ICRISAT Science with a human face International Crops Research Institute for the Semi-Arid Tropics

Reference Set

To make the Pigeonpea collection more suitable for exploitation a subset of 300 accessions Click here for details on Accessions was developed. Based on the genotypic data of composite collection, a subset of 300 diverse accessions were chosen from the composite collection using ‘max length sub tree’ option of DARwin5.0, which creates the subset of units minimizing the redundancy between units and limiting the loss of diversity (Table 4). The reference set captured 83.2% (164 alleles) of the 197 alleles of the composite collection, representing diversity from the entire spectrum of composite collection. The reference set will be profiled with additional markers and extensively phenotyped for traits of economic importance to identify accessions for beneficial traits for utilization in pigeonpea breeding and genomics (Upadhyaya et al. 2006). The plant breeders will have access to genotypically diverse accessions to enhance the yield potential of pigeonpea. Seeds of reference set are available to the bona fied users of germplasm from ICRISAT genebank upon signing Seed Material Transfer Agreement (SMTA).

For more information contact:

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