

DEVELOPMENT AND GENOMIC CHARACTERIZATION OF A COMMON BEAN SEGREGANT POPULATION TARGETING DOMESTICATION TRAITS

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To capitalize the benefits of genetics in crop improvement, geneticists and breeders need to identify genes and molecular variants responsible for phenotypic variations, and to map them on the genome of the targeted crops. The domestication process of plants and animals represents not only a milestone in the history of the human being but it is also a unique tool for the study of evolutionary processes, and a crucial model to discover genes and genomic regions related to important agronomic traits and to exploit the genetic diversity of the wild relative. Many studies have clearly indicated that the use of wild relatives can have a tremendous impact on crop improvements.

For the reason above we have developed an introgression population segregating for domestication syndrome traits in the common bean, *Phaseolus vulgaris*. The wild donor was the Mesoamerican wild G12873 from Molerols (Mexico), while the recurrent parent is the Andean variety Midas. Here we present the genomic characterization of this population obtained by using a combination of Next Generation Sequencing techniques.