

TG190, 36.3 cM, Chromosome 7 (potato-TXB 1992 map)

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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 CT226 and TG572 (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

Table 1. PCR primers on chromosome 7 (primers from Hemming et al., 2004)

Primer Name	Primer Sequence (5'-3')
PTG190F1	GCAGTACACTTCTCCTTATCATGTG
PTG190R1	AGTTTCAGTAGTTGTTCCAAATCC

*PCR at an annealing temperature of 53°C (TGEN53), ~765-bp fragment.

Sequence

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

GENBANK ACCESSION NUMBER: EU926659

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1      GCAGTACACT TCTCCTTATC ATGTGAACTC ATTTCTTATG TATTCATTGG CAGATTCCAC
61     CAAAACCAGA ACCAAAGCAT TGTACAAAAC CAGAACCTTT CCAACTGGAG AGTCTGGTCA
121    GGCATGAAAG AGAGATGCAG AGGGAATGG AAGAACGGCG AAGATTGGAG AAGGAAGAAG
181    CAATGATGAG GACTTTTATA GCACAACCAA TCTTGATCGA GTAAGACCCC TCAAAGAATG
241    ACTATTTATG AACTATATCT TTTCTGCTAG TGAATCTGAA AGATAAATCA TGTTCCTTTA
301    AATGTATAGG GATCCAATTC CAGTTCCTGA GAAAGTACGT AAGCCCCTCA CTCAAGTTCA
361    GGAATTTAAT CTACACGTAG ATCATCGTGC ACCAGATAGA GCTGAGTTTG ATAAGAAGGT
421    AAAACTTTT GTCAATTGGCG TACCACTTTC TCTGAGAAGC CTATATATAGC CACTACTCACT
481    CATATTATAA GCTGTTGTGC AGATTAAGGA GAAAGAAATG ATGTATCAAA AATACAGAGA
541    GGAGGCAGAA ACTGCAAGAT TGGTATGCAT ATTATTATAA ACTATGGTGT TATTTCCGAGC
601    ACCGCTAATG ATATGATTAG ACTAATCTC TTAATGGTGG TTAGATGGAA GAAGAGCTGG
661    CCCTGAAACA ACTACGGAAA ACCTTGGTGC CTCATGCAAG ACCTTTGCCT AAATTTGATC
721    ATCCTTTCTT GCCACAAAAG TAAGAATAAT TCTTTGTTTT TCTTTTACAT AATTGGAATT
781    TGAACAACCT ACTGAAACT
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NC EBR-8, I3/I3 (Partial Sequence) (from R. Gardner)

GENBANK ACCESSION NUMBER: EU926658

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1      GCAGTACACT TCTCCTTATC ATGTGAACTC ATTTCTTATG TATTCATTGG CAGATTCCAC
61     CAAAACCAGA ACCAAAGCAT TGTACAAAAC CTGAACCTTT CCAACTGGAG AGTCTGGTCA
121    GGCATGAAAG AGAGATGCAG AGGGAAATGG AAGAACGGCG AAGATTGGAG AAGGAAGAAG
181    CAACGATGAG GACTTTTATA GCGCAACCAA TCTTGATCGA GTAAGACCCC TCAAAGAATG
241    ACTATTTATG AACTATATCT TTTCTGCTAG TGAATCTGAA AGATAAATCA TGTTTCTTAA
301    ATGTATAGGG ATCCAATTCC AGTTCCTGAG AAAGTACGTA AGCCCTCAC TCAAGTTCAG
361    GAATTTAGTC TACACGTAGA TCATCGTGCA CCAGATAGAG CTGAGTTTGA TAAGAAGGTA
421    AACCTTTTTG TCAGTGGCGT ACCACTTTCT CTGAGAGGCC TATTATAGCC AACTCACTC
481    ATATTATAAG CTGTTGTGCA GATCAAGGAG AAAGAAATGA TGTATCAAAA ATACAGAGAG
541    GAGGCAGAAG CTGCAAGAAT GGTATGCATA TTATAAACTA TGGTGTATT TCGAGCACCG
601    CTAATGATAT GATTAGACTA ATTCTCTTAA TGGTGGTTAG ATGGAAGAAG AGATGGCCCT
661    GAAACAACCTA CGGAAAACCT TGGTGCCTCA TGCAAGACCT TTGCCTAAAT TTGATCATCC
721    TTTCTTGCCA CAAAAGTAAG AATAATTCAT GCTGCTACTC TTTGTTTTTC TTTTACATAA
781    TATTGGAATT TGGAACAACCT ACTGAAACT
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Comparison of Purple Russian (top sequence) with NC EBR-8 (bottom sequence)

Identity= 97.61%(776/795) gap=2.21%(18/813)

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1      GCAGTACACTTCTCCTTATCATGTGAACTCATTCTTATGTATTTCATTGGCAGATTCCAC
      |||
1      GCAGTACACTTCTCCTTATCATGTGAACTCATTCTTATGTATTTCATTGGCAGATTCCAC

61     CAAAACCAGAACCAAAGCATTGTACAAAACCAAGAACCTTTCCAAGTGGAGAGTCTGGTCA
      |||
61     CAAAACCAGAACCAAAGCATTGTACAAAACCTGAACCTTTCCAAGTGGAGAGTCTGGTCA

121    GGCATGAAAGAGAGATGCAGAGGGAAATGGAAGAACGGCGAAGATTGGAGAAGGAAGAAG
      |||
121    GGCATGAAAGAGAGATGCAGAGGGAAATGGAAGAACGGCGAAGATTGGAGAAGGAAGAAG

181    CAATGATGAGGACTTTTATAGCAACAACCAATCTTGATCGAGTAAGACCCCTCAAAGAATG
      |||
181    CAACGATGAGGACTTTTATAGCGCAACAACCAATCTTGATCGAGTAAGACCCCTCAAAGAATG

241    ACTATTTATGAACTATATCTTTCTGCTAGTGAATCTGAAAGATAAATCATGTTTCTTTA
      |||
241    ACTATTTATGAACTATATCTTTCTGCTAGTGAATCTGAAAGATAAATCATGTTTCTT.A

301    AATGTATAGGGATCCAATCCAGTTCCCTGAGAAAGTACGTAAGCCCTCACTCAAGTTCA
      |||
300    AATGTATAGGGATCCAATCCAGTTCCCTGAGAAAGTACGTAAGCCCTCACTCAAGTTCA

361    GGAATTTAATCTACACGTAGATCATCGTGACCAGATAGAGCTGAGTTTGATAAGAAGGT
      |||
360    GGAATTTAGTCTACACGTAGATCATCGTGACCAGATAGAGCTGAGTTTGATAAGAAGGT

421    AAAACTTTTTGTCAATGGCGTACCCTTTCTCTGAGAAGCCTATTATAGCCACACTCACT
      |||
420    AAACCTTTTTGTCAAGTGGCGTACCCTTTCTCTGAGAGCCTATTATAGCCACACTCACT

481    CATATTATAAGCTGTTGTGCAGATTAAGGAGAAAGAAATGATGTATCAAAAATACAGAGA
      |||
480    CATATTATAAGCTGTTGTGCAGATCAAGGAGAAAGAAATGATGTATCAAAAATACAGAGA
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