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Managing soybean aphid virulence: a genetic perspective

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After the soybean aphid (*Aphis glycines*) invaded North America in 2001, it rapidly became the most important insect pest of soybean in the North Central Region. The soybean aphid is usually controlled using insecticides, but emerging evolution of resistance may limit this traditional approach. Soybean varieties with resistance to the soybean aphid (i.e. *Rag* genes) have been developed, but their use is limited due to some soybean aphid populations that have broken this resistance (i.e. virulence). To extend the durability of aphid resistant soybean, we must develop strategies that can manage virulent aphids, as well as virulence evolution. We developed molecular markers that distinguish virulent aphid colonies reared in the laboratory. These markers were then used to monitor the frequency of virulent and avirulent aphids in microcosms that contained a mixture of resistant and susceptible soybean. We found that the presence of susceptible soybean allowed the soybean aphid population to retain avirulence, thereby slowing the increase of virulent soybean aphid. Additionally, we compared genomic variation among virulent and avirulent soybean aphids collected across the North-Central region to determine if any single nucleotide polymorphisms were distinct. We found that aphids differing in their ability to survive on soybean containing 2 *Rag* genes (*Rag1* and *Rag 2*) showed genetic differences among transcription factors and transposable elements, possibly related to virulence. Our data will provide new understanding on how virulence can be managed while still using aphid resistant soybean.