

MK00003=Q1/850

Marker: Q1/850

Type: Codominant

Description: STS primers (derived from a subset of RAPD markers) that were tested for polymorphisms at the *Mj-1* locus in carrot. Linked to *Mj-1*.

Reference: [Leonardo Ph.D. Thesis](#) page 201, 213

Primers: Q1/800 Forward 5'-GGA CGA TGG CCA GGG AAA GC-3'
Q1/800 Reverse 5'-AAC CAA GTC ACG CCA ACA GTA AAT-3'

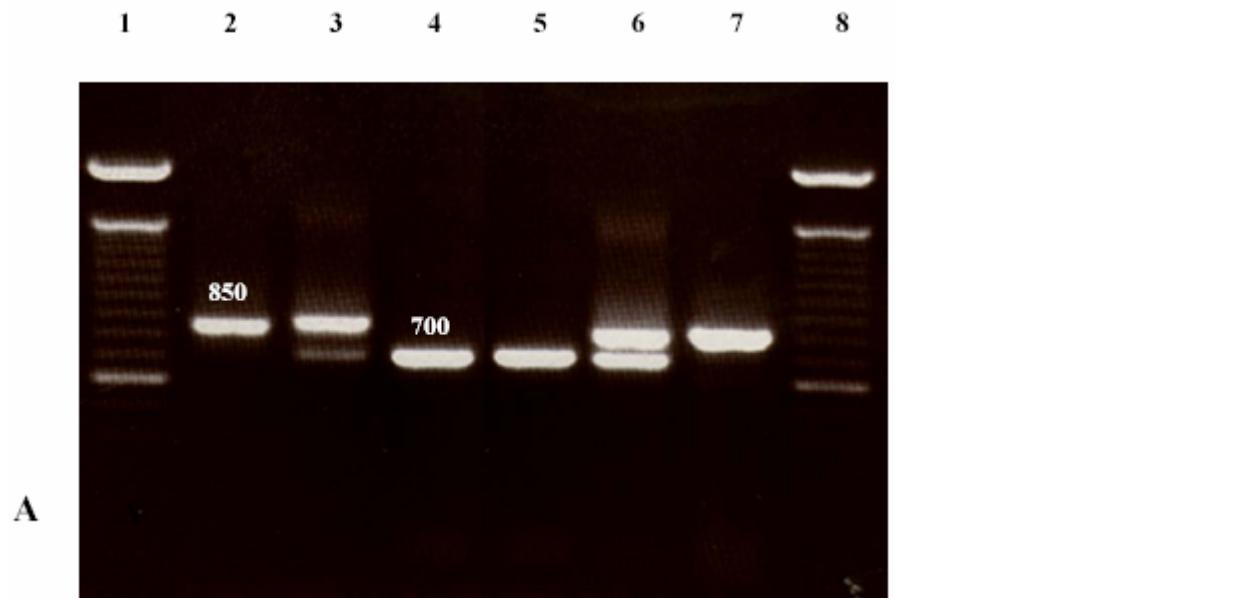
PCR Reaction: "DNA amplification reaction was done with 23µl master mix reaction + 2µl DNA template. The master mix consisted of 11.32µl of milliQ water, 2.5µl of 10x DNA polymerase buffer, 2.3µl of MgCl₂ (25mM), 5.7µl of deoxynucleotide triphosphates (0.5mM of each), 1µl of primer (5mM), and 0.18µl (5 units/µl) of thermostable DNA polymerase (Perkin Elmer). PCR was done with either Perkin Elmer Cetus 9600 or 9700 thermocyclers."

PCR Program: 94°C 2:00; 40 cycles of {94°C 0:30; 59°C 1:00; 72°C 1:30}; 68°C 10:00

Screening Method: Agarose Gel, size difference

Product Sizes: Susceptible: 700 b.p.
Resistant: 850 b.p.

Example: Leonardo Ph.D. Thesis page 204=Figure 4.2. Agarose gel electrophoresis of the codominant sequence-tagged site (STS) marker SQ1850 / SQ1700. Lanes 1 and 8 = 100bp ladder; Lane 2 = 'Brasília-1252'; Lane 3 = 'HCM'; Lane 4 = 'USDA 6274B'; Lane 5 = homozygous susceptible; Lane 6 = heterozygous and Lane 7 = homozygous resistant F2 individual from the cross 'Brasilia-1252' x '6274B'.



Sequence Information:

The sequence of the Q1 (OPQ-01) RAPD primer is GGGACGATGG

Leonardo's Ph.D. thesis has two relevant sequences, these have been placed in our database as VC000025 (Original title OP-Q1/800) and as VC000026 (Original title SQ1/700 US)

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>VC000025 OP-Q1/800 BR Sequenced RAPDs from Leonardo Ph.D. Thesis Table 8.25
GAATTCCGCCCTAACCAAGTCACGCCAACAGTAAATTATGGATTTGCAAATATTGTGTTATGACCATCAGCAATTGGTATATGTTATGTGTG
GTTTGTGGAAGACAATGTTAATCAGCCCATTGTTAGCAATTGTGCTTATAGTGCAGAAAGTTCTGTTGACATGATGGTCTTCCCTAATTTCAG
CAACTATAGGAAACCAACAAACAAAATTACAGTCAGAGTAGTATGGTATGCCGTTCTGTGAGTCTGGGATGTAGCTAGCACTGCATAGCATGA
ATATATAGAAGTTGTCTCTAATCATGAAGCTGTACATGTTAGGTTATGATTAATACTTATGCTGTGACAAAGTTCTGATGGCAAGTTGCCGA
GTATCACCCCTTTGCATATGATCGCTTTTGAGGCTCGGAGCCTCAAATGGTACACAGAACAAAATTGGATACTGCACCAATAGGTAGTA
TGGAGCCTCCAATAATGCCGAACTGCCATTCCCTGACATCATTGAAAATGCACCAAATAATGACAATACAGGTACACTATAAGAATTATCATCTCG
TTAAGAAAATAAGTTGAGTTATGCCCTAGCCAATTGGTATGATACAATGTTATTGACTTTATGGTAAACAATGTTATTACATAAAAGTCAG
GATAGCAAAATTGAAATTGATGATGATATTGGTACCCACACATAGAATGATGAGAATGTTCTCCATGGTAAAGGTATGGAAGA
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TTCCCGTGGACGTGATGTCAACTTCGTAATACTAACACCGAGCTTCCCTGGCCATCGTCCAAGGGCGAATT

>VC000026 SQ1/700 US Sequenced RAPDs from Leonardo Ph.D. Thesis Table 8.25
GAATTGCCCTTAACCAAGTCACGCCAACAGTAAATTACAGATTGTAAATATTGTGTTATGACCATTAGCAATATGGTATATGTTATGTGTA
GTTGTGGAAGACAATGTTAATCAGCCATTGTTAGCAATTGTCCTTATAGTGCAAAGGTTCTGTTGACATGATGGCTTCCCTAATTTCAG
CAACTATAGGAAACCAACAACAAATTACAGTCAGAGTAGTATGGTATGCTGTTGAGTCTGGGATGTAGCTGACACTGCATAGCATGA
ATATATAGAAGTTGCTCTAATCATGAAGCTGTACATGCTTAGGTTAGTTAATGCTGACAAGGTTCTGATGGCAAGTGCCGA
GTATCACCCCTCTTGCAATGATGTTTTGTTAGGCCGAGCCTAAATGGTACACGGAAACAAAATTGGGAACTGACCAATAGGTAGTA
TGGAGCCTCCAAATAATGCGAACTGCCTATTCTGACATCATTGAAAGGAAATGCAACATAGGTTAACTATAAGAATTATCATCTCG
TTAAGAAAAAAATAGTTGAGTTATGCTCAGCCAAATTGTTAGTATGACATACAGGTTAACTATAAGAATTATCATCTCG
ACTAACACCGAGCTTCCCTGGCCATCGTCCAAGGGCGAATT

Q1/800 US nema from file Q1_800.doc 5/9/2000 = sequence of original RAPD band. **Green** marks the RAPD primer location:

Q1/800 US nema

>VC012706 The original full sequence of the Q1-800 RAPD band, from file Q1_800.doc 5/9/2000; has been reverse complemented to match Leonardo Thesis orientation

GAATTGCCCTTGGACGATGCTACAATATAATGCTCTTATAAATCTGAAAGTATAAATTGATTTGCTGATAATATATATTGAATGCT
TAAATAGATGATTAGAGAACGATTATTGTTTATAACCTTATATTACAGGATTAGTCATTAGTCATAGTTATTCTGAGGTGTTGCA
TTGTTGGGATAATGGATGCTAGGAGATTAAGTTTACATTCACTTACAGTAAACCAAGTCACGCCAACAGTAAATTTCAGAGATTGTA
TGTGTTATTGACCATAGCAATTGTTATGTTGTTAGTGTAGTTGTTGGAAGAACATACTGCTTGTGACATGAGGTTGCTTATAGTG
CAAAGTCTGTGTTGATGATGGTCTTTCCCTAATTTCAGTACAGTACAGCAACTATAGGAAACCaACAAATTACAGTACAGTAGTATGGT
CGTGTGAGTCTGGATGATGATAGCTAGCACTGCATAGCATGAATATAAGAAGTTGCTCTAATCATGAAGCTGTACATGCTTAGGTTAGT
AATACTTATTGCTGACAAAGTCTGATGGCAAGTGGCAGTACACCCCTCTTGCAATATGATCGCTTTTGAGGCTCGGAGCCTAAATG
GTGACACGAAACAAAATTGGATACTGCACCAATAGGAGTATGGAGCTCCAAATAATGCCAATGCTTACATTGACATCATTGAAAGCACC
AAATAATGACAACACAGGTTAACTATAAGAATTATCATCTGTTAAGAAAATAAGTGTGAGTTATGCTCAGCCAAATTGTTAGTATGATA
TATTGACTTTATGTTGAAACAATGTTTACATAAGGTAATACTAACACCGAGCTTCCCTGGCCATCGTCCAAGGGCGAATT
698 bp primer to primer

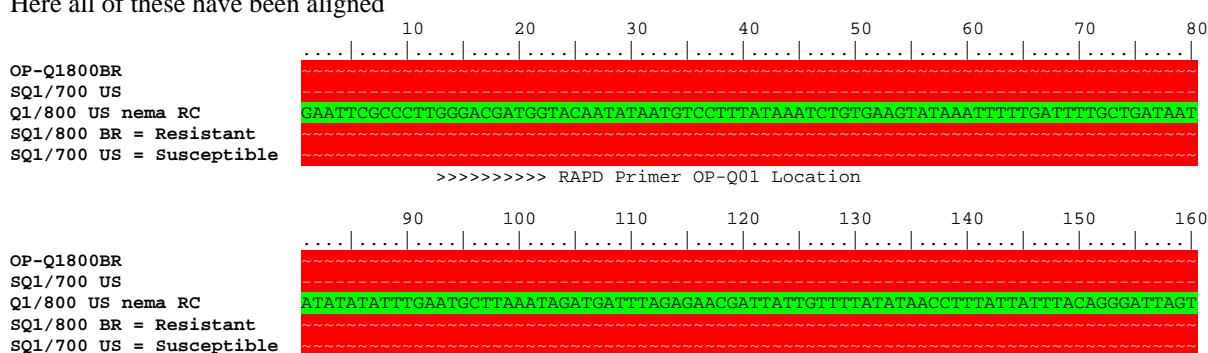
SQ1/800 BR = Resistant

GAATTGCCCTTAACCAAGTCACGCCAACAGTAAATTACAGATTGCAAATATTGTGTTATGACCATTAGCAATTTGGTATATGTTATGTGTA
GTTGTGGAAGACAATGTTAATCAGCCATTGTTAGCAATTGTCCTTATAGTGCAAAGGTTCTGTTGACATGATGGCTTCCCTAATTTCAG
CAACTATAGGAAACCAACAACAAATTACAGTCAGAGTAGTATGGTATGCTGTTGAGTCTGGGATGTAGCTGACACTGCATAGCATGA
ATATATAGAAGTTGCTCTAATCATGAAGCTGTACATGCTTAGGTTAGTTAATGCTGACAAGGTTCTGATGGCAAGTGCCGA
GTATCACCCCTCTTGCAATGATGCTTTTGTTAGGCCGAGCCTAAATGGTACACGGAAACAAAATTGGGAACTGACCAATAGGTAGTA
TGGAGCCTCCAAATAATGCCAACTGCCTATTCTGACATCATTGAAAGGAAATGCAACATAGGTTAACTATAAGAATTATCATCTCG
TTAAGAAAAAAATAGTTGAGTTATGCTCAGCCAAATTGTTAGTATGACATACAGGTTAACTTGTGAAACAAATGTTATTACATAAGGT
CAGGATAGCAAATTGAGTTGAGTAAATGATAATTGTTAGGTCACCCACACATAGAATGATGAGAATGTTCTCCATGGTGAAGGTATGGAAGA
TTCCCGTGGACGTGATGTCACTTCGTTAACTAACACCGAGCTTCCCTGGCCATCGTCCAAGGGCGAATT
826 bp primer to primer

SQ1/700 US = Susceptible

GAATTGCCCTTAACCAAGTCACGCCAACAGTAAATTACAGATTGCAAATATTGTGTTATGACCATTAGCAATTTGGTATATGTTATGTGTA
GTTGTGGAAGACAATGTTAATCAGCCATTGTTAGCAATTGTCCTTATAGTGCAAAGGTTCTGTTGACATGATGGCTTCCCTAATTTCAG
CAACTATAGGAAACCAACAACAAATTACAGTCAGAGTAGTATGGTATGCTGTTGAGTCTGGGATGTAGCTGACACTGCATAGCATGA
ATATATAGAAGTTGCTCTAATCATGAAGCTGTACATGCTTAGGTTAGTTAATGCTGACAAGGTTCTGATGGCAAGTGCCGA
GTATCACCCCTCTTGCAATGATGCTTTTGTTAGGCCGAGCCTAAATGGTACACGGAAACAAAATTGGGAACTGACCAATAGGTAGTA
TGGAGCCTCCAAATAATGCCAACTGCCTATTCTGACATCATTGAAAGGAAATGCAACATAGGTTAACTATAAGAATTATCATCTCG
TTAAGAAAAAAATAGTTGAGTTATGCTCAGCCAAATTGTTAGTATGACATACAGGTTAACTTGTGAAACAAATGTTATTACATAAGGT
ACTAACACCGAGCTTCCCTGGCCATCGTCCAAGGGCGAATT
698 bp primer to primer

Here all of these have been aligned



The figure displays two genomic sequence alignments. The top alignment shows the OP-Q1800BR sequence (Q1/800 US nema RC) and the Q1/800 sequence (Q1/800 BR = Resistant, Q1/700 US = Susceptible). The bottom alignment shows the OP-Q1800BR sequence and the Q1/800 sequence. Both alignments have a scale from 970 to 1040 on the top and 1050 to 1120 on the bottom. Green boxes highlight specific regions: a long segment from approximately 975 to 1035 in the top alignment and a shorter segment from approximately 1055 to 1105 in the bottom alignment. Below the alignments, arrows indicate the locations of RAPD primers: an arrow pointing left labeled "RAPD Primer OP-Q01 Location" and another arrow pointing left labeled "Q1/800 Reverse Primer Location".