

Clustering of Rice Genotypes - *A Multivariate Approach*

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ABSTRACT

An important step in plant breeding programs is identification of parents that are genetically distant from each other, to find crossing combinations with better prospects of hybrid vigor. The potential of identifying genetically distant parents depends on genetic diversity of population. 60 Rice genotypes from diverse origins have been employed to study genetic variation in order to identify the most effective components of grain yield. Using cluster analysis, the genotypes were grouped into 8 clusters of which clusters II was the largest cluster consisting of 21 genotypes while cluster III, IV, VII and VIII are the smallest clusters with only a single genotype each. The maximum intra cluster distance ($D = 371.74$) was found in cluster VI consisting of 8 genotypes NLR 33358, ADT 45, ADT 37, JGL 1118, IR 10F221, NLR 3367, IR 64197 and ADT 43. From the inter cluster D^2 values of eight clusters, it can be seen that the highest divergence occurred between cluster V and cluster VI (1651.37) While the minimum inter cluster distance was noticed between cluster IV and cluster VII (94.06). Out of 17 characters studied the maximum contribution (79.66 %) towards total divergence is by 5 characters only. They are days to maturity, test weight, flag leaf width, flag leaf length, Days to 50% flowering. These characters should be taken into consideration while selecting parents for hybridization.

Key words: *Genotypes, Genetic diversity, Cluster analysis, Mahalanobis D^2*