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Alignment of sequences for the Mi23 locus for: M82, M82-1-8, mi/mi; LA1606, *S. pimpinellifolium*; LA2184, *S. pimpinellifolium*; Gc9, resistant to begomoviruses, introgression from *S. chilense* LA2779; TY52, resistant to TYLCV, with introgression from *S. chilense* LA1969 for the *Ty-1* gene; LA2779, *S. chilense*; LA1932, *S. chilense*; LA0392, *S. arcanum*; LA3858, *S. peruvianum*; LA3900, *S. peruvianum*; Gh2, Mi/Mi, resistant to root-knot nematode and also resistant to begomoviruses.

M82	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
LA1606	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
LA2184	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
Gc9	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
TY52	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
LA2779	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
LA1932	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTtAAAaTATGAAAACAAGTATT	60
LA0392	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
LA3858	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
LA3900	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
Gh2	TGGAAAAATGTTGAATTTCTTTTGTAAGTGTACAAAGTTAAAATTATGAAAACAAGTATT	60
Consensus	tggaaaaatgttgaatTTCTTTTGTAAGTGTACAAAGTT aaa tatgaaaacaagtatt	

M82	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCAAATTTGAGCGGAGAAATGTGACAGTTC	120
LA1606	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCAAATTTGAGCGGAGAAATGTGACAGTTC	120
LA2184	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCAAATTTGAGCGGAGAAATGTGACAGTTC	120
Gc9	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCtAAATTTGAGCGGAGAAATGTGACAGTTC	120
TY52	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCtAAATTTGAGCGGAGAAATGTGACAGTTC	120
LA2779	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCtAAATTTGAGCGGAGAAATGTGACAGTTC	120
LA1932	TGGAGTTTCTAAAATTTTGGAAATATTCTagCtAAATTTGAGCGGAGAAATGTGACAGTTC	120
LA0392	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCAAATTTGAGCGGAGAAAT.....	110
LA3858	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCAAATTTGAGCGGAGAAAT.....	110
LA3900	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCAAATTTGAGCGGAGAAAT.....	110
Gh2	TGGAGTTTCTAAAATTTTGGAAATATTCTGGCAAATTTGAGCGGAGAAAT.....	110
Consensus	tggagtttctaaaatTTTGGAAATATTct gc aaatttgagcggagaaat	

M82	ACGTCCAAATCTCCAGAGTCTTCATACATAGAAGTGTCAAACAAATTGGCAGGTTCTTAC	180
LA1606	ACGTCCAAATCTCCAGAGTCTTCATACATAGAAGTGTCAAACAAATTGGCAGGTTCTTAC	180
LA2184	ACGTCCAAATCTCCAGAGTCTTCATACATAGAAGTGTCAAACAAATTGGCAGGTTCTTAC	180
Gc9	ACGTCCAAATCTCCAGAGTCTTCATACATAGAAGTGTCAAACAAAtttaGCAGGTTCTTAC	180
TY52	ACGTCCAAATCTCCAGAGTCTTCATACATAGAAGTGTCAAACAAAtttaGCAGGTTCTTAC	180
LA2779	AtGTCCAAATCTCCAGAGTCTTCATACATAGAAGTGTCAAACAAATTGGCtGGTTCTTAC	180
LA1932	ACGTCCAAATCTCCAGAGTCTTCATACATAGAAGTGTCAAACAAATTGGCAGGTTCTTAC	180
LA0392TGGCAGGTTCTTAC	124
LA3858TGGCAGGTTCTTAC	124
LA3900TGGCAGGTTCTTAC	124
Gh2TGGCAGGTTCTTAC	124
Consensus	t gc ggttcttac	

M82	A.CCTTTTACTGTTCTAAAAAGATGTCTACAATT T GTTTCATCAAAGCCCCGACGGAACT	239
LA1606	A.CCTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTTCATCAAAGCCCCGACGGAACT	239
LA2184	A.CCTTTTACTGTTCTAAAAAGATGTCTACAATT T GTTTCATCAAAGCCCCGACGGAACT	239
Gc9	AtCtTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTTCATCAAAGCCCCGACGGAACT	240
TY52	AtCtTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTTCATCAAAGCCCCGACGGAACT	240
LA2779	AtCtTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTTCATCAAAGCCCCGACGGAACT	240
LA1932	AtCtTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTTCATCAAAGCCCCGACGGAACT	240
LA0392	AtCtTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTTCATCAAAGCCCCGACGGAACT	184
LA3858	AtCtTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTT g ATCAAAGCCCCGACGGAACT	184
LA3900	AtCtTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTT g ATCAAAGCCCCGACGGAACT	184
Gh2	AtCtTTTTACTGTTCTAAAAAGATGTCTACAATTcGTTT g ATCAAAGCCCCGACGGAACT	184
Consensus	a c ttttactgttctaaaaagatgtctacaatt gttt atcaaagccccgacggaact	
M82	ATTAAGTAGACGACGTTAGTAAAATAACAAGCAACCAAAGCAGTT AC GAGAGATCACTTT	299
LA1606	ATTAAGTAGACGACGTTAGTAAAATAACAAGCAACCAAAGCAGTT AC GAGAGATCACTTT	299
LA2184	ATTAAGTAGACGACGTTAGTAAAATAACAAGCAACCAAAGCAGTT AC GAGAGATCACTTT	299
Gc9	ATTAAGTAGACG g GTTAGTAAAATAACAAGCAACCAAAtCAGTTtaGAGAGATCACTTT	300
TY52	ATTAAGTAGACG g GTTAGTAAAATAACAAGCAACCAAAtCAGTTtaGAGAGATCACTTT	300
LA2779	ATTAAGTAGACG g GTTAGTAAAATAACAAGCAACCAAAGCAGTTtaGAGAGATCACTTT	300
LA1932	ATTAAGTAGACGACGTTAGTAAAATAACAAGCAACCAAAtCAGTTtaGAGAGATCACTTT	300
LA0392	ATTAAGTAGACGACGTTAGTAAAATAACAAGCAACCAAAGCAGTTtaGAGAGATCACTTT	244
LA3858	ATTAAGTAGACG g GTTAGTAAAATAACAAGCAACCAAAGCAGTTtaGAGAGATCACTTT	244
LA3900	ATTAAGTAGACG g GTTAGTAAAATAACAAGCAACCAAAGCAGTTtaGAGAGATCACTTT	244
Gh2	ATTAAGTAGACG g GTTAGTAAAATAACAAGCAACCAAAGCAGTTtaGAGAGATCACTTT	244
Consensus	attaagtagacga gtttagtaaaataacaagcaacccaaa cagtt gagagatcacttt	
M82	TTTCCCA GGGG ATTTTTCTAGTAAGATTTTTAA TCAAGCA CATTATCT ACT AAATATATAG	359
LA1606	TTTCCCA GGGG ATTTTTCTAGTAAGATTTTTAA TCAAGCA CATTATCT ACT AAATATATAG	359
LA2184	TTTCCCA GGGG ATTTTTCTAGTAAGATTTTTAA TCAAGCA CATTATCT ACT AAATATATAG	359
Gc9	TTTCCCAcGG a ATTTTTCTAGTAAGATTTTTAAcC Ag GCAtATTATCTtCTAAATATATAG	360
TY52	TTTCCCAcGG a ATTTTTCTAGTAAGATTTTTAAcC Ag GCAtATTATCTtCTAAATATATAG	360
LA2779	TTTCCCAcGGGATTTTTCTAGTAAGATTTTTAAcC Ag aCatATTATCTtCTAAATATATAG	360
LA1932	TTTCCCAcGGGATTTTTCTAGTAAGATTTTTAAcC Ag GCAtATTATCTtCTAAATATATAG	360
LA0392	TTTCCCA t GGGATTTTTCTAGTAAGATTTTTAAcC Ag GCAtATTATCTtCTAAATAT g TAG	304
LA3858	TTTCCCAcGGGATTTTTCTAGTAAGATTTTTAAcC Ag GCAtATTATCTtCTAAATAT g TAG	304
LA3900	TTTCCCAcGGGATTTTTCTAGTAAGATTTTTAAcC Ag GCAtATTATCTtCTAAATAT g TAG	304
Gh2	TTTCCCAcGGGATTTTTCTAGTAAGATTTTTAAcC Ag GCAtATTATCTtCTAAATAT g TAG	304
Consensus	tttccca gg atttttctagtaagattttaa ca ca attatct ctaaatat tag	
M82	CGAGTTAGTATCATTATACTTTGT G TACAAATTAATTTTCGATTACTCTGGGTAAACAAG	419
LA1606	CGAGTTAGTATCATTATACTTTGT G TACAAATTAATTTTCGATTACTCTGGGTAAACAAG	419
LA2184	CGAGTTAGTATCATTATACTTTGT G TACAAATTAATTTTCGATTACTCTGGGTAAACAAG	419
Gc9	CGAGTTAGTAT t ATTATACTTTGTcTACAAATTAATTTTCGATTACTCTGGGTAAACAAG	420
TY52	CGAGTTAGTAT t ATTATACTTTGTcTACAAATTAATTTTCGATTACTCTGGGTAAACAAG	420
LA2779	CGAGTTAGTATCATTATACTTTGTcTACAAATTAATTTTCGATTAC g CTGGGTAAACAAG	420
LA1932	CGAGTTAGTATCATTATACTTTGTcTACAAATTAATTTTCGATTACTCTGGGTAAACAAG	420
LA0392	CGAGTTAGTATCATTATACTTTGTcTACAAATTAATTTTCGATTACTCTGGGTAAACAAG	364
LA3858	CGAGTTAGTATCATTATACTTTGTcTACAAATTAATTTTCGATTACTCTGGGTAAACAAG	364
LA3900	CGAGTTAGTATCATTATACTTTGTcTACAAATTAATTTTCGATTACTCTGGGTAAACAAG	364
Gh2	CGAGTTAGTATCATTATACTTTGTcTACAAATTAATTTTCGATTACTCTGGGTAAACAAG	364
Consensus	cgagttagtat attatactttgt tacaatataattttcgattac ctgggtaacaag	

M82	CCATATAGTATGC	432
LA1606	CCATATAGTATGC	432
LA2184	CCATATAGTATGC	432
Gc9	CCATATAGTATGC	433
TY52	CCATATAGTATGC	433
LA2779	CCATATAGTATGC	433
LA1932	CCATATAGTATGC	433
LA0392	CCATATAGTATGC	377
LA3858	CCATATAGTATGC	377
LA3900	CCATATAGTATGC	377
Gh2	CCATATAGTATGC	377
Consensus	ccatatagtatgc	

M82, mi/mi GenBank no. EU033926

SEQ: 432 bp;
Composition 152 A; 67 C; 74 G; 139 T; 0 OTHER
Percentage: 35.2% A; 15.5% C; 17.1% G; 32.2% T; 0.0%OTHER
Molecular Weight (kDa): ssDNA: 133.54 dsDNA: 266.25

ORIGIN

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1      TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAGTATT
61     TGGAGTTTCT AAAATTTTGG AATATTCTGG CAAAATTTGA GCGGAGAAAT GTGACAGTTC
121    ACGTCCAAAT CTCCAGAGTC TTCATACATA GAAGTGTCAA ACAAATTGGC AGGTTCTTAC
181    ACCTTTTACT GTTCTAAAAA GATGTCTACA ATTTGTTTCA TCAAAGCCCC GACGGAACTA
241    TTAAGTAGAC GACGTTAGTA AAATAACAAG CAACCAAAGC AGTTACGAGA GATCACTTTT
301    TTCCCAGGGG ATTTTCTAG TAAGATTTTA ATCAAGCACA TTATCTACTA AATATATAGC
361    GAGTTAGTAT CATTATACTT TGTGTACAAA TTAAATTTTCG ATTACTCTGG GTAAACAAGC
421    CATATAGTAT GC

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***S. pimpinellifolium* LA1606**

SEQ: 432 bp;
Composition 152 A; 68 C; 74 G; 138 T; 0 OTHER
Percentage: 35.2% A; 15.7% C; 17.1% G; 31.9% T; 0.0%OTHER
Molecular Weight (kDa): ssDNA: 133.53 dsDNA: 266.25

ORIGIN

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1      TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAGTATT
61     TGGAGTTTCT AAAATTTTGG AATATTCTGG CAAAATTTGA GCGGAGAAAT GTGACAGTTC
121    ACGTCCAAAT CTCCAGAGTC TTCATACATA GAAGTGTCAA ACAAATTGGC AGGTTCTTAC
181    ACCTTTTACT GTTCTAAAAA GATGTCTACA ATTCGTTTCA TCAAAGCCCC GACGGAACTA
241    TTAAGTAGAC GACGTTAGTA AAATAACAAG CAACCAAAGC AGTTACGAGA GATCACTTTT
301    TTCCCAGGGG ATTTTCTAG TAAGATTTTA ATCAAGCACA TTATCTACTA AATATATAGC
361    GAGTTAGTAT CATTATACTT TGTGTACAAA TTAAATTTTCG ATTACTCTGG GTAAACAAGC
421    CATATAGTAT GC

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***S. pimpinellifolium* LA2184 GenBank no. EU033930**

SEQ: 432 bp;
Composition 152 A; 67 C; 74 G; 139 T; 0 OTHER
Percentage: 35.2% A; 15.5% C; 17.1% G; 32.2% T; 0.0%OTHER
Molecular Weight (kDa): ssDNA: 133.54 dsDNA: 266.25

ORIGIN

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1      TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAGTATT
61     TGGAGTTTCT AAAATTTTGG AATATTCTGG CAAAATTTGA GCGGAGAAAT GTGACAGTTC
121    ACGTCCAAAT CTCCAGAGTC TTCATACATA GAAGTGTCAA ACAAATTGGC AGGTTCTTAC
181    ACCTTTTACT GTTCTAAAAA GATGTCTACA ATTTGTTTCA TCAAAGCCCC GACGGAACTA
241    TTAAGTAGAC GACGTTAGTA AAATAACAAG CAACCAAAGC AGTTACGAGA GATCACTTTT
301    TTCCCAGGGG ATTTTCTAG TAAGATTTTA ATCAAGCACA TTATCTACTA AATATATAGC
361    GAGTTAGTAT CATTATACTT TGTGTACAAA TTAAATTTTCG ATTACTCTGG GTAAACAAGC
421    CATATAGTAT GC

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Gc9, resistant to begomoviruses with introgression from *S. chilense* LA2779, susceptible to root-knot nematode, mi/mi, Ty1/Ty1; **GenBank no. EU033925**
SEQ: 433 bp;

Composition 150 A; 66 C; 71 G; 146 T; 0 OTHER
Percentage: 34.6% A; 15.2% C; 16.4% G; 33.7% T; 0.0%OTHER
Molecular Weight (kDa): ssDNA: 133.77 dsDNA: 266.87

ORIGIN

```
1   TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAAGTATT
61  TGGAGTTTCT AAAATTTTGG AATATTCTGG CTAAATTTGA GCGGAGAAAT GTGACAGTTC
121 ACGTCCAAAT CTCCAGAGTC TTCATACATA GAAGTGTCAA ACAATTTAGC AGGTTCTTAC
181 ATCTTTTTTAC TGTTCTAAAA AGATGTCTAC AATTCGTTTC ATCAAAGCCC CGACGGAACT
241 ATTAAGTAGA CGAGGTTAGT AAAATAACAA GCAACCAAAT CAGTTTAGAG AGATCACTTT
301 TTTCCCACGG AATTTTTTCTA GTAAGATTTT AACCAGGCAT ATTATCTTCT AAATATATAG
361 CGAGTTAGTA TTATTATACT TTGTCTACAA ATTAAATTTT GATTACTCTG GGTAACAACAG
421 CCATATAGTA TGC
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TY52, resistant to begomoviruses (TYLCV) with introgression from *S. chilense* LA1969, Ty1/Ty1 (near isogenic line from Dani Zamir, Hebrew University of Jerusalem)

SEQ: 433 bp;
Composition 150 A; 66 C; 71 G; 146 T; 0 OTHER
Percentage: 34.6% A; 15.2% C; 16.4% G; 33.7% T; 0.0%OTHER
Molecular Weight (kDa): ssDNA: 133.77 dsDNA: 266.87

ORIGIN

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1   TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAAGTATT
61  TGGAGTTTCT AAAATTTTGG AATATTCTGG CTAAATTTGA GCGGAGAAAT GTGACAGTTC
121 ACGTCCAAAT CTCCAGAGTC TTCATACATA GAAGTGTCAA ACAATTTAGC AGGTTCTTAC
181 ATCTTTTTTAC TGTTCTAAAA AGATGTCTAC AATTCGTTTC ATCAAAGCCC CGACGGAACT
241 ATTAAGTAGA CGAGGTTAGT AAAATAACAA GCAACCAAAT CAGTTTAGAG AGATCACTTT
301 TTTCCCACGG AATTTTTTCTA GTAAGATTTT AACCAGGCAT ATTATCTTCT AAATATATAG
361 CGAGTTAGTA TTATTATACT TTGTCTACAA ATTAAATTTT GATTACTCTG GGTAACAACAG
421 CCATATAGTA TGC
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LA2779, *S. chilense*, this accession was source of resistance for begomoviruses (J. W. Scott, University of Florida); **GenBank no. EU033931**

SEQ: 433 bp;
Composition 149 A; 66 C; 74 G; 144 T; 0 OTHER
Percentage: 34.4% A; 15.2% C; 17.1% G; 33.3% T; 0.0%OTHER
Molecular Weight (kDa): ssDNA: 133.83 dsDNA: 266.87

ORIGIN

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1   TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAAGTATT
61  TGGAGTTTCT AAAATTTTGG AATATTCTGG CTAAATTTGA GCGGAGAAAT GTGACAGTTC
121 ATGTCCAAAT CTCCAGAGTC TTCATACATA GAAGTGTCAA ACAAATTGGC TGGTTCTTAC
181 ATCTTTTTTAC TGTTCTAAAA AGATGTCTAC AATTCGTTTC ATCAAAGCCC CGACGGAACT
241 ATTAAGTAGA CGAGGTTAGT AAAATAACAA GCAACCAAAG CAGTTTAGAG AGATCACTTT
301 TTTCCCACGG GATTTTTTCTA GTAAGATTTT AACCAGACAT ATTATCTTCT AAATATATAG
361 CGAGTTAGTA TCATTATACT TTGTCTACAA ATTAAATTTT GATTACGCTG GGTAACAACAG
421 CCATATAGTA TGC
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LA1932, *S. chilense*, this accession was source of resistance for begomoviruses (J. W. Scott, University of Florida); **GenBank no. EU033929**

SEQ: 433 bp;

Composition 150 A; 68 C; 71 G; 144 T; 0 OTHER

Percentage: 34.6% A; 15.7% C; 16.4% G; 33.3% T; 0.0%OTHER

Molecular Weight (kDa): ssDNA: 133.74 dsDNA: 266.87

ORIGIN

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1      TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTT AAAATATGAA AACAAGTATT
61     TGGAGTTTCT AAAATTTTGG AATATTCTAG CTAAATTTGA GCGGAGAAAT GTGACAGTTC
121    ACGTCCAAAT CTCCAGAGTC TTCATACATA GAAGTGTCAA ACAAATTGGC AGGTTCTTAC
181    ATCTTTTTTAC TGTTCTAAAA AGATGTCTAC AATTTCGTTT ATCAAAGCCC CGACGGAAC
241    ATTAAGTAGA CGACGTTAGT AAAATAACAA GCAACCAAAT CAGTTTGTAG AGATCACTTT
301    TTTCCCACGG GATTTTTTCTA GTAAGATTTT AACCAGGCAT ATTATCTTCT AAATATATAG
361    CGAGTTAGTA TCATTATACT TTGTCTACAA ATTAAATTTT GATTACTCTG GGTAACAACG
421    CCATATAGTA TGC
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LA0392, *S. arcanum*, closely related to *S. peruvianum*; **GenBank no. EU033928**

SEQ: 377 bp;

Composition 129 A; 54 C; 65 G; 129 T; 0 OTHER

Percentage: 34.2% A; 14.3% C; 17.2% G; 34.2% T; 0.0%OTHER

Molecular Weight (kDa): ssDNA: 116.58 dsDNA: 232.35

ORIGIN

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1      TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAGTATT
61     TGGAGTTTCT AAAATTTTGG AATATTCTGG CAAAATTTGA GCGGAGAAAT TGGCAGGTTT
121    TTACATCTTT TTACTGTTCT AAAAAAGATGT CTACAATTCG TTTCATCAAA GCCCCGACGG
181    AACTATTAAG TAGACGACGT TAGTAAAATA ACAAGCAACC AAAGCAGTTT AGAGAGATCA
241    CTTTTTTCCC ATGGGATTTT TCTAGTAAGA TTTTAACCAG GCATATTATC TTCTAAATAT
301    GTAGCGAGTT AGTATCATT TACTTTGTCT ACAAATTAATA TTTTCGATTAC TCTGGGTAAA
361    CAAGCCATAT AGTATGC
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LA3858, *S. peruvianum*, this species is the reported source of resistance for Mi gene; **GenBank no. EU033932**

SEQ: 377 bp;

Composition 129 A; 53 C; 67 G; 128 T; 0 OTHER

Percentage: 34.2% A; 14.1% C; 17.8% G; 34.0% T; 0.0%OTHER

Molecular Weight (kDa): ssDNA: 116.65 dsDNA: 232.35

ORIGIN

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1      TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAGTATT
61     TGGAGTTTCT AAAATTTTGG AATATTCTGG CAAAATTTGA GCGGAGAAAT TGGCAGGTTT
121    TTACATCTTT TTACTGTTCT AAAAAAGATGT CTACAATTCG TTTGATCAAA GCCCCGACGG
181    AACTATTAAG TAGACGAGGT TAGTAAAATA ACAAGCAACC AAAGCAGTTT AGAGAGATCA
241    CTTTTTTCCC ACGGGATTTT TCTAGTAAGA TTTTAACCAG GCATATTATC TTCTAAATAT
301    GTAGCGAGTT AGTATCATT TACTTTGTCT ACAAATTAATA TTTTCGATTAC TCTGGGTAAA
361    CAAGCCATAT AGTATGC
```

LA3900, *S. peruvianum*, this species is the reported source of resistance for Mi gene

SEQ: 377 bp;

Composition 129 A; 53 C; 67 G; 128 T; 0 OTHER

Percentage: 34.2% A; 14.1% C; 17.8% G; 34.0% T; 0.0%OTHER

Molecular Weight (kDa): ssDNA: 116.65 dsDNA: 232.35

ORIGIN

```
1      TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAGTATT
61     TGGAGTTTCT AAAATTTTGG AATATTCTGG CAAAATTTGA GCGGAGAAAT TGGCAGGTTT
121    TTACATCTTT TTACTGTTCT AAAAAAGATGT CTACAATTCG TTTGATCAAA GCCCCGACGG
181    AACTATTAAG TAGACGAGGT TAGTAAAATA ACAAGCAACC AAAGCAGTTT AGAGAGATCA
241    CTTTTTTCCC ACGGGATTTT TCTAGTAAGA TTTTAACCAG GCATATTATC TTCTAAATAT
301    GTAGCGAGTT AGTATCATT TACTTTGTCT ACAAATTAATA TTTTCGATTAC TCTGGGTAAA
361    CAAGCCATAT AGTATGC
```

Gh2, Mi/Mi, resistant to root knot nematode and also begomoviruses with Ty1/Ty1, Ty3/Ty3; **GenBank no. EU033926**

SEQ: 377 bp;

Composition 129 A; 53 C; 67 G; 128 T; 0 OTHER

Percentage: 34.2% A; 14.1% C; 17.8% G; 34.0% T; 0.0%OTHER

Molecular Weight (kDa): ssDNA: 116.65 dsDNA: 232.35

ORIGIN

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1      TGGAAAAATG TTGAATTTCT TTTGTAAGTG TACAAAGTTA AAATTATGAA AACAAGTATT
61     TGGAGTTTCT AAAATTTTGG AATATTCTGG CAAAATTTGA GCGGAGAAAT TGGCAGGTTT
121    TTACATCTTT TTACTGTTCT AAAAAAGATGT CTACAATTCG TTTGATCAAA GCCCCGACGG
181    AACTATTAAG TAGACGAGGT TAGTAAAATA ACAAGCAACC AAAGCAGTTT AGAGAGATCA
241    CTTTTTTTCCC ACGGGATTTT TCTAGTAAGA TTTTAACCAG GCATATTATC TTCTAAATAT
301    GTAGCGAGTT AGTATCATT TACTTTGTCT ACAAATTAAT TTTTCGATTAC TCTGGGTAAA
361    CAAGCCATAT AGTATGC
  
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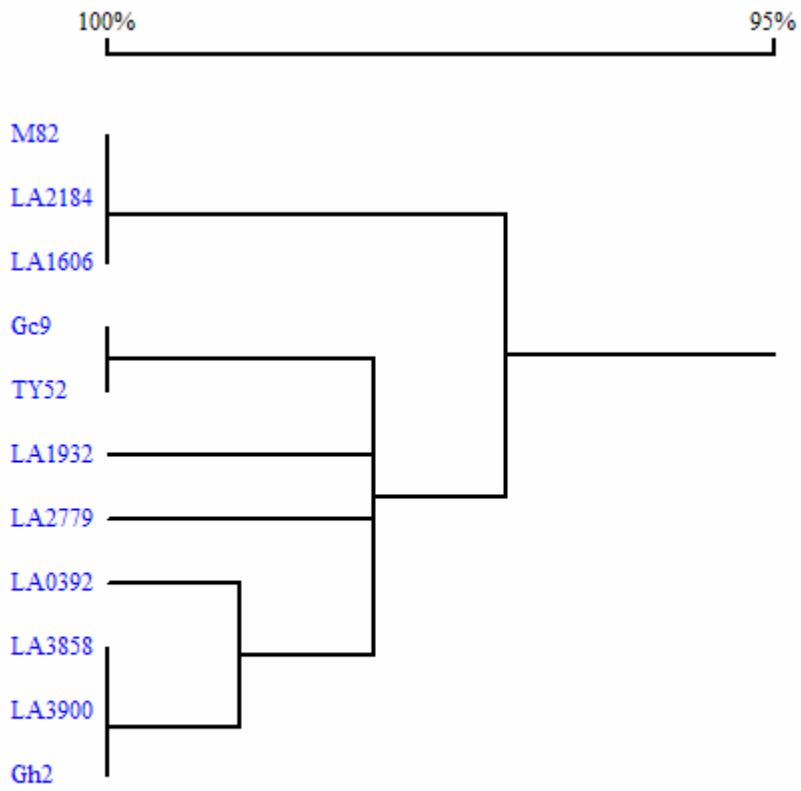
Calculations from DNAMAN software:

Distance matrix of 11 sequences

M82	0									
LA1606	0.002	0								
LA2184	0.000	0.002	0							
Gc9	0.039	0.037	0.039	0						
TY52	0.039	0.037	0.039	0.000	0					
LA2779	0.037	0.035	0.037	0.021	0.021	0				
LA1932	0.035	0.032	0.035	0.018	0.018	0.021	0			
LA0392	0.029	0.027	0.029	0.021	0.021	0.019	0.019	0		
LA3858	0.035	0.032	0.035	0.019	0.019	0.016	0.021	0.008	0	
LA3900	0.035	0.032	0.035	0.019	0.019	0.016	0.021	0.008	0.000	0
Gh2	0.035	0.032	0.035	0.019	0.019	0.016	0.021	0.008	0.000	0.000

Homology matrix of 11 sequences (does not consider the large indel)

M82	100%									
LA1606	99.8%	100%								
LA2184	100.0%	99.8%	100%							
Gc9	96.1%	96.3%	96.1%	100%						
TY52	96.1%	96.3%	96.1%	100.0%	100%					
LA2779	96.3%	96.5%	96.3%	97.9%	97.9%	100%				
LA1932	96.5%	96.8%	96.5%	98.2%	98.2%	97.9%	100%			
LA0392	97.1%	97.3%	97.1%	97.9%	97.9%	98.1%	98.1%	100%		
LA3858	96.5%	96.8%	96.5%	98.1%	98.1%	98.4%	97.9%	99.2%	100%	
LA3900	96.5%	96.8%	96.5%	98.1%	98.1%	98.4%	97.9%	99.2%	100.0%	100%
Gh2	96.5%	96.8%	96.5%	98.1%	98.1%	98.4%	97.9%	99.2%	100.0%	100%



Homology Tree from DNAMAN software