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Genetic diversity analysis of Zinc, Iron, Grain Protein content and yield components in Rice

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Abstract
The genetic diversity among 85 land races were evaluated for ten characteristics by using Mahalanobis D^2 Statistics. The genotypes were grouped into six clusters based on relative magnitude of D^2 values. Cluster-I was the largest comprising of forty three landraces,and cluster-V and -VI were monogenotypic clusters**.** Maximum inter-cluster distance was exhibited between clusters-II and -VI. The five prominent characters, total number of filled grains per panicle, grain zinc concentration, days to fifty per cent flowering, plant height and protein content, mainly contributed towards total divergence. Cluster-V has highest mean value for panicle length and number of tillers per plant.Cluster-III hashighest grain yield per plant and cluster-VI has highergrain iron concentration and protein percentage.The maximum contribution towards genetic divergence was observed in number of grains per panicle followed by grain zinc concentration. Thus, this study evaluated the diverse landraces useful in selection of parents during hybridization.

Keywords: Rice, Genetic diversity, Fe, Zn and Protein.

Introduction

Rice (*Oryza sativa* L.) is one of the agronomically and nutritionally important cereal crops. It is a major source of food for more than 2.7 billion people on a daily basis and is planted on about one-tenth of the earth's arable land. It is the single largest source of food energy to half of the humanity in the world, most of them in developing countries. Rice is the major food crop in India occupying nearly 43.97 million hectares with an annual production of 104.32 million tonnes and productivity of 2372 kg ha^{-1} (India stat, 2012-2013). In the last two decades, new research findings generated by the nutritionists revealed the importance of micronutrients, vitamins and proteins in maintaining good health, adequate growth and even acceptable levels of cognitive ability apart from the problem of protein energy malnutrition.

Quantification of the degree of divergence in a given experimental materials is vital for the identification of divergent genotypes for further use in hybridization to create new variability. Mahalanobis D^2statistic has been used as a powerful tool for quantifying genetic divergence in a given population. The Divergent genotypes could be obtained either by collectionfrom different eco-geographical regions or it could be induced by combination breeding.. The main objective of this research work is the evaluation of genetic diversity among the land races of ricefor yield and yield contributing characteristics to identify the parents for hybridization program.

Materials and Methods

The experimental material consisted of eighty five landraces of rice obtained from the plant breeding division, crop improvement section, Indian Institute of Rice Research (formally, Directorate of Rice Research), Rajendranagar, Hyderabad. Experiment was carried out during *Kharif*2014-2015 at Directorate of Rice Research Farm, ICRISAT campus, Patancheru, Hyderabad, India. All the genotypes were sown separately on raised beds in the nursery on 3rd July, 2014. Twenty five days old seedlings of each genotype were transplanted in 2 rows of 3 m length by adopting a spacing of 20 cm x 15 cm in a Randomized Block Design replicated twice. Recommended agronomic and plant protection measures for raising a healthy nursery and main crop were taken up during the experiment. Five plants of each genotype in each replication selected randomly were used to record data. Ten characteristics, which include seven quantitative characters and three nutritional traits, were recorded. Grain iron and zinc concentrations were determined by X-Ray Fluorescence Spectrometry. Protein/Nitrogen content was estimated by Combustion Method using protein analyzer.

Results and Discussion

The significance of 85 land races of rice in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

All landraces of rice under study were distributed into six clusters based on D^2values using Tocher's method (Rao, 1952) such that the genotypes belonging to different clusters. The distribution of genotypes into various clusters is presented in Table 1 and Figure 1. Out of six clusters, cluster I was the largest comprising of forty three landraces, followed by cluster IV with sixteen, cluster III with fourteen, cluster II with ten and cluster V and cluster VI were monogenotypic clusters. It indicates the existence of high degree of heterogeneity among the genotypes.

It is evident from the clustering pattern shownin Table.1 and Figure.1 that the landraces originating from similar geographical regions were classified into different clusters and it also indicates that geographical diversity and genetic diversity were not related due to differences in adaption, selection criteria, selection pressure and environmental conditions.

The average intra and inter cluster D^2 values and statistical distance among 85 genotypes are presented in Table 2. Intra cluster D^2 values ranged from zero (cluster V, VI) to 39.77 (cluster IV).Maximum intra cluster distance was observed in cluster IV (39.77), followed by cluster III (38.98), cluster II (35.36), cluster and cluster I (32.93), indicating that some genetic divergence still existed among the genotypes. Selection within such clusters might be executed based on maximum mean value for the desirable characters. This could be made use of in the yield improvement through recombination breeding.

From the inter cluster D^2 values of the six clusters, the inter cluster distance was higher than intra cluster distance indicating the presence of wide genetic diversity among the landraces under study. it can be seen that the highest divergence occurred between cluster II and VI (100.30) followed by cluster IV and VI (78.61), cluster I and VI (77.77), cluster III and IV (77.45), cluster II and V (73.74), cluster III and VI (68.76), cluster IV and V (68.55) suggesting that the crosses involving varieties from these clusters would give wider and desirable recombination in order to get high heterotic recombinants. While the lowest was noticed between cluster I and II (43.83), followed by cluster I and III (50.79), cluster III and V (52.33), cluster II and IV (54.34), cluster V and VI (59.93) cluster I and II (59.10).

The cluster means for each of ten characters are presented in Table 3. It can be observed from the data shown in table that the considerable differences existed for all the characters under study. The data indicated that the cluster mean for days to 50 per cent flowering was highest in cluster VI (101.00) and the lowest in cluster V (41.00). Plant height was highest in cluster V (140.10 cm) and lowest in cluster II (91.39cm). Cluster V recorded the highest panicle length (26.50) and the lowest number in cluster II (19.34). Cluster V and cluster VI recorded the highest number of tillers per plant (12.70cm) and the lowest was recorded in cluster II (9.46 cm). The number of grains per panicle was highest in cluster V (211.00) and the lowest in cluster IV (70.56). Highest 1000 grain weight was recorded in cluster I (23.63 g) and the lowest in cluster VI (19.60g). Cluster III recorded the highest grain yield per plant (25.58 g) while in cluster II it was low (14.17 g). Cluster II recorded low Grain iron concentration (9.00) whereas it was high in cluster VI (11.95). High grain zinc concentration was recorded in cluster VI (25.35) while it was low in cluster II (6.81). cluster VI recorded high grain protein content (9.90) where it was lowest in cluster II (6.81).Therefore, this result indicates that selection of landraces having high values for particular trait could be made and used in the hybridization programme for improvement of that character.

The cluster V is having highest mean value for panicle length, number of tillers per plant and 1000 grain weight and plant height. Cluster III has higher grain yield per plant, and the grain iron concentration and protein percentage is higher in cluster VI. Thus,the clusters having high mean values observed in this study may be directly used for adaptation or may be used as parents in future hybridization programme.

The results showed in Table 4 indicates that the contribution of No. of grains per panicle was highest towards genetic divergence (42.91%) by taking 1532 times ranking first, followed by grain zinc concentration (24.71%) by 882 times, Days to 50% flowering (13.00%) by 464 times, grain protein content (8.99%) by 321 times, plant height (7.62%) by 272 times, grain iron concentration (2.04%) by 73times, 1000 grain weight (0.53%) by 19 times, grain yield per plant (0.20%) by 7 times, number of tillers per plant and panicle length each by zero times, respectively to the genetic divergence in decreasing order. Similar result were conformity with Ramya and Kumar (2008) for number of filled grains per panicle, number of productive tillers per plant and grain yield per plant; Banumathy*et al*. (2010) for grain yield, days to 50 per cent flowering, total grains per panicle and plant height; Padmaja*et al*. (2010) who

reported major contribution to diversity through total number of grains/panicle; Sandhya *et al.* (2014) characters like number of number of spikelets per panicle, biological yield per plant, test weight, harvest index and days to 50 percent flowering contributed maximum towards genetic diversity.

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Table 1: Clustering pattern among 85 landraces of rice (Tocher's method**)**

Cluster No	Number of land races	Name of the land races
I	43	GP-9043, GP-9119,GP-9034,GP-9192, GP-9200, GP-9157, GP-9623, GP-9850, GP-10047,GP-9729 ,GP-9917, GP-9047 ,GP-9913, GP-9055, GP-9788, GP-9166, GP-9007, GP-9025, GP-9048 ,GP-9019, GP-9797, GP-9825, GP-9916, GP-9801, GP-9022, GP-9053, GP-9807, GP-9811, GP-9814, GP-9932, GP-9926, GP-9920, GP-9051, GP-9929, GP-9790, GP-9868, GP-9200, GP-9255, GP-9006 ,GP-9928, GP-9847, GP-9927, GP-9812
II	10	GP-9820, GP-9856, GP-9855, GP-9957, GP-9859, GP-9867, GP-9024, GP-9861, GP-9949, GP-9933
III	14	GP-9195, GP-9255, GP-9848, GP-9202, GP-9986,GP-9937,GP-9207, GP-9202, GP-9036, GP-9111,GP-9390GP-9070, GP-9210, GP-9846
IV	16	GP-9817, GP-9835, GP-9865, GP-10056, GP-9901GP-9153,GP-9152, GP-9863, GP-10122, GP-9703, GP-10038, GP-9725, GP-9064 ,GP-9555, GP-9223
V	1	GP-9244
VI	1	GP-9634

Table 2: Intra (diagonal) and inter-cluster average of D^2 values of 85 landraces of rice

CLUSTER	**I**	**II**	**III**	**IV**	**V**	**VI**
I	**32.93**	43.83	50.79	52.33	60.34	77.77
II		**35.36**	66.44	59.10	73.74	100.30
III			**38.98**	77.45	54.34	68.76
IV				**39.77**	68.55	78.61
V					**0.00**	59.93
VI						**0.00**

Table 3: Cluster means for 10 characters in 85 landraces of rice (cluster analysis).

Cluster No	Days to 50% flowering	Plant height (cm)	Panicle Length (cm)	No. of tillers/plant	Number of grains/panicle	1000 grain weight(g)	Grain yield/ plant (g)	Grain iron concentration(mg/kg)	Grain zinc concentration (mg/kg)	Grain Protein Content%
Cluster I	84.29	116.31	22.73	11.15	107.71	23.63	24.79	9.05	17.03	7.21
Cluster II	63.95	91.39	19.34	9.46	89.35	20.77	14.17	9.55	14.96	6.81
Cluster III	91.68	121.79	22.65	11.11	186.82	22.27	25.58	9.35	16.41	6.90
Cluster IV	68.47	106.32	22.21	10.88	70.56	23.45	19.14	11.28	21.78	8.33
Cluster V	41.00	140.15	26.50	12.75	211.00	23.62	19.33	11.55	19.05	9.41
Cluster VI	101.00	115.70	21.95	12.75	201.00	19.65	16.86	11.95	25.35	9.90

Table 4: Relative contribution of different characters to genetic diversity in 85 landraces of rice.

S.No	Characters	Times Ranked 1st	Contribution %
1	Days to 50% Flowering	464	13.00%
2	Plant Height (cm)	272	7.62%
3	Panicle Length (cm)	0	0.00%
4	No. of tillers/plant	0	0.00%
5	Number of grains/ panicle	1532	42.91%
6	1000 grain weight (g)	19	0.53%
7	Grain yield/ plant (g)	7	0.20%
8	Grain iron concentration (mg/kg)	73	2.04%
9	Grain zinc concentration (mg/kg)	882	24.71%
10	Grain Protein Content	321	8.99%

Figure

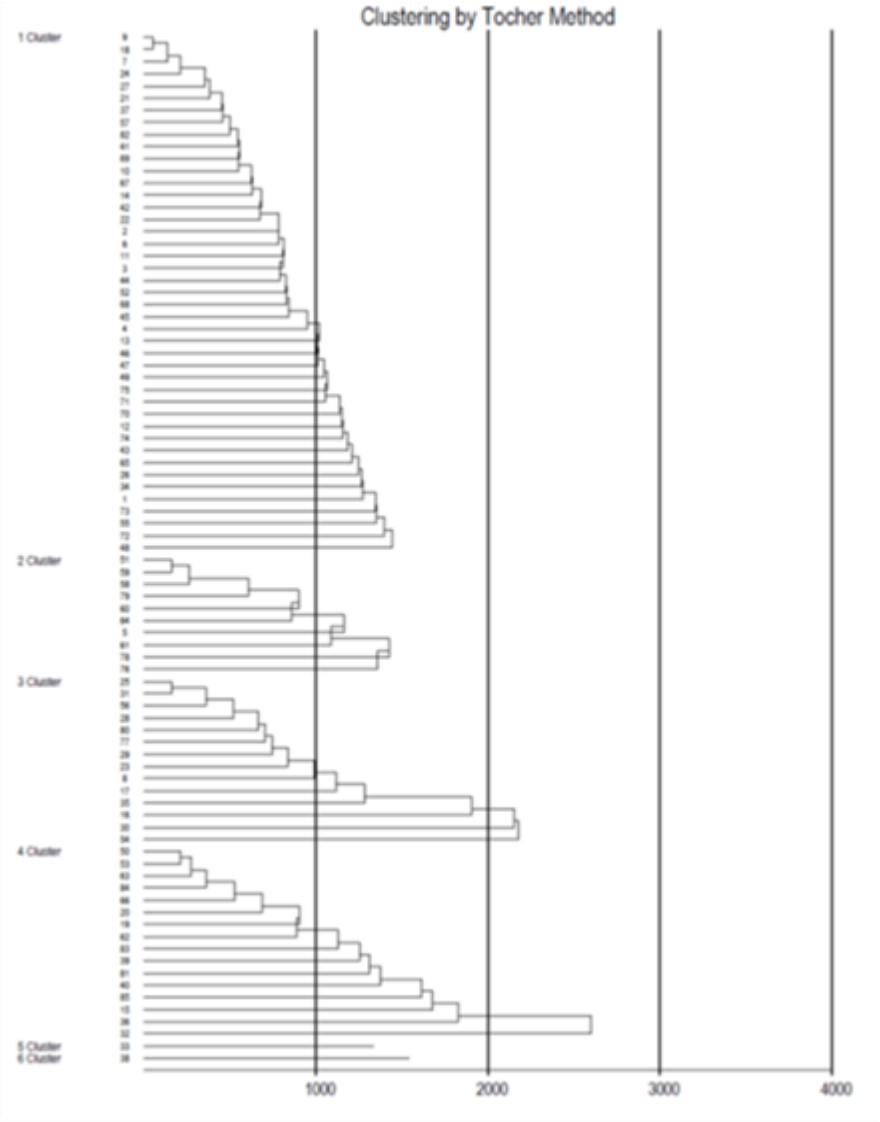

Figure 1: Clustering pattern by Tocher's Method