EVOLUTION OF THE EUROPEAN BEAN FROM THEIR AMERICAN ANCESTORS

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INTRODUCTION

Microsatellite markers have been enough proved to be ideal markers to distinguish the fine-scale relationships within bean gene pools and between lines or populations in many species (Kwan and Gepts 2009, Diaz and Blair et al. 2006, 2007). They may help to reveal the history of bean introduction in the Iberian Peninsula and its widespread to other countries of the Mediterranean area. This research could help to give support, with experimental data derived from microsatellite polymorphisms, to the existence of a new European genetic pool in common bean. Increasing the knowledge about the variability of the Mediterranean bean genotypes is essential in order to select the most suitable for breeding, both for hybridization and selection of lines, from populations. As well as this, it is quite important to gain a better understanding about what part of the genome of bean varieties from the New World are still present in nowadays Mediterranean bean varieties. With this aim, a set of microsatellite markers was analysed in a large and representative set of common bean populations of both American and European origins. Investigation of genetic similarity between populations from both continents made it possible to identify various types of American common bean introduced into Europe at different times or in different places and which have given rise to distinctive intermediate or recombinant types (Santalla et al. 2002).

MATERIAL AND METHODS

The set of analysed populations consisted of a total of 532 of white seeded *Phaseolus vulgaris* accessions collected from different countries of the Mediterranean area, genotypes from America, and the gene pool check controls: ICA Pijao, Calima and California Dark Red Kidney. We have genotyped 62 polymorphic microsatellite markers by standard procedures. The analysis of population structure was accomplished by using STRUCTURE software. The genetic diversity analysis of both the studied loci and groups defined by STRUCTURE software was performed with PowerMarker V3.2. Genetic relationships among entire accessions were analysed by Principal Component Analysis (PCA) using the DARwin 5.0.158 program.

RESULTS AND DISCUSSION

After applying STRUCTURE software to the genotypes of the total set of accessions, Mesoamerican and Andean accessions were defined based on their membership coefficient (MC). Population structure of Mesoamerican and Andean set of accessions was analysed independently running structure at K from 1 to 12 and the optimal values of K were estimated by following the procedure of Evanno and collaborators (2005). K=3 was estimated as an optimal clustering number for each one of Mesoamerican and Andean set of accession. Clusters performed by STRUCTURE in both sets were named as follows: Andean - Nueva Granada/Turkey (which also included the cDRK control), Nueva Granada (NG) accessions (not Turkey NG ), Peru accessions from the whole Mediterranean area-; Mesoamerican – Pure Mesoamerican from South-Western Europe, Pure Mesoamerican from
Eastern Europe and Middle Orient countries and a final group of Intermediate Mesoamerican accessions. PCA of microsatellite diversity showed the genetic relationships among bean Mesoamerican and Andean populations (figure 1) and displayed similar results to those found with STRUCTURE software. As diversity concerns, the lowest values were found for the Nueva Granada/Turkish group (0.37) and the highest differentiation was shown between Eastern and Western Mesoamerican accessions and Turkish ones (0.28). The highest flow (Nm) was found between Mesoamerican accessions from both East and West geographic Mediterranean areas (7.03). The study also highlights the large percentage of accessions that are carrying alleles from both original American pools and the broad genetic diversity shown by European common bean populations.

![Figure 1: Genetic relationships among Andean and Mesoamerican accessions of white seeded common bean from the Mediterranean area.](image)

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