

RUDÁ × AND 277 RILS: A POTENTIAL NEW CORE MAPPING POPULATION FOR COMMON BEAN

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The main population used for genetic mapping in common bean (*Phaseolus vulgaris*) is the BAT 93 × Jalo EEP 558 RIL (Recombinant Inbred Lines) population, reported by Nodari *et al.* (1993) and Freyre *et al.* (1998), which is currently composed of 75 lines. BAT 93 and Jalo EEP 558 belong to the Mesoamerican and Andean gene pools, respectively. These parents contrast for many important traits, such as disease and insect reactions, grain nutritional quality and other morphological and agronomical traits. Another important common bean RIL mapping population that has been used by the bean research community was developed by CIAT (Cali, Colombia) from crosses between DOR 346 (Mesoamerican) and G 19833 (Andean). This population is currently composed of 87 lines (Blair *et al.*, 2003; Galeano *et al.*, 2009). Several other bean mapping populations have also been developed and used by different groups. However, a serious limitation of most of these populations is their reduced size, which drastically affects the accuracy of the estimates of recombination rates and consequently the precision of the resulting genetic maps.

According to Silva *et al.* (2007), the minimum population size and respective genome saturation level to develop reliable genetic maps using a RIL mapping population should be 200 lines/5.0 cM, 300 lines/10.0 cM or 500 lines/20 cM. For this reason, a core mapping population with appropriated size is still lacking for common bean. In addition, with the ongoing *P. vulgaris* genome sequencing projects, a large number of molecular markers are being developed and will be available soon for the bean research community. In this sense, the fine-mapping of candidate genes and QTLs will become possible and highly demanded.

In an attempt to develop a potential new core mapping population for common bean, the BIOAGRO/UFV and Embrapa bean research groups developed a RIL population with 500 lines from crosses between Rudá (Mesoamerican) and AND 277 (Andean). These parents present considerable phenotypic contrast for many morphological and agronomical traits, in addition to disease reactions (Table 1). The genetic variability among them has also been checked at the molecular level. The estimated genetic distance based on a set of 126 SSR markers discovered by Embrapa group, most of them reported by Grisi *et al.* (2007), was 78.6%, and 71.3% using 677 SNP markers reported by Souza *et al.* (2012). Rudá is a ‘carioca’ seeded cultivar (beige background with brown stripes) developed by CIAT and released in Brazil by Embrapa. It derived from crosses between the cultivars Carioca and Rio Tibagi. Although it is a high yielding cultivar, Rudá is susceptible to the main bean diseases occurring in Brazil. AND 277 is a ‘manteigão’ seeded line (cream background with light red stripes) also developed by CIAT from multiple crosses [(Cargabello × (Pompadour Checa × Linea 17) × (Linea 17 × Red Cloud)]. It is resistant to different pathotypes of the angular leaf spot (ALS), anthracnose and rust pathogens (Table 1), harboring the ALS and anthracnose resistance genes *Phg-1* and *Co-1^f*, respectively.

Crosses and generation advancement from F₂ to F₉ generations, using the SSD (Single Seed Descent) method, were performed under greenhouse conditions. To identify the true hybrids, all F₁ plants and F₂ seeds were analyzed morphologically. Rudá × AND 277 RILs have been grown in the field for seed multiplication and phenotyping for important morphological and agronomical traits. In addition, these RILs are being genotyped at Embrapa using SSR and SNP markers, and also GBS. Seeds of the Rudá × AND 277 RIL mapping population should be available soon upon request. We expect that a cooperative use of these RILs as a reference mapping population should help the development of a reliable, integrated and saturated core genetic map for common bean.

Table 1. Reactions of the common bean lines Rudá and AND 277 to some of the main bean diseases.

Disease	Pathogen	Pathotype	Disease Reaction ^a	
			Rudá	AND 277
Angular leaf spot	<i>Pseudocercospora griseola</i>	7-15 ^b ; 15-7 ^b ; 23-23 ^b ; 31-7 ^b 47-39 ^b ; 63-6 ^b 63-7 ^b ; 63-23 ^b 63-31 ^b ; 63-47 ^b 63-63 ^b	S	R
		7 ^c ; 55 ^c ; 87 ^c	S	S
Anthracnose	<i>Colletotrichum lindemuthianum</i>	8 ^c ; 9 ^c ; 64 ^c ; 65 72 ^c ; 73; 77; 81; 453 ^c ; 1609; 2047 ^c	S	R
		71 ^c ; 89 ^c	R	R
Rust	<i>Uromyces appendiculatus</i>	21-3; 53-19 29-3	S S	R S
White mold	<i>Sclerotinia sclerotiorum</i>	SsEpamig01	S	S

^aResistant (R) and susceptible (S) reaction. ^bDisease reaction reported by Balbi *et al.* (2009) and ^c by Arruda (2009).

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