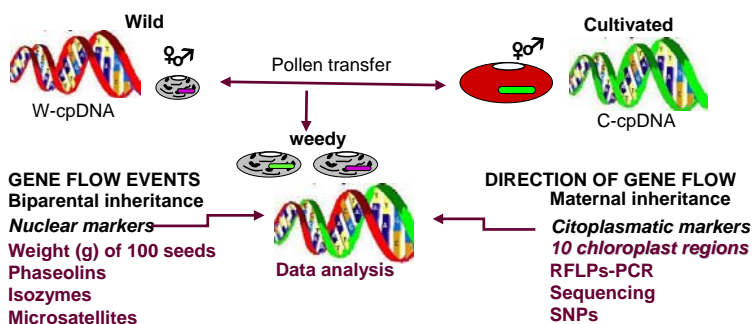


Introduction

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* spp.) 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), Apurimac (Perú) and Tarija (Bolivia).



In addition, we selected a total of 150 materials probably resulting from interspecific hybridizations 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*

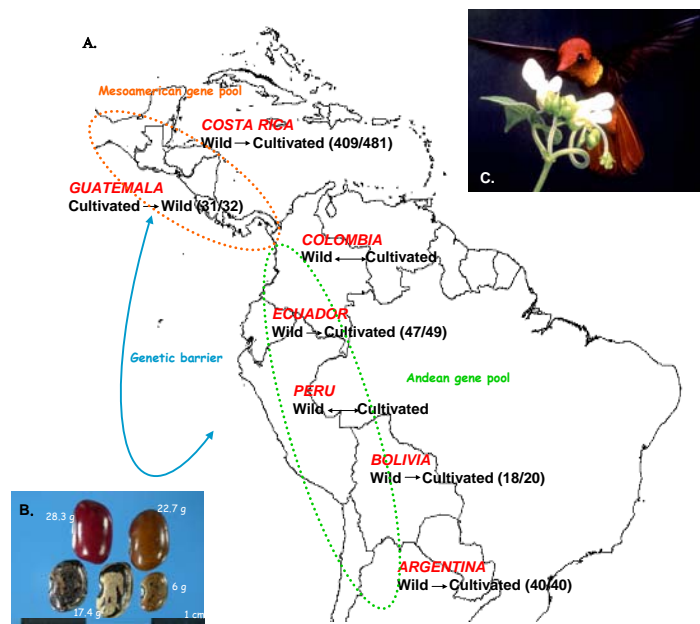
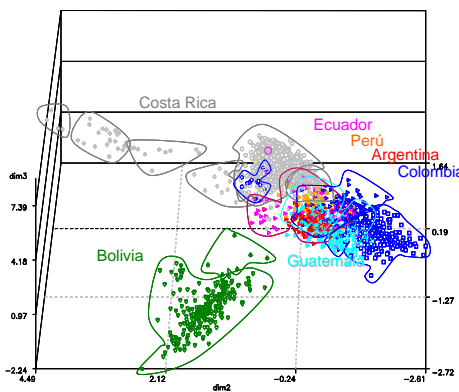


Figure 1. A. Found directions of gene flow and their frequencies through the geographical range of common bean. B. Possible wild-weed-crop complex. The weedy materials are not typical cultivated or wild beans. They are intermediate genetically as result of gene flow events among cultivated and wild types. C. Humming-bird pollinating a flower of common bean

The data analysis showed that 98% of the individuals were indeed hybrids. The results shown 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.



The gene flow was mostly in materials belonging to the Andean gene pool. However, outcrossing between Andean and Mesoamerican gene pools were evidenced in 12% of the weedy individuals

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

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).

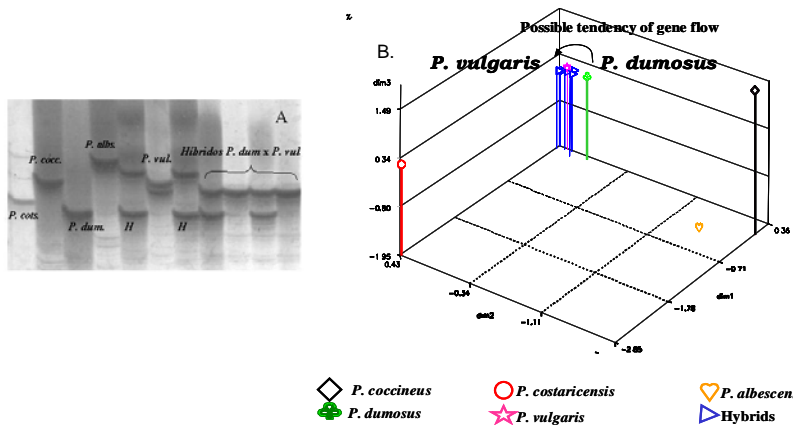


Figure 3. A. Specific microsatellites characterizing each species and observed in the evaluated interspecific hybrids. *Loci* of microsatellites BM181 show different allelic forms in all species and the shared alleles in hybrids individuals between *P. vulgaris* and *P. dumosus*. B. Spatial distribution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

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