

TG360, Chromosome XII, Oct. 5, 2006

Primers designed by Aliya Momotaz, U of FL

Sequence: C. T. Martin and D. P. Maxwell, UW-Madison

SEQ Heinz-TG360-FR: 939 bp;

Composition 360 A; 182 C; 147 G; 250 T; 0 OTHER

Percentage: 38.3% A; 19.4% C; 15.7% G; 26.6% T; 0.0%OTHER

Molecular Weight (kDa): ssDNA: 289.64 dsDNA: 578.75

ORIGIN

```
1 CTCTCCATAT CCTCAATAAT TACAACCACT GGTTCCTCAT ACTTGCCATG GTCACTATAC
61 CATGATGCTA AGAGCGAAAC ATCAGCTGCC TTAGAATAAA AAACAATGAC GATAGTGAAT
121 AACATAAAG ATGTCACACA AGACTTAGTT CTAATTAAT ATGTGCATAA TTATAGAGTT
181 AATTGTCTAC TTACTTCAAT GTC AACCCATA AGTAATTGTC TCAGAAATGC TCTGAGACAG
241 CCCCCTAATGC CATTCTTGGT AGAAAAATCA AAGGAGGAAA TATTAGCCAC ATAGCATCCA
301 TGAGATTTCA AGTGTAACC AAGTTCAGCA AAAGTTAATA TGTCATCGAC AGTTTCAATA
361 TTCTCTGCAA ATAATCCAAG AATGTACTGA TCAACACGGG TGAACAACCTA CCCATTCATA
421 AAATTTTATT AACAGGAACA ATCAGGTAAA GTTGGGAATC GGAAATCAGG GTTAGGTGGT
481 CTGGCCATAA TTCACACAAT TGAACAACAT TCTTGAAAAG GAACACAACA AATTTATGGG
541 AGGAGTTGAG ATAAGAAATC TTTTCAGAAA AACAAAATAG AAGATCTCAG ATATTGGTTA
601 CCATCAGCAT AGTTTCATAT TTGCAAACCTA AACGTCTAAA ATAAATGAAA AATGAACTTA
661 CTGGTGAAGA CCAGACCAGT GAAGAGCTTT TTAACATAAC CACCATTATG GACAAAAGGG
721 TATGGAAGAC TTGACTTTGA TGGATCAACA GGCCTCTGC ACGAACAAAT TTCATTAAAA
781 GATTCACGAA CCCATGTGCC TATCTCATCA AACACGCCGG CATTTTACT CCTCAAGACA
841 TCCTAAATTC AATTCTCAA CATCAAGAAA TAAGCAATTT AGCATCACTT AATTTACT
901 GAATTGGATC AACGAAAATA TCTATAACAT TTCAGGACA
```

SEQ 902b-TG360FR: 940 bp; (902 is Gh902-b, selected from Ih902 in Guatemala, and is resistant to begomoviruses in Guatemala) Ih902 is the resistant parent for FAVI9, the source of Gh13.

SEQ 902b-TG360FR: 939 bp;

Composition 360 A; 182 C; 147 G; 250 T; 0 OTHER

Percentage: 38.3% A; 19.4% C; 15.7% G; 26.6% T; 0.0%OTHER

Molecular Weight (kDa): ssDNA: 289.64 dsDNA: 578.75

ORIGIN

```
1 CTCTCCATAT CCTCAATAAT TACAACCACT GGTTCCTCAT ACTTGCCATG GTCACTATAC
61 CATGATGCTA AGAGCGAAAC ATCAGCTGCC TTAGAATAAA AAACAATGAC GATAGTGAAT
121 AACATAAAG ATGTCACACA AGACTTAGTT CTAATTAAT ATGTGCATAA TTATAGAGTT
181 AATTGTCTAC TTACTTCAAT GTC AACCCATA AGTAATTGTC TCAGAAATGC TCTGAGACAG
241 CCCCCTAATGC CATTCTTGGT AGAAAAATCA AAGGAGGAAA TATTAGCCAC ATAGCATCCA
301 TGAGATTTCA AGTGTAACC AAGTTCAGCA AAAGTTAATA TGTCATCGAC AGTTTCAATA
361 TTCTCTGCAA ATAATCCAAG AATGTACTGA TCAACACGGG TGAACAACCTA CCCATTCATA
421 AAATTTTATT AACAGGAACA ATCAGGTAAA GTTGGGAATC GGAAATCAGG GTTAGGTGGT
481 CTGGCCATAA TTCACACAAT TGAACAACAT TCTTGAAAAG GAACACAACA AATTTATGGG
541 AGGAGTTGAG ATAAGAAATC TTTTCAGAAA AACAAAATAG AAGATCTCAG ATATTGGTTA
601 CCATCAGCAT AGTTTCATAT TTGCAAACCTA AACGTCTAAA ATAAATGAAA AATGAACTTA
661 CTGGTGAAGA CCAGACCAGT GAAGAGCTTT TTAACATAAC CACCATTATG GACAAAAGGG
721 TATGGAAGAC TTGACTTTGA TGGATCAACA GGCCTCTGC ACGAACAAAT TTCATTAAAA
781 GATTCACGAA CCCATGTGCC TATCTCATCA AACACGCCGG CATTTTACT CCTCAAGACA
841 TCCTAAATTC AATTCTCAA CATCAAGAAA TAAGCAATTT AGCATCACTT AATTTACT
901 GAATTGGATC AACGAAAATA TCTATAACAT TTCAGGACA
```

Fast alignment of DNA sequences Heinz-TG360-FR and 902b-TG360FR

Ktuple=2 Gap\_penalty=7

Upper line: Heinz-TG360-FR, from 1 to 938

Lower line: 902b-TG360FR, from 1 to 938

Heinz-TG360-FR:902b-TG360FR identity= 100.00%(939/939) gap=0.00%(0/939)

```
1 CTCTCCATATCCTCAATAAATTACAACCACTGGTTTCTCATACTTGCCATGGTCACTATAC
|
|
|
1 CTCTCCATATCCTCAATAAATTACAACCACTGGTTTCTCATACTTGCCATGGTCACTATAC
|
|
|
61 CATGATGCTAAGAGCGAAACATCAGCTGCCTTAGAATAAAAAACAATGACGATAGTGAAT
|
|
|
61 CATGATGCTAAGAGCGAAACATCAGCTGCCTTAGAATAAAAAACAATGACGATAGTGAAT
```

121 AACAAATAAGATGTCACACAAGACTTAGTTCTAATTAATATGTGCATAATTATAGAGTT  
|||  
121 AACAAATAAGATGTCACACAAGACTTAGTTCTAATTAATATGTGCATAATTATAGAGTT  
  
181 AATTGTCTACTTACTTCAATGTCAACCATAAGTAATTGTCTCAGAAATGCTCTGAGACAG  
|||  
181 AATTGTCTACTTACTTCAATGTCAACCATAAGTAATTGTCTCAGAAATGCTCTGAGACAG  
  
241 CCCCCAATGCCATTCTTGGTAGAAAAATCAAGGAGGAAATATTAGCCACATAGCATCCA  
|||  
241 CCCCCAATGCCATTCTTGGTAGAAAAATCAAGGAGGAAATATTAGCCACATAGCATCCA  
  
301 TGAGATTTCAAGTGTAACAAGTTCAGCAAAAGTTAATATGTCATCGACAGTTTCAATA  
|||  
301 TGAGATTTCAAGTGTAACAAGTTCAGCAAAAGTTAATATGTCATCGACAGTTTCAATA  
  
361 TTCTCTGCAAATAATCCAAGAATGACTGATCAACACGGGTGAACAACACTACCCATTATA  
|||  
361 TTCTCTGCAAATAATCCAAGAATGACTGATCAACACGGGTGAACAACACTACCCATTATA  
  
421 AAATTTTATTAACAGGAACAATCAGGTAAAGTTGGGAATCGGAAATCAGGGTTAGGTGGT  
|||  
421 AAATTTTATTAACAGGAACAATCAGGTAAAGTTGGGAATCGGAAATCAGGGTTAGGTGGT  
  
481 CTGGCCATAATTCACACAATTGAACAACATTCTTGAAAAGGAACACAAACAAATTTATGGG  
|||  
481 CTGGCCATAATTCACACAATTGAACAACATTCTTGAAAAGGAACACAAACAAATTTATGGG  
  
541 AGGAGTTGAGATAAGAAATCTTTTCAGAAAAACAAAATAGAAGATCTCAGATATTGGTTA  
|||  
541 AGGAGTTGAGATAAGAAATCTTTTCAGAAAAACAAAATAGAAGATCTCAGATATTGGTTA  
  
601 CCATCAGCATAGTTTCATATTTGCAAACATAACGTCTAAAAATAAATGAAAAATGAACTTA  
|||  
601 CCATCAGCATAGTTTCATATTTGCAAACATAACGTCTAAAAATAAATGAAAAATGAACTTA  
  
661 CTGGTGAAGACCAGACCAGTGAAGAGCTTTTAACTAAACCACCATTATGGACAAAAGGG  
|||  
661 CTGGTGAAGACCAGACCAGTGAAGAGCTTTTAACTAAACCACCATTATGGACAAAAGGG  
  
721 TATGGAAGACTTGACTTTGATGGATCAACAGGCCCTCTGCACGAACAAATTCATTAAAA  
|||  
721 TATGGAAGACTTGACTTTGATGGATCAACAGGCCCTCTGCACGAACAAATTCATTAAAA  
  
781 GATTCACGAACCCATTGTCTATCTCATCAAACACGCCGGCATTATACTCCTCAAGACA  
|||  
781 GATTCACGAACCCATTGTCTATCTCATCAAACACGCCGGCATTATACTCCTCAAGACA  
  
841 TCCTAAATTCAATTCTCAAACATCAAGAAATAAGCAATTTAGCATCACTTAATTTACT  
|||  
841 TCCTAAATTCAATTCTCAAACATCAAGAAATAAGCAATTTAGCATCACTTAATTTACT  
  
901 GAATTGGATCAACGAAAATATCTATAACATTTTCAGGACA  
|||  
901 GAATTGGATCAACGAAAATATCTATAACATTTTCAGGACA