

## M31751, near 54.00 cM on Chr. 11

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Primer Name	Sequence (5' to 3')
M37151-exoF3	GTTCGTATAACTGGACTTGCTC
M37151-exoR4	GGT AAG ACT GAG TTC ATG GC

### 100a M37151exoF3-exoR4: 954 bp:

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1      CTGCTCCTGG ACTCACGGGT TTCATTTAGT AAGTTATGGT TGCTACTATT GAATTATACT
61     GCTTCTTGTA TGTACTTGTC CTTGTGGCAA TTATGGTGAA TTTTGGTTAA TGTTATGCTT
121    TGGCTTGTGT TGTAGCATGA ATATGGTGAC ACTACAAACG GATGTATGTC TACAGGTTAG
181    CTTCTGATTT AGTTTGAAGT TTGAGTTAAT CGAAATGTTG ATGAATTGGA ACTCCTCTTG
241    TAATGTACTA AAATAAAATT GGAACCTTTC TAGTAGCTAG TTGGAAATGA TGTGTTTAGT
301    TCTAGTTTCG CTGGTACTAG TTTGAAATTT GTTCCCTTTT GATTACTGCA GGAGCCCATT
361    TTAATCCGAA TAAATTGACA CATGGAGCTC CTGGAGATGA AATCCGTCAT GCGGGTGACC
421    TGGGAAACAT AGTGGCCAAT GCCGATGGTA AAGTACATCT TTTCTATTCT TTCATAGCGC
481    TTTGATTCTG TATTTGTTTG TTAAGATGGA TGATGACTTT CTAGATTCTT AATTGCGCTT
541    ACTGTATGCA GGCGTGGCTG AAGTGACACT TGTAGATAAT CAGGTTGTTA CATTACCTT
601    GTCTGGTCAT CGTCATTCGA TGTCACTTTA TGTGCTCTAT GTTTGCTATT GTTATAGTTT
661    TAGGATAATT TACTGACTCT AAATCTTGTG CACCAATTAG ATACCATTGA CCGGTCCAAA
721    CTCAGTTGTT GGACGAGCAC TTGTGGTTCA TGAGCTTGAG GATGACCTCG GAAAGGGTAA
781    GGTTCTACAT TTTGTATTTG ATCCATCTTA ATCTGTAAAT TTGAAAAGGT TATTTCTGCG
841    AGTGTATCAA ATTTTATTTG GTGCATGCTA TACTACCTTT ACATTTTTTTT TGGAGGTCTC
901    TATGGTGCCT TCATCTAACC TCATTTGGTG GTCTCTCTGT AAGGTGGCCA TGAA
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### Blast Search-The sequence matches with a 96% identity to the following:

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DEFINITION L.esculentum (cherry tomato) SOD Cp;Le:1 gene (part 1).
ACCESSION  X77175 X77165
AUTHORS     Kardish,N., Magal,N., Aviv,D. and Galun,E.
TITLE       The tomato gene for the chloroplastic Cu,Zn superoxide dismutase:
            regulation of expression imposed in transgenic tobacco plants by
            a short promoter
JOURNAL     Plant Mol. Biol. 25 (5), 887-897 (1994)
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### SGN BAC Clone search

No Match

### Comparison With Other Breeding Lines From Guatemala

Both 100a and Purple Russian produced good sequence with the forward and reverse primers. Upon alignment 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 11.