

Chromosome 6, 28 cM

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Primers

The Gene (GTH-SGN_E_tom_potato_gene_2_AGS_804) of BAC clone C06HBa0167M06 was compared with GenBank sequences and it matched the *Capsicum annuum* putative isopropylmalate synthase mRNA (EU616568). This match was used to design primers for exons, which would amplify two introns and one exon.

P6-28 F1: CAGAACGATCTTGGGCTTTCTACTGC
P6-28 R2: CCATCTTGCTTGACATGAGTATATG

Annealing Temperature: 53°C, a single PCR fragment was produced, which was directly sequenced.

RIL Families:

Gh13 was the source of resistance for the RILs and it is known to have an introgression from about 19 cM to 32 cM. RIL34 (W312) has the Ty3 introgression marker at 25 cM and is resistant to begomoviruses; and RIL5 (W316) does not have the Ty3 introgression marker and is susceptible.

Partial Sequence of P6-28 F1/R2 W316 (Sequence from RIL316, *S. lycopersicum* sequence)

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1      GTCAGAACGA TCTTGGGCTT TCTACTGCCA ACACCTTAGC TGTATGTGGT TCAATGTTGA
61     TGAGAACCTT AGATGTTTAT GCCATCTTAA GTTGTATGCA CATTAAAGCG TGTCCAATTT
121    CAGGGAGCAT GTGCAGGTGC AAGACAATTG GAAGTGACCA TCAATGGAAT TGGTGAAAGA
181    GCTGAAAATG CTTCTTTAGA GGAGGTGTGT GAGGGCTTTC CGCTGAGAAA TTTCAGTTCT
241    CTTATGTGCA TGATTTGGGC TCCAAAATTT GAGGGGTGGA ATCACTAATT AAACAACCTT
301    GACTATAAGT TCCCCTCTGT TCTTTCCTTG AAAAAAAGTT AGGTCTTCAA AGAAATTTCC
361    CATAATTGCG TAAGGCATTC TCCACACAAA AGGAACTATT CCACCTCTTC CTAGAGTAAA
421    TTAACATCTT TAATTTAGAC TGAATGACTG AACTAGAGT AGAAGTTGTG TGGTATGTAA
481    TATTATTCTT TTGCAAAAACA ATAGTTGCAA ACATGCAACC GTATTTTGCC ATTTTGGTCT
541    TTGGAGCCAA TTTCTGCCAT TGGTTGTGTT ATGTGCTGTT TAAACTGACA AACTACTGAC
601    GTTCATGAGA CTCCTTTTTT CTTCTGTGGT CTTGTTTGTG TTTGGTTTTT ATCTTGGCAT
661    GTCGGGCCTT CATTTTCTAA CCTTTTACCA TGNNNNNNNA ATAGGTTGTA ATGGCCTTAA
721    AGTGTCTGGG AGAGCAAGTA CTAGGGTGCC C
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Partial Sequence of P6-28 F1/R2 W312

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1      GTCAGAACGA TCTTGGGCTT TCTACTGCCA ACACCTTAGC TGTATGTGGT TCAATGTTGA
61     TGAGAACCTA GTTGTTTTATG CCAACTTAAG TTGTATGCAC ATTAAGCGT GTCCAATTTT
121    AGGGAGCATG TGCAGGTGCA AGACAATTGG AAGTGACCAT CAATGGAATT GGTGAAAGAG
181    CTGAAAATGC TTCTTTAGAG GAGGTGCGTG AGGGCCTTTT GCTGAGAAAT TTCAGTTCTC
241    TTATGTGCAT GATTTGGGCT CCAGAATTG GAGGGTGGA TCACTAATTA AACACCTTG
301    ACTATAAGTT CTCTCTGTT CTTTCTTGA CAAAAAGTTA GGCTTCAA GAAATTTCC
361    ATAATCTCGT AAGGCATTTT CCGCACAAA GGAACCTATC CACCTTCC TAGACTAAAT
421    TAACATCTTT AATTTAGACT AACTAGAG TAGAAGTTGT GTGGTACGTA ATATTATTCT
481    TTTGCAAAAC AATAGTTGCA AACATGCAAC CGTATTTTGC CATTTTGGT TTTGGAGCCA
541    ATTTCTGCCA TTGGTTGTGT TATGTGCTGT TAAAACTGAC AAACACTGA CGTTCATGAG
601    ACTCCTTTTT CCTCTGTGGT ACTTGTGTTG CTTTGGTTTT CATCTTGGGC ATGTCGGCCT
661    TCATTTTCTA ACCTTTTACC A
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Comparison of W312 with W316

Upper line: W312, from 1 to 684

Lower line: 316, from 1 to 690

W312:316 identity= 97.65%(665/681) gap=1.73%(12/693)

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1      GTCAGAACGATCTTGGGCTTTCTACTGCCAACACCTTAGCTGTATGTGGTTCAATGTT
      |||
1      GTCAGAACGATCTTGGGCTTTCTACTGCCAACACCTTAGCTGTATGTGGTTCAATGTT

61     GATGAGAACCTAGTTGTTTATGCCAACTTAAGTTGTATGCACATTAAGCGTGTCCAAT
      |||
59     GATGAGAACCTAGATGTTTATGCCATCTTAAGTTGTATGCACATTAAGCGTGTCCAAT

120    TTCAGGGAGCATGTGCAGGTGCAAGACAATTGGAAGTGACCATCAATGGAATTGGTGAAA
      |||
119    TTCAGGGAGCATGTGCAGGTGCAAGACAATTGGAAGTGACCATCAATGGAATTGGTGAAA

180    GAGCTGGAAATGCTTCTTTAGAGGAGGTGCGTGAGGGCCTTTGCTGAGAAATTCAGTT
      |||
179    GAGCTGGAAATGCTTCTTTAGAGGAGGTGTGTGAGGGCTTCCGCTGAGAAATTCAGTT

240    CTCTTATGTGCATGATTTGGGCTCCAGAATTTGAGGGGTGGAATCACTAATTAACAACC
      |||
239    CTCTTATGTGCATGATTTGGGCTCCAATAATTTGAGGGGTGGAATCACTAATTAACAACC

300    TTGACTATAAGTTCCTCTGTCTTTCTTGA CAAAAAGTTAGGTCTTCAAAGAAATTT
      |||
299    TTGACTATAAGTTCCTCTGTCTTTCTTGA AAAAAAGTTAGGTCTTCAAAGAAATTT

360    CCCATAATCTCGTAAGGCATTCTCCGCACAAAAGGA ACTATTCACCTCTCCTAGACTA
      |||
359    CCCATAATGCGTAAGGCATTCTCCACACAAAAGGA ACTATTCACCTCTCCTAGAGTA

420    AATTAACATCTTTAATTTA.....GACTAATACTAGAGTAGAAGTTGTGTGGTACGT
      |||
419    AATTAACATCTTTAATTTAGACTGAATGACTGATACTAGAGTAGAAGTTGTGTGGTATGT

472    AATATTATTCTTTTGCAAAACAATAGTTGCAAACATGCAACCGTATTTTGCCATTTGGT
      |||
479    AATATTATTCTTTTGCAAAACAATAGTTGCAAACATGCAACCGTATTTTGCCATTTGGT

532    CTTTGGAGCCAATTTCTGCCATTGGTTGTGTTATGTGCTGTTAAACTGACAACTACTG
      |||
539    CTTTGGAGCCAATTTCTGCCATTGGTTGTGTTATGTGCTGTTAAACTGACAACTACTG

592    ACGTTCATGAGACTCCTTTTTCTCTGTGGTACTTGTGTTGCTTTGGTTTTTCATCTTGG
      |||
599    ACGTTCATGAGACTCCTTTTTCTCTGTGGTACTTGTGTTGCTTTGGTTTTTCATCTTGG

652    CATGTCGGGCCTTCATTTTCTAACCTTTTACCA
      |||
658    CATGTCGGGCCTTCATTTTCTAACCTTTTACCA
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Blast Search: (search sequence = W316, susceptible genotype)

Matched nothing with greater than 90% nucleotide identity on NCBI database.

Matched the following BAC clone on SGN website: [C06HBa0261A18.1](#)

(AC211067.1)

```
Query: 3      cagaacgatccttgggcttttctactgccaacaccttagctgtatgtggttcaatggtgatg 62
              |||
Sbjct: 43490  cagaacgatccttgggcttttctactgccaacaccttagctgtatgtggttcaatggtgatg 43549

Query: 63      agaaccctagatggtttatgccatcttaagttgtatgcacattaaagcgtgtccaatttca 122
              |||
Sbjct: 43550  agaacc-tagatggtttatgccatcttaagttgtatgcacattaaagcgtgtccaatttca 43608

Query: 123     gggagcatgtgcaggtgcaagacaattggaagtgacctcaatggaattggtgaaagagc 182
              |||
Sbjct: 43609  gggagcatgtgcaggtgcaagacaattggaagtgacctcaatggaattggtgaaagagc 43668

Query: 183     tggaaatgcttcttttagaggaggtgtgtgagggctttccgctgagaaatttcagttctct 242
              |||
Sbjct: 43669  tggaaatgcttcttttagaggaggtgtgtgagggctttccgctgagaaatttcagttctct 43728

Query: 243     tatgtgcatgatttgggctccaaaatttgaggggtggaatcactaattaacaaccttga 302
              |||
Sbjct: 43729  tatgtgcatgatttgggctccaaaatttgaggggtggaatcactaattaacaaccttga 43788

Query: 303     ctataagttcccctctgttctttccttgaaaaaaagttaggctcttcaaagaaatttcca 362
              |||
Sbjct: 43789  ctataagttcccctctgttctttccttgaaaaaaagttaggctcttcaaagaaatttcca 43848

Query: 363     taattgcgtaaggcatttctccacacaaaaggaactattccacctcttcttagagtaaatt 422
              |||
Sbjct: 43849  taattgcgtaaggcatttctccacacaaaaggaactattccacctcttcttagagtaaatt 43908

Query: 423     aacatctttaatttagactgaatgactgatactagagtagaagttgtgtggtatgtaata 482
              |||
Sbjct: 43909  aacatctttaatttagactgaatgactgatactagagtagaagttgtgtggtatgtaata 43968

Query: 483     ttattcttttgcaaaaacaatagttgcaaacatgcaaccgtattttgccattttggtcttt 542
              |||
Sbjct: 43969  ttattcttttgcaaaaacaatagttgcaaacatgcaaccgtattttgccattttggtcttt 44028

Query: 543     ggagccaatttctgccattggttgtgttatgtgctgtttaaactgacaaactactgacgt 602
              |||
Sbjct: 44029  ggagccaatttctgccattggttgtgttatgtgctgtttaaactgacaaactactgacgt 44088

Query: 603     tcatgagactccttttctctgtggtacttgtttgtctttgggttttcatctt-ggcatg 661
              |||
Sbjct: 44089  tcatgagactccttttctctgtggtacttgtttgtctttgggttttcatcttgggcatg 44148

Query: 662     tcgggccttcattttctaaccttttaccatg 692
              |||
Sbjct: 44149  tcgggccttcattttctaaccttttaccatg 44179
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