

Classification of genetic diversity and choice of parents for hybridization in cowpea *Vigna unguiculata* (L.) Walp for humid savanna ecology

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Abstract

Thirty-one accessions of cowpea of diverse eco-geographic origins were evaluated for genetic diversity using principal component analysis (PCA), single linkage cluster analysis (SLCA) and canonical techniques. The accessions were classified into six groups by PCA and SLCA while canonical technique identified five vector groups. There was no relationship between the clustering pattern and eco-geographic distribution. PCA and canonical techniques can be jointly used in multivariate analysis

as both techniques performed complimentary role in identifying characters responsible for variation in cowpea. SLCA alone provided a clearer and more informative display of the group of accessions based

on character performance. The three techniques revealed most distant accessions as having widest variation and possible choice of parent stocks in hybridization.