An Allelic Series at the *Co-1* Locus for Anthracnose Resistance in Common Bean

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Introduction. Broad-based resistance to bean anthracnose can be achieved if both Andean and Middle American genes are combined in the same cultivar (Young and Kelly 1996). However, Andean sources of anthracnose resistance have not been studied as extensively as Middle American sources. There is limited information available on the independence of the individual genes present in Andean cultivars or on the relationship of these genes to other previously characterized anthracnose resistance genes. To date only one Andean anthracnose resistance gene has been described, the *Co-1* gene. In two published studies (Cardenas et al 1964; Muhalet et al 1981) reverse of dominance in populations segregating at this locus has been reported. Change of dominance depending on the genotypes involved in those crosses can be explained by a multiple allelic series at that specific locus. For instance, if a race such as beta (race 130) possesses multiple virulent genes such that it is virulent to some alleles at the *Co-1* locus but not all the alleles, either 3R:1S or 1R:3S ratios would be observed depending on the specific combinations of alleles segregating in the different crosses. In this study, we report additional evidence for existence of an allelic series at the *Co-1* locus.

Materials and Methods. Segregating populations were developed to study anthracnose resistance genes present in Kaboon, Perry Marrow, and Flor de Mayo M38 (Table 1). Crosses were made with the Andean genotypes Cardinal and Michigan Dark Red Kidney (MDRK) and the Middle American genotype Cornell 49-242. Cardinal possesses no known gene for anthracnose resistance, whereas MDRK carries the *Co-1* gene and Cornell 49-242 carries the *Co-2* gene. F_2 plants and F_3 families from these crosses were used to determine inheritance and independence of Andean genes for anthracnose resistance. The parents and segregating populations were inoculated with a spore suspension of the pathogen and disease evaluation was performed as described by Young and Kelly (1996). Specific races of *C. lindemuthianun* were chosen based on the different phenotypic reaction observed in parental genotypes.

Results and Discussion. Based on the segregation ratio (3R:1S) observed in the F_2 populations MDRK x Kaboon and Cardinal x Kaboon (Table 1) we conclude that Kaboon carries one dominant gene conferring resistance to races 7 and 73 of *C. lindemuthianum*. This gene is independent from the *Co-2* locus as indicated by the segregation ratio 15R:1S (p=0.51) observed in a cross between Cornell 49-242 and Kaboon. This gene in Kaboon also proved to be an allele of the *Co-1* gene present in MDRK since no segregation was observed in a R x R cross. Support for allelism is based on the differential reaction of these genotypes to a range of anthracnose races. Therefore we propose the symbol $Co\text{-}1^2$ for this gene. This allele is very important for the bean breeding program as it confers resistance to both Andean and Middle American races of anthracnose recently identified in Michigan. To determine whether Kaboon has other

resistance genes we inoculated the F_2 progeny of Cardinal and Kaboon with a less virulent race, the Andean race 5. The observed segregation ratio (57R:7S; p=0.38) indicate that Kaboon may have other dominant resistance genes with complementary mode of action, since Cardinal possesses no known genes for anthracnose resistance. Therefore, at least two of the three dominant genes segregating in this cross must come from Kaboon.

Perry Marrow, an Andean genotype, appears to have another anthracnose resistant allele at the Co-1 locus. In R x R crosses between Perry Marrow and MDRK or Kaboon, no susceptible F_2 plants were found when inoculated with race 73. In contrast, the genotype Flor de Mayo 38 appears to posses an independent dominant gene for resistant to race 73 as a ratio 15R:1S was obtained in a cross with Kaboon. The anthracnose resistance present in Flor de Mayo 38 could have originated from its Middle American background (Acosta-Gallegos et al 1995).

These findings have major implication in developing breeding strategies for durable anthracnose resistance. If different alleles occurs at the same locus, breeders may not have many sources of Andean resistance genes available for gene pyramiding.

Table 1. Crosses used for the genetic characterization of anthracnose resistance in Kaboon (K), Perry Marrow (PM) and Flor de Mayo M38 (FM38).

Population	Race	Reaction*	Observed ratio in the F_2	Observed ratio in the F_3	Expected ratio	P value
MDRK x K	73	R x R	174R		all R	1
MDRK x K	7	S x R	80R:22S		3:1	0.42
MDRK x K	7	S x R		21RR:55Rr:25rr	1:2:1	0.57
Cornell x K	7	R x R	55R:5S		15:1	0.51
Cardinal x K	5	S x R	60R:10S		57:7	0.38
Cardinal x K	73	S x R	125R:49S		3:1	0.34
Cardinal x K	7 + 73	S x R	70R:28S		3:1	0.41
FM38 x K	73	R x R	90R:5S		15:1	0.70
PM x K	73	R x R	152R		all R	1
MDRK x PM	73	R x R	143R		all R	1

*R = resistant reaction and S = susceptible reaction.

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