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**Esterase, Total Protein and Seed Storage Protein Diversity in Okra  
(*Abelmoschus esculentus* L. Moench)**

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**Abstract**

Twenty-two accessions of okra (*Abelmoschus esculentus*), maintained at the Plant Genetic Resources Centre, Bunso, Ghana, were assayed for diversity in esterases, and total and storage proteins. A total of 34 reproducible and easily scorable bands were exposed with the number of bands per accession ranging from one to 21. All but nine of the bands were polymorphic. Storage proteins were the most diverse while esterases revealed the least diversity. Similarity matrices were calculated using the Jaccard coefficient, and input into cluster analysis. The phenogram produced by the UPGMA of the Jaccard similarity matrix from the pooled data of the esterases, and total and storage proteins revealed three major clusters at the 55% level of similarity. Accession 5 collected from Nyinguto was relatively distant from the other main clusters and separated at the 42% level of similarity. The second and third clusters comprised 11 and 10 accessions, respectively. It was observed that 18 out of the 22 accessions were distinct accessions. Similarity indices ranged from 29% to 100%. The wide range of similarity indices, coupled with the clustering of accessions, suggests useful variability in the collection for genetic conservationists and plant breeders.