

Chromosome 3, 76 cM

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Primers

P3-76F2, CAA TGG TGT GCT CGT CGA ATC AGA ATC GGA G

P3-76R2, GTT CCT TTT CAG CAT AGG CAG TAT TCC ATT TCG

Partial Sequence of Gc171, P3-76 F2R2: 936 bp . Gc171 is resistant to begomoviruses in Guatemala and the resistance gene was introgressed from *S. chilense* LA1932 by Jay Scott (University of Florida) and associates. HUU-VF is susceptible to begomoviruses and does not have an introgression in this region.

Gc171-1 (partial sequence):

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CAATGGTGTGCTCGTCGAATCGAATCGGAGCATGGAGTCCCATTGTCNACTGNAAAGGGA      60
GGGCTTTGATGTGGCCTCCATATGGCACTGGGCAACATGTAAAGCTTCCTGGTCCTTCTA      120
TTAGGGAACCAAATGTTTACGACTTCGGCACTCCTTATAAGCAGATGTTTCGATGACCTC      180
CGCCGCAAAGACGTGCAACTGTAAGCCAAAATTGCATTTATGCCTTTTCTAATTATCGTC      240
TCCTTTTGCTAATTCCTTGAACCTCTCTGTGTTTAAAATTTTCGTGTGTCGCTCAATTCAGT      300
TACCATTAAATAACCCTAATATGTGTAGAGTCTGTTATTTGCGCTGCACGAAGTGAATTT      360
AAGGATTTTCCATCTGCTAGGATTTGTATGATCTTCTTGAAGCTTTTGGATGCCTAATAT      420
CCTGTTCTAGTTTCCTTACCTTAATGGACAATTAGCATAATAAAAATCGGAGGAGTTAATG      480
TAAGGGTATTCATACAAGTATAAATTTTACAAGAACTTCTCGTTTCGTTAGACGCCAATG      540
GAGGTTTCTTTTAGGGAAAAAGTGTCTATCATTATTTCAAATGAGACAGGGGTCTGTAA      600
CAGGATTTCTATGTGATTTGGAGTTGTTTTATTCTTGCGGATAAAATTTTAGAACTTTGT      660
TTAGTTTTTGTACTTCTGAATACGGGTAAAGTTGCATATTTTGAATACGAAATTCCTCAA      720
TGTTCACGCCATGATAATGTGGTGTGTTCCTTTTTCAGGACAAAAGTCAACCTCCACC      780
GTGTTTCTATGCTTTGAGATGGCTATTATACCTAGAATTGTTGGCAAATATTGCTTTATT      840
TTCAGAATCCTCTGTTTTAATTCAAATTAGGGTTGAGCCTCAGTTTCATTTCCAGGTAC      900
AAACGAAATGGAATACTGCCTATGCTGAAAAGGAAC      936
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HUU-VF (partial sequence):

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CAATGGTGTGCTCGTCGAATCAGAATCGGAGCATGGAGTCACATTGTCTACTGAAAAGGG      60
AGGGATTTGATGTGGCCTCATATGGCACTGGGCAACATGtaaaagcttcCTGGTCCTTCTA      120
TTAGGGAACCAAATGTTTACGACTTCGGCACTCCTTATAAGCAGATGTTTCGATGACCTCC      180
GCCGCAAAGACGTGCAACTGTAAGCCAAAATTGCATTTATGCCTTTTCTAATTATCGTCT      240
CCTTTTGCTAATTCCTTGAACCTCTCTGTGTTTAAAATTTTCGTGTGTTACTCAATTCAGTT      300
ACCATTAAATAACCCTAATATGTGTAGTGTCTGTTATTTGCGCTGCACGAAGTGAATTTA      360
AGGATTTTCCATCTGCTAGGATTTGAATGATCTTCTTGAAGCTTTTGGATGCCTAATATC      420
CTGTTCTAGTTTCCTTACCTTAATGGACAATTAGCATAATAAAAATCGGAGGAGTTAATGT      480
AAGGGTATTCATATAAGTATAAATTTTACAAGAACTTCTCGTTTCGTTAGACGCCAATGG      540
AGGTTTCTTTTAGGGAAAAATGTGTCTATCATTATTTACATGAGACAGGGGTCTGTAA      600
CAGGATTTTCTATGTGATTTGGAGTTGTTTTATTCTTGCGGATAAAATTTTAGCACTTGT      660
TAGTTTTTGTACTTCTGAATATGGGTAAAGTTGCATATTTTGAATACGAAATTCCTCAA      720
GTTCCACGCCATGATAATGTGGTGTGTTCCTTTTTCAGGACAAAAGTCAACCTCCACC      780
GTGTTTCTATACCTTTGAGATGGCTGATATTGCTTTATTTTTCAGAATCCTCTGTTTTAAT      840
TCAAATTAGGGTTGAGCCTCAATTTCAATTTCCAGGTACAAACGAAATGGAATACTGCCT      900
ATGCTGAAAAGGAAC      915
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Comparison of Gc171 (bottom sequence) with HUI-VF (Top Sequence)

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1 CAATGGTGTGCTCGTCGAATCAGAATCGGAGCATGGAGTCACATTGTCTACTGAAAAGGG
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1 CAATGGTGTGCTCGTCGAATC.GAATCGGAGCATGGAGTCCCATTGTCNACTGNAAAGGG

61 AGGGATTGATGTGGCCT.CATATGGCACTGGGCAACATGTAAAGCTTCCTGGTCCTTCT
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60 AGGGCTTTGATGTGGCCTCCATATGGCACTGGGCAACATGTAAAGCTTCCTGGTCCTTCT

120 ATTAGGGAACCAAATGTTTACGACTTC.GGCACTCCTTATAAGCAGATGTTTCGATGACCT
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120 ATTAGGGAACCAAATGTTTACGACTTCGGGCACTCCTTATAAGCAGATGTTTCGATGACCT

179 CCGCCGCAAAGACGTCGAACTGTAAGCCAAAATTGCATTTATGCCTTTTCTAATTATCGT
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180 CCGCCGCAAAGACGTCGAACTGTAAGCCAAAATTGCATTTATGCCTTTTCTAATTATCGT

239 CTCCTTTTGCTAATTCTTGAACCTCTCTGTGTTTAAAATTTTCGTGTGTACTCAATTCAG
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240 CTCCTTTTGCTAATTCTTGAACCTCTCTGTGTTTAAAATTTTCGTGTGTGCTCAATTCAG

299 TTACCATTAAATAACCCTAATATGTGTAGTGTCTGTTATTTGCGCTGCACGAAGTGAATT
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|
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300 TTACCATTAAATAACCCTAATATGTGTAGAGTCTGTTATTTGCGCTGCACGAAGTGAATT

359 TAAGGATTTTCCATCTGCTAGGATTTGATGATCTTCTTGAAGCTTTTGGATGCCTAATA
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360 TAAGGATTTTCCATCTGCTAGGATTTGTATGATCTTCTTGAAGCTTTTGGATGCCTAATA

419 TCCTGTTCTAGTTTCCTTACCTTAATGGACAATTAGCATAATAAAAATCGGAGGAGTTAAT
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420 TCCTGTTCTAGTTTCCTTACCTTAATGGACAATTAGCATAATAAAAATCGGAGGAGTTAAT

479 GTAAGGGTATTCATAAAGTATAAAATTTACAAGAACTTCTCGTTTCGTTAGACGCCAAT
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480 GTAAGGGTATTCATAAAGTATAAAATTTACAAGAACTTCTCGTTTCGTTAGACGCCAAT

539 GGAGGTTTCTTTTTAGGGAAAAAGTGTCTATCATTATTTCAATGAGACAGGGGGTCTGT
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540 GGAGGTTTCTTTTTAGGGAAAAAGTGTCTATCATTATTTCAATGAGACA.GGGGTCTGT

599 AACAGGATTTTCATGTGTATTTGGAGTTGTTTTATTCTTGCGGATAAAATTTAGCAC.TT
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599 AACAGGATTTCTATGTGTATTTGGAGTTGTTTTATTCTTGCGGATAAAATTTAGAACTTT

658 GTTTAGTTTTTGACTTCTGAATAAGGGTAAAGTTGCATATTCTGGAATACGAAATTCTCA
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659 GTTTAGTTTTTGACTTCTGAATAAGGGTAAAGTTGCATATTTGGAATACGAAATTCTCA

718 AATGTTCCACGCCATGATAATGTGGTGTGTTCTTTTTCAGGACAAAACGTCACAACCTCC
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719 AATGTTCCACGCCATGATAATGTGGTGTGTTCTTTTTCAGGACAAA.GTCACAACCTCC
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778  ACCGTGTTTCTATACTTTGAGATGGCTG.....ATATTGCTTT
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778  ACCGTGTTTCTATGCTTTGAGATGGCTATTATACCTAGAATTGTTGGCAAATATTGCTTT

816  ATTTTCAGAATCCTCTTGTTTTAATTCAAATTAGGGTTGAGCCTCAATTTCAATTTCCAG
      |||||
838  ATTTTCAGAATCCTCTTGTTTTAATTCAAATTAGGGTTGAGCCTCAGTTTC.ATTTCCAG

876  GTACAAACGAAATGGAATACTGCCTATGCTGAAAAGGAAC
      |||||
897  GTACAAACGAAATGGAATACTGCCTATGCTGAAAAGGAAC

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Blast Search

The sequence matched [SGN-M7043 C2_At1g73820 \(COSII marker\)](#).

Summary

The sequence for Gh13, Glh902 and M82 were equal to HUI-VF. Both Gh13 and Glh902 are resistant to begomoviruses in Guatemala. M82 and HUI-VF are susceptible to begomoviruses in Guatemala. Analysis of F2 plants indicated that there was a positive correlation between the presence of this introgression in chromosome 3 and the PCR-Marker for Ty4 gene (introgression) (Brenda Esperanza and Luis Mejia, University of San Carlos, Guatemala, personal communication).