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—Scientific Note—

# Quantitative Trait Loci Identification and Marker Development for Papaya Ringspot Virus Resistance in Squash

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**Papaya Ringspot Virus (PRSV) is an aphid transmitted pathogenic plant virus threatening squash production worldwide. Viruses being obligate intracellular parasites, chemical and cultural practices for their control are not fully effective. Using a genetic source of resistance is the most effective way to minimize crop loss due to virus. Current study identified quantitative trait loci (QTL) and molecular markers associated with PRSV resistance using whole genome sequencing based on bulked segregant analysis technique. An $F_2$ population derived from a cross between 'Nigerian Local' (PRSV resistant) and 'Waltham Butternut' (susceptible) were mechanically inoculated with PRSV and disease ratings were recorded. At 28 days after inoculation 30% of the $F_2$ individuals were found to be resistant. Two DNA bulks, each from 10 resistant and 10 susceptible $F_2$ individuals were selected for whole genome resequencing and subsequent QTL mapping. QTL mapping using *QTLseqr* identified one major QTL significantly associated with PRSV resistance on chromosome 9 ($P < 0.05$) which was designated as QtlPRSV-C09. Thirteen kompetitive allele specific PCR (KASP) markers were developed within the QTL region and two KASP markers were found to be tightly linked with resistance. Overall, QTL and associated markers identified in the study will facilitate accelerated breeding of stable PRSV resistance in squash through marker assisted selection.**

Papaya Ringspot Virus (PSRV) is one of the major constraints in all of the squash growing regions worldwide. However, genomic regions associated with PRSV resistance remain unknown in squash making virus resistance breeding tedious and time-consuming with rigorous phenotypic assays.

## Materials and Methods

Mapping $F_2$ population was developed by crossing 'Nigerian Local' (PRSV resistant) × 'Waltham Butternut' (susceptible). $F_2$ plants were mechanically inoculated with PRSV and screened phenotypically. The 10 most resistant and the 10 most susceptible individuals were selected. DNA from the 10 most resistant and the 10 most susceptible individuals were pooled together to prepare a resistant and a susceptible bulk, respectively. Resistant and susceptible parents, and resistant and susceptible bulks were sent for whole genome re-sequencing. Sequencing results were used for variant calling and quantitative trait loci (QTL) analysis.

## Results

QTL associated with PRSV resistance were identified on Chromosome 9 that extended from 785,532 bp to 5,093,314 bp and harbored 12,245 SNPs. Thirteen kompetitive allele specific PCR (KASP) markers were developed from the region out of which two were found to be significantly associated with resistance. The markers can be used for accelerated selection of PRSV resistance individuals.

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