ANTHRACNOSE RESISTANCE SOURCES TO BE EXPLORED BY THE COMMON BEAN BREEDING PROGRAMS IN BRAZIL

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The attack of pests and pathogens is one of the main causes of yield and quality losses in the common bean (*Phaseolus vulgaris* L.) crop worldwide. This is especially true for small farmers with low-technology inputs in Brazil. Among the most destructive diseases that attack the crop we find anthracnose (ANT), caused by the fungus *Colletotrichum lindemuthianum*. The pyramiding of different race-specific resistance (R) alleles could be used as a strategy for developing broad and durable resistance to a large number of pathogen races (Ragagnin *et al.* 2009). However, it is necessary to check what R alleles are still effective and, for this reason, really useful to the breeding programs. Thus, the main goal of the present work was to evaluate common bean anthracnose resistance sources for disease reaction under greenhouse and field conditions. In addition, the tested genotypes were also screened with SCAR markers linked to R genes presented as useful for the breeding programs in Brazil.

Artificial inoculations were carried out according to Pastor-Corrales *et al.* (1995), using three *C. lindemuthianum* pathotypes selected based on the criteria prevalence (races 73 and 81) and virulence (race 2047). At least 16 plants per genotype were screened with each one of the pathotypes. The field trial was conducted during the growing season of winter/2013, in a disease endemic area (ANT screening site) located at Embrapa Rice and Bean Experimental Station (Santo Antônio de Goiás, GO, Brazil), using a randomized complete block (RCB) design with three replications. Each plot consisted of two rows each 3.0 m long, spaced by 0.5 m, with 15 plants per meter. Pathogen inoculation was done by natural infection. At both greenhouse and field screening, ANT severity was scored using a 1-to-9 scale, where 1= no symptoms and 9= dead plants. The molecular marker screening followed standard methods, using available SCAR markers previously identified (http://www.css.msu.edu/bic/PDF/SCAR_Markers_2010.pdf).

'G 2333' (*Co-4*^{2}, *Co-5* and *Co*-7) was the only genotype resistant in the field and to all tested *C. lindemuthianum* pathotypes. 'MDRK' (*Co-1*), 'Kaboon' (*Co-1*^{2}), 'Perry Marrow' (*Co-1*^{3}), 'AND 277' (*Co-1*^{4}), 'TO' (*Co-4*), 'PI 207262' (*Co-4*^{3} and *Co-9*), 'TU' (*Co-5*) and 'AB 136' (*Co-6* and *co-8*) were resistant in the field and in the greenhouse screening with the pathotypes 73 and 81. 'SEL 1308' (*Co-4*^{2}) showed to be resistant to the pathotypes 73 and 2047, being also resistant in the field (Table 1). The results demonstrated that the R alleles *Co-3*, *Co-3*^{3}, *Co-7*, *Co-10*, *Co-11* and *Co-13* were not effective to the tested pathotypes, although *Co-10* conferred resistance in the field screening (Table 1). *Co-4*^{2} ('SEL 1308') was the only allele conferring resistance to the pathotype 2047, although it was supplanted by the pathotype 81, what can be controlled by other alleles, e.g. *Co-5* ('G 2333' and 'TU') and *Co-6* ('AB 136'). For this reason, the combination of *Co-4*^{2} with *Co-5* or *Co-6* should be useful for the common bean breeding programs in Brazil. As shown in Table 1, in addition to race-specific reactions, the pyramiding of the mentioned R alleles can be also supported in some way by available SCAR markers linked to these target alleles.

Table 1. Reaction of common bean lines to anthracnose (*Colletotrichum lindemuthianum*) at greenhouse and field testes, and molecular screening of those lines with SCAR markers linked to resistance genes.

Genotype	Resistance (R) gene	*C. lindemuthianum* pathotype[a]			Field[a]	SCAR marker[b]			
		73	81	2047		SY20/ *Co-4*	SH18/ *Co-4*^{2}	SAB3/ *Co-5*	SAZ20/ *Co-6*
MDRK	*Co-1*	1.0	1.0	6.0	1.6	0	0	0	0
Kaboon	*Co-1*^{2}	1.0	1.0	5.0	1.6	0	0	0	0
Perry Marrow	*Co-1*^{3}	1.0	1.0	5.0	1.3	0	0	0	0
AND 277	*Co-1*^{4}	3.0	3.0	4.0	2.6	0	0	0	0
Widusa	*Co-1*^{5}	1.0	9.0	6.0	1.6	0	0	0	0
Cornell 49-242	*Co-2*	9.0	1.0	9.0	5.6	0	0	0	0
Mexico 222	*Co-3*	9.0	9.0	6.0	3.3	0	0	0	0
BAT 93	*Co-3*^{3}	9.0	5.0	6.0	8.6	0	0	0	0
TO	*Co-4*	1.0	1.0	5.0	1.6	1	0	0	0
SEL 1308	*Co-4*^{2}	1.0	5.5	2.0	1.0	1	1	0	0
PI 207262	*Co-4*^{3} and *Co-9*	1.0	1.0	6.0	1.6	1	0	0	0
G 2333	*Co-4*^{2}, *Co-5* and *Co-7*	1.0	1.0	2.0	1.3	1	0	1	0
TU	*Co-5*	1.0	1.0	5.0	3.0	0	0	1	0
SEL 1360	*Co-5*^{2}	1.5	6.0	3.5	-	0	0	1	0
AB 136	*Co-6* and *co-8*	1.0	1.0	5.0	1.0	0	0	0	1
H1	*Co-7*	9.0	4.5	5.0	-	0	0	0	0
Ouro Negro	*Co-10*	3.5	4.0	6.5	1.0	0	0	0	0
Michelite	*Co-11*	9.0	9.0	9.0	8.3	0	0	0	0
Jalo Vermelho	*Co-12*	1.5	8.5	3.5	-	0	0	0	0
Jalo Listras Pretas	*Co-13*	6.5	7.0	8.0	-	0	0	0	0
Rosinha G2[c]	-	8.0	9.0	6.5	8.6	0	0	0	0

[a] Mean scores of disease severity based on a 1-to-9 scale, where resistance reaction= 1-to-3 (1= no symptoms and 9= dead plants).
[b] Presence (1) or absence (0) of SCAR marker.
[c] Susceptible cultivar control.

REFERENCES

Pastor-Corrales *et al.* (1995) *Plant Disease* 79:63-67.
Ragagnin *et al.* (2009) *Plant Breeding* 128:156-163.