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WHOLE-GENOME SCAN FOR THE SIGNATURE OF SELECTION IN *PHASEOLUS VULGARIS* L.

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The molecular screening of the whole genome for the signature of selection is a very promising approach to identify genes and genomic regions with adaptive role. "Natural selection mapping" or "Genomic scans for the signature of selection" can be useful in order to validate the role of previously identified genes of agronomic importance or to identify genes or genomic regions without any prior information. Here, we present the map-based analysis of genetic diversity in wild and domesticated accessions of Andean and Mesoamerican *Phaseolus vulgaris* L. (common bean) using different classes of molecular markers: chloroplast SSR, AFLPs, and STS. AFLP and STS have been mapped in the *P. vulgaris* core map BAT93 x Jalo EEP558, in which several genes and QTLs of agronomic relevance have already positioned, including loci involved in the domestication syndrome. Several statistical methods were used in order to identify loci that show a pattern of diversity and divergence departing from neutral expectations. The map location of these outlier loci were compared with the positions of the genes and QTLs already available in the consensus map allowed an indirect validation of the result. Our results show that, in common bean, the genome-scan approach is a very promising approach to map and identify genes of interest.