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Using genomics to manage the invasive guava root-knot nematode

May 18, 2026



Microscopic image of two juvenile guava root-knot nematodes (GRKN), one newly hatched and one unhatched. Image colorized. Photo by William Rutter, USDA-ARS.

Root-knot nematodes (RKN) are devastating pests of many crop plants, including watermelon. These parasites infect and damage plant roots, reducing growth and yield. In recent years, a new hypervirulent species of root-knot nematode—the Guava Root-Knot Nematode (GRKN)—has been spreading across the southeastern U.S., infecting and damaging crop varieties that are typically RKN-resistant. Growers need new resistant crop varieties to help manage GRKN, but breeding new watermelon lines for resistance can take decades, as resistance is controlled by multiple genes.

To speed up the process, Clemson and USDA researchers screened a panel of wild watermelon lines to identify resistance to GRKN. They then tested the ability of genomic selection to predict which breeding lines are most likely to contain the best combination of genes to provide GRKN resistance.

Their results demonstrate that by genotyping their breeding lines and applying genomic selection models, watermelon breeders can avoid much of the laborious resistance screening involved in traditional variety development, thereby reducing the time needed to develop GRKN-resistant watermelon varieties. These results also serve as proof of concept for applying genomic selection to breed for RKN resistance in other crops.

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Biswas, A., Regmi, H., Waldo, B. D., Branham, S., Wechter, P., Kousik, S., Jarquin, D., Levi, A., & Rutter, W. B. (2026). Genomic selection of root-knot nematode (*Meloidogyne enterolobii*) resistance in watermelon wild relatives (*Citrullus amarus*). *The Plant Genome*, 19, e70203. <https://doi.org/10.1002/tpg2.70203>

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