

THE EFFECT OF SELECTION ON LOCI WITHIN CLOSE PROXIMITY OF DOMESTICATION LOCI IN COMMON BEAN (*PHASEOLUS VULGARIS* L.)

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Identifying regions of the genome that have been the targets of selection will provide important insights into the evolutionary history and facilitate the identification of important agronomic genes. The structure of genetic diversity of modern crops is deeply influenced by the processes of domestication and plant breeding. Both domestication and plant breeding reduced genetic diversity due to random genetic drift (bottlenecks) and because of selection for target genes. World-wide common bean (*Phaseolus vulgaris* L.) is the most important source of proteins for direct human consumption, and the identification of genes of agronomic importance may facilitate improved productivity and quality of this important crop. We sequenced gene fragments spanning 6 cM of a genomic region of the linkage group B8 where several major QTLs related to the domestication syndrome have been previously located. We compared three sets of accessions representing the various stage of common bean improvement (wild, landraces and improved cultivars). Gene fragments representing other genomic regions were sequenced for comparison. Overall, we analysed 48 genotypes chosen on the basis of SSR data in order to represent the largest diversity within each set of accessions. We performed several statistical tests to identify the signature of selection due to domestication and crop improvement. This research is very promising because we may be able to identify genes of potential agronomic importance and to determine the effect of domestication and breeding on the structure of genetic diversity in the common bean genome.