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INTRA - AND INTER-SPECIES VARIABILITY AND GENETIC RELATIONSHIPS IN WILD AND CULTIVATED BEANS FROM MEXICO

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Beans (Phaseolus spp.) and maize are major staples in Mexican food. Studying the genetic diversity of wild and cultivated Phaseolus species is a major challenge for conservation and exploitation. We suggest that new information should contribute to improving our knowledge of intra and inter-species genetic variability as well as the genetic relationships among domesticated species of Phaseolus in México. In addition, the increased knowledge could improve the conservation of Phaseolus genetic resources throughout Mexico and provide a global overview of the importance of an integrative use of Phaseolus in common bean breeding (Hernández-Delgado et al., 2015). This work had two aims: to characterize the genetic variability among and within four domesticated species of Phaseolus, and to estimate the relationship and genetic structure of populations in germplasm of P. acutifolius, P. coccineus, P. lunatus and P. vulgaris.

The intra- and inter-species variability and genetic relationships in germplasm from P. acutifolius, P. coccineus, P. lunatus, and P. vulgaris was analyzed. Twelve accessions of each species were collected from throughout Mexico and compared with the following controls: P. albescens, P. coccineus subsp. striatus var. purpurascens, P. parvifolius, and P. xolocotzii as well as the bred cultivars (P. vulgaris) Negro Jamapa, Negro Papaloapan, Pinto Centauro, and Pinto Coloso. Germplasm was analyzed with 15 simple sequence repeat (SSR) markers, six genic and nine inter-genic, which amplified 292 alleles (225 intergenic and 67 genic markers). Values of expected (Hₑ) and observed (Hₒ) heterozygosity per accession and SSR were calculated, and Molecular Analysis of Variance (AMOVA) was performed. Genetic structure of populations and coancestry values were determined using STRUCTURE V 2.3.3 (Pritchard et al., 2010) and STRUCTURE HARVESTER V 0.6.92 (Earl and vonHoldt, 2011).

No associations among genetic and geographic distances were identified. In total, 74% of the molecular genetic variance was identified within species with the other 26% identified among species; genetic differentiation among species was high (FST = 0.26). Population structure analysis (Fig. 1) indicated robust clustering by each species and controls; however, species P. lunatus and P. vulgaris were more closed as P. acutifolius and P. coccineus. Between these two groups were located the controls and (P. xolocotzii, P. albescens, P. coccineus subsp. striatus var. purpurascens, P. parvifolius, and bred controls). Hamann et al. (1995) reported increased intra-specific variation in P. vulgaris and P. lunatus compared with P. coccineus and P. acutifolius. Angioi et al. (2009) used chloroplast simple sequence repeats (cpSSR) to analyze the domesticated species of Phaseolus (vulgaris, coccineus, lunatus, acutifolius and dumosus) and found a clear separation of each species, particularly P. coccineus from all others with a particularly close relationship between P. vulgaris and P. dumosus. Our results confirmed the hypothesis that P. vulgaris exhibits the highest values of genetic variability compared with the
other three species, *P. coccineus*, *P. acutifolius* and *P. lunatus*, based on allele range and heterozygosity values. In addition, wild *Phaseolus* germplasm collected throughout México exhibits increased genetic variability than bred *P. vulgaris* germplasm.

**Fig. 1.** Graph of the Bayesian population structure of Mexican *Phaseolus* species (*K* = 5), where each bar represents an individual accession. Each color represents membership coefficient groups determined using the Structure software package, version 2.3.1 (Pritchard *et al.*, 2010).

**REFERENCES**