

## ORIGINS AND DOMESTICATION OF *PHASEOLUS VULGARIS*, AS REVEALED BY CHLOROPLAST AND NUCLEAR MOLECULAR MARKERS

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### *Phaseolus vulgaris*, domestication, plastidial and nuclear diversity

The common bean (*Phaseolus vulgaris* L.) is the most important legume for direct human consumption, and in some countries it is the primary source of protein in the human diet. From a population genetics perspective, the major subdivisions of wild common bean progenitors are known, and the domesticated gene pools have been defined. Two major domestication events, one in Mesoamerica and the other in the southern Andes, appear to have resulted in the Mesoamerican and Andean gene pools that mirror the geographic distribution of the wild progenitors. In the present study, we have analyzed 190 genotypes of *P. vulgaris*, which are representative of all of the different gene pools and forms (wild and domesticated). All of the individuals were analyzed using 17 chloroplast microsatellites (cpSSRs); due to their relatively high levels of polymorphism and their generally uniparental inheritance, cpSSRs represent a useful tool for the study of genetic variation and evolution in plants. A subset of 131 genotypes was also analysed by nuclear markers, such as AFLP (300 polymorphic markers), distributed along the whole genome, and two STS designed on the genomic sequence of *Pv*-SHATTERPROOF1, which is similar to SHATTERPROOF1 of *Arabidopsis thaliana*. The results are discussed in relation to the origins and domestication of *Phaseolus vulgaris*.