

COSII Marker C2_At5g37850, 119.5 cM, Chr. 2

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University of Wisconsin-Madison: July 20, 2006

Primer Name	Primer Sequence (5' to 3')
BG2F-10	TGGACCCAATCAATTCTGTACAGTTCTC
BG2R-10	TCCCTTAAAGGTTGGGTATCCTGTG

Cerasifforme BG2F10-R10: 185 bp;

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1      TGGACCCAAT CAATTCTGTA CAGTTCTCAA ATCACACAGG CAAGCTGCTT ATATCACTTC
61     ATTCAAAGAA TCTGAGGCCT GAAATACGGT GCGAGGTCAT CTGTTAACCT GTAAAATCAT
121    GTGAACTGGA TTATGTTATG GNTTNTNAGC TGAAGCACTC CACAGGATAC CCAACCTTTA
181    AGGGA
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Blast Search

This sequence matches for two stretches of 40 base pairs to the following mRNA. The gap between the stretches may be an intron.

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DEFINITION  Lycopersicon esculentum clone 133015R, mRNA sequence.
ACCESSION  BT013971
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
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SGN BAC Clone Search

No Match

Comparison With Other Breeding Lines

Both 902h and Cerasifforme produced good sequence with both the forward and reverse primers. Upon alignment Cerasifforme matched exactly with 902h. Therefore, there are no SNP or INDEL that distinguish the begomovirus resistant genotypes from the susceptible at this location on chromosome two.