

## UTILIZATION OF WILD GERMPLASM FOR PLANT BREEDING IN COMMON BEAN (*PHASEOLUS VULGARIS* L.)

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Random genetic drift and selection during domestication and plant breeding have strongly reduced the level of genetic variation in modern crops. Recently, the work conducted in tomato and rice has shown that the use of wild relatives associated with the use of molecular tools could have a tremendous impact on crop improvement. However, several problems are associated with the introduction of exotic germplasm such as the occurrence of deleterious traits that tend to mask useful variants, the presence of various level of incompatibility between domesticated crops and their wild relatives, and the need to develop an efficient identification system of the most promising wild genotypes to build segregating populations. For autogamous species, in particular, the regions of the genome surrounding the major domestication genes appear to be particularly interesting to tag the introgression from wild relatives into modern cultivars. Because of the combined action of selection and recombination, these “domestication regions” have probably experienced a higher level of isolation between domesticated and wild forms. Indeed, farmers and breeders selecting for domesticated alleles, have probably selected also against tightly linked genes. As shown recently in *P. vulgaris*, the domestication regions of the genome appear to harbour a much higher level of genetic variation in the wild populations in comparison with other regions not involved in domestication. To develop breeding strategies aimed at exploiting wild germplasm, the following elements are needed: a deep understanding of the population history and structure of both domesticated and wild populations, the identification of the loci that have been the target of selection during domestication and breeding episodes, and knowledge of the level and structure of diversity along the genome. Here we present an ongoing project aimed at utilizing the genetic diversity of wild *P. vulgaris*. This project includes the analysis of the genetic diversity using various molecular tools, the identification of genomic regions related to the domestication process, the identification of a set of wild genotypes to be used as donors parents and the analysis of segregating populations for QTL analysis, in the short term, and breeding purposes, in the longer term.