

T1329, 43 cM, Chromosome 7

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Introduction

The goal for this research was to develop a co-dominant CAPS or SCAR marker for the I3 gene, which conditions resistance to *Fusarium oxysporum* f. sp. *lycopersici* race 3. PCR primers for markers in the chromosomal region between the molecular markers TG183 (42 cM) and TG639 (43.3 cM) (Hemming et al., 2004) were evaluated on homozygous susceptible, and homozygous resistant tomato inbred lines as well as heterozygous F1 hybrids obtained from J. W. Scott, University of Florida, R. Gardner, North Carolina State University or commercial hybrids.

Reference:

Hemming, M. N., S. Basuki, D. J. McGrath, B. J. Carroll, and D. A. Jones. 2004. Fine mapping of the tomato *I-3* gene for Fusarium wilt resistance and elimination of a co-segregating resistance gene analogue as a candidate for *I-3*. Theor. Appl. Gen. 109:409-418.

Primers

The sequence of T1329 was compared with sequences at GenBank. Putative exons were identified by the match with *Vitis vinifera*, AM441937, and a forward primer and a reverse primer were designed from the putative exon regions to amplify a genomic region, which should include at least one intron.

Table 1. PCR primers on chromosome 7

Primer Name	Primer Sequence (5'-3')
P7-43CF2	GGTGTCCGAGGTATTGAGGCAGAAG
P7-43CR2	CAAATTCCTGATAGCTTGAACCCG

*PCR annealing temperature at 53°C (TGEN53), ~980 bp fragment.

Sequence

M82 (Partial Sequence), (i3/i3)

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1      TGGCCAGGTA TGAAAACCAC GAGTGCGATG ATCACCCCTT ATTCCCTGTG GAATCCGGGT
61     TTATTCATGT ATTGCTGCAA AGAATAGATA GCTATGCCTT TTTGCTAAGC TGCCCCACTC
121    TGCTCTCTCT ACACGTGTTC ATATCTGCAT TTTGTCAAAT TTCTAGTGTA GAATATGACT
181    GGCACGTGTA GAAGTTAATG GAGGGACATC AATCAGTGTA TATAGTTACA CAAGTTTAAG
241    ATGTAATATG TTGGCACAAT GTTCTCCTAA TTAGAGACTA AACATGAAAT TTTTAACACT
301    CATATATAAC TATGCCAAAT CCGAGCAAGG GAGTAAAGTT TTTCTTTACC CTTAATTTTC
361    TAGATTAGAG AGAAGTATGA TAGTGAATCA TGTAGGGCGT TTCCTTGCCCT CATTGTCTG
421    ACCTTGATTT TCTTCTTTCC TTATGGATGG TCTTAGATTG CATCCACTGA CCCATTTCTA
481    ATTCTAATTT TTGGGCTCTT TCCAAAATTC TATTTATCC TGAAAGCTAA TTTTGGTGAT
541    CATGAGGTCA TCCGAATGAA GAATTTTATT CGTGAGTCTT TCTGTAGTCG ATGCATTCGA
601    CTGGTTTCGT ATGTCAATTT GACAATAATG AAAAAGAGAG AGAATCCCTA ATTGTGAGA
661    AAAAGAGTTT TGGTTATACT TTTTCTATTC AGCATTTAGT GCTTGTAGCC AGCTATCTTC
721    CAATAAAAAT CAGAACAAGT TGGAAATATGA TGTATTTTTT CCTCATCTTA GAATAGGATG
781    CACTGTGTTT CACTTAATCT GAGCGTGAAA CAATACTTCT TTTCTGTGG CTTTGTCTG
841    TGCCTGTTCT TCTGTTTGCT TCATGTCTGT AAAAGAATAT GTATTCTGAT ATTTGTAATT
901    AGGATGGCAC TTTTGTAATG TTTCTTTCTG GATCCTGACA GCCAATGAGG CCTGGGTGCC
961    GAT
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NC EBR-8, I3/I3 (Partial Sequence), inbred from R. Gardner

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1      GGTGTCGGAG GTATTGAGGC AGAAGCTGCA ATGCTTTGGC CAGGTATGAA AACTACGAGT
61     GCGATGATCA CCCTTTTATT CCTCTGTGAA TCCGGGTTTA TTCATGTATT GCTGCAAAAA
121    ATAGAAAGCT ATGCCTTTTT GCTAAGGTGC CCCACTCTGC TCTTCTGACA CGTGTTCATA
181    TCTGCATTTT GTCAAATTTT TAGTGTAGAA TATGACTGGC ACGTGTAGAA GTTAATGGAG
241    GGACATCAAT CAGTGTATAC AGTTACACAA GTTAAAGATG TAATATGTTG GCACAATGTT
301    CTCCTTATTA GAGACTAAAC ATGAAATTTT TAACACTCAT ATATAACTAT GCCAAATCGG
361    AGCAAGGGAG TAAAGTTTTT CTTTACCCTT AATGCTCTAG ATTAGAGAGG AGTATGATAG
421    TGGATCATGT AGGGCGTTCC TTGCCTCATT TGTCTGACCT CGTATTTCTT CTTTCCTTAT
481    GGATGTCCTT AGATTGCATC CACTGACCCA TTTCTAATTC TAATTTTGGG CTCTTCCCAA
541    AATTCTATGT ATTCTGAAA GCTAATTTTG GTGATCATGA GGTCAATCCG ATGAAGAATT
601    TTATCCGTGA GTCTTCTGTG AGTCGATGCA TTCGACTAGT TTCGTATGTC AATTTGACAA
661    TAATGAAAAA GAGAGAGAAT CCCTCACTTG TTGAGAAAAA GAGTTTGGT TATACTTTTT
721    CTATTTGAGC ATTTAGTGCT TGTAGCCAGC TATCTTCCTA TAAAAATCAG ATCAAGTCGG
781    AATATGATGT TATTTTTCCT CATCTTAGAA TAGGATGCAC TGTGTTCCAC TCAATCTGAG
841    CGCGAAACAA TACTTCTTTT CCTGTGGCTT TGCTGCTTGC CTGTTCTTCT GTTTGCTTTA
901    TGTCTGTAAT AGAATATGTA TTCTGATATT GGTACTTCGG ATGGCAATTT TGTAATGTTT
961    CTTTCTGGAT CCTGTCAGCC AATGAGGCCT GGTGCCGAT

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Comparison of M82 (top sequence) with NC EBR-8 (bottom sequence)

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1      .....TGGCCAGGTATGAAAACCACGAGT
1      GGTGTCGGAGGTATTGAGGCAGAAGCTGCAATGCTTTGGCCAGGTATGAAAACTACGAGT
25     GCGATGATCACCC.TTTATTCTCTGTGAATCCGGGTTTATTCATGTATTGCTGCAAAAGA
61     GCGATGATCACCCTTTTATTCTCTGTGAATCCGGGTTTATTCATGTATTGCTGCAAAAAA
84     ATAGATAGCTATGCCTTTTTGCTAAGCTGCCCCACTCTGCTCTTCTGACACGTGTTCATA
121    ATAGAAAAGCTATGCCTTTTTGCTAAGGTGCCCCACTCTGCTCTTCTGACACGTGTTCATA
144    TCTGCATTTTGTCAAATTTCTAGTGTAGAATATGACTGGCACGTGTAGAAGTTAATGGAG
181    TCTGCATTTTGTCAAATTTCTAGTGTAGAATATGACTGGCACGTGTAGAAGTTAATGGAG
204    GGACATCAATCAGTGTATATAGTTACACAAGTTAAGATGTAATATGTTGGCACAATGTT
241    GGACATCAATCAGTGTATACAGTTACACAAGTTAAGATGTAATATGTTGGCACAATGTT
264    CTCCTAATTAGAGACTAAACATGAAATTTTTAACACTCATATATAACTATGCCAAATCGG
301    CTCCTTATTAGAGACTAAACATGAAATTTTTAACACTCATATATAACTATGCCAAATCGG
324    AGCAAGGGAGTAAAGTTTTTCTTTACCCTTAATTTTCTAGATTAGAGAGAAGTATGATAG
361    AGCAAGGGAGTAAAGTTTTTCTTTACCCTTAATGCTCTAGATTAGAGAGGAGTATGATAG
384    TGAAATCATGTAGGGCGTTTCCCTGCCTCATTGTCTGACCTTGTATTTCTTCTTCCCTTA
421    TGGATCATGTAGGGCG.TTCCTTGCCCTCATTGTCTGACCTCGTATTTCTTCTTCCCTTA
444    TGGATGTCCTTAGATTGCATCCACTGACCCATTTCTAATCTAATTTTTGGGCTCTTTCC
480    TGGATGTCCTTAGATTGCATCCACTGACCCATTTCTAATCTAA.TTTTTGGGCTCTTCCC
504    AAAATTCATTTATTCTGAAAGCTAATTTTGGTGATCATGAGGTCATCCGAATGAAGAA
539    AAAATTCATGTATTCTGAAAGCTAATTTTGGTGATCATGAGGTCATCCGAATGAAGAA
564    TTTTATTCGTGAGTCTTTCTGTAGTCGATGCATTGACTGTTTCGTATGTCAATTTGAC
599    TTTTATCCGTGAGTCTTTCTGTAGTCGATGCATTGACTAGTTTCGTATGTCAATTTGAC

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624 AATAATGAAAAAGAGAGAGAATCCCTAA.TTGTTGAGAAAAAGAGTTTGGTTATACTTT
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659 AATAATGAAAAAGAGAGAGAATCCCTCACCTTGTTGAGAAAAAGAGTTTGGTTATACTTT

683 TTCTA.TTCAGCATTTAGTGCTTGTAGCCAGCTATCTTCCAATAAAAAATCAGAACAAAGTT
|||
719 TTCTA.TTCAGCATTTAGTGCTTGTAGCCAGCTATCTTCCATATAAAAAATCAGATCAAGTC

742 GGAATATGATGTTATTTTCCCTCATCTTAGAATAGGATGCACTGTGTTCCACTTAATCTG
|||
779 GGAATATGATGTTATTTTCCCTCATCTTAGAATAGGATGCACTGTGTTCCACTCAATCTG

802 AGCGTGAAACAATACTTCTTTTCCCTGTGGCTTTGCTGCTTGCTGTCTTCTTCTGTTTGCTT
|||
839 AGCGCGAAACAATACTTCTTTTCCCTGTGGCTTTGCTGCTTGCTGTCTTCTTCTGTTTGCTT

862 CATGTCGTGTAAGAAGAAATATGTATTCTGATATTGTACTTAGGATGGCCTTTTGTAATGT
|||
899 TATGTCGTGTAAGAAGAAATATGTATTCTGATATTGGTACTTCGGATGGCAATTTTGTAATGT

922 TTCTTTCTGGATCCTGACAGCCAATGAGGCCTGGGTGCCGAT
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959 TTCTTTCTGGATCCTGTCAGCCAATGAGGCCTGGGTGCCGAT

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Comments

Partial sequences were obtained for four tomato samples. M82 (susceptible) and NC EBR-8 (resistant) sequences had differences of approximately 25 SNPs and 5 indels. The M82 sequence was the same as the other susceptible line, Purple Russian; and the NC EBR-8 sequence was the same as the other resistant line sequence, NC123S.

The sequence of M82 matched the clone C07HBa0073N22 with a 99% nt identity in both GenBank and SGN sites. NC EBR-8 matched this clone with a 96% nt identity. M82 also matched SL_FOS0059I01_pIBR_449241 with a 99% nt identity and SL_EcoRI0098D07_T7_310033 with a 98% identity at the SGN site, as did NC EBR-8 with a 96% and a 95% nt identity, respectively.