

## T1329, 43 cM, Chromosome 7

Ana Cristina Barillas and Douglas P. Maxwell, University of Wisconsin-Madison  
July 20, 2008

### 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')
P7-43CF3	CATGCTTGCCTAGATAACAAAGTTGG
P7-43CR3	GAAGCAACAGATTCATCCAAGTCCCCAG

\*PCR annealing temperature at 53°C (TGEN53), ~710-bp fragment.

### Sequence

#### M82 (Partial Sequence), (i3/i3)

```
1      CATGCTTGCC TAGATAACAA AGTTGGATTC AAGGTGAGCG AGCTATTCAT TTTGATATTT
61     ACCATTAGTT CTCTTGGTTG ATCAACTTGT AACATAAATT GTTGTGAGAC TAAATTACCC
121    AACCCAGAT  TCTGACTTCT GGAATGCTA ATCCAAGTGG CTTTACATCG ATTTAGGGAT
181    TTGCTGTGCC AAAAGAGGTG CAAGATAAAG TGGCCAAGTT TTCCTTCCAT GGGCAACCTG
241    CAGAGCTCAA ACATGGCAGT GTTGTGATTG CTGCTATCAC AAGTTGCACA AATACATCCA
301    ATCCCAGTGT TATGCTAGGA GCAGCTCTGG TTGCCAAAAA GGCATCTGAG CTGGGTCTAC
361    ATGTTAGTGC TACTCCATAT ACTTGCCTTA TCATTTGATT GTAATTCAGG CATGCCATCT
421    TAATCCTTGT TCCTGATTAT TTTTCAGGTT AAGCCATGGG TTAAAACTAG CCTTGCCCCA
481    GGCTCTGGTG TTGTTACAAA ATATTTACTC AAGAGGTATT GATTGGAAGT TTGTTAAAGA
541    GCAAAGTTCT ACTAACCAG ACCATTGTTA CTGAAAAACA TTGTGATATG TCATTTCTCG
601    CATGTAACAG TGGTCTACAG AAGTATTTAA ATCAGCAAGG TTTCAACATT GTTGGCTATG
661    GCTGCACCAC TTGTATAGGG AACTCTGGGG ACTTGGATGA ATCTGTTGCT TC
```

NC EBR-8, I3/I3 (Partial Sequence), inbred from R. Gardner

```
1      CATGCTTGCC TAGATAACAA AGTTGGATTG AAGGTGAGCG AGTTATTCAT TTTGATATTT
61     ACCATTAGTT CTCCTGGTTG ATCAACTTGT AACATAAATT GTTGTGAGAC TATAAATTAC
121    CCAACCCAG ATTCTGACTT CTGGAAATGC TAATCCAAC TGTCTACAT CGATTAGGG
181    ATTTGCTGTG CCAAAGAGG TGCAAGATAA AGTGCCAAG TTTTCCTCC ATGGGCAACC
241    TGCAGAGCTC AAACATGGCA GTGTGTGAT TGCTGCTATC ACAAGTTGCA CAAATACATC
301    CAATCCAGT GTTATGCTAG GAGCAGCTCT GGTGCCAAA AAGGCATCTG AGCTGGGTCT
361    ACATGTTAGT GCTACTCCAT ATACTGCTT TATCATTGA TTGTAATCA GGCATGCCAT
421    CTTAATCCTT GTTCCTGATT ATTTTTCAGG TTAAGCCATG GGTAAAACT AGCCTTGCCC
481    CAGGCTCTGG TGTGTTACA AAATATTTAC TCAAGAGGTA TTGATTGGAA GTTTGTAAA
541    GAGCAAAGTT CTAATAACCC AGACCATTGT TACTTGAAA CATTGTGATA TGTCAATTTT
601    TGCATGTAAC AGTGTCTAC AGAAGTATT AAATCAGCAA GGTTTCAACA TTGTTGGCTA
661    TGGCTGCACC ACTTGTATAG GAACTCTGG GGACTTGGAT GAATCTGTTG CTTC
```

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

```
1      CATGCTTGCC TAGATAACAAAGTTGGATTCAAGGTGAGCGAGCTATTCATTTTGATATTT
      |||
1      CATGCTTGCC TAGATAACAAAGTTGGATTCAAGGTGAGCGAGTTATTCATTTTGATATTT
      |||

61     ACCATTAGTTCTCTTGGTTGATCAACTTGTAACATAAATTGTTGTGAGAC..TAAATTAC
      |||
61     ACCATTAGTTCTCTTGGTTGATCAACTTGTAACATAAATTGTTGTGAGACTATAAATTAC
      |||

119    CCAACCCAGATTCTGACTTCTGGAAATGCTAATCCAACCTGCTTTACATCGATTTAGGG
      |||
121    CCAACCCAGATTCTGACTTCTGGAAATGCTAATCCAACCTGCTCTACATCGATTTAGGG
      |||

179    ATTTGCTGTGCCAAAAGAGGTGCAAGATAAAGTGGCCAAGTTTTCCTTCCATGGGCAACC
      |||
181    ATTTGCTGTGCCAAAAGAGGTGCAAGATAAAGTGGCCAAGTTTTCCTTCCATGGGCAACC
      |||

239    TGCAGAGCTCAAACATGGCAGTGTGTTGATTGCTGCTATCACAAGTTGCACAAATACATC
      |||
241    TGCAGAGCTCAAACATGGCAGTGTGTTGATTGCTGCTATCACAAGTTGCACAAATACATC
      |||

299    CAATCCAGTGTATGCTAGGAGCAGCTCTGGTTGCCAAAAGGCATCTGAGCTGGGTCT
      |||
301    CAATCCAGTGTATGCTAGGAGCAGCTCTGGTTGCCAAAAGGCATCTGAGCTGGGTCT
      |||

359    ACATGTTAGTGTACTCCATATACTTGCCTTATCATTGATTGTAATTCAGGCATGCCAT
      |||
361    ACATGTTAGTGTACTCCATATACTTGCCTTATCATTGATTGTAATTCAGGCATGCCAT
      |||

419    CTTAATCCTTGTTCCTGATTATTTTTCAGGTTAAGCCATGGGTTAAAACTAGCCTTGCCC
      |||
421    CTTAATCCTTGTTCCTGATTATTTTTCAGGTTAAGCCATGGGTTAAAACTAGCCTTGCCC
      |||

479    CAGGCTCTGGTGTGTTACAAAATATTTACTCAAGAGGTATTGATTGGAAGTTTGTAAA
      |||
481    CAGGCTCTGGTGTGTTACAAAATATTTACTCAAGAGGTATTGATTGGAAGTTTGTAAA
      |||

539    GAGCAAAGTTCTACTAACCAGACCATTGTTACTTGAAAACATTGTGATATGTCATTTTC
      |||
541    GAGCAAAGTTCTACTAACCAGACCATTGTTACTTGAAAACATTGTGATATGTCATTTTC
      |||

599    TGCATGTAACAGTGGTCTACAGAAGTATTTAAATCAGCAAGGTTTCAACATTGTTGGCTA
      |||
601    TGCATGTAACAGTGGTCTACAGAAGTATTTAAATCAGCAAGGTTTCAACATTGTTGGCTA
      |||

659    TGGCTGCACCACCTTGTATAGGGAACCTGGGGACTTGGATGAATCTGTTGCTTC
      |||
661    TGGCTGCACCACCTTGTATAGGGAACCTGGGGACTTGGATGAATCTGTTGCTTC
      |||
```

**Comments**

Partial sequences were obtained for four tomato samples. M82 (susceptible) and NC EBR-8 (resistant) sequences had differences of approximately 2 SNPs and 1 indel. The M820 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 100% nt identity in both GenBank and SGN sites. NC EBR-8 also matched this clone with a 99% nt identity.