

Exploring genetic diversity in blackgram (*vigna mungo* (L.) Hepper) through D² statistics and principal component analysis

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ABSTRACT

Genetic diversity is an essential prerequisite for crop improvement, enabling the identification of divergent parents for hybridization. The present study evaluated fifty-five blackgram genotypes for yield and quality traits using multivariate analysis. Mahalanobis D² statistics grouped the genotypes into six clusters, with Cluster I containing the maximum of 35 genotypes, followed by Cluster II with nine genotypes and Cluster III with eight genotypes, while Clusters IV, V and VI were solitary. The distribution of genotypes across clusters was random, suggesting distinct genetic backgrounds. The highest inter-cluster distance was observed between Clusters III and VI, followed by Clusters III and V, indicating wide genetic divergence. Principal component analysis identified five components with eigenvalues greater than one, explaining 76.71% cumulative variance. The first two PCs alone accounted for 56.04% of total variability. Seed yield per plant, test weight, protein content, and number of pods per plant were the major contributors to divergence. The results suggest that hybridization involving genotypes from distantly related clusters could yield superior segregants for yield and quality improvement.

Keywords: *Blackgram, Genetic diversity, Mahalanobis D² Statistics and Principal component analysis*