MARKER-ASSISTED PREVENTIVE PLANT BREEDING FOR SOYBEAN APHID (*APHIS GLYCINES*) RESISTANCE

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The development of cultivars resistant to quarantine organisms anticipates action against potential risks in agriculture. The Brazilian Program for Preventive Plant Breeding is part of a plant protection effort to guard the country against damage caused by quarantine organisms. The soybean aphid (SA) (*Aphis glycines*) is a common soybean pest in Asia. It was recently introduced in North America, where it quickly became one of the most important soybean pests. SA decreases yield, causes stunting and is a vector of many soybean viruses. There are no reports of SA in Brazil. Sources of SA resistance have been identified in the USDA soybean germplasm collection and can be used as donors of resistant genes in breeding programs. The objectives of this work were to (i) identify new SNP markers associated with the resistance gene detected in Dowling (*Rag1*) for use in marker assisted selection, (ii) initiate the development of genetic stocks adapted to Brazil containing SA resistance genes detected in three germplasm accessions (Dowling, PI 200538 and PI 567543C). Molecular marker linkage analysis was based on a Dowling x BRSGO 8360 RIL population. RILs were screened for SA Biotype I resistance in a greenhouse choice test. GBS (genotyping-by-sequencing) and the SoySNP6K Illumina Infinium assay were used to genotype the RILs, as well as a TaqMan assay specific for *Rag1*. Linkage and QTL maps were built using R/qtl and ASMap. The *Rag1* TaqMan assay successfully detected RILs containing the resistant allele. Genotypes were significantly correlated with the resistant phenotype (X^2 = 70.096, p-value = 6.008e-16). The GBS linkage map included 5,727 SNPs distributed in 20 soybean chromosomes, while the SoySNP6K linkage map included 1,621 SNPs. Both maps presented the *Rag1* QTL, as expected, in soybean chromosome 7. A smaller set of SNPs distributed throughout the soybean genome, including markers for the detection of SA resistance genes, has been developed for backcross marker-assisted selection.

Key-words: SNPs, genotyping-by-sequencing, marker-assisted backcrossing

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