Introduction

The genetic compatibility between crops and their wild relatives has important implications for conservation of genetic diversity and for the introduction and management of transgenic crops. The gene flow event, distribution of receptor populations, gene transfer effectiveness, and long-term effects (namely in fitness) are being studied in natural populations of common bean in a center of origin and genetic diversity.

Our project has been conducted since 1987 in populations of Phaseolus vulgaris of the Central Valley of Costa Rica with financial support of the Bundesministerium für Wirtschaftliche Zusammenarbeit und Entwicklung (BMZ) of Germany.

Materials and Methods

For the disclosure of wild populations, we applied a technique of ecoregographic surveying (Araya et al. 2001). For the molecular characterization, 2000 individuals were selected based on a morphoagronomic evaluation, and 794 of them were weedy types possibly resulting from gene flow events (González-Torres et al. 2003). We used phaseolin, isozymes and microsatellites as nuclear markers (González-Torres et al., 2004). The gene flow direction was detected by RFLPs-PCR, sequencing and SNPs on chloroplast DNA (Chacón 2001).

Results and Discussion

We documented the geographical distribution of each wild population as well as the biological complexes of "wild-weedy-cultivated" materials (Figure 1b). Twenty-two populations of wild common bean are known for Costa Rica, and distributed in four watersheds in the central part of that country representing at least 90% of the found populations (González Torres et al. 2004).

Figure 1. Distribution of wild common bean in the Central Valley of Costa Rica (base map: IGN-IGN, 1991). Solid square: Reventazón, one population; solid heart: Perís, one population; closed circles: Vírlita north, 3 populations; solid triangles: Vírlita south, 7 populations; crosses: Candelaria north, 8 populations; and closed stars: Candelaria south, 4 populations. Dotted line represents the continental divide, while the other lines limit the different watersheds. Red closed stars: Distribution of complex weedy-cultivated. The results obtained in the characterization of the populations are summarized in Table 1. The red underline fonts are ‘wild’ characteristics and the green fonts are ‘cultivated’ characteristics. The blue fonts are specific characteristics found in a biological status.

The data analysis showed that 98% of the putative hybrids were indeed hybrid. The direction of gene flow was mainly wild pollen towards the cultivated materials (82%). However, the other direction was observed at lower frequency but as significant percentage. The gene flow was mostly in materials belonging to the Mesoamerican gene pool (the one prevailing in the area). However, outcrossing between Mesoamerican and Andean gene pools were identified in 8% of the weedy individuals (Figure 2). The figure 2 demonstrates repeated events of gene flow of wild pollen toward cultivated forms (individuals 1 to 3). Individual 4 has been events of repeated outcrossings resulting a weedy with nuclear genome of a wild form biological form with cytoplasmic genome of the cultivated (Chloroplast capture); however, it keeps a high seed weight as a cultivated type.

![Table 1](image)

Table 1. Morphological, biochemical and molecular markers used and No. individuals analyzed for each parameter

![Figure 2](image)

Figure 2. Graphic representation of markers used on a selection of individuals

The individual 6 illustrates a case of outcrossing between Andean and Mesoamerican genepools. It has a chloroplast haplotype ‘Mesoamerican cultivated’ and phaseolin Andean type. In contrast with its SSR alleles are ‘wild’ and ‘cultivated’.

Our results provide an update about the distribution of wild common bean in Costa Rica, its ecology and conservation status. In addition, they allowed us to reliably establish the existence of simple or complex events of gene flow among different biological forms. Obviously, domestication has not yet altered the reproductive system of common bean up to prevent gene exchange between such forms. This in turn is also important for the production of certified seeds, or the management of genetic resources on-farm.

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Literature Cited


