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Research Article

Biometrical studies on genetic variability and diversity in upland rice (*Oryza sativa* L.)

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Abstract

The study was conducted with thirty seven advanced rice cultures during *Rabi* 2016-17 under upland rice ecosystem. The analysis of variance revealed that all the treatments were significant for various characters *viz.*, days to 50% flowering, plant height, number of productive tillers per plant, number of panicles/m^2, panicle length, number of filled grains per panicle, grain yield/ha, straw yield/ha and harvest index. The higher magnitude of PCV and GCV were recorded for number of panicles /m^2, grain yield/ha and straw yield/ha. High heritability coupled with high genetic advance was recorded for number of panicles/m^2 which indicated the major role of additive gene action in the inheritance of this trait. Based on the D^2 analysis, the genotypes were grouped into eight clusters. Maximum number of genotypes (21 genotypes) was grouped in cluster I. Maximum inter cluster distance was observed between cluster III and VIII (7.75) followed by between cluster III and VI (7.11) indicating wider genetic diversity between genotypes. The intra cluster distance was maximum in cluster I (4.07) followed by cluster II (3.88) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the nine traits studied, number of panicles/m^2 has contributed maximum divergence (22.22%) followed by panicle length (17.12%), plant height (14.41%), filled grains per panicle (11.26%) and days to fifty per cent flowering (10.96%). Hence these altogether contribute more than seventy five per cent towards total divergence. Therefore these characters may be given importance during selection programme in upland rice ecosystem.

Key words
Variability, heritability, genetic advance, diversity, upland rice.

Introduction

Rice (*Oryza sativa* L.) is the most important cereal food crop of the world and about 90 per cent of the people of South-East Asia consume rice as staple food. Upland rice has been gaining popularity, because current high-yielding varieties have led to an increase in genetic vulnerability, a scarcity of water for irrigation, and a breakdown of resistance genes against emerging races of pathogen due to intensive cultivation. It is important in cropping systems, because of the lack of irrigation facilities and lower cost of production (Fageria *et al*., 2014). Further, a majority of area under upland rice cultivation suffer from poor productivity due to lack of promising rice cultivars under such eco-climatic condition. Thus, in order to improve the productivity level, a breakthrough would be desirable by way of increasing biological efficiency through hybridization and the productivity of new varieties suited to upland condition. Perhaps there is no other single crop possessing as enormous variation as in rice. However, due to the ever-increasing demand of food grains, there is still a great scope to develop rice varieties suited to upland conditions for higher production.

The success of this to a large extent would depend on the exploitation of existing variability and therefore it is desirable to collect, evaluate and utilize the available diversity to suit specific need with regards to specific ecosystem. Yield is a complex character, which is highly influenced by the environment, hence direct selection for yield alone limit the selection efficiency and ultimately results in limited success in yield improvement. Study of variability parameters and D^2-statistics are expected to provide reliable basis for selecting out desirable elite and diverse parents for hybridization and exploitation of variability. Grouping of genotypes on the basis of genetic distance finally provides a clear picture about the inter-relationship of the genotypes and helps to pick up appropriate genotype. This study was therefore conducted to select potential genotypes and to identify the most important characters for breeding programmes by exploiting the genetic variation, heritability and diversity analysis of yield and related attributes of 37 upland rice genotypes.

Materials and Methods

The experimental material comprised of 37 advanced rice cultures collected from various research institutes which were evaluated in a randomized block design with three replications at Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi during *Rabi* 2016-17. The experimental site is located at 9” 21’ N latitude, 78” 22’ E longitude and an altitude of 242 m above mean sea level with average annual rainfall of 840 mm. This site has clay loam soil texture with pH of 8.0. Each genotype was raised in 5 mx2 m plot keeping 15 x 10 cm spacing. The recommended agronomic practices were followed to raise good crop stand. The data were recorded on ten randomly selected plants from each replication for various quantitative traits studied were *viz*, days to 50% flowering, plant height (cm), number of productive tillers per plant, number of panicles/m^2, panicle length, number of filled grains per panicle, grain yield (kg/ha), straw yield (kg/ha) and harvest index. Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse & Sukhatme (1967). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated using the formula given by Burton (1952), heritability in broad sense and genetic advance were calculated as per Johnson *et al.*, (1955). The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao, 1952.

Results and Discussion

Genetic variability

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating existence of variability among the genotypes (Table 1.). The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non-heritable components to assess the true breeding nature of the particular trait under study. The perusal of coefficient of variability indicated that wide range of variability was present at both phenotypic and genotypic levels for all the characters under studied. The magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits which may be due to higher degree of interaction of genotypes with the environment (Kavitha & Reddy 2002). The differences in the magnitude of PCV and GCV for number of productive tillers per plant, number of panicles/m^2, number of filled grains per panicle, grain yield, straw yield and harvest index were of high order. The higher magnitude of PCV and GCV were recorded for number of panicles /m^2 , grain yield/ha and straw yield/ha (Table 2.).

Burton (1952) pointed out that the heritability in combination with intensity of selection and amount of variability present in the population influences gains to be obtained from selection. Thus, genetic advance is yet another important selection parameter which although independent, represents the expected genetic advance under selection. It measures the differences between the mean genotypic values of the selected lines and the mean genotypic values of original population from which these were selected. According to Panse (1957) if a character is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action, high heritability along with high genetic advance provided good scope for further improvement. In the present study, high broad sense heritability estimates were obtained for plant height (62%), number of panicles/m^2 (67%) and panicle length (61%) (Table 2.), indicating the major role of additive gene action in inheritance of these traits. High heritability alone does not guarantee large gain from selection unless sufficient genetic advance (GA) attributed to additive gene action is present. High heritability coupled with high genetic advance was recorded for number of panicles /m^2 (Table 2.). It indicates that most likely the heritability is due to additive gene effects and selection may be effective. This finding is in close agreement with the findings of Babu *et al.* (2012) and Allam *et al.* (2015).

Genetic diversity

Based on the relative magnitude of D^2 values, thirty seven genotypes were grouped into eight clusters (Table 3). Maximum number of genotypes (21 genotypes) was grouped in cluster I. Cluster II consists of ten genotypes and others were represented by a single genotype each. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Similar findings of non- correspondence of geographic origin with genetic diversity was also reported by Shanmugasundaram *et al.* (2000) and Nayak *et al.* (2004). The intra and inter cluster distance are presented in Table 4. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster III and VIII (7.75) followed by between cluster III and VI (7.11) indicating wider genetic diversity among the genotypes between these groups. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. Surprisingly the clusters identified with maximum inter cluster distance were possessed a single genotype in each cluster. Hence selection of parents for hybridization is already over. The minimum inter cluster distance was found between cluster III and V (3.44) followed by between cluster II and VI (4.55). These genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give fruitful result.

The maximum intra cluster distance was observed in cluster I (4.07) followed by cluster II (3.88). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through inter-varietal hybridization (Joshi *et al.*, 2008). A perusal of results of cluster means (Table 5) revealed that cluster I with twenty one genotypes had exhibited highest mean value for panicle length (21.41 cm) and plant height (78.32). Cluster II had genotypes with maximum number of panicles /m^2 (185.87) and the genotype in Cluster III (PM 16003) had taken more days for fifty per cent flowering (63.67). Cluster IV was characterized by lowest grain yield (666.67), while the cluster V had maximum number of filled grains per panicle (142.33) and grain yield (1943.33). The genotype PM 14041 with more straw yield (6800) and highest productive tillers per plant (8.33) was grouped in cluster VI. The Genotype IET 25111 (Cluster VII) had shown short stature (59.60). The genotype IET 25134 possessing lowest mean values for productive tillers per plant (4.33), number of panicles /m^2 (77.33), filled grains per panicle (57.67) and straw yield/ha (700) but highest harvest index (0.54) was grouped in cluster VIII. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster II has recorded desirable mean value for maximum number of traits *viz.*, productive tillers per plant, number of panicles /m^2, panicle length, filled grains per panicle and grain yield. Similar results were also reported by Banumathy *et al.* (2010) and *Rai et al.* (2014), thereby underlining the fact that the hybridization 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.

The contribution of each trait to total divergence is presented in table 6. Among the traits studied, number of panicles /m^2 has contributed maximum divergence (22.22%) followed by panicle length (17.12%), days to 50 % flowering (14.41), filled grains per panicle (11.26) and plant height (10.96%). The minimum percentage of contribution was observed in harvest index (3.75%) followed by productive tillers per plant (5.41%), grain yield/ha (6.76%) and straw yield (8.11%). The traits *viz.*, number of panicles /m^2 , panicle length, plant height, filled grains per panicle and days to 50 % flowering had contributed more than seventy five per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

It is concluded from the variability studies that high heritability coupled with high genetic advance was recorded for number of panicles/m^2 and the major role of additive gene action involved in the inheritance of this trait. Thus, this trait may serve as an effective selection parameter during breeding programme in the upland rice ecosystem. Divergence studies suggested that cluster II has recorded desirable mean value for maximum number of productive traits and best genotypes within this cluster may be directly selected or may be used as potential parents in hybridization programme by giving importance to the characters (number of panicles/m^2, panicle length, plant height, filled grains per panicle and days to 50 % flowering) which are contributing more to the total divergence.

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Table 1. Analysis of variance for different traits in upland rice

Source of variation	Degrees of freedom	Days to 50% flowering	Plant Height	Productive tillers per plant	Panicles /m^2	Panicle length	Filled grains per panicle	Grain yield/ha	Straw yield/ha	Harvest index
Replication	2	22.60	83.91	1.95	2256.83	2.47	213.30	448395	12409279	0.02
Treatment	36	59.35*	154.67*	3.63*	5590.47*	8.25*	931.20*	732036*	6698078*	0.01*
Error	72	12.41	26.34	1.05	1108.58	1.44	285.39	209681	2390945	0.00

*significant at P=0.05 level

Table 2. Estimates of mean, variability, heritability and genetic advance in upland rice

Traits	Mean	PV	GV	PCV	GCV	h^2(%)	GA	GAM
Days to 50% flowering	55.44	28.05	15.64	9.55	7.13	56	7.79	14.07
Plant height	74.00	69.12	42.77	11.23	8.84	62	13.58	18.35
Productive tillers per plant	6.71	3.21	0.21	26.70	6.83	7	0.31	4.62
Panicles /m^2	137.29	2602.55	1493.96	37.16	28.15	67	77.31	56.31
Panicle length	20.50	3.71	2.27	9.39	7.35	61	3.11	15.18
Filled grains per panicle	83.04	500.66	215.27	26.94	17.67	43	25.39	30.58
Grain yield	1519.82	383800.06	174118.44	40.76	27.46	45	741.98	48.82
Straw yield	4350.45	3826656.75	1435710.75	44.96	27.54	37	1937.58	44.54
Harvest index	0.27	0.01	0.01	31.57	18.19	33	0.07	27.67

GV=Genotypic Variation; **PV**=Phenotypic Variation; **GCV**=Genotypic Co-efficient of Variation; **PCV**=Phenotypic Co-efficient of Variation; $\mathbf{h^2}$=Heritability (Broad sense); **GA**=Genetic Advance; **GAM**=Genetic Advance as % of Mean.

Table 3. Clustering pattern of 37 genotypes

Cluster	No. of genotypes	Name of genotypes
I	21	IR12-L369 (G3), IR13-L382 (G6), IR13-L391 (G7), IR12-L356 (G2), IR13-L114 (G4), IR13-L137 (G5), IR12-L353 (G1), IR14-L235 (G12), IR13-L406 (G9), IR13-L400 (G8), IR13-L413 (G10), IET 25106 (G18), PM 14048 (G34), IET 25114 (G21), IET 24690 (G16), PM 14032 (G27), PM 14046 (G33), IR14-L177 (G11), PM 14049 (G35), PM 16002 (G14) and PM 16001 (G13).
II	10	PM 14030 (G26), PM 14044 (G32), PM 14018 (G25), PM 14038 (G28), Anna(R)4 (G37), PM 14050 (G36), IET 25107 (G19), PM 13017 (G24), PM 14042 (G30) and PM 14043 (G31).
III	1	PM 16003 (G15)
IV	1	IET 25118 (G22)
V	1	IET 25105 (G17)
VI	1	PM 14041 (G29)
VII	1	IET 25111 (G20)
VIII	1	IET 25134 (G23)

Table 4. Intra (diagonal) and inter cluster average distance of yield traits in 37 genotypes

	I	II	III	IV	V	VI	VII	VIII
I	4.07	5.85	6.31	5.05	5.81	5.78	6.61	6.65
II		3.88	5.75	5.75	6.05	6.65	5.80	6.54
III			0.00	6.83	3.44	7.11	4.55	7.75
IV				0.00	6.64	4.65	6.42	6.46
V					0.00	6.96	5.97	6.55
VI						0.00	5.17	6.28
VII							0.00	6.09
VIII								0.00

Table 5. Cluster mean of different yield characters in 37 rice genotypes

Cluster	Days to 50% flowering	Plant Height (cm)	Productive tillers per plant	No. of panicles /m^2	Panicle length (cm)	Filled grains / panicle	Grain yield (kg/ha)	Straw yield (kg/ha)	Harvest Index
I	53.92	78.32	6.84	121.71	21.41	84.49	1420.32	4247.62	0.27
II	58.20	67.80	6.27	185.87	19.58	77.53	1931.33	4966.67	0.28
III	63.67	71.73	7.00	137.33	20.63	130.33	1533.33	3933.33	0.30
IV	52.00	77.27	7.67	104.33	17.17	57.67	666.67	2333.33	0.22
V	58.00	72.47	6.67	102.33	21.27	142.33	1943.33	3600.00	0.41
VI	46.67	73.87	8.33	118.67	16.83	64.00	1233.33	6800.00	0.15
VII	59.67	59.60	8.00	125.33	18.33	71.00	983.33	4733.33	0.24
VIII	57.00	60.47	4.33	77.33	18.90	57.67	733.33	700.00	0.54

Table 6. Percentage of contribution of each character towards total divergence

Character	No. of Times Ranked First	Contribution (%)
Plant Height (cm)	73	10.96
Days to 50% flowering	96	14.41
Productive tillers per plant	36	5.41
No. of panicles /m^2	148	22.22
Panicle length (cm)	114	17.12
Filled grains / panicle	75	11.26
Grain yield (kg/ha)	45	6.76
Straw yield (kg/ha)	54	8.11
Harvest Index	25	3.75
Total	**666**	**100**