

## T1329, 43 cM, Chromosome 7

Ana Cristina Barillas and Douglas P. Maxwell, University of Wisconsin-Madison  
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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 forward and reverse primers 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')
P7-43CF1	GGTTCCTGTCGACCTAGTTATTG
P7-43CR1	CTTCTGCCTCAATACCTCCGACACC

\*PCR annealing temperature at 53°C (TGEN53), ~550-bp fragment.

### Sequence

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

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1      GGTTCCTGTC GACCTAGTTA TTGATCACTC AGTTCAAGTT GATGTAACAA GGTCAGAAAA
61     TGCAGTCCAG GCTAATATGG AGCTTGAATT CCAAAGGAAT AAGGAGAGAT TTGCCTTCCT
121    TAAGTGGGGA TCCAATGCTT TCCAAAACAT GCTTGTGTGT CCACCTGGGT CTGGTATTGT
181    GCATCAGGTA TTGTACCTGA AACTGAATG TGACTTAGCT GCTTGTGCTT CTGGATTTGG
241    TCAATGTGAT AGTTGTGCTG AGCTCTAACT ATTTCTTGAA TCATGAATTC TTCAGCTTTG
301    CATGCTCTTA CTTATCTTCC CTCGTTAGAG GATTGGAGT GAGTTTCCAC TTCTGAAACA
361    GTGGATTTGC AAAACTGATA ATATTTTCTT CTATTGTAAT TTTAGGTGAA TCTTGAATAT
421    CTTGGAAGGG TTGTGTTCAA TAGGGAAGGC TTGCTCTACC CAGATAGCGT GGTCGGAACA
481    GATTCCCACA CCACTATGAT TGATGGGTTA GGANTTGTCT GCTGGGGTGT CGGAGGTATT
541    GAGGCAGAAG
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## NC EBR-8, I3/I3 (Partial Sequence), inbred from R. Gardner

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1      GGTTCCTGTC GACCTAGTTA TTGATCACTC AGTTCAAGTT GATGTAACAA GGTCAGAAAA
61     TGCAGTCCAG GCTAATATGG AGCTTGAATT CCAAAGGAAT AAGGAGAGAT TTGCCTTCCT
121    TAAGTGGGGA TCCAATGCTT TCCAAAACAT GCTTGTGTTT CCACCTGGGT CTGGTATTGT
181    GCATCAGGTA TTGGACCTGA AACTGAATG TGACTTAGCT GCTTGTGCTT CTGGATATGG
241    TCAATGTGAT AGTTGTGCTG AGCTCTAGCT ATTTCTTGAA TCATGAATTC TTCAACTTTG
301    CATGCTCTTA CTTATCTTCC CTTGTTGGAG GATTTGGAGT GAGTTCCAC TTCTGAAACA
361    GTGCATTTGC AAAACTGATA ATATTTTCT CTATTGTAAT TTTAGGTGAA TCTTGAATAT
421    CTTGGAAGGG TTGTGTTCAA TAGGGAAGGC TTGCTCTACC CAGATAGCGT GGTCGGAACA
481    GATTCCCACA CCACTATGAT TGATGGGTTA GGANTTGCTG GCTGGGGTGT CGGAGGTATT
541    GAGGCAGAAG
```

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

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1      GGTTCCTGTCGACCTAGTTATTGATCACTCAGTTCAAGTTGATGTAACAAGGTCAGAAAA
|||
1      GGTTCCTGTCGACCTAGTTATTGATCACTCAGTTCAAGTTGATGTAACAAGGTCAGAAAA

61     TGCAGTCCAGGCTAATATGGAGCTTGAATTCCAAAGGAATAAGGAGAGATTTGCCTTCCT
|||
61     TGCAGTCCAGGCTAATATGGAGCTTGAATTCCAAAGGAATAAGGAGAGATTTGCCTTCCT

121    TAAGTGGGGATCCAATGCTTTCCAAAACATGCTTGTGTTCCACCTGGGTCTGGTATTGT
|||
121    TAAGTGGGGATCCAATGCTTTCCAAAACATGCTTGTGTTCCACCTGGGTCTGGTATTGT

181    GCATCAGGTATTGTACCTGAAAACCTGAATGTGACTTAGCTGCTTGTGCTTCTGGATTGG
|||
181    GCATCAGGTATTGTGACCTGAAAACCTGAATGTGACTTAGCTGCTTGTGCTTCTGGATATGG

241    TCAATGTGATAGTTGTGCTGAGCTCTAACTATTTCTTGAATCATGAATTCCTCAGCTTTG
|||
241    TCAATGTGATAGTTGTGCTGAGCTCTAGCTATTTCTTGAATCATGAATTCCTCAACTTTG

301    CATGCTCTTACTTATCTTCCCTCGTTAGAGGATTTGGAGTGAGTTTCCACTTCTGAAACA
|||
301    CATGCTCTTACTTATCTTCCCTTGTGAGAGGATTTGGAGTGAGTTTCCACTTCTGAAACA

361    GTGGATTGCAAAACTGATAATATTTTCTCTATTGTAATTTAGGTGAATCTTGAATAT
|||
361    GTGCATTTGCAAAACTGATAATATTTTCTCTATTGTAATTTAGGTGAATCTTGAATAT

421    CTTGGAAGGGTTGTGTTCAATAGGGAAGGCTTGCTCTACCCAGATAGCGTGGTCGGAACA
|||
421    CTTGGAAGGGTTGTGTTCAATAGGGAAGGCTTGCTCTACCCAGATAGCGTGGTCGGAACA

481    GATTCCCACACCACTATGATTGATGGGTTAGGANTTGCTGGCTGGGGTGTCCGAGGTATT
|||
481    GATTCCCACACCACTATGATTGATGGGTTAGGANTTGCTGGCTGGGGTGTCCGAGGTATT

541    GAGGCAGAAG
|||
541    GAGGCAGAAG
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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 7 SNPs. 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 (28,687 nt) with a 99% nt identity, as did NC EBR-8 with a 98% nt identity, at the GenBank (AC212624) and SGN sites. M82 also matched the clones SL\_EcoRI0098D07\_T7\_310033 with a

99% nt identity, and LE\_HBa0006P10\_SP6\_3042 with 100% nt identity. NC EBR-8 matched the same clones with a 97% and a 98% nt identity, respectively.