

RESEARCH ARTICLE :

Analysis of genetic divergence for yield contributing traits in Pumpkin (*Cucurbita moschata* Duch. ex Poir.)

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SUMMARY : Genetic divergence among 23 pumpkin genotypes was estimated using Mahalanobis's D^2 statistic. Analysis of variance studies indicates significant differences among all the genotypes for all the characters under study. Based on D^2 analysis, the genotypes were grouped into 6 different clusters, where cluster II contained the highest number of genotypes (6) followed by I (5), III (5), IV (4), VI (2) and cluster V contained the lowest (1). Clustering pattern revealed that geographical diversity was not associated with genetic diversity *i.e.*, genotypes collected from same location were grouped into different clusters. The maximum intra-cluster distance was observed for cluster VI (6.07) and the minimum for cluster I (4.67). The maximum inter-cluster distance was observed between cluster V and VI (8.31) and that of minimum was observed in between the cluster I and II (5.80). Cluster V recorded the highest mean values for the characters vine length at 90 days (m), number of primary branches at 90 days, sex ratio, days to fruit harvest, fruit set %, fruit length (cm), rind thickness (cm), flesh thickness (cm), test weight (100 seed wt.(g).)

KEY WORDS :

Cluster, D^2 analysis, Genetic diversity, Pumpkin

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