

COSII Marker C2-At3g27310, 138.0 cM, Chr. 2

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Primer Name	Primer Sequence (5' to 3')
BG2F-12	AGCCCGAAGACTTCTATGAGTTCAC
BG2R-12	TCTGCCTCACGAATTTTCTTCGTC

Cerasiforme BG2F12-R12: 427 bp;

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1      AGCCCGAAGA CTTCTATGAG TTCACACCAG AGGATTATTA TCGACTTTTG GGAACTAAAA
61     AAGAAGGTAA GATACACTTG TATAGACTTT CAGATGAAAA ATGGCTTCAA GTATTTGCTA
121    AAGTGAAATT TCTAGCTGAC CTCTAACAGA AGAACAAAAA AACATGTCAA TTAGTTGTCT
181    GTCGATTTAT TTGACAAATT AACTAGAAC  TCCAGACTCT ATTATTTTTC TTTTATGCTT
241    GCGCCTTGGG TATATTCACC GTGTCTTCCA CATTTTTTACC TTCTTCAATG GATCTTGTTT
301    ATTATTATAG ATCTGTAGAA ATGTATACAG GAATTTGGTT ATTTTAATGA TTCTGCTTAT
361    TCTAACTGGT GTTGGGAAAA TTTTCAACAG AGAAGCACTT GAAGACGAAG AAAATTCGTC
421    AGGCAGA
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Blast Search

There is a partial match to the following mRNA. The gaps may be introns.

DEFINITION *Lycopersicon esculentum* clone 113655F, mRNA sequence.
ACCESSION BT012727
AUTHORS Kirkness,E.F., Wang,W. and Vazeille,A.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-2004) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20850, USA

SGN BAC Clone Search

This sequence matched with 100% identity to the following BAC clone:

Clone name: LE_HBa0194L19

Name: Tomato HindIII BAC Library

Organism: *Solanum lycopersicum*

Comparison With Other Breeding Lines

Cerasiforme, Gc9, and 902h each gave good sequence with both the forward and reverse primers. Upon alignment all of the sequences matched identically. Therefore, there are no SNP or INDEL that distinguish the begomovirus resistant genotypes from the susceptible at this location on chromosome two.