Development of a Bambara Groundnut Core Collection from IITA Germplasm Based on Characterisation and Evaluation Data

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Abstract

An important step towards the improvement of the productivity of Bambara Groundnut (*Vigna subterranea* (L.) Verdc.), an underutilised African grain legume, is the development of improved cultivars. In order to maintain the existing genetic diversity and fully utilise the available germplasm, a core collection from germplasm held at the genebank of the International Institute of Tropical Agriculture (IITA) was developed. To estimate genetic diversity within the collection, characterisation and evaluation data available from the "International Bambara Groundnut Database" were analysed.

Based on this data set a hierarchical cluster analysis was performed to identify groups of accessions with minimal within and maximal between group variability. Reliable cluster levels were selected based on stability of the clusters and distance between levels. At each selected level the most typical accession of each group was chosen as an entry in a core collection and representative of the group. Thus, a high genetic diversity is retained within the core collection at each level. Core collections were defined so that entries of each core collection are contained in the next bigger collection defined at the next level. The resulting set of core collections is called a "hierarchical nested core collection". By using this structure the total number of entries does not increase, which facilitates the management and use of the core collections.

Since each entry in the core collection is regarded a representative of a group of accessions, there is strong linkage between the main collection and the core collection. This facilitates the use of all accessions of the genebank.

Information on agronomic and physiological traits can be linked with entries to the core collection and groups of accessions. For each cluster a profile of trait values can be assigned either based on means of all members or based on data collected from the core entry. These cluster profiles can be used to identify groups of accessions with desired features. Thus promising accessions can easily be identified, including genotypes with no available data for the given traits.

Keywords: Bambara Groundnut, breeding, core collection, genetic diversity, germplasm, neglected crop

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