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Evaluation of the Genetic Architecture of Soybean Cyst Nematode Resistance at the Rhg1 Locus

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Plant genetic resistance is the most sustainable management strategy to combat soybean cyst nematode (SCN). Traditionally, both PI 90763 and Peking were classified into Peking-type resistance sources, yet they show differences in the degree of resistance to virulent SCN populations including TN22. Thus, a recombinant inbred line (RIL) population of 144 $F_{3:4}$ individuals was developed crossing PI 90763 and Peking to investigate the allele status at the *Rhg1* locus. The seeds from each of the F*3* plants were individually harvested and phenotyped for SCN resistance. After extracting the DNA from the $F_{3:4}$ population, QTL mapping confirmed that both parents carried the same *rhg1-a* allele and revealed two novel QTL for SCN resistance in PI 90763. This research contributes to understanding Peking-type resistance and provides more genetic diversity for breeding superior SCN-resistant soybean cultivars in the future.