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Pyramids of QTLs enhance host-plant resistance to leaf-chewing insects in soybean
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Plant resistance to leaf-chewing insects minimizes the need for insecticide applications, reducing crop production costs and pesticide concerns. In soybean [*Glycine max* (L.) Merr.], resistance to a broad range of leaf-chewing insects is found in PI 229358 and PI 227687. PI 229358's resistance is conferred by three quantitative trait loci (QTLs): M, G, and H. QTL-M is the major source of resistance in PI229358, and is required for the expression of QTL-H and QTL-G. PI 227687's resistance is conferred by QTL-E. The near-isogenic lines (NILs) Benning^{ME}, Benning^{MGHE}, and Benning^{ME+cry1Ac} were developed to determine if novel QTL pyramids would enhance soybean resistance to leaf-chewing insects, and if pyramiding these QTLs with Bt (*cry1Ac*) enhances resistance against Bt-tolerant pests. In field-cage conditions, Benning^{ME} and Benning^{MGHE} suffered 61% less defoliation by soybean looper [SBL, *Chrysodeixis includens* (Walker)] than Benning. In detached-leaf assays Benning^{ME+cry1Ac} was more resistant than Benning^{ME} and Benning^{cry1Ac} against the Bt-resistant Southern armyworm [SAW, *Spodoptera eridania* (Cramer)]. To determine the QTL introgressions in Benning^{ME} and Benning^{MGHE}, high-density SNP genotypes were obtained using the SoySNP50K iSelect BeadChip (Illumina, San Diego, USA). To facilitate selection of lines carrying a specific QTL pyramid, KASP markers were developed for high-throughput genotyping. These NILs are valuable genetic resources for breeding host-plant resistance to insects in soybean. The combination of QTL-M and QTL-E provides agriculturally relevant levels of resistance, and with only two loci, the use of this pyramid is feasible in a breeding program.