IDENTIFICATION OF GENOMIC REGIONS ASSOCIATED TO RESISTANCE TO NEMATODE *Meloidogyne javanica* IN HEXAPLOID SWEETPOTATO

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Root-knot nematodes (*Meloidogyne* spp.) cause damage to roots and tubers of sweetpotato (*Ipomoea batatas,* $2n = 6x = 90$), resulting in financial losses. *Meloidogyne javanica* stands out as one of the most aggressive species. The most efficient way to control root-knot nematodes is by developing of resistant cultivars. Marker-assisted selection (SAM) is a relevant tool for this purpose, as the phenotyping is laborious and expensive. The objective of this study was finding genomic regions related to resistance to *M. javanica* using a Genome-Wide Association Study (GWAS). We used a population from Embrapa Hortaliças with 193 clones (191 experimental clones and 2 commercial clones) genotyped using a DArTag platform with 3,120 single nucleotide polymorphisms. Two sequential trials in completely randomized design were conducted, each with four replications per clone, and one plant per plot. Each plot was inoculated with 1,000 individuals of *M. javanica* and evaluated 90 days after inoculation. There were five traits: gall score using two scales (0 to 10 for *NBP*, and 0 to 5 for *NN*), total number of specimens per plot (*total*), number of nematodes per gram of vegetal tissue (*nemag*), and reproduction factor (*fr*). GWAS using the Q + K model adapted for polyploids, which is implemented on the R package GWASpoly v.2.13. In this step, markers were tested in an additive model and three dominance models. The GWAS detected significant association in three genomic regions for *nemag* in the dominance model. The site located at the chromosome 3 is related to the expression of Leucine-Rich Repeat Receptor Kinases (LRR-RKs), known for their role in vegetal defence and growth. The other sites, located at chromosomes 11 and 12, are associated to the expression of regulators involved in the response to biotic and abiotic stresses. In addition to *nemag*, we detected significant associations for the *NN* trait at chromosomes 9 and 12. Significant genomic regions in these chromosomes codify proteins like Armadillo Repetitions and Ubiquitin-Conjugating enzymes, which play roles in defence mechanisms in plants. This study identified 5 regions, at chromosomes 3, 9, 11 and 12 associated to the resistance to *M. javanica*, which can be leveraged towards SAM for *M. javanica* resistance in sweetpotato.

Keywords: GWAS; polyploid; marker-assisted selection; *Ipomoea batatas;* root-knot nematodes.