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NUCLEOTIDE DIVERSITY IN WILD AND DOMESTICATED *PHASEOLUS VULGARIS* L. FROM MESOAMERICA

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The common bean (*Phaseolus vulgaris*) is a diploid (2n = 2x = 22), annual species that is predominantly self-pollinating and is the most important grain legume for direct human consumption. For *P. vulgaris*, many aspects of its molecular and phenotypic diversity, migration dynamics and population structure are well known. To date, in contrast, little information is available on the level and extent of its nucleotide diversity. The common bean was domesticated independently in Mesoamerica and in the Andes, and the largest diversity of its wild and domesticated forms is found in Mesoamerica, where a single domestication event is believed to have occurred. The main aims of the present study were to develop SNP markers and to identify genes and genomic regions that are related to the adaptive processes during domestication of *P. vulgaris*. We developed 30 primer combinations to amplify and sequence the orthologous counterparts of genes previously studied in wild and domesticated soybean. All of the primer combinations were used for a preliminary selection of 10 loci. A sample of 24 genotypes was developed to represent the wild and domesticated Mesoamerican populations (18), including six additional genotypes from the Andean and phaseolin I gene pools. Here, we present and discuss the results from the sequencing of 15 gene fragments (including five loci previously identified as potentially under selection during the domestication process in Mesoamerica).