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DISCERNING GENETIC VARIABILITY AND DIVERSITY IN PADDY HYBRIDS THROUGH MULTIVARIATE TECHNIQUES

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ABSTRACT

Twenty-five paddy hybrids were evaluated in randomized block design with three replications at Regional Agricultural Research Station, Nandyal to estimate the genetic variability, heritability and genetic advance as per cent of mean for eight yield and yield attributes during *kharif*, 2024. The Phenotypic coefficient of variation (PCV) was higher than Genotypic Coefficient of variation (GCV) for all the traits studied suggesting that environment effects influence these characters. In the current study, moderate PCV and GCV were observed for yield and yield attributes *viz.*, effective bearing tillers/m² (14.09 % and 13.04%), test weight (14.90% and 14.56%) and grain yield (Kg per hectare) (15.82% and 13.11%). Heritability was high for the characters studied except for panicle length (PL). High heritability coupled with high genetic advance as *per cent* of mean was displayed by effective tillers/m² (85.66% and 24.87), test weight (95.58% and 29.32) and grain yield (Kg per hectare) (68.72% and 22.39) implying that these traits were mainly governed by additive gene effects and response to selection could be affected for further yield improvement through simple selection. The cluster analysis revealed that genotypes from Cluster IV can be crossed with genetically distant genotypes from Cluster VI to combine high yield potential with desirable phenological traits. Correlation analysis revealed that grain yield had a strong and positive association with ear bearing tillers per m², spikelet fertility, and test weight indicating that these traits are key determinants of yield and can be used as reliable selection criteria in breeding programmes.

Keywords : Rice, genetic variability, correlation and cluster analysis

Introduction

Rice (*Oryza sativa* L.) is one of the most important staple food crops in the world, providing a major share of calories for a large proportion of the global population. Improvement in rice productivity, quality, and adaptability depends largely on the availability of sufficient genetic variability, since diverse germplasm serves as the basic raw material for crop breeding and selection. India, which ranks second in the world after China in terms of rice production, produces 22% of the world's rice (Vasudev *et al.*, 2023). However, due to its vulnerability to environmental factors, the direct evaluation of grain yield, a multifaceted trait influenced by numerous

characteristics and frequently polygenic in nature faces difficulties.

The global demand for rice is projected to increase from 490 million tonnes in 2020 to 555 million tonnes by 2035. To face the upcoming challenge, hybrids are need to be developed. However, hybrid lines play a vital role in modern agriculture by harnessing hybrid vigour (heterosis) to achieve higher yields, *i.e.*, 15-20% increase in yield when compared with pure lines. Assessment of variability, heritability, and genetic advance and cluster analysis allows breeders to determine the extent of exploitable variation and to distinguish traits that are mainly governed by genetic factors from those strongly influenced by the environment.

Material and Methods

The present experiment was laid out Regional Agricultural Research Station (RARS), Nandyal, Andhra Pradesh, India during *kharif*, 2024. The experimental material was comprised of 25 paddy hybrids tested in Randomized Block Design, with three replications having a plot size of 10 m² per variety with a spacing of 20 cm x 15 cm. All the recommended agronomic practices by Acharya N.G. Ranga Agricultural University are followed during crop growth period. Twenty five hybrids are studied for the eight yield and yield attributes *viz.*, Days to 50% flowering (DFF), Days to maturity (DM), Plant height (PH), Effective bearing tillers/m² (EBT/m²), Panicle length (PL), Spikelet fertility% (SF), Test weight (TW) and grain yield GY (Kg/ha). Data was collected from five competitive and randomly selected plants for recording yield and yield component traits except DFF and DM that were recorded on plot basis. The phenotypic and genotypic coefficients of variation were estimated as per the method outlined by Burton and De Vane (1953). Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was estimated on genotype mean basis as described by Allard (1960). Genetic advance as percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated as per the procedure given by Johnson *et al.* (1955). The data generated by evaluation of hybrids is forwarded to statistical analysis to estimate genetic diversity through hierarchical clustering using JMP 17.0 statistical software (SAS Institute Inc., Cary, NC, USA).

Results and Discussions

The estimates of range, variance, phenotypic and genotypic co-efficient of variation (GCV, PCV), heritability in broad sense and genetic advance as percent of mean for eight yield and yield attributes in 25 paddy hybrids are furnished in Table 1. The PCV showed high magnitude than the GCV for all the characters indicating the influence of environment in the expression of these traits. Moderate PCV and GCV were registered by EBT/m², TW and GY indicated that these characters have moderate genetic variability with some environmental influence on its expression and can be improved through selection in advanced generations. This was inconformity with the results of Adjah *et al.* (2020) and Debsharma *et al.* (2022). Low PCV and GCV was noted for the traits *viz.*, DFF, DM, PH, PL and SF implying that these traits shown narrow genetic base which can be altered through hybridization followed by rigorous selection in advanced generations.

High heritability observed for all the traits ranging from 51.23% for PL to 97.99% for SF indicating least influence of environment on the genetic expression of the characters under study. The traits *viz.*, DFF (95.61%), DM (97.90%), PH (88.22%), EBT/m² (85.65%), SF (97.99%), TW (95.58%) and GY (Kg/ha) (68.72%) displayed higher estimates of heritability. On the other hand, PL expressed moderate heritability.

However, the estimates of heritability alone will not be of much value for selection and genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.*, 1955) to estimate realized genetic improvement possible in the character through simple selection methods. High heritability and high genetic advance estimates registered for EBT/m² ($h^2(b) = 85.65\%$, GAM = 24.87%), TW ($h^2(b) = 95.58\%$, GAM = 29.32%) and GY ($h^2(b) = 68.72\%$, GAM = 22.39%) indicating additive gene effects in inheritance of these characters and simple selection would be effective to augment further genetic improvement of these traits. These were inconformity with results of Ravikumar *et al.* (2015), Satyanarayana *et al.* (2024). High heritability coupled with moderate genetic advance as per cent of mean was observed for the traits PH (88.22%, 12.56%), DFF (95.61%, 10.49%) and SF (97.99%, 15.95%) indicating the role of both additive and non-additive gene effects in their genetic control and simple selection methods may not be rewarding to effect further genetic gain in these traits. The results are inconsistent with the findings of Barhate *et al.* (2021). From the foregoing discussion, it can be concluded that more heritability and genetic advance as per cent of mean were observed for EBT/m², TW and GY indicating that variation in above traits was most-likely due to additive gene effects, hence simple selection may be effective to improve these traits in the present material under study.

Hierarchical cluster analysis was conducted with 25 rice hybrids using Wards method which provides the best result to get the finest possible classification. The cluster analysis revealed the aggregation of hybrids into six clusters (Table 2 and Figure 2) This clearly infers the existence of ample amount of genetic divergence in the hybrids of these clusters. Crosses between genotypes belonging to the same cluster are less likely to produce desirable variability due to genetic similarity. In contrast, hybridization between genotypes from widely separated clusters is expected to generate greater heterosis and a higher frequency of transgressive segregants. From a breeding perspective, the identification of divergent clusters provides a strategic framework for parent selection. For instance, genotypes from Cluster IV (which exhibited superior

mean performance for yield traits) can be crossed with genetically distant genotypes from Cluster VI (early maturity group) to combine high yield potential with desirable phenological traits. Such crosses increase the likelihood of recombination of favorable alleles governing yield, adaptability, and maturity, thereby enhancing the probability of obtaining superior transgressive segregants due to increased heterotic potential.

Further, among the six divergent clusters, the highest numbers of hybrids were grouped in cluster I with 9 hybrids followed by 5 hybrids in cluster III and IV. The hybrids in cluster IV showed highest mean values for GY and PL (Table 3). The hybrids of cluster V showed maximum value for EBT/m² and GP. Ravikumar *et al.* (2015), Tejaswani *et al.* (2016), Tejaswini *et al.* (2018) and Kumari *et al.* (2021) also documented same kind of clustering of accessions into distinct clusters. These findings are consistent with the reports of Rahimi *et al.* (2013), Pandit *et al.* (2016), Sharafi *et al.* (2018), and Divya *et al.* (2022) in rice

The correlation analysis of eight traits (Fig. 2) revealed that DFF displayed high and positive association with DM, PH and EBT/m². The trait DM correlated positively with PH and EBT/m². PH was positively associated with EBT/m² and PL was positively associated with PH and TW. Similarly, SF% was positively associated with EBT/m² and GY.

Likewise, TW was associated with PL and GY. Furthermore, GY was positively associated with EBT/m², SF% and TW and negatively associated with DFF, DM, PH and PL. Similar kind of association results were also in congruence with Sudeepthi *et al.* 2020, Roy *et al.* 2024 and Howlader *et al.* 2025.

Conclusion

The present study revealed substantial genetic variability among the 25 rice hybrids for yield and yield-related traits, indicating ample scope for improvement through selection and hybridization. Traits such as EBT/m², TW, and GY showed moderate to high variability with high heritability and high genetic advance, suggesting that additive gene action predominantly governed these characters and that simple selection would be effective for their improvement. Correlation analysis showed that grain yield had positive associations with EBT/m², SF%, and TW, while it was negatively associated with DFF, DM, PH, and PL. This suggests that selection for higher effective tillers, spike fertility, and test weight can indirectly contribute to yield improvement. Overall, the combined evidence from variability, correlation, and cluster analyses suggests that these diverse and superior genotypes can be effectively utilized to exploit heterosis and develop improved rice hybrids with higher yield potential.

Table 1: Mean, Range, Coefficient of variation, Heritability, Genetic Advance as per cent of mean in 62 advanced rice cultures

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%) h ² (bs)	Genetic advance as % of mean (GAM)
			Minimum	Maximum	GCV (%)	PCV (%)		
1	Days to 50 per cent flowering	98.64	80	106	5.21	5.32	95.61	10.49
2	Days to maturity	128.82	110	138	4.02	4.06	97.9	8.19
3	Plant height (cm)	115.24	104.41	128.21	6.49	6.91	88.22	12.56
4	Ear bearing tillers/ m ²	392.57	280	514	13.04	14.09	85.65	24.87
5	Panicle length (cm)	25.93	23.81	28.18	3.72	5.19	51.23	5.48
6	Spikelet fertility	83.43	65.67	93.75	7.83	7.91	97.99	15.95
7	Test weight (g)	17.29	11.90	22.14	14.56	14.90	95.58	29.32
8	Grain yield (Kg/ha)	5739.29	4166.40	7301.12	13.11	15.82	68.72	22.39

PCV and GCV: Phenotypic and genotypic coefficients of variation, h² (bs): Broad-sense heritability, GAM: Genetic advance as a percentage of the mean

Table 2: Grouping of different hybrids into six distinct clusters

Cluster	No. of Paddy hybrids	Paddy hybrids
I	9	NDLRH 564, NDLRH 574, NDLRH 565, NDLRH 578, NDLRH 573, NDLRH 566, NDLRH 580, NDLRH 581, NDLRH 588
II	3	NDLRH 567, NDLRH 579, NDLRH 587
III	5	NDLRH 568, NDLRH 569, NDLRH 570, NDLRH 576, NDLRH 572
IV	5	NDLRH 575, NDLRH 583, NDLRH 584, NDLRH 577, NDLRH 582
V	2	NDLRH 571, NDLRH 586
VI	1	NDLRH 585

Table 3 : Cluster means of various characters of rice advanced breeding lines under study

Cluster No.	DFF	DM	PH	PL	EBT/m ²	GP	TW	GY (Kg/ha)	Mean
Cluster I	100.33	130.78	118.14	389.11	26.38	76.62	16.96	4943.21	725.19
Cluster II	104.67	135.33	115.77	388.33	24.11	87.60	12.68	5684.22	819.09
Cluster III	99.20	129.20	120.56	398.00	26.42	83.92	18.60	6213.89	886.22
Cluster IV	98.60	128.20	108.90	445.00	25.34	89.38	17.27	6583.77	937.06
Cluster V	92.50	124.00	109.35	312.00	27.36	90.33	21.57	6011.52	848.58
Cluster VI	80.00	110.00	104.40	310.00	24.85	86.32	19.19	5929.49	833.03
Mean values	95.88	126.25	112.85	373.74	25.74	85.70	17.71	5894.35	

Bold figures indicate maximum and minimum values in each character.

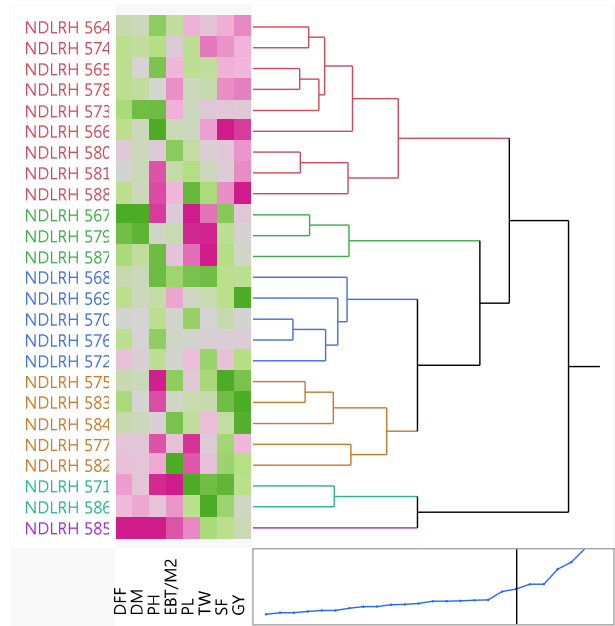


Fig. 1 : Dendrogram showing clustering by Wards method

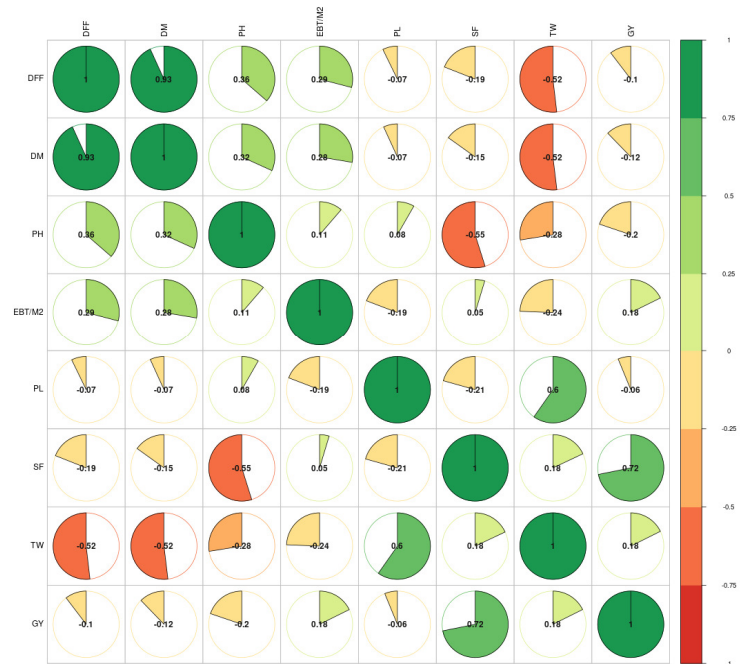


Fig. 2 : Correlation for yield and its components in rice hybrids

References

- Adjah, K.L., Abe, A., Adetimirin, V.O. and Asante, M.D. (2020). Genetic variability, heritability and correlations for milling and grain appearance qualities in some accessions of rice (*Oryza sativa* L.). *Physiology and molecular biology of plants*, **26**, 309-1317.
- Allard, R. W. (1960). Principles of Plant Breeding. John Wiley & Sons, Inc., New York, 485.
- Barhate, K.K., Jadhav, M.S and Bhavasar, V.V. (2021). Genetic variability, heritability and genetic advance in aromatic lines of rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry*, **10**(3), 360-362.
- Burton G W and Devane E H. (1993). Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*, **45** : 478-481.
- Debsharma, S.K., Syed, Md. A., Ali, Md. H., Maniruzzaman, S., Roy, P.R., Brestic, M., Gaber, A and Hossain, A. (2022). Harnessing on Genetic Variability and Diversity of Rice (*Oryza sativa* L.) Genotypes Based on Quantitative and Qualitative Traits for Desirable Crossing Materials. *Genes*. **14**: 1-21.
- Divya M, Singh PK, Rabiya P, Sareeta N and Mankesh K. (2022). Estimation of Genetic Diversity by Principal Component Analysis of Yield Attributing Traits in Katarni Derived Lines. *Journal of Rice Research*, **15**(2): 63-69
- Howlader, N.C., Bulbul, M.T.A., Islam, M.Z., Arafat, E., Rana, M.S. and Hasan, M.Z. (2025). Assessing rice genotypes based on agro-morphological characterization and diversity analysis in southern Bangladesh. *Discover Plants*, **2**(1): 1-19.
- Johnson, H.W., Robison, H.F and Comstock, R.E. (1955). Genotypic and phenotypic correlations in soybean and their implications in selection. *Agronomy Journal*, 477-83.
- Kumari, B.K., Ravi Kumar, BNVSRR, Jyothula, DPB and Rao, M.K. (2021). Diversity analysis in rice breeding lines for yield and its components using principal component analysis. *Journal of Pharmacognosy and Phytochemistry*. **10**(1), 905-909.
- Pandit, E., Barik, S.R., Mohanty, S.P., Mohanty, D.P., Das, L., Singh, O.N. and Pradhan, S.K. (2016). Principal component analysis for selection of heterotic hybrids for yield component traits in mid and mid-early duration rice genotypes. *ORYZA-An International Journal on Rice*, **53**(3), 255-261.
- Rahimi, M., Dehghani, H., Rabiei, B. and Tarang, A.R. (2013). Evaluation of rice segregating population based on drought tolerance criteria and biplot analysis. *International Journal of Agriculture and Crop Sciences*, **5**(3), 194-199.
- Ravi Kumar, B.N.V.S.R., Kumari, P.N., Rao, P.V.R., Rani, M.G., Satyanaryana, P.V., Chamundeswari, N., Vishnuvardhan, K.M., Satyanarayana, Y., Bharatalakshmi, M. and Reddy, A.V. (2015). Principal component analysis and character association for yield components in rice (*Oryza sativa* L.) cultivars suitable for irrigated ecosystem. *Current Biotica*. **9**(1), 25-35.
- Roy, T.K., Sannal, A., Tonmoy, S.S., Akter, S., Roy, B., Rana, M.M., Alam, Z. and Hasan, M.R. (2024). Trait analysis of short duration boro rice (*Oryza sativa* L.) varieties in northern region of Bangladesh: insights from heatmap, correlation and PCA. *Nova Geodesia*, **4**(2), 175-175.
- Satyanarayana, P.V., Kumar, K.M., Babu, P.U., Srinivasa, T. and Manoj Kumar D. (2024). Genetic Architecture, Studies to Identify the Selection Criteria for Yield in Long Duration Rice Lines (*Oryza sativa* L.). *International Journal of Environment and Climate Change*. **14**(4), 842-851.
- Sharifi, P. and Ebadi, A.A. (2018). Relationships of rice yield and quality based on genotype by trait (GT) biplot. *Anais da Academia Brasileira de Ciencias*, **90**, 343-356.
- Sudeepthi, K., Srinivas, T., Kumar, BNVSRR, Jyothula, D.P.B. and Umar, S.N. (2020). Genetic divergence studies for anaerobic germination traits in rice (*Oryza sativa* L.). *Current Journal of Applied Science and Technology*, **39**(1), 71-78.
- Tejaswini KLY, Manukonda S and Rao PR. 2018. Genetic divergence and cluster analysis studies in rice (*Oryza sativa* L.) using D² statistics. *Journal of Pharmacognosy and Phytochemistry*, **7**(4S): 108-116.
- Tejaswini, K.L.Y., Manukonda, S., Rao, P.R., Kumar, B.R., Mohammad, L.A. and Raju, S.K. (2016). Cluster analysis studies in rice (*Oryza sativa* L.) using wards minimum variance method. *Journal of Agricultural and Crop Research*, **4**(9), 129-139.
- Vasudeva Reddy, D., Suneetha, Y., Ravi Kumar, BNVSRR and Ramesh, D. (2023). Evaluation of experimental hybrids for yield and yield component traits in rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*, **70**(1), 050-061.