

## GENETIC DIVERSITY AND RELATIONSHIPS AMONG 192 PUBLIC COMMON BEAN INBRED LINES ASSESSED BY SSR MARKERS

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Knowledge of germplasm diversity and of relationships among elite breeding materials has a significant impact on the improvement of crop plants and on the development of strategies for genetic resources management and exploration. The present study was conducted to determine the level of genetic variation and relatedness among some selected common bean varieties by using microsatellite markers. In this investigation, we used 61 SSRs to fingerprint 192 common bean inbred public lines released over the last 50 years in the U.S.A. All the lines are commercial seed type classes that are grown in the USA and include both dry bean classes and snap beans for the fresh and processing markets. The 344 alleles identified were used as raw data for estimating the amount of diversity and to describe the genetic structure of the commercial bean gene pool. A model-based clustering analysis placed the varieties in six clusters that correspond to major breeding groups plus a set of lines showing evidence of mixed origins. Neighbor-joining tree was constructed to further assess the genetic structure of common bean lines, showing good agreement with the pedigree information and the cluster analysis. A significant fixation index  $F_{ST}$ , also revealed genetic substructure within the U.S. common bean gene pool with Kidney and Pinto-Great Northern beans being the most different from the other varietal groups. The results of this study - based on a much larger number of SSRs - confirm a previous observation indicating a relatively low level of genetic variation and a molecular variability that parallels phenotypic characters distinguishing different commercial groups. Our results indicate also a strong subpopulation structure and provide additional tools for breeding and breeder's rights implementation.