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Gene Flow and its Effect on Agrobiodiversity: Common Bean as a Model for Future Considerations in Biosafety

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Abstract

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, pollination activity and long-term effects (namely in fitness) are being studied in natural populations of common bean in a centre of origin and genetic diversity.

Our project has been conducted since 1987 in populations of *Phaseolus vulgaris* in central Costa Rica with financial support of the Bundesministerium für Wirtschaftliche Zusammenarbeit und Entwicklung (BMZ) of Germany. We documented the geographical distribution of each wild population and the biological complexes of “wild-weedy-cultivated” materials. Twenty-two populations of wild common bean are known for Costa Rica, and distributed in four watersheds in the central part representing at least 90 % of the possibly existing populations.

For the disclosure of wild populations, we applied a technique of ecogeographic surveying. For the molecular characterisation, 1,232 individuals were selected based on a morphoagronomic evaluation, and 417 of them were weedy types possibly resulting from gene flow event. We used phaseolin, isozymes, and microsatellites as markers. The gene flow direction was detected by RFLPs-PCR, sequencing and SNPs on chloroplast-DNA.

The data analysis showed that 98 % of the individuals were indeed hybrids. The direction of gene flow was mainly wild pollen towards the cultivated materials (82 %). However, the other direction was observed at lower but significant percentage. The gene flow was mostly in materials belonging to the Mesoamerican gene pool. However, outcrossing between Mesoamerican and Andean gene pools were evidenced in 8 % of the weedy individuals.

Our results provide an update about the distribution of wild common bean in Costa Rica, its ecology and conservation status. Additionally, 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 *P. vulgaris* 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.

Keywords: Introgression, outcrossing, *Phaseolus vulgaris*, SNPs, SSRs