

ISLANDS OF DOMESTICATION IN THE COMMON BEAN (*PHASEOLUS VULGARIS* L.) GENOME

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AFLP, domestication, Phaseolus vulgaris, population genomics, selection

The main aim of this study was to use an AFLP-based, large-scale screening of the whole genome of *Phaseolus vulgaris* L. to determine the effects of selection on the structure of the genetic diversity in wild and domesticated populations.

We first used pooled DNA samples, seven each of wild and domesticated populations of *P. vulgaris* were studied using 2,506 AFLP markers (on average, one every 250 kb). About 10% of the markers were also analysed on individual genotypes and were used to empirically infer allelic frequencies from bulk data. In both datasets, we tested the departure from neutral expectation for each marker using an F_{ST} -based method.

Moreover, we tested with 19 AFLP primer combination a large set of accession from the three known gene pool of *P. vulgaris* (Andean, Mesoamerican and ancestral) in order to highlight the signature of selection under domestication within and between gene pools.

The most important outcome is that a large fraction of the genome of the common bean appears to have been subjected to effects of selection during domestication. We also mapped and classified the markers obtained in individual genotypes according to their proximities to known genes and QTLs of the domestication syndrome. Most of the markers that were found to be potentially under the effects of selection were located in the proximity of previously mapped genes and QTLs related to the domestication syndrome.

Overall, our results indicate that domestication appears to have affected not only target genes, but also a large portion of the genome around these genes. These “domestication islands” have probably experienced a higher level of isolation between the wild and the domesticated forms in comparison with the rest of the genome probably because of linkage to the loci selected during domestication.

Thus, the regions of the genome surrounding the major domestication genes are particularly interesting to tag the introgression from wild relatives into modern cultivars

As most of the markers that are under the effects of selection are linked to known loci related to the domestication syndrome, we conclude that population genomics approaches are efficient in

detecting QTLs. We also present a method based on bulk DNA samples that is effective in pre-screening for a large number of markers to determine selection signatures.