BACKCROSS ASSISTED BY RAPD MARKERS TO DEVELOP COMMON BEAN LINES WITH CARIOCA TYPE GRAINS CONTAINING THE *Ur-11* RUST RESISTANCE GENE

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Rust, caused by the fungus *Uromyces appendiculatus*, may cause serious losses to the common bean culture mainly in regions with mild temperatures and high humidity (Paula Júnior & Zambolim, 1998). The BIOAGRO/UFV bean breeding program has been using cv. Ouro Negro as the only source for rust resistance. However, more recently new sources were characterized and cultivar Belmidak RR-3 (*Ur-11*) has been shown to be an important resistant source to *U. appendiculatus* races prevalent in the state of Minas Gerais, Brazil (Faleiro et al.,1999; Faleiro et al., 2001). Allelism studies involving Ouro Negro and Belmidak RR-3 showed that these cultivars possess distinct rust resistance genes that can be pyramided to develop bean materials adapted to Central Brazil with complementary resistant (Alzate-Marin et al., 2002).

In our backcross breeding program for the creation of common bean cultivars resistant to rust we usually develop near-isogenic lines containing the individual resistance genes and then they are intercrossed. Rudá, the recurrent parent that we have been using, is a "carioca" type cultivar, with good yield potential but susceptible to rust. Here we report on the transfer of *Ur-11* from Belmidak RR-3 to Rudá, in a process assisted by molecular markers.

Materials and Methods

Common bean cultivar Belmidak RR-3 (pollen donor) was crossed with Rudá, in the greenhouse under controlled environmental conditions. In each backcross generation BC_nF_1 plants were inoculated with spore suspensions of a mixture of races of *U. appendiculatus* (2 x 10^4 spores/ml). The plants were then incubated for two days in a mist chamber kept at 20 - 22 ^{o}C and 100% relative humidity. After this period, each plant was scored visually for the disease symptoms using a 1-to-6 scale (Stavely et al., 1983) in which 1 was attributed to plants with no visible symptoms and 6 to severely diseased or dead plants. Leaf DNA was extracted from the progenitors and the resistant BC_nF_1 plants by a mini-prep procedure based on Doyle and Doyle (1990). RAPD amplification reactions were according to Williams et al. (1990) using different primer sets in each backcross cycle. Genetic similirities based on the RAPD data and cluster analyses were determined by the SPSS program and the Euclidian method for binary data (Wilkinson et al., 1992).

Results and Discussion

The relative genetic similarities between the BC_2F_1 resistant plants and the recurrent parent varied between 75.8 and 97%. The plants genetically closer to the recurrent parent were used in the next backcross cycle. The genetic similarities between the BC_3F_1 resistant plants and Rudá varied from 82.1 to 97.4%. Three BC_3F_1 lines bearing the *Ur-11* gene which were phenotypically undistinguishable from the recurrent parent (Figure 1) will now be selfed to select homozygous plants to be used in the pyramidation of different rust resistance genes in the background Rudá.

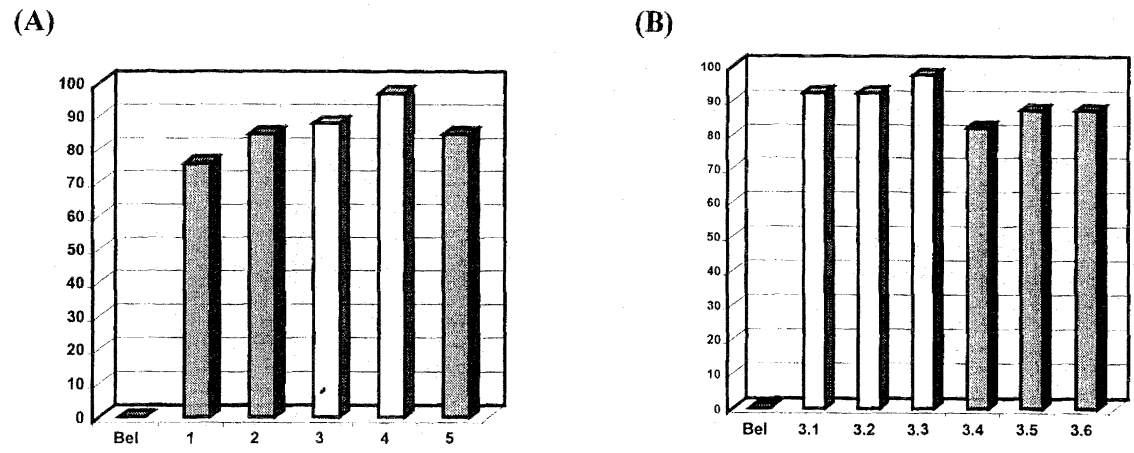

Figure 1. Relative genetic similarity (%) between BC_2F_1 (A) and BC_3F_1 (B) resistant plants and the recurrent parent Rudá. The relative distance between the recurrent and the donor parent Belmidak RR-3 (Bel) was considered to be 0%. Plants represented by white bars were selected based on their higher similarities in relation to Rudá.

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