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First report on the identification and inheritance of an *Rdc* gene conferring resistance to soybean stem canker (*Diaporthe phaseolorum* var. *caulivora*)

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Conventional plant breeding is an effective tool that contributes to the development of sustainable agriculture. In soybean, breeding for disease resistance has contributed to effective management of many important diseases. Soybean stem canker (SSC) is caused by two varieties of the fungus *Diaporthe phaseolorum*: var. *meridionalis* (Dpm) and var. *caulivora* (Dpc). Five resistance genes for SSC-Dpm (*Rdm1-5*) were identified in soybean germplasm. However, the genotypes carrying these *Rdm* genes were not effective against SSC-Dpc. The objective of this work was to identify and characterize the inheritance of *Rdc* genes for resistance to SSC-Dpc through a classical Mendelian analysis. Resistant (R) and susceptible (S) genotypes were used to make 288 RxS and 132 RxR crosses, including their reciprocals. The segregating F<sub>2</sub> generations were obtained by self-fertilization of the respective F<sub>1</sub>. The incorporation of codominant molecular markers (Single Nucleotide Polymorphism, SNP) allowed to detect polymorphisms between differential parents and to validate molecularly the F<sub>1</sub> heterozygous individuals. Those F<sub>2</sub> derived from molecularly validated F<sub>1</sub> were selfed to obtain F<sub>3</sub> seeds. F<sub>2:3</sub> families, which included 10 F<sub>3</sub> individuals derived from the same F<sub>2</sub> plant, were planted. Parents (R and S), F<sub>1</sub> individuals, and families F<sub>2:3</sub> (Progeny Test, PT) were inoculated with an isolate of Dpc (Dpc16), which had been previously identified morphologically and molecularly. The chi-square goodness of fit test verified that phenotypic segregation for individual plants in F<sub>3</sub> adjusted to a 5:3 ratio (live resistant: dead susceptible plants) and that the PT results corresponded to the genotypic ratios (1RR: 2Rr: 1rr) of F<sub>2</sub> individuals. These results allowed the identification of at least one major disease resistance gene of simple Mendelian inheritance, for which the symbol *Rdc1* is proposed. To our knowledge, this is the first report on resistance genes *Rdc* identified for SSC caused by Dpc.