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RESEARCH ARTICLE

Genetic diversity using principal component analysis and hierarchical cluster analysis in rice

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SUMMARY

A set of 100 germplasm lines with four checks *viz*., BPT-5204, PSB-68, Siri1253 and MGD-101 were evaluated in augmented block design during *Kharif* 2020. The observations were documented for 5 quantitative traits *viz*., days to 50% flowering, panicle length, number of panicles per square meter, 1000 grain weight and grain yield by principal component analysis and cluster analysis to determine the relationship and genetic divergence among the individuals. The cumulative variance of 55.60% was explained by 1st two principal components (PC1 and PC2) with eigen values greater than 1. Component 1 with variance of 32.10% had contribution from days to 50% flowering, panicle length, panicles per square meter and grain yield while principal component 2 accounting 23.50% total variability has contribution from days to 50% flowering and panicles per square meter. The remaining variability of 17.68%, 16.10% and 10.60% was consolidated in PC3, PC4 and PC5. Results from cluster analysis grouped 100 germplasm lines into four clusters with minimum individuals constituted in cluster 1 and maximum individuals were found in cluster 4. The lines in cluster 1 (2.62) showed maximum divergence followed by cluster 3 (2.23). The maximum inter cluster Euclidean distance was observed between clusters 2 and cluster 3 followed by cluster 1 and cluster 2 giving a scope for selection of parents for hybridization programme from these clusters to realize high genetic variation and novel combinations for yield increment.

Key Words : Principal component analysis, Hierarchical cluster analysis, Rice

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