



Molecular characterization of high performance inbred lines of Brazilian common beans

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ABSTRACT. The identification of germplasm genetic variability in breeding programs of the common bean (*Phaseolus vulgaris*) is essential for determining the potential of each combination of parent plants to obtain superior genotypes. The present study aimed to estimate the extent of genetic diversity in 172 lines and cultivars of the common bean by integrating five tests of value for cultivation and use (VCU) that were conducted over the last eight years by the breeding program of Embrapa Arroz e Feijão in Brazil. Nine multilocus genotyping systems composed of 36 fluorescent microsatellite markers distributed across 11 different chromosomes of the common bean were used, of which 24 were polymorphic. One hundred and eighty-seven alleles were identified, with an average of 7.79 alleles per locus and an average gene diversity of 0.65. The combined probability of identity for all loci was 1.32×10^{-16} . Lines that are more genetically divergent

between the selection cycles were identified, allowing the breeding program to develop a crossbreed between elite genotypes with a low degree of genetic relatedness. H_E values (ranging from 0.31 to 0.63) and the genetic differentiation among the VCU tests (F_{ST} of 0.159) supports for new strategies to increase the genetic base from which the program is conducted. Private alleles (26%) were identified and can be directly incorporated into the gene pool of cultivated germplasm, thereby contributing effectively to the expansion of genetic diversity in this bean-breeding program.

Key words: *Phaseolus vulgaris*; Breeding; Genetic diversity; SSR markers