

Multivariate Analyses of Genetic Divergence Based on Metric and Physiological Traits in Pigeonpea (*Cajanus cajan* (L.) Millsp.).

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ABSTRACT

Forty five genotypes of pigeonpea collected from different research centres across the country were subjected to Mahalanobis' D^2 Statistic, cluster analysis and principal component analyses based on 21 metric and physiological traits. Considerable genetic divergence among the 45 genotypes resulted into seven clusters as per D^2 analysis and also in case of cluster analysis. The grouping of genotypes into clusters was at random which suggested that geographical isolation might not be the only factor causing genetic diversity. Out of 21 characters studied, seed yield per plant contributed maximum towards divergence followed by grain protein content, relative water content at flowering stage, relative water content at vegetative stage, number of secondary branches per plant and specific leaf weight at flowering stage. Principal component analysis identified seven principal components (PCs) which explained 78.0% of the variability. The genotypes LRG-69, JSA-66, LRG-73, TAT 9629 and 11969 showed maximum inter-cluster distance and wide genetic distance in all the three divergence methods with each other and hence these genotypes could be exploited in hybridization programme for identification of desirable segregants.

Key words : Cluster analysis, D^2 analysis, Pigeonpea, Principal Component Analysis.