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Exploring the molecular basis of new sources of resistance and the effects of gene pyramiding to control soybean aphids

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Soybean aphids are one of the main pests of soybean. Current control strategies rely heavily on insecticides, but commercial varieties carrying host resistance genes are starting to be available. However, the discovery of biotypes of soybean aphids that are virulent on available resistant soybean genotypes, greatly threatens the sustainability of aphid resistance in integrated pest management systems. Thus, new sources of resistance and a better understanding of the molecular bases of these traits are needed to develop novel control strategies.

In a screening of 308 plant introduction (PI) lines selected to represent soybean diversity, we identified 15 lines with increased resistance to soybean aphids. Using genome-wide association analyses we found six new loci contributing to resistance, and identified potential candidate genes. Characterization of the type of resistance determined that five PI lines had antibiosis and antixenosis based resistance, five had antibiosis only, and two had only antixenosis. Interestingly, no direct correlation was observed between the resistant alleles in the six loci and each type of resistance, suggesting that genomic context may be important to determine the trait outcome. We also used transcriptome analysis to assess the molecular basis of increased resistance after gene pyramiding in a soybean line carrying the *Rag1* and *Rag2* soybean resistance genes. We expected an additive effect manifested as a combination of the molecular changes observed in lines carrying the *Rag1* or *Rag2* genes individually. However, we found that gene pyramiding leads to a synergistic interaction between resistant genes, resulting in a novel defense response in the pyramid line. Again, genomic context seems to be an important determinant of the molecular phenotype. Our findings could have important consequences for integrated management strategies based on plant host resistance.