Multivariate Analysis in Rice (Oryza sativa L.)

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ABSTRACT

Thirty five genotypes of rice were evaluated for 18 characters to study genetic divergence by using Mahalanobis' D^2 statistic, cluster analysis and principal component analysis. On the basis of these three clustering methods six clusters were obtained for D^2 statistic and cluster analysis for each method. Absolute growth rate showed maximum contribution towards genetic divergence in D^2 statistics. PCA identified six components with eigen value more than one which contributed 79.526 per cent of cumulative variance. Highest inter - cluster distance was observed between cluster IV *viz.,* IR 8 and VI *viz.,* MTU 1061 followed by clusters V *viz.,* CSR 4 and VI *viz.,* MTU 1061 and clusters IV *viz.,* IR 8 and V *viz.,* CSR 4. Whereas cluster I *viz.,* MTU 1075, TELLA HAMSA, MTU 1061, ACC. No. 11081 and cluster VI viz., KAVYA, IR 8 And PR 109 etc followed by cluster IV *viz.,* NLR 28523 and NLR 145 and clusters V *viz.,* MTU 1002, WGL 186 and CSR 4 and cluster II *viz.,,* PR 106, BPT 5204, BPT 2270 and NLR 3041 etc and cluster V *viz.,* MTU 1002, WGL 186 and CSR 4 showed maximum inter cluster distance in hierarchical cluster analyses. For varietal improvement strains from these clusters were important on the basis of their genetic distance and highest cluster means. Divergence studies indicated that selection for hybridization should be more based on genetic diversity rather than the geographic diversity**.**

Key words : Cluster analysis, D^2 analysis, Principal component analysis, Rice.