study suggested that selection of swelling capacity and hydration capacity must be given preference along with optimum dry seed density in breeding for grain quality improvement.

PX-3

ASSESSMENT OF RICE VARIETIES FOR FLOUR AND MARKET PREFERENCE

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Farmers were requested to introduce the new rice variety suitable for flour making as well as market preference. Hence this assessment was undertaken by KrishiVigyan Kendra, Aruppukottaiunder on farm testing during Rabi 2011-12 with new rice varieties (TRY 3 and TPS 3) along with their practicing variety (ASD 16). The yield recorded by TRY 3 is better than other two varieties. Market preference for TRY 3 is good and sold at the market with higher price. Idly preparation is mainly depends on properties of flour. This fact is in line with TRY 3 rice. Among the three rice varieties assessed for flour and market preference, TRY 3 recorded more number of filled grains of 109. The test weight was least in TRY 3 indicating that the variety is relatively medium bold than other two varieties. The grain yield recorded was high in TRY 3 *i.e.* 56 q/ha which is 3.7 % higher than ASD 16 and 8.9 % over TPS 3. The net return and B:C ratio was higher in TRY 3 compared to the other two assessed varieties. Farmers realized that TRY 3 is suitable for idly making and better choice of variety in the problem soils.

PX-4

FREE RADICAL SCAVENGING ACTIVITY OF BARK OF *Terminalia bellirica*

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Terminalia bellirica Roxb belongs to the family *Combretaceae* commonly known as myrobalan, is a deciduous tree found throughout the Indian forests and plains. Antioxidants from plant materials terminate the action of free radicals thereby protecting the body from various diseases. There is a growing interest all over the world for discovering the untapped reservoir of medicinal plants. The petroleum ether, chloroform, ethanol and aqueous extracts of bark of *Terminalia bellirica* were screened for free radical scavenging activity using DPPH, ABTS, superoxide, nitric oxide, hydroxyl and hydrogen peroxide scavenging activity using standard procedure and it was compared with the standard ascorbic acid. The scavenging activity was found to be dose dependent. The ethanol extract exhibits maximum scavenging activity while compared to chloroform, petroleum ether and aqueous extract. From the present study, it can be concluded that the bark extract of *Terminalia bellirica* posses good inhibitory activity. Hence it can be used to treat various diseases such as diabetes mellitus, cancer, neurodegenerative disorders and aging which are caused by free radicals.

PX-5

EVALUATING RICE GERMPLASM FOR HIGH IRON AND ZINC CONCENTRATION IN POLISHED RICE

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Rice is mainly consumed in polished form and it contains only 20 per cent of the daily requirement of zinc and a small amount of iron. Hence, in countries where rice is a major staple food, Fe and Zn deficiencies are the most prevalent with almost three billion people affected worldwide especially in developing and least developed nations. Biofortification of rice varieties with iron and zinc is one of the significant strategies to manage micronutrient malnutrition. Initial step of any breeding program involves the screening of available germplasm stock to identify the source of high iron and zinc rice accessions. In the current study, rice grains of 150 accessions were dehulled and polished with laboratory dehusker and polisher and analyzed for micronutrient content using X-ray fluorescence. Iron concentration ranged from 1.3 µg/g in the genotype RG120 (Thataan samba) to 12.9 µg/g in RG147 (IG 58 - CI 11011). Zinc content varied from 5 µg/g in the genotypes *viz.,* RG22 (IR36), RG102 (Varakkal) to 29.2 µg/g in the genotype RG130 (Honduras). Thus, wide variation existing in this germplasm accessions serve as a genetic source for biofortification in rice with various breeding strategies.

PX-6

ASSESSING THE ANTIOXIDANT ACTIVITY, NUTRACEUTICAL AND FUNCTIONAL PROPERTIES OF SELECTED MILLETS AND PULSES

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Neutraceuticals are health enhancing physiologically active food components which are also called as phytochemicals. Phytochemicals (phenolic compounds andphytates) are responsible for higher

antioxidant activity in whole grain. Millets are rich in phenolics acids, tannins and phytate which act as antinutrients and these antinutrients are known to reduce the risk of oxidative damage in the human body, prevent many diseases such as atherosclerosis, cancer, diabetes etc. Hence, this study was carried out to determine the antioxidant activities, neutraceutical properties of millets (kodo millet, little millet, pearl millet, proso millet) and pulses (horse gram and soybean). Among the millets and pulses, the little millet contained (373.67 mg GAE /100 g) higher content of polyphenols than kodo millet, proso millet, pearl millet (368.77, 361.87 and 333.63 mg GAE /100 g). Soybean and horse gram contained 171.54 and 143.46 mg GAE /100 g, respectively. Antioxidant activity was high in pearl millet 83.2 mg/100g) followed by kodo millet, little millet, proso millet (70.82, 67.63 and 65.74 mg/100g). Soybean and horse gram was 35.14 and 33.27 mg/100grespectively. The tannin content was high in proso millet and soybean (22.67 and 34.47 mg TAE/100g) than kodo millet, little millet, pearl millet, horse gram (22.53, 17.62, 13.45 and 16.12 mg TAE/100g). Thephytate content was maximum in kodomillet and soybean contained and the value was 35.17 and 36.58 mg/100g whereas in pearl millet, prosomillet, little millet and horse gram contained 33.42, 27.17, 24.42 and 10.23 mg/100g, respectively.

PX-7

STUDIES ON PREPARATION OF MORINGA INSTANT SOUP MIX AND ANALYSIS OF ITS NUTRITIONAL COMPOSITION

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Moringa is truly a miracle plant. The most incredible thing about moringa is the amount of nutritional and medicinal chemicals and compounds found in this plant. To increase the utility of such a wonderful plant, a value added product *i.e.*moringa instant soup mix has been prepared and its nutritional composition were analyzed at Horticultural College and Research Institute, Periyakulam during 2011. Matured and sound moringa pods were selected and cut into pieces of 5cm length wise. They are steam blanched for 10 minutes and the pulp has been scooped out. The scooped pulps were immersed into one per cent Potassium Metabisulphite solution for 30 minutes. Then they were dried in cabinet drier at 50°C for 13 hrs. The dried pulp was ground into fine powder by using mixer. Tomato powder (20g), onion powder (20g), pepper owder (10g) turmeric powder (4g), corn flour (4g) and required amount of salt (12g) were prepared and mixed well with moringa pulp powder (100g). They were stored in glass bottles and they were used as instant soup mix. Organoleptic evaluation obtained the initial scores for colour (7.0), flavour (7.5), taste (7.0) consistency (7.5) overall acceptability (8) which had decreased to 6.89, 7.38, 6.74, 7.12 and7.6 respectively during storage period (120 days).The iron (27.4mg/100g), calcium (1.5g/100g) and protein (26.7g/100g) content of moringa instant soup mix were analyzed.

PX-8

DEVELOPMENT OF A NOVEL HEALTH DRINK FROM MILLETS

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Small millets have immense health benefits as they are rich in phytochemicals and nutrients, particularly beneficial to overcome the current life style diseases.On the other hand, in India more than 50 per cent of children are malnourished.Millet based foods help to overcome these two extremes.Millet based products is economically viable and also it highlights the excellent medicinal and nutritional qualities.An attempt was made to develop millet health drink using germinated pearl millet, kodo millet and whole wheat along with pulses.The grains were soaked in water for 3 h and allowed to germinate for 24 h followed by shade dried for 10 h.The dried germinated millets were roasted until husks spilt open and then milled in a burr mill to obtain a fine flour.The flour was then blended with green gram flour, roasted bengal gram flour and skim milk powder.The nutritive value of the health mix and sensory evaluation was conducted for the health drink. The drink had high consumer acceptability.The standardized mix had 17.08 percent protein, 4.05 percent fibre, 20.68 mg calcium and 7.57 mg of iron in 100 g. The mix can be stored for six months in poly propylene (PP) bags without much change in the nutrient content.The nutrient rich health drink was suitable for all groups of people.The mix can be used for preparation of different snacks like sweet ball, steamed food etc.

सत्यमेव जयते
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Indian Society of Plant Breeders (ISPB) was established during 1995. It has more than five hundred breeders as life members working in both State Agricultural Universities including Foreign Universities ICAR Institutes, Private Companies and Senior Plant Breeders. ISPB involved in conducting seminars and symposia and publication of research articles through its electronic journal.

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