

COSII Marker C2_At4g18810, 58.00 cM, Chr. 2

Luis Montes, Brenda Garcia, and Douglas Maxwell
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| Primer Name | Sequence (5' to 3') |
|-------------|----------------------------|
| BG2F-6 | TTCGATCAAGGCGACAATATCACG |
| BG2R-6 | AGCAATTTCTTCACTGGATATTTTCC |

902h BG2F6-R6: 297 bp;

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1      TTCGATCAAG GCGACAATAT CACGGTATTT GCTCAGAAAT TAGAAATTTA TCTTCTGATT
61     TATAAAGCCT TGTATAATTT CATGGTATAT GCTCAGAATT AGAGAGTTGT TTTCTTATTT
121    ATTAAGTCTT GTGGAGTCTG TATAATTCTT TTTAGGTCCT CCATAAAGTC TAGCTGAAGA
181    TCACTTCTCG AATCATGTTG ATAGCGTTGA ACTTTCTTTC TAATTTTCTC ATGCGAACAT
241    TTGTATCTGA TTTGTATCTG GTATGTACAG GGAAAAATAT CCAGTGAAGA AATTGCT
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Blast Search

No Match

SGN BAC Clone Search

No Match

Comparison With Other Breeding Lines From Guatemala

902h and Cerasiforme each produced good sequence with both the forward and reverse primers. Gc9 produced useable sequence with only the reverse primer. 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 2.