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Poster Abstract - B.10

MOLECULAR AND GENETIC DIVERSITY OF A GENOMIC SEQUENCE SIMILAR TO *SHATTERPROOF* (*SHP1*) IN *PHASEOLUS VULGARIS* L.

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Compared with their wild progenitors, domesticated crops show marked phenotypic differences even if they belong to the same biological species. These differences, known as the domestication syndrome, results from selection for adaptation to cultivates environments. One of the key traits of the domestication syndrome is the seed dispersal mechanism (shattering), which was lost in common bean and in many other domesticated species. Two MADS-box genes involved in the control of silique shattering have been identified in *Arabidopsis thaliana* (*SHP1* and *SHP2*). Based on EST sequences, we identified in *Phaseolus vulgaris* two genomic sequences similar to *SHATTERPROOF* (*SHP1*) of *Arabidopsis thaliana*. We were also able to amplify and sequence a single product (*PvSHP1*) from several genotypes of *Phaseolus* spp. and a few other legumes, which appears to be an interesting sequence for phylogenetic studies. We developed two markers spanning indels that were used to locate the identified sequence on the *Phaseolus vulgaris* core linkage map (BAT93 X Jalo EEP558) and study its molecular diversity in a larger sample of wild and domesticated accessions from both Andean and Mesoamerican gene pools.

Current work in progress includes a study of the gene expression of Pv*SHP1* and identification of other candidate genes potentially involved in seed dispersal in *P. vulgaris*.