

Multivariate Analyses and Genetic Divergence in Pigeonpea (*Cajanus Cajan* (L.) Millsp.).

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ABSTRACT

Forty one genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.] collected from different research centres across the country were subjected to Mahalanobis' D^2 Statistic, cluster analysis and principal component analyses based on 13 traits. Considerable genetic divergence among the 41 genotypes resulted into six clusters as per D^2 analysis and seven clusters in the 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 thirteen characters studied, number of pods per plant contributed maximum towards divergence followed by grain protein content. Principal component analysis identified four principal components (PCs) which explained 77.65% of the variability. The genotypes SM 13, SM 114, Perennial 1 and TT 02 showed maximum inter-cluster distance and wide genetic distance with each other in all the three divergence methods. So they can be exploited in hybridization programme for identification of desirable segregants.

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