

POPULATION STRUCTURE AND LINKAGE DISEQUILIBRIUM IN COMMON BEAN (*PHASEOLUS VULGARIS* L.)

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Common bean (*Phaseolus vulgaris* L.) is the world's most important grain legume for direct food consumption, especially in Latin America and Africa. Although little is known about its genomic organization, the evolution and domestication history of this species that has been intensively studied over the last few years.

P. vulgaris is thought to have originated in a region encompassing Ecuador and northern Peru, and dispersed both northwards and southwards establishing the Mesoamerican and Andean gene pools, respectively. Independent domestication took place in these two gene pool.

The main objectives of this study were to (1) investigate genetic diversity within and among populations of common bean, (2) examine the population structure, and (3) determine the extent and genomic distribution of Linkage disequilibrium (LD) using AFLP markers.

We have analyzed the DNA of 199 genotypes of *Phaseolus* from the three known gene pool (Andean, Mesoamerican and Ancestral) with 418 AFLPs fragments resulting from 19 primer combinations.

Population structure was investigated using different model-based inference framework. Overall, a clear separation was found between Andean and Mesoamerican gene pools. Moreover the results showed a very high level of LD in domesticated compared to the wild forms in both Andean and Mesoamerican gene pools.