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Genetic linkage mapping of quantitative trait loci for soybean aphid resistance in PI 606390A

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Andy Michel, Department of Entomology, The Ohio State University, Ohio, USA The soybean aphid (Aphis glycines Matsumura) is among the most damaging insect pests of soybean (Glycine max (L.) Merr.) in North America. Host plant resistance is an important management strategy to control the soybean aphid. Several major resistance loci (Rag1, Rag2, Rag3 and rag4) to soybean aphid biotypes 1, 2, and 3 have been identified; however, soybean aphid biotypes have evolved the capacity to defeat single host-plant resistance genes. While pyramiding Rag1, 2,3 is effective on aphid biotypes 1 and 2, biotypes 3 and 4 are less susceptible to this resistance gene stacking. This study was conducted to map quantitative trait loci (QTL) for aphid resistance in PI 606390A which has strong antibiosis resistance to aphid biotypes 1, 2, and 3. Using 125 F6:7 recombinant inbred lines from a cross of HR09-018 × PI 606390A we identified novel QTLs on chromosome 4 and 18 which confer resistance to aphid biotype 3. These QTLs were detected on chromosomes where no gene for soybean aphid resistance has been reported thus far. Moreover, these are the first QTLs other than the Rag1, 2,3 pyramid to confer resistance to aphid biotype 3. The molecular markers closely linked to the QTLs reported here will be useful for developing elite cultivars with broader and more durable resistance against soybean aphids.