

Got-2 locus, 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 corresponds to 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. The isozyme for glutamate oxaloacetate transaminase has been used as a marker for the *I3* gene and Wang et al. (2007) developed a PCR-based marker associated with this isozyme.

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.

Wang, G.-P., G. T. T. Lim, and D. A. Jones. 2007. Development of PCR-based markers from the tomato glutamate oxaloacetate transaminase isozyme gene family as a means of revitalizing old isozyme markers and recruiting new ones. Mol. Breeding 19:209-214.

Primers

Table 1. PCR primers on chromosome 7 from Wang et al. (2007) for GOT-B

Primer Name	Primer Sequence (5'-3')
PGot-2 F1	AGTGGCAGTGAAAAGTCAGTTG
PGot-2 R1	CCAAGTAACCAACATTTCCAGTAG

*PCR at an annealing temperature of 53°C (TGEN53), ~636 bp fragment.

Sequences:

Purple Russian, i3/i3 (Partial Sequence); Purple Russian is a heritage tomato (OP) from Seed Savers Exchange, Decorah, Iowa

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1      AGTGGCAGTG AAAAGTCAGT TGCAGCAACT TGCCAGGCC ATGTACAGTA ATCCACCTCT
61     TCATGGTGCT CTTGTTGTTT CTACAATCCT TGGAGATCCA AACTTGAAAA CTCTATGGCT
121    CGGGGAAGTG AAGGTTAGTT AATGGTGCTC TGGCTGCTCT TTAGCTTGGT ACTCGTTTTT
181    AGAACATCAT ATGTTAAGCG TAAATTTTCA ATGACTTAAA GAGTTTTTTT CCAGGGCATG
241    GCTGATCGTA TCATCGGGAT GAGAACTGCT TTAAGGGGAA ATCTTGAGAA GTTGGGCTCA
301    CCTCTATCTT GGGAACACAT AACCACCAG GTATTGAGA TCAACGACTT CCTTCACTTT
361    CTGTAATAGT ACGTAACTAT AAGAATTCAC CTATTGTCCC CTTAATGTTC GATCCTTCCT
421    ACAGATTGGC ATGTTCTGCT ACAGTGGGAT GACACCGGAA CAAGTAGACC GATTGACAAA
481    AGAGTATCAC ATCTACATGA CTCGTAATGG TCGTATCAGG TATAATTATT GAGTCGTCAA
541    GTTCAAGCTT TTAAGCACCT GTATTGAT AAAAGTTTAT ATCTGATTGT TTTTTTCCCA
601    ATCTATTTCT TTTGCTTCTT GTATGGTGCA GTATGGCAGG AGTTACTACT GGAAATGTTG
661    GTTACTTGG
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NC EBR-8, I3/I3 (Partial Sequence), inbred from R. Gardner

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1      AGTGGCAGTG AAAAGTCAGT TGCAGCAACT TGCCAGGCCC ATGTACAGTA ATCCACCTCT
61     TCATGGTGCT CTTGTTGTTT CTACCATCCT TGGAGATCCA AACTTGAAAA CTCTATGGCT
121    CGGGGAAGTG AAGGTTAGTT AATGGTGCTC TGGCTGCTCT TTAGCTTGGT ACTCGTTTTT
181    AGAACATCAT ATGTTAAGCT TAAAATTTCA ATGACTTAAA GAGTTTTTAT CCAGGGCATG
241    GCTGATCGTA TCATCGGGAT GAGAACTGCT TTAAGGGAAA ATCTTGAGAA GTTGGGCTCA
301    CCTCTATCTT GGGAACACAT AACCAACCAG GTATTTGAGA TCAATGACTT CCTTCACTTT
361    CTGTAGTAGT ACGTAACTAT AAGAATTCAC CTATTGTCCC CTTAATGTTT GATACTTCCT
421    ACAGATTGGC ATGTTCTGCT ACAGTGGGAT GACATCGGAA CAAGTAGACC GATTGACAAA
481    AGAGTATCAC ATCTACATGA CTCGTAATGG TCGTATCAGG TATAATTATT GAGTCGTCAA
541    GTTCAAGCTT GTAAGCACCT GTATTCATAT GTACAAGTTT ATATCTGATT ATTTTTTTCC
601    CAATCTGTTT CTTTTGCTTC TTGTATGGTG CAGTATGGCA GGAGTTACTA CTGGAAATGT
661    TGGTACTTG G
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Comparison of Purple Russian (top sequence) with NC EBR-8 (bottom sequence)

Identity= 98.06%(656/669) gap=0.30%(2/671)

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1      AGTGGCAGTGAAAAGTCAGTTGCAGCAACTTGCCAGGCCCATGTACAGTAATCCACCTCT
      |||
1      AGTGGCAGTGAAAAGTCAGTTGCAGCAACTTGCCAGGCCCATGTACAGTAATCCACCTCT

61     TCATGGTGCTCTTGTTGTTTCTACAAATCCTTGAGATCCAAACTTGAAAACCTCTATGGCT
      |||
61     TCATGGTGCTCTTGTTGTTTCTACCAATCCTTGAGATCCAAACTTGAAAACCTCTATGGCT

121    CGGGGAAGTGAAAGGTTAGTTAATGGTGCTCTGGCTGCTCTTTAGCTTGGTACTCGTTTTT
      |||
121    CGGGGAAGTGAAAGGTTAGTTAATGGTGCTCTGGCTGCTCTTTAGCTTGGTACTCGTTTTT

181    AGAACATCATATGTTAAGCTAAAATTTCAATGACTTAAAGAGTTTTTTTCCAGGGCATG
      |||
181    AGAACATCATATGTTAAGCTTAAAATTTCAATGACTTAAAGAGTTTTTTATCCAGGGCATG

241    GCTGATCGTATCATCGGGATGAGAACTGCTTTAAGGGGAAATCTTGAGAAGTTGGGCTCA
      |||
241    GCTGATCGTATCATCGGGATGAGAACTGCTTTAAGGGGAAATCTTGAGAAGTTGGGCTCA

301    CCTCTATCTTGGGAACACATAACCAACCAGGTATTTGAGATCAAAGACTTCCTTCACTTT
      |||
301    CCTCTATCTTGGGAACACATAACCAACCAGGTATTTGAGATCAATGACTTCCTTCACTTT

361    CTGTAATAGTACGTAACATAAGAATTCACCTATTGTCCCCTTAATGTTTCGATCCTTCCT
      |||
361    CTGTAGTAGTACGTAACATAAGAATTCACCTATTGTCCCCTTAATGTTTCGATATCTTCCT

421    ACAGATTGGCATGTTCTGCTACAGTGGGATGACACCGGAACAAGTAGACCGATTGACAAA
      |||
421    ACAGATTGGCATGTTCTGCTACAGTGGGATGACATCGGAACAAGTAGACCGATTGACAAA

481    AGAGTATCACATCTACATGACTCGTAATGGTCGTATCAGGTATAATTATTGAGTCGTCAA
      |||
481    AGAGTATCACATCTACATGACTCGTAATGGTCGTATCAGGTATAATTATTGAGTCGTCAA

541    GTTCAAGCTTTAAGCACCTGTATTCTAT..AAAGTTTATATCTGATTGTTTTTTTCC
      |||
541    GTTCAAGCTTGTAAAGCACCTGTATTCTATGTACAAGTTTATATCTGATTATTTTTTTCC
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599  CAATCTATTCTTTTGCTTCTTGTATGGTGCAGTATGGCAGGAGTTACTACTGGAAATGT
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
601  CAATCTGTTCTTTTGCTTCTTGTATGGTGCAGTATGGCAGGAGTTACTACTGGAAATGT

659  TGGTTACTTGG
      |||||  |||||
661  TGGTTACTTGG

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Comments

Partial sequence was obtained for the six samples tested. Purple Russian and NC EBR-8 sequences differed by 13 SNPs and one two-nucleotide indel. An F2 plant from Llanero (i3/i3) had the same sequence as Purple Russian. Fla7547 and NC123S had the identical sequence to NC EBR-8, which was as expected. The hybrids, NC07196, had a sequence that was a mixture of the Purple Russian and the NC EBR-8 sequences, which indicated that it was heterozygous for the I3 gene, ie I3/i3.

For the sequence of Purple Russian there was a 100% nt identity with BAC clones LE_HBa0115A16_T7_38815 and C07SLm0075L20.1 (AC212652) at the SGN site. The NC EBR-8 sequence matched with clone LE_HBa0115A16_T7_38815 at 94% nt identity, and with clone C07SLm0075L20.1 at 97% identity at the SGN site.