OUTCROSSING IN MEXICAN WILD AND DOMESTICATED POPULATIONS OF COMMON BEAN

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Gene flow is one of the major evolutionary factors shaping the organization of genetic diversity in gene pools from crop or wild plants. In the case of common bean, gene flow between wild and domesticated beans may be responsible for the racial diversification observed in the two cultivated gene pools. The marked reduction in genetic diversity induced by domestication (Sonnante et al. 1994) could be alleviated at least partially by gene flow from wild beans. Conversely, gene flow from domesticated to wild beans could displace gene from local adaptation in wild beans and, by displacing wild bean alleles, represent a genetic “contamination” of the wild gene pool. Finally, gene flow from domesticated to wild beans is a necessary, although not sufficient condition for escape of transgenes. It has been proposed that such escape might increase the potential weediness of wild crop relatives. In spite of its importance, gene flow has often been neglected in genetic diversity. This can be attributed to technical difficulties such as identifying the appropriate markers capable of differentiating between wild and domesticated types and distinguishing similarities due to gene flow from those due to common ancestry.

Common bean is generally considered to be a predominantly self-pollinated species. All estimates of outcrossing published so far were obtained from sites outside actual domestication centers of the crop (reviewed in Ibarra-Perez et al. 1997). In the experiments presented here, we have investigated whether bean germplasm from Mexico has been shaped by gene flow between wild and domesticated. In a first experiment, we sought to construct a dendrogram of AFLP diversity in a sample of Mexican wild and domesticated beans representative of their distribution in that country. We reasoned that if gene flow were prevalent, we would observe a series of regional clusters, containing wild and domesticated types from the respective regions. If, on the contrary, gene flow were very limited we would observe separate clusters for wild and domesticated beans. In fact, we observed the latter topology for the tree, suggesting that gene flow might not have played an important role in shaping bean genetic diversity. Closer inspection of the dendrogram, however, showed that a number of wild and domesticated forms from the Sierra Norte of the state of Puebla clustered together. This observation raised the possibility that under certain local conditions gene flow migh actually take place.

In a second experiment, we therefore examined more closely the genetic diversity of wild and domesticated P. vulgaris from the Sierra Norte of Puebla. In that region, the two types grow together within the same field. Genetic diversity was assessed with Inter Simple Sequence Repeats (ISSR) (Gonzalez et al. 1998). ISSRs proved to be a desirable marker type as they were able to distinguish wild from cultivated beans, four local landraces among themselves, and individuals within populations. A dendrogram showed separate clusters for wild and domesticated beans, again suggesting that gene flow might be fairly limited. However, some subclusters in the general cultivated cluster suggested that gene flow might actually be taking
place. We therefore decided to analyze the data in a different way by investigating individual markers especially those that were predominantly homozygous recessive (i.e., no ISSR band). We assumed that individuals that showed a dominant allele (i.e., a ISSR band) had experienced an outcross at some stage in their pedigree. The power of this analysis was increased by combining data from several loci (approximately 15 per population). Depending on the threshold chosen for homozygous recessiveness, outcrossing levels thus determined ranged from 20-55% (90% recessive homozygosity) or around 20% (95%). Two reasons can be proposed for these relatively high outcrossing levels. First, these represent outcrossing events accumulated over many years of sympatry. Kaplan and Lynch (1999) have recently revised the dates for Mesoamerican archaeological remains to 2500 years BP. Although we do not know for how long the wild and domesticated beans from Puebla have been grown together, beans are a traditional crop grown by náhuatl (Aztec)-speaking natives suggesting that there has been plenty of opportunity for gene flow. Second, P. vulgaris is grown with two other, outcrossing species, P. polyanthus and P. coccineus. The latter species may play a major role in attracting insect pollinators such as bumblebees inside the fields. Once in the fields, these pollinators may be less discriminating and may pollinate selfing and outcrossing species alike.

Because wild beans grew exclusively within fields in Puebla, there was no opportunity to investigate the role of spatial separation. A third experiment was then conducted with materials recently collected in Chiapas. In this state of Mexico, wild beans grow under different regimes of spatial separation from domesticated beans: within the same field, at the edge of fields, and separated from fields. A dendrogram based on AFLP diversity again showed a separation between wild and domesticated beans even for materials that grow within the same field and with the same phenology. Taking a cue from our results in Puebla, we reanalyzed the marker data based on individual marker data. This time, however, we established three categories of AFLP markers: those linked to genes of QTLs for domestication (Koinange et al. 1996), those linked to genes or QTLs controlling traits other than those of domestication (Nodari et al. 1993; unpubl. data), and those apparently unlinked to any genes. Population genetic parameters showed marked differences between these three categories of markers. The maximum population differentiation (FST) was observed for markers linked to domestication genes, followed by those linked to non-domestication genes. Unlinked genes showed no differentiation. This observation suggested that gene flow is taking place between wild and domesticated beans but that selection after the initial outcross for adaptation to the respective environments (wild or domesticated) counteracts the effects of gene flow. This hypothesis was confirmed by the genetic diversity data (H), which show the strongest reduction of diversity for markers linked to the domestication syndrome.

In summary, our results show that gene flow between wild and domesticated beans is taking place in spite of the predominantly self-pollinated nature of the reproductive system of common bean. In retrospect, our failure to identify outcrossing by multivariate techniques such as dendrograms can be attributed to the large number of markers, which tends to obscure the information provided by a few key markers. Finally, information on map location is a key element in evaluating patterns of genetic diversity.