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Short Communication

Genetic Diversity Analysis of Yield and Lodging Related Traits in Different Landraces of Rice (*Oryza sativa* L.)

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Rice is a universal food crop which feeds over several million people in the world. The exponential growth in world's population demands an increase in production and productivity of rice. Rice crop's broad genetic could be utilized to break the yield barrier. For this purpose, various germplasm lines and cultivars should be evaluated to study the extent of variability present in them which could be further employed in plant breeding programmes. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme [1]. Keeping this in view, the present study was determined to evaluate the genetic diversity of 30 rice genotypes using Mahalanobis D^2 statistics.

Twenty-four landraces and six improved rice cultivars were raised during 2020 at Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University. Twenty-eight days old seedlings were transplanted in the main field in Randomized Block Design (RBD) with three replications each. Each entry was transplanted in plot of 2.55 m length and width of 1.20 m as spacing of 15 cm between rows, 10 cm between plants and 60 cm between plots. The standard agronomic practices were followed. They were evaluated for sixteen yield and lodging related characters viz., days to 50% flowering, plant height, panicle length, culm length, flag leaf length, flag leaf width, number of internodes, lodging index, number of productive tillers, grain length, grain breadth, grain L/B ratio, culm diameter, total spikelets per panicle, thousand grain weight, grain yield per plant. Five (three for lodging related characters) random plants from each plot were taken for recording data. The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis [2] and grouping of varieties into clusters was done following the Tochers method as detailed by Rao [3].

Analysis of variance showed significant differences for all the sixteen characters studied among the genotypes. Based on D^2 value, 30 genotypes were grouped into 8 clusters (Table 1). Maximum number of genotypes (18 genotypes) was grouped in cluster I. Cluster II, III, IV, V and VI composed of two genotypes each and cluster VII and VIII with one genotype each.

Table 1 Clustering pattern of 30 genotypes

Cluster number	No. of genotypes	Genotypes
I	18	Amman ponni, Mapillai samba, Karuppu kavuni, Arupadham kuruvai, Zeeraga samba, Iluppai poo samba, Kudaivaazhai, Atchaya ponni, Manjal Ponni, Chella White ponni, Kichedi samba, Thooyamalli, Andhra ponni, Poonkar
II	2	IR 20, CO R 50
III	2	Thengai poo samba, Kaalan namak
IV	2	Bhavani, Karunguruvai
V	2	Vaishnavi, Salem sanna
VI	2	Kuthiraival samba, ADT 43
VII	1	Sornamasuri
VIII	1	TKM 13

The intra and inter cluster distance are presented in (Table 2). Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the

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genotypes. The highest inter cluster distance was found between cluster VII and cluster VIII (46.72) which was followed by cluster V and cluster VIII (46.68) and cluster II and cluster V (37.81) indicating wider genetic diversity among the genotypes between these groups [4]. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. The least inter cluster distance was found between cluster II and IV (14.83) which indicates genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give appreciable result.

Table 2 Intra and inter cluster averages of D^2 values among 8 clusters of rice genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	20.80	26.46	23.05	24.44	28.40	26.52	29.57	34.98
II		9.74	21.27	14.83	37.81	15.31	39.54	20.42
III			11.88	15.66	36.63	27.44	37.67	27.52
IV				12.68	33.84	22.07	35.32	20.85
V					13.42	35.25	16.67	46.68
VI						18.01	37.66	26.66
VII							0.00	46.72
VIII								0.00

Table 3 Contribution of different characters to diversity in rice

Character	Number of first rank	Percentage of contribution
Days to 50% flowering	17	3.90
Plant height	100	22.98
Panicle length	5	1.14
Culm length	0	0.00
Flag leaf length	1	0.22
Flag leaf width	0	0.00
Number of internodes	5	1.14
Lodging incidence	137	31.49
Number of productive tillers	36	8.27
Grain length	3	0.68
Grain breadth	17	3.90
Grain L/B ratio	8	1.83
Culm diameter	13	2.98
Total spikelets per panicle	16	3.67
1000 grain weight	5	1.14
Grain yield per plant	72	16.55

Cluster I recorded the maximum intra cluster distance (20.8) followed by cluster VI (18.01) and cluster V (13.42). Hence, selection within these clusters may be done for the desirable traits [5].

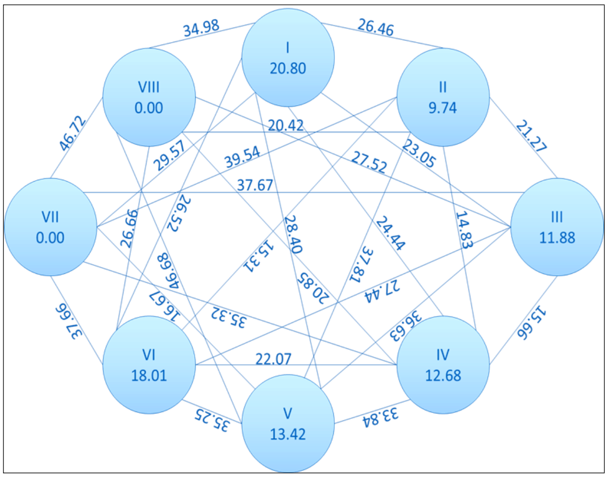

Fig 1 Cluster diagram indicating inter and intra cluster distances among the clusters formed using D^2 analysis

The results of the cluster mean (Table 3) revealed that cluster VIII exhibited maximum mean values for characters like grain yield per plant, thousand grain weight, grain length, grain breadth and minimum values for lodging index, plant height and days to 50% flowering. Cluster III showed maximum mean values for grain yield per plant, total spikelets per panicle, grain breadth, panicle length and number of internodes. Thus, by crossing genotypes included in the above clusters a wide spectrum of variability for the above-mentioned panicle and grain density characters could be obtained in the segregating generation. Based on the per se performance of the beat genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme [6].

The contribution of each trait to total divergence is presented in (Table 3). Lodging index (31.49 per cent) contributed maximum towards genetic divergence followed by plant height (22.98 per cent) and grain yield per plant (16.55). Selection based on plant height and lodging index will be effective in improving the grain yield per plant in rice due to the existing vast genetic divergence. Kuthiraival samba and Thengai Poo Samba could be used as a base genotype for improving lodging resistance. Characters like culm length and flag leaf width do not have any divergence among the genotypes used for this study.

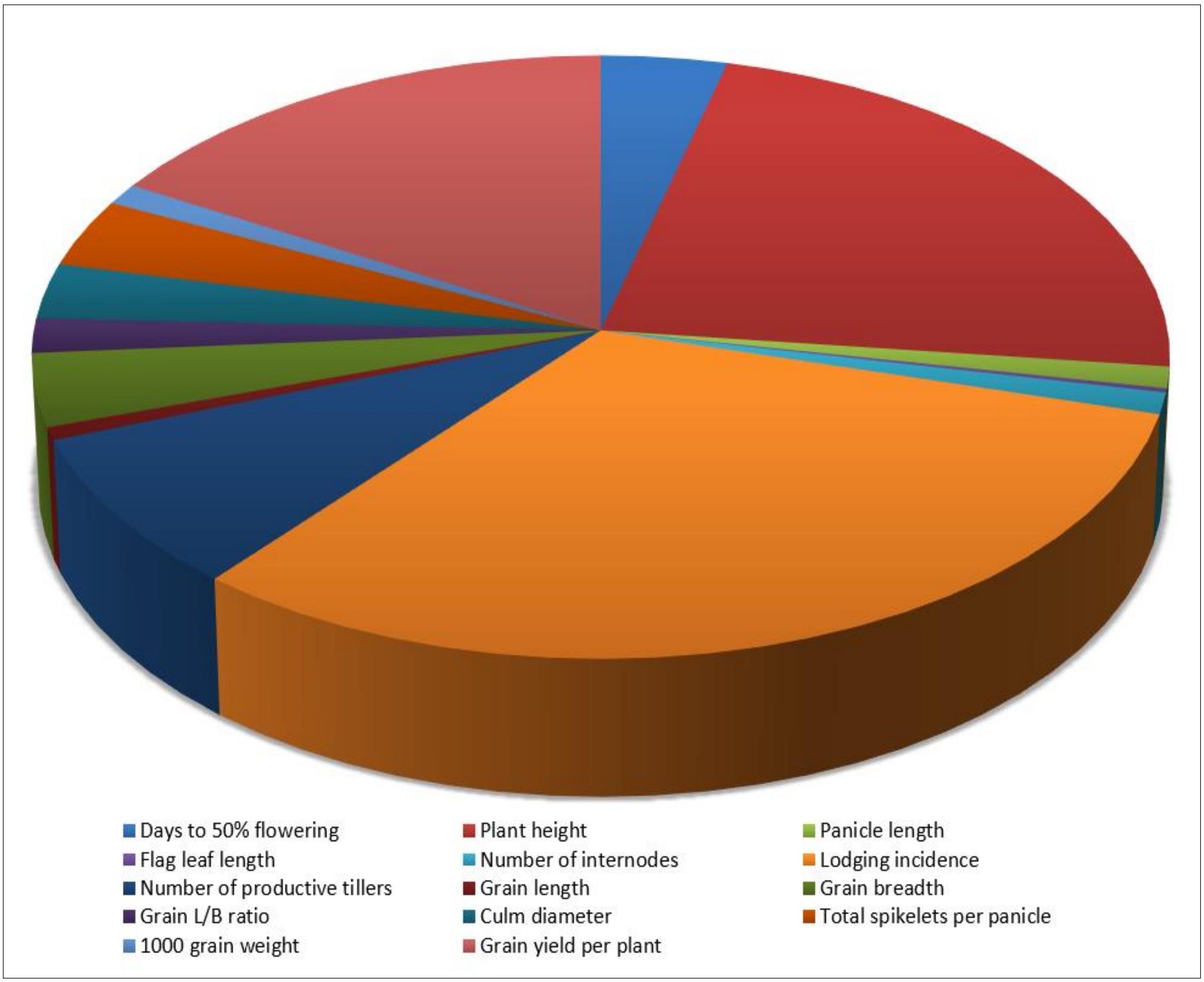

Fig 2 Contribution of various characters to divergence

CONCLUSION

From the afore mentioned investigation genetic divergence was analyzed for different yield and lodging related traits for 24 landraces and 6 improved varieties of rice. The analysis of variance revealed significant differences among the genotypes for all the characters studied. Based on Mahalanobis D^2 analysis all the 30 genotypes were grouped into eight different clusters. Among the 8 clusters, cluster I was the largest with eighteen genotypes. Cluster II, III, IV, V and VI composed of two genotypes each and cluster VII and VIII with one genotype each. Cluster I recorded the maximum intra cluster distance followed by cluster VI and cluster V. The highest inter cluster distance was found between cluster VII and cluster VIII which was followed by cluster V and cluster VIII. Selection of genotypes in these clusters can be done which may serve as potential donors for future hybridization programmes to develop potential recombinants with high yield paired with desirable traits. The characters like lodging index, plant height and grain yield per plant contributed maximum towards genetic divergence.

LITERATURE CITED

1. Joshi MA, Singh P, Sarao NK, Sharma RC, Bharaj TS. 2008. Genetic diversity among the rice varieties cultivated in Punjab. *Oryza* 45(4): 277-279.
2. Mahalanobis PC. 1936. On the generalized distance of statistics. In the proceedings India: National Institute of Science. pp 49-55.
3. Subudhi HN, Meher J, Bose LK, Das S. 2009. Genetic diversity studies of promising varieties of eastern India based on quality characters. *Oryza* 46(4): 271-274.
4. Rao CR. 1952. *Advanced Statistical Methods in Biometrics Research*. New York: John Wiley and Sons.
5. Singh J. 2010. Genetic diversity for sustainability of rice crop in Indian Punjab and its implications. *Journal of Plant Breeding and Crop Science* 2(9): 293-298.
6. Banumathy S, Manimaran R, Sheeba A, Manivannan N, Ramya B, Kumar D, Ramasubramanian GV. 2010. Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electronic Journal of Plant Breeding* 1(4): 500-504.