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Diverse Nematode Collection Aids Researchers: Transcript

Waukesha, Wis. (April 12, 2021) – Media can use the following transcript to personalize the accompanying “Diverse Nematode Collection Aids Researchers” press release issued by The SCN Coalition.

The following quotes can be attributed to University of Georgia Soybean Breeder and Geneticist Zenglu Li:

“The soybean cultivars with resistance are the most economically efficient way to control parasitic nematodes in soybean fields. We need to find new sources of SCN and root-knot nematode resistance so we can deploy the new genes into the soybean breeding program.”

“The soybean breeding program at the University of Georgia has released many cultivars of the soybean germplasm lines. We have a goal to develop the soybean cultivars and release to the farmers who see the yield protection benefits.”

“I am grateful for the sponsorship from the United Soybean Board that provides great support for our research. We use a team approach at the University of Georgia between the nematologists, plant pathologists, plant geneticists and the breeders to deliver new tools to soybean growers.”

The following quotes can be attributed to University of Georgia Nematologist Melissa Mitchum:

“30 years ago, we only knew that SCN genes were dominant or recessive – that they could be inherited. Three decades later, we have the genetic and molecular tools to not only sequence the nematode genome but sequence a wide variety of SCN populations. The Tode Farm is being used to compare the genomes to pinpoint the genes for virulence.”

“The nematode genome sequencing project has many benefits to soybean growers. First, as we use it to identify the virulence genes, we also identify key targets to potentially engineer novel forms of resistance to SCN. Virulence genes likely encode proteins found in SCN spit, which is a tool the nematode uses to establish an elaborate feeding structure on soybean roots.” Second, once we know what the virulence genes are, this will open the door to developing a molecular diagnostic tool to more quickly determine the virulence of a SCN field population and prescribe the most effective type of resistance for the grower to plant and to manage SCN in their field.

“For prescriptive management to become a reality for growers, we need to integrate our knowledge of the genetics of plant resistance genes with the knowledge of the SCN virulence genes.”

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