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How the soybean aphid genome and transcriptomics provides insight into molecular mechanisms of adaptation to aphid resistant soybean

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The soybean aphid (*Aphis glycines*) is an invasive pest seriously damaging soybean in 80% of the North American soybean production region. Using traditional breeding, 5 genes provide resistance to *A. glycines* (i.e. Rag resistance), but, as early as 2005, certain soybean aphid population adapted to survive on resistant soybean (i.e. virulence). Currently 4 soybean aphid biotypes are known that have differential survival on different Rag genes. The durability of Rag genes can be extended if we understand the molecular mechanisms that allow soybean aphid to overcome resistance. Using a combination of Illumina short read and Pac-Bio long read sequencing, we sequenced 302 Mb of the soybean aphid genome, representing 95% of the total genome size based on flow cytometry. Our soybean aphid genome is the smallest known for an aphid, and shows a reduction in genes for detoxification and putative salivary effectors. Next, we compared gene expression among virulent and avirulent soybean aphid biotypes exposed to susceptible and resistant plants using RNA-sequencing. Aligning reads to our genome, we found between 2,500 and 1,900 genes differentially expressed when reared on susceptible and resistant varieties, respectively. A large portion of genes differentially expressed were effectors and transposable elements; interestingly most effectors showed decreased expression but transposable elements showed increased expression in virulent biotypes. Genomics and transcriptomics suggests a pathway for virulence may be mediated by effectors.