Two Linked Genes for Soybean Mosaic Virus Resistance

Soybean mosaic virus (SMV) causes significant yield loss and seed quality deterioration in soybean. In the United States, SMV was classified into seven strains, G1 through G7, and three host resistance loci—Rsv1, Rsv3, and Rsv4—were identified. Rsv1 is the most common and diverse locus with 10 different alleles conferring differential plant reactions to SMV strains, and it was mapped to a very complex resistance-gene-rich region on chromosome 13 (LG F).

A recent study published in *Crop Science* evaluated whether the Rsv1-y allele in York soybean belongs to the Rsv1 locus. The researchers provided the first evidence that Rsv1 and Rsv1-y are two tightly linked loci conferring resistance to different SMV strains. The Soybean Genetic Committee approved a new symbol of Rsv5 designated for the resistance gene in York to replace the original Rsv1-y allele assignment.

Due to the tight linkage between Rsv1 and Rsv5, the two genes most likely act as one genetic unit and can be easily transferred to the progeny. The two-gene combination provides multiple resistance and durable protection against constantly evolving SMV strains.

Adapted from Klepadlo, M., P. Chen, A. Shi, R.E. Mason, K.L. Korth, V. Srivastava, and C. Wu. 2017. Two tightly linked genes for soybean mosaic virus resistance in soybean. *Crop Sci.* 57. View the full article online at http://dx.doi.org/doi:10.2135/cropsci2016.05.0290

Sampled U.S. Sugarcane Aphids on Sorghum Are Primarily One Clone

Since 2013, the sugarcane aphid (*Melanaphis sacchari*) on sorghum has been rapidly spreading from state to state in the southern United States and, in 2016, reached 19 states. These aphids often become so abundant in numbers that most sorghum fails to develop the main heads, and for many, plant death occurs. There is uncertainty if there are multiple sugarcane aphid genotypes on sorghum in the U.S. or if all aphids are one genotype.

In an article recently published in *Crop Science*, researchers with the USDA-ARS performed high-throughput sequencing of the sugarcane aphid, generating 1.44 Gb of nucleotides. From this data, as well as a previous study, 52 microsatellite markers were utilized to genotype 48 samples from 17 locations across seven states and one U.S. territory. All samples were one genotype with the exception of a single sample collected from Sinton, TX, which had the predominant genotype as well as another genotype. Thus, the invasive sugarcane aphid is spreading on sorghum in these locations as primarily one “superclone.” Knowledge of the number of sugarcane aphid genotypes is important for identifying resistant sorghum plants and for insecticide use.


Foliar symptoms of SMV infection (left to right): resistant (symptomless), susceptible (mosaic), and necrotic (systemic necrosis). Source: Picture collection from the University of Arkansas, Soybean Breeding and Genetics Laboratory.

Sugarcane aphids feeding on a leaf of *Sorghum bicolor* in Tifton, GA.