

Studies in *Phaseolus* germplasm diversity: a review of work at CIAT

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Both wild and cultivated *Phaseolus* germplasm were characterized over several years using RAPD and/or AFLP to determine the genetic structure of the species and the association of genetic structure with phenotypic traits. In most cases, multivariate analysis was carried out using Multiple Correspondence Analysis (MCA), which adjusts the weight of each datum inversely to its frequency in the population. For present purposes this implies that rare DNA polymorphisms that occur together get especially high value in the analysis, a phenomenon that is interpreted evolutionarily as reflecting descent from a common ancestor.

A core collection of wild *P. vulgaris* was created, based on geographic distribution and seed protein classification of phaseolin, lectins and alpha-amylase inhibitors (Tohme et al, 1996). A total of 114 accessions were analyzed by AFLP. Reported gene pools of Andean, Mesoamerican and northern Andean (Ecuador and northern Peru) origins were recognized, and additional diversity was found in Colombia, suggesting a fourth wild bean gene pool. This latter pool has been incorporated into a breeding program together with other wild accessions, and one Colombian accession appears to have contributed yield genes that are expressed in the temperate region of the United States (J. Kelly, pers. comm., 2002). Wilds from Guatemala separated only slightly from Mexican wilds, but relatively discreet groups were observed in the Andean pool. It is suggested that the rugged Andean terrain serves to isolate genetic groups more effectively than the topography of Middle America.

Diversity in cultivated bean as revealed by RAPD analysis mirrored the structure of the wild bean gene pools and was largely consistent with results reported by other authors. Two major gene pools, one Middle American and one Andean, were revealed (Gepts et al, 1986). Within the Middle American gene pool, races Durango, Jalisco and Mesoamerica were distinguishable, and groups formed by DNA analysis were consistent with morphological traits associated with these races (Singh et al, 1991). However, a fourth race was distinguished among climbing beans in the south of Mexico and in Guatemala, which separated from race Jalisco climbers in the MCA (Beebe et al, 2000). This race was designated as race Guatemala and was characterized by having several sources of resistance to angular leaf spot. G2333, a widely studied source of anthracnose resistance, also pertains to this race. The distinction of races Jalisco and Guatemala may reflect the a geographical separation created by the isthmus of Tehuantepec in southern Mexico, with a maximum altitude of about 1000 m above sea level

Furthermore, some internal structure was distinguished within races Mesoamerica and Durango (Beebe et al, 2000). Race Mesoamerica separated into two closely related subgroups, one designated M1 that consisted of type 2 habit genotypes (largely black seeded) and one with wide diversity in seed color and type 3 growth habits. Race Durango presented two subgroups with differences in seed size, color and growth habit. Sub-group D1 represented the more commercial types, while subgroup D2 presented less attractive (black or cream) colors, and more type 4 growth habits.

The Andean pool of cultivated bean displayed a surprisingly narrow genetic base (Beebe et al, 2001). Thus, races in the Andean pool have a different meaning that in the

Middle American pool, and reflect relatively few loci that govern physiological adaptation and growth habit, and not broad evolutionary patterns at the genome level. However, about 10% of accessions from the Andean zone that were assumed to be Andean types based on typical Andean phaseolin, presented significant introgression from Mesoamerican beans. Furthermore, this introgression was associated with detectable changes in phenotype. It is suggested that this phenomenon has implications when screening Andean germplasm for superior traits, for example, for disease resistance genes. One must be careful when assuming that genes are Andean in origin, since elite accessions might in fact contain introgression from Middle American beans.

The northern Andes and especially Colombia, is a region with a very complex genetic structure of common bean. Here one can find land races of both major gene pools that have been cultivated for many generations, introgressed types, local wild populations, and local domesticates. A wild-weedy-crop complex permits gene flow among all these groups (Beebe et al, 1997). Evidence suggests an incipient northern Andean cultivated pool, based on a broad analysis of morphological and biochemical traits (Islam et al, 2001a), and which presents a pattern of reaction to pathogens more typical of Andean beans (Islam et al, 2001b). A few accessions of cultivated bean are to be found with phaseolin types that are typical of Colombian wild beans (CH and L; Beebe et al, 1997).

Physiologically, *Phaseolus* from lower latitudes including Colombia and the northern Andes would appear to be quite different from accessions from Mexico or Argentina. At higher latitudes photoperiod response governs flowering of wild bean but no such daylength difference exists to stimulate flowering at low latitudes. We do not understand what stimulates flowering in this environment, but locally collected wild beans in Colombia are notoriously difficult to bring to flower in Colombia. Locally collected *P. polyanthus* shows a similar phenomenon with regard to difficulty of flowering and seed production in Colombia, and also separates from Middle American accessions in an analysis of AFLP. These observations highlight a knowledge gap with regard to *Phaseolus* genetic resources from low latitudes.

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