

Gene flow and its effect on agrobiodiversity: Common bean as a model for future considerations in biosafety

González-Torres¹, R.I., Araya-Villalobos² & D.G. Debouck¹

¹Genetic Resources Unit, Centro Internacional de Agricultura Tropical, AA 6713, Cali, Colombia ² Estación Experimental FBM, Universidad de Costa Rica, Apartado 183-4050, Alajuela, Costa Rica
✉ rgonzalez@ciat.or.cr

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 ecogeographic 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).

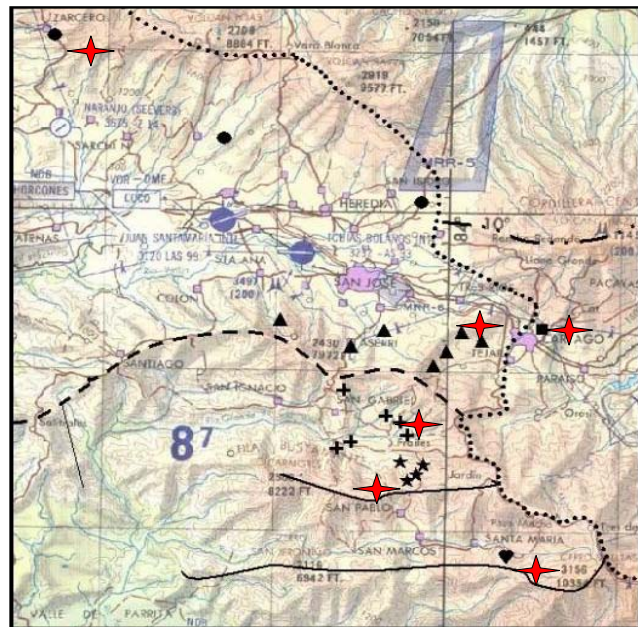


Figure 1. Distribution of wild common bean in the Central Valley of Costa Rica (base map: IGN-DGAC, 1991). Solid square: Reventazón, one population; solid heart: Pirris, one population; closed circles: Virilla north, 3 populations; solid triangles: Virilla south, 7 populations; crosses: Candelaria north, 6 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 wild-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 evidenced 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.

Tropentag 2005

International Research on Food Security, Natural Resource Management and Rural Development
University of Hohenheim, Stuttgart
Centre for Agriculture in the Tropics and Subtropics
October 11 - 13, 2005
Gießen

Biological form	Seed average weight (g)	Phaseolin type	Isozymes		Microsatellites		Chloroplast haplotype
			Pattern ¹	Allele ²	Primer	Allele	
Wild	6 (2.5-7) N=1399	<u>"S-4"</u> <u>"S"</u> <u>"MI"</u> <u>"S-3"</u> N=907	<u>DIA -1</u> N=229	<u>PRX 100</u> N=197	BM140 BM172 BM175 BM183 BM187 BM188 BM189 BM205 GATS91 N=316	<u>160</u> 80 <u>164</u> 110 <u>165</u> <u>147</u> <u>138</u> <u>122</u> <u>224</u>	H N=540
Weedy	13 (8-21.3) N=794	<u>"C"</u> <u>"CH"</u> <u>"H"</u> <u>"S"</u> <u>"X-7"</u> <u>"S-4"</u> N=548	<u>DIA-1</u> <u>DIA-2</u> <u>DIA-4</u> N=157	<u>PRX 100</u> <u>PRX 98</u> N=182	BM140 BM172 BM175 BM183 BM187 BM188 BM189 BM205 GATS91 N=408	<u>160</u> , <u>177</u> 80 <u>164</u> , <u>185</u> 110 <u>165</u> , <u>189</u> <u>147</u> , <u>150</u> <u>138</u> , <u>148</u> <u>127</u> , <u>136</u> <u>224</u> , <u>243</u>	G, H J, K, L, F N=669
Cultivated	23 (22-46) N=225	<u>"S"</u> <u>"MI"</u> <u>"X-7"</u> <u>"CH"</u> N=205	<u>DIA -2</u> <u>DIA -4</u> N=64	<u>PRX 98</u> N=29	BM140 BM172 BM175 BM183 BM187 BM188 BM189 BM205 GATS91 N=67	<u>180</u> 80 <u>183</u> 110 <u>189</u> <u>150</u> <u>148</u> <u>136</u> <u>243</u>	J, K, L N=53

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

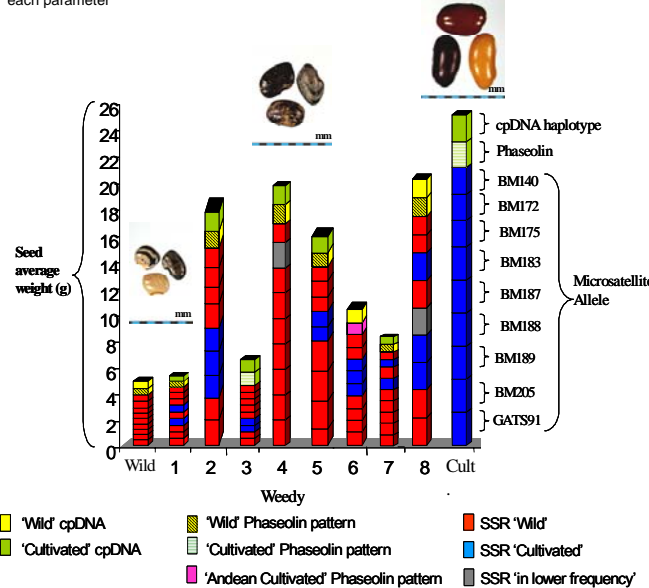


Figure 2. Graphic representation of markers used on a selection of individuals

The individual 6 illustrates a case of outcrossing between Andean and Mesoamerican gene pools. 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.

Acknowledgments

The field and lab activities have been supported by grants of BMZ, Germany. The authors thank specially CONAGEBIO, and Orlando Toro, Myriam Cristina Duque, Cesar Ocampo, Antonio Hernández and Dr. Joe Tohme of CIAT.

Literature Cited

- Araya Villalobos, R., W. G. Gonzalez Ugalde, F. Camacho Chacón, P. Sanchez Trejos & D. G. Debouck. 2001. Genetic Resources and Crop Evolution 48: 221-232.
Chacón Sánchez, Ml. 2001. Ph.D. Thesis. Dep. of Agricultural Botany. Univ. of Reading, UK.
González-Torres RI, E Gaitán, MC Duque, O Toro, C Ocampo, J Tohme & DG Debouck. 2003. BIC 46:1-2.
González-Torres, R.I, E Gaitán, R Araya, O Toro, J Tohme & DG Debouck. 2004. BIC 47:167-168.
González-Torres, R.I, R Araya, E Gaitán & DG Debouck. 2004. Agronomía Mesoamericana 15(2):145-153.