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Bogged down in caterpillar-killing QTLs: Mapping resistance to defoliating insects in soybean

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The impact of genetics-based resistance to defoliating insects in crops is highlighted by the success of transgenic Bt lines. Efforts are ongoing to supplement or substitute Bt with soybean-derived resistance alleles. The deployment of non-transgenic defoliating insect resistance in soybean currently centers on the isolation and introgression of large-effect QTLs from two highly resistant landraces, leaving other major alleles latent in elite lines unexploited. Boggs contains additional major QTLs for resistance and is as resistant to defoliators as the combination of the two largest QTLs isolated from resistant landraces. The QTLs in Boggs were mapped using an existing RIL population of Boggs x PI 494851 (highly susceptible) genotyped with the Soy6k SNP chip. Two QTLs from Boggs affect insect growth rate (antibiosis); one of these collocates with a QTL for Japanese beetle resistance, while the other was not previously known to exist in US germplasm. Boggs carries a single QTL for insect non-preference that was previously detected in a susceptible background. Selection and phenotyping for all 3 QTLs is underway in a separate population to validate these QTLs and provide suitable markers for selection. Validated alleles from Boggs will add to those already available to improve cultivars to complement other insect control measures.