

DIVERSITY OF COMMON BEAN (*Phaseolus vulgaris* L) GERMPLASM IN UGANDA

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ABSTRACT

Common bean (*Phaseolus vulgaris* (L.) is a diploid, self-pollinated species with $2n = 2x = 22$ chromosomes and the most important legume grown in Uganda. A large collection of 320 common bean accessions obtained from different parts of Uganda is maintained at the National Crops Resources Research Institute (NaCRRI) and occasionally used for different breeding purposes. The genetic diversity within this germplasm was phenotyped using 22 traits planted in a Randomised Complete block design (RCBD) replicated twice, for two seasons in the fields at NaCRRI. Due to economic reasons 100 superior accessions was genotyped using Polymerase Chain Reaction (PCR) based markers that included, Phaseolin marker and 22 fluorescently labeled microsatellites (SSRs) in the laboratory at University of California, Davis, U.S.A. The level of morphological variation estimated using the Shannon Weaver diversity index (H), ranged from 0.47 to 0.58 with an overall mean of 0.56 ± 0.19 , an indicator of high genetic diversity. Cluster analysis using Principal component analysis (PCA) showed that all the 320 accessions were morphologically distinct but grouped into three major groups (G1, G2 and G3) with many admixtures between these groups. The genotypes differed mostly for growth habit, pod cross-section, pod curvature, hypocotyl colour, days to flowering, node number on the main stem, number of flower buds, and 100 seed weight. The phaseolin analysis found 49 Mesoamericans and 51 Andeans. The SSR markers used in this study to assess the genetic relationships and structure among genotypes within the gene pools was highly informative with average polymorphism information content (PIC) of 0.8. The model based analysis for the level of population structuring and differentiation found three groups (K3.1, K3.2 and K3.3.) with differences in the phenotypes. The level of genetic differentiation (F_{ST}) among the predicted subpopulations was 0.14, 0.12 and 0.09, which indicate a moderate level of genetic differentiation of beans in Uganda. Comparisons between groups formed by PCA and Structure analyses found some accessions independently grouping in the same cluster regardless of the method used. The Andean genotypes dominating the G1 group correlated to K3.1, G2 and G3 with mostly Mesoamerican genotypes to K3.2 to K3.3 respectively. This study provided the first joint approach involving, morphological and molecular analysis of common bean germplasm in Uganda. It sets the stage for further analyses and conservation of the genetic diversity for agronomic traits such as yield and resistance to biotic and abiotic stresses.