Molecular Characterization and Phylogeny of Thirty Common Bean Varieties

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Molecular characterization of varieties of potential use in research programs involving gene mapping, marker search or plant breeding can facilitate the choice of the most appropriate crosses. It can also be used to develop a phylogenetic analysis that can more accurately establish the centre of origin of such varieties.
In the present study the results of a molecular characterization of thirty common bean varieties are reported.

The following varieties were studied: the anthracnose differential cultivars, Michelite, MDRK, Perry Marrow, Cornell49-242, Widusa, Kaboon, Mexico222, PI207262, TO, TU, AB136 and G2333; nine breed lines or varieties carrying anthracnose resistance genes, A493, A321, A252, SEL1360, SEL1308, Sanilac, Catrachita, V204, and V225; seven bean varieties currently grown in Spain, Andecha, Xana, Cimera, Canela, Tolosana, Riñón and Ganxet; and the parent lines of a RIL mapping population taking part of the integrated genetic map, BAT93 and jaloEPP558.

Eighty-one molecular markers were analyzed, including 4 CAPs (Geffroy et al. 1998, Murray et al. 2002), 2 ISSRs (Hamann et al. 1995), 1 RAPD (Gonçalves-Vidigal and Kelly 2003), 19 SCARs previously described by different authors, 25 SCARs recently obtained in our laboratory (Pañeda et al. in preparation) and 30 microsatellites (Yu et al. 2000, Blair et al. 2003). Most of the SCARs were linked to disease resistance genes or other genes of interest. The markers were distributed among the eleven linkage groups (fig. 1).

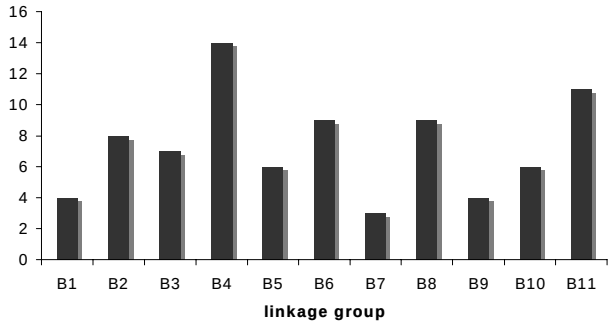

Figure 1. Number of markers located in each linkage group.

In summary, the 81 primer pairs used amplified a total number of 219 different polymorphic DNA fragments, microsatellites being the most efficient in this respect.

Figure 2 shows the phylogenetic tree resulting from the data obtained. It was built using the Wagner parsimony method for discrete traits (Eck and Dayhoff 1966, Kluge and Farris 1969). This was carried out using the PARS program from the PHYLIP package (Felsenstein 1989), using the default options (unrooted trees, ordinary parsimony and no weighted sites).

The varieties analyzed are distributed in two main groups, most probably related to their centers of origin, Andean (left) and Mesoamerican (right). In addition, when considered in some detail, the results are consistent with the previously known pedigrees. For example, Xana proceed from Andecha, and this variety, together with Cimera are very similar landraces from Asturias, Spain; BAT93 and AB136 proceed from PI207262 and Catrachita, respectively; Sanilac was obtained after X-irradiation from Michelite; and A493 proceed from a cross between Alubia (Andean) and BAT93. Finally, the relative positions of the twelve anthracnose differential cultivars are consistent with their previously known geographical origins.

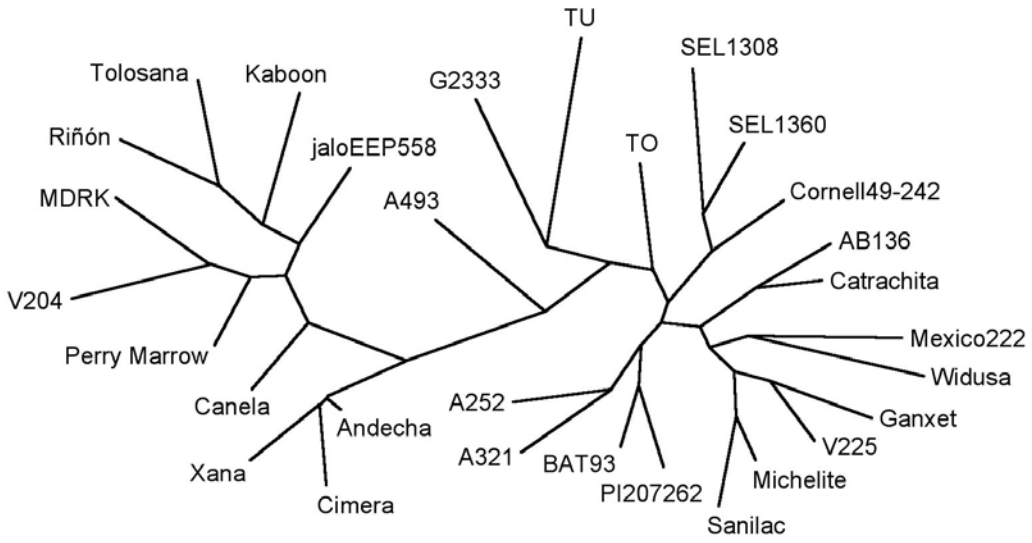

Figure 2. Phylogenetic tree of thirty common bean varieties. The length of the different lines in the drawing is proportional to genetic distances.

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