

Multivariate analysis in Upland Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

An experiment was conducted to analyze the genetic diversity among 60 genotypes for 16 quantitative characters in upland cotton. The 60 genotypes were grouped into 15 clusters based on Mahalanobis D^2 analysis with cluster I being largest with 15 genotypes followed by 13 genotypes in cluster II, 11 genotypes in cluster XII and 10 genotypes in cluster VII. Based on Hierarchical cluster analysis all the genotypes were grouped into 8 clusters with cluster I being largest with 23 genotypes followed by 9 genotypes in cluster II and 8 genotypes in cluster IV. This random distribution of genotypes indicated that the genetic diversity and geographical diversity are not related. In Principal component analysis first six principal components with eigen value more than one contributed 87.315 per cent towards the total variability with PC_1 alone showing maximum of 22.27 per cent variability.

Key words: *Cotton, Hierarchical cluster analysis, Mahalanobis D^2 analysis, Principal component analysis.*