Gene flow events in Phaseolus vulgaris and among species of section Phaseoli along their distribution range

R.I. González-Torres2, M.C. Duque2, O. Toro1, R. Araya3, D.G. Debouck1 & J. Tohme2
CIAT 1Genetic Resources Unit, 2Biotechnology Research Unit, AA 6713 Cali COLOMBIA; 3EEFBM Universidad de Costa Rica COSTA RICA

Introduction

Although common bean has long been considered as an autogamous plant, it can outcross naturally with its wild relative or even with sister species leading to the formation of complexes “wild-weedy-cultivated”. With the aim to evidence the gene flow event, its direction, and their implications on genetic biodiversity, genetic resources conservation, and for the introduction and management of transgenic crops in centers of origin. In addition, we present evidence of gene flow events among bean species (Phaseolus ssp.) in natural conditions of Colombia and Costa Rica.

Materials and Methods

We evaluated 715 wild types, 413 cultivated types, and 901 weedy types belonging to natural complexes from Oaxaca (México), El Progreso (Guatemala), San José (Costa Rica), Boyacá (Colombia), Azuay (Ecuador), Apurímac (Perú) and Tarija (Bolivia).

We evaluated a total of 150 materials probably resulting from interspecific hybrids and 21 materials as controls of possible species involved in gene flow events with 56 nuclear SSR (González-Torres et al., 2006).

Results and Discussion

Gene flow events on Phaseolus vulgaris

The data analysis showed that 98% of the individuals were indeed hybrids. The results showed the diversity of chloroplast haplotypes in elements of the complexes and the direction of the flow. The wild and cultivated populations were characterized with such markers allowing then to infer about weedy individuals. The main direction was that of wild pollen towards cultivated materials, although the other direction was also evidenced at lower frequency in many places.

In addition, we present evidence of gene flow events among bean species (Phaseolus ssp.) in natural conditions of Colombia and Costa Rica.

In addition, 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.

Gene flow events among species of section Phaseoli along their distribution range

The microsatellites were powerful enough to separate the species though they belong to the same evolutionary phylum. The characterization of the different bean species through microsatellite loci evaluation according to Gaitán-Solís et al. (2002) is confirmed and extended to P. albescens and P. costaricensis for the first time. The molecular markers indicated that the putative natural interspecific hybrids actually were hybrids (González-Torres et al., 2006).

Figure 2. Multiple correspondence analyses (MCA) of morphological, biochemical and molecular markers used to understand the population structure and its dispersion.

Figure 3. A. Specific microsatellites characterizing each species and observed in the evaluated interspecific hybrids. Loci of microsatellites BM181 show different allelic forms in all species and the shared alleles in hybrids individuals between P. vulgaris and P. dumosus. B. Spatial distribution of individuals using multiple correspondence analyses.

The data indicate that the evaluated hybrids result from gene flow between the common bean and P. dumosus (as pollen donor) in the Central Valley of Costa Rica as well as in Boyacá, Colombia. A different allelic frequency, namely of P. dumosus, suggests that the hybrids are of different generations. The cluster obtained using MCA established the hybrid group structure. This group is spatially near to P. vulgaris and P. dumosus indicating that the evaluated loci have been a recombination among these species by gene flow events. The natural interspecific hybrids are rare, and their reduced fertility might imply that the species of this phylum are “good biological species”. They can be valued as natural genetic bridges in improvement programs (Singh 2001).

Acknowledgments

The field and lab activities have been supported by grants of BMZ, Germany.

Literature Cited