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Comparative analysis of soybean genotype resistance to *Heterodera glycines* and *Meloidogyne* species via resistance gene analogs

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ABSTRACT. Nematodes are important pests of soybean throughout the world and cause high yield losses. As a control strategy, the identification of resistance genes is an important aim of breeding studies. Plants possess resistance genes (R), which are responsible for the recognition of pathogens and activation of the defense system. R genes and resistance gene analogs (RGAs) possess conserved domains, from which nucleotide-binding site is the most common. Using degenerate primers originating from these domains, it is possible to identify and isolate sequences of R and RGA genes. In this study, soybean genotypes resistant to the nematodes *Heterodera glycines*, *Meloidogyne incognita*,

M. javanica, and *M. enterolobii* were compared by the use of RGAs and simple sequence repeat (SSR) markers. Forty-six soybean genotypes were studied, including plant introductions (PIs), commercial crops, and source of resistance genotypes. Thirteen combinations of RGA primers and different SSRs linked to QTLs were used to confirm resistance to soybean cyst nematodes (SCN). Fragments associated with resistance to the studied nematodes were amplified in the source of resistance and PI genotypes. RGA markers were efficient at distinguishing groups of genotypes that were resistant and susceptible to *Meloidogyne* spp and SCN. Combinations of specific primers were identified through their ability to amplify nucleotide sequences from possible resistance candidate genes. SSR markers contributed to the analysis of SCN race specificity, showing that the QTLs identified by these markers are distinct from those identified by RGA markers.

Key words: Soybean resistance; Nematode; Resistance gene analogs; Conserved domains; Molecular markers