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## ResearchArticle

# Genetic diversity studies in pigeonpea (Cajanus cajan L. Millsp.) 

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#### Abstract

SUMMARY Genetic diversity using Mahalanobis D-square ( $\mathrm{D}^{2}$ ) techniques was studied for yield and yield contributing traits of 100 genotypes of pigeonpea. These genotypes were grouped into nine clusters. The greatest distance between two clusters was existed between cluster VII and III (727.38) indicating greatest divergence, followed by cluster VIII and III (630.51), cluster IX and $V$ ( 604.66 ), cluster $V$ and III (580.32) and cluster VIII and $V(573.60)$. Whereas the least distance was recorded between cluster V and IV (71.57) followed by cluster III and II (122.10), cluster IV and I (217.85), cluster II and I (219.33) indicating least genetic divergence among genotypes. The intra cluster values varied from 0.00 to 139.00 . The maximum intra-cluster distance was noticed in cluster I (139.00).


Key Words : Pigeonpea, Genetic diversity, Clustering pattern, $\mathrm{D}^{2}$ statistics
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