Chromosome 3, 76cM

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BACKGROUND: Dr. Y. Ji, University of Florida, indicated that there was an introgression associated with Ty4 gene on chromosome 3 near 76-85 cM. Originally, Ty4 was thought to be on chromosome 6 between 40-80 cM. Our UW-team scanned this region at 5-cM intervals and did not find any evidence for an introgression in Gc171, which gives the SCAR marker for Ty4. With this new information and the information form Dr. Ji, our group starting scanning chr. 3 from 66 - 85 cM to check for an introgression. Begomovirus resistant inbred used was G70, which was a selection from Gc171 by a susceptible hybrid. The susceptible germplasm was HUJ-VF (lab code, W168, an inbred from Hebrew University of Jerusalem, F. Vidavski and H. Czosnek) and M82.

Primers
P3-76F1, TGA AGC TCC GGT ATG CAA TGG TGT GCT CG
P3-76R1, CGA AGG GAC CAT CAG CAG CAT TAT CCT GCC

Partial Sequence of Gc171, P376F1-R1: 894 bp;

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                                                          CTGG   120
GCAACATGTAAAGCTTCCTGGTCCTTCTATTAGGGAACCAAATGTTTACGACTTCGGCAC   180
TCCTTATAAGCAGATGTTCGATG CCTCCGCCGCAAAGACGTCGAACTGTAAGCCAAAAA   240
TTGCATTTATGCCTTTTCTAAT A TCGTCTCCTTTTGCTAATTCCTTGAACTCTCTGTG   300
TTTAAAATTTCGTGTGTCGCTCAATTCAGTTACCATTAAATAACCCTAATATGTGTAGAG   360
TCTGTTATTTGCGCTGCACGAAGTGAATTTAAGGATTTTCCATCTGCTAGGATTTGTATG   420
ATCTTCTTGAAGCTTTTGGATGCCTAATATCCTGTTCTAGTTTCCTTACCTTAATGGACA   480
ATTAGCATAATAAAATCGGAGGAGTTAATGTAAGGGTATTCATACAAGTATAAATTTTAC   540
AAGAACTTCTCGTTTCGTTAGACGCCAATGGAGGTTTCTTTTTAGGGAAAAAGTGTCTAT   600
CATTATTTCAAATGAGACAGGGGTCTGTAACAGGATTTCTATGTGTATTTGGAGTTGTTT   660
TATTCTTGCGGATAAATTTTAGAACTTTGTTTAGTTTTTGACTTCTGAATACGGGTAAAG   720
TTGCATATTTTGGAATACGAAATTCTCAAATGTTCCACGCCATGATAATGTGGTGTGTTC   780
CTTTTCAGGACAAAAGTCACAACCTCCACCGTGTTTCTATGCTTTGAGATGGCTATTATA   840
CCTAGAATTGTTGGCAAATATTGCTTGAAGCTCCgGTAtGCaATGGTGTGCTCG         894
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Partial Sequence of M82, P376F1-R1: 856 bp;

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                                              AAAAGGGAGGGATTTGATGTGGCCT    60
CATATGGCACTGGGCaACATGTAAAGCtTCCTGGTCCTTCTATTAGGGAACCAAATGTTT   120
ACGACTTCGGCACTCCTTATAAGCAGATGTTCGATGACCTCCGCCGCAAAGACGTCGAAC   180
TGTAAGCCAAAATTGCATTTATGCCTTTTCTAATTATCGTCTCCTTTTGCTAATTCCTTG   240
AACTCTCTGTGTTTAAAATTTCGTGTGTTACTCAATTCAGTTACCATTAAATAACCCTAA   300
TATGTGTAGTGTCTGTTATTTGCGCTGCACGAAGTGAATTTAAGGATTTTCCATCTGCTA   360
GGATTTGAATGATCTTCTTGAAGCTTTTGGATGCCTAATATCCTGTTCTAGTTTCCTTAC   420
CTTAATGGACAATTAGCATAATAAAATCGGAGGAGTTAATGTAAGGGTATTCATATAAGT   480
ATAAATTTTACAAGAACTTCTCGTTTCGTTAGACGCCAATGGAGGTTTCTTTTTAGGGAA   540
AATGTGTCTATCATTATTTCACATGAGACAGGGGGTCTGTAACAGGATTTTCATGTGTAT   600
TTGGAGTTGTTTTATTCTTGCGGATAAATTTTAGCACTTGTTTAGTTTTTGACTTCTGAA   660
TATGGGTAAAGTTGCATATTCTGGAATACGAAATTCTCAAATGTTCCACGCCATGATAAT   720
GTGGTGTGTTCCTTTTCAGGACAAAAGTCACAACCTCCACCGTGTTTCTATACTTTGAGA   780
TGGCTGATATTGCTTTATTTTCAGAATCCTCTTGTTTAATTCAAATTAGGGTTGAGCCTC   840
AATTTCAATTTCCAGG                                               856
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Partial Sequence of HUJ, P376F1-R1: 963 bp;

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CAATGGTGTGCTCGTCGAATCAGAATCGGAGCATGGAGTCACATTGTCTACTGAAAAAGG    60
GAGGGATTTGATGTGGCCTCATATGGCACTGGGCAACATGTAAAGCTTCCTGGTCCTTCT   120
aTTAGGGAACCAAATGTTTACGACTTCGGCACTCCTTATAAGCAGATGTTCGATGACCTC   180
CGCCGCAAAGACGTCGAACTGTAAGCCAAAATTGCATTTATGCCTTTTCTAATTATCGTC   240
TCCTTTTGCTAATTCCTTGAACTCTCTGTGTTTAAAATTTCGTGTGTTACTCAATTCAGT   300
TACCATTAAATAACCCTAATATGTGTAGTGTCTGTTATTTGCGCTGCACGAAGTGAATTT   360
AAGGATTTTCCATCTGCTAGGATTTGAATGATCTTCTTGAAGCTTTTGGATGCCTAATAT   420
CCTGTTCTAGTTTCCTTACCTTAATGGACAATTAGCATAATAAAATCGGAGGAGTTAATG   480
TAAGGGTATTCATATAAGTATAAATTTTACAAGAACTTCTCGTTTCGTTAGACGCCAATG   540
GAGGTTTCTTTTTAGGGAAAATGTGTCTATCATTATTTCACATGAGACAGGGGGTCTGTA   600
ACAGGATTTTCATGTGTATTTGGAGTTGTTTTATTCTTGCGGATAAATTTTAGCACTTGT   660
TTAGTTTTTGACTTCTGAATATGGGTAAAGTTGCATATTCTGGAATACGAAATTCTCAAA   720
TGTTCCACGCCATGATAATGTGGTGTGTTCCTTTTCAGGACAAAAGTCACAACCTCCACC   780
GTGTTTCTATACTTTGAGATGGCTGATATTGCTTTATTTTCAGAATCCTCTTGTTTTAAT   840
TCAAATTAGGGTTGAGCCTCAATTTCAATTTCCAGGTACAAACGAAATGGAATACTGCCT   900
ATGCTGAAAAGGAACTTGGGTGTAAAGCTTGCACCTCAACGTTtGGCAGGATAATGCTGC   960
TGA                                                            963
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Comparison of Gc171 with HUJ

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1     CTGGGCAACATGTAAAGCTTCCTGGTCCTTCTATTAGGGAACCAAATGTTTACGACTTCG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
89    CTGGGCAACATGTAAAGCTTCCTGGTCCTTCTATTAGGGAACCAAATGTTTACGACTTCG

61    GCACTCCTTATAAGCAGATGTTCGATG.CCTCCGCCGCAAAGACGTCGAACTGTAAGCCA
      |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
149   GCACTCCTTATAAGCAGATGTTCGATGACCTCCGCCGCAAAGACGTCGAACTGTAAGCC.

120   AAAATTGCATTTATGCCTTTTCTAA.TATCGTCTCCTTTTGCTAATTCCTTGAACTCTCT
      ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
208   AAAATTGCATTTATGCCTTTTCTAATTATCGTCTCCTTTTGCTAATTCCTTGAACTCTCT

179   GTGTTTAAAATTTCGTGTGTCGCTCAATTCAGTTACCATTAAATAACCCTAATATGTGTA
      ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
268   GTGTTTAAAATTTCGTGTGTTACTCAATTCAGTTACCATTAAATAACCCTAATATGTGTA

239   GAGTCTGTTATTTGCGCTGCACGAAGTGAATTTAAGGATTTTCCATCTGCTAGGATTTGT
      | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
328   GTGTCTGTTATTTGCGCTGCACGAAGTGAATTTAAGGATTTTCCATCTGCTAGGATTTGA

299   ATGATCTTCTTGAAGCTTTTGGATGCCTAATATCCTGTTCTAGTTTCCTTACCTTAATGG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
388   ATGATCTTCTTGAAGCTTTTGGATGCCTAATATCCTGTTCTAGTTTCCTTACCTTAATGG

359   ACAATTAGCATAATAAAATCGGAGGAGTTAATGTAAGGGTATTCATACAAGTATAAATTT
      |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
448   ACAATTAGCATAATAAAATCGGAGGAGTTAATGTAAGGGTATTCATATAAGTATAAATTT

419   TACAAGAACTTCTCGTTTCGTTAGACGCCAATGGAGGTTTCTTTTTAGGGAAAAAGTGTC
      |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
508   TACAAGAACTTCTCGTTTCGTTAGACGCCAATGGAGGTTTCTTTTTAGGGAAAATGTGTC

479   TATCATTATTTCAAATGAGACA.GGGGTCTGTAACAGGATTTCTATGTGTATTTGGAGTT
      |||||||||||| |||||||| |||||||||||||||||||  ||||||||||||||||
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568   TATCATTATTTCACATGAGACAGGGGGTCTGTAACAGGATTTTCATGTGTATTTGGAGTT

538   GTTTTATTCTTGCGGATAAATTTTAGAACTTTGTTTAGTTTTTGACTTCTGAATACGGGT
      ||||||||||||||||||||||||| || |||||||||||||||||||||||| ||||
628   GTTTTATTCTTGCGGATAAATTTTAGCAC.TTGTTTAGTTTTTGACTTCTGAATATGGGT

598   AAAGTTGCATATTTTGGAATACGAAATTCTCAAATGTTCCACGCCATGATAATGTGGTGT
      ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
687   AAAGTTGCATATTCTGGAATACGAAATTCTCAAATGTTCCACGCCATGATAATGTGGTGT

658   GTTCCTTTTCAGGACAAAAGTCACAACCTCCACCGTGTTTCTATGCTTTGAGATGGCTAT
      |||||||||||||||||||||||||||||||||||||||||| ||||||||||||
747   GTTCCTTTTCAGGACAAAAGTCACAACCTCCACCGTGTTTCTATACTTTGAGATGGCTGA

718   TATACCTAGAATTGTTGGCAAATATTGCTTGAAG
      |||  ||  | ||   |     | ||| || ||
807   TATTGCTTTATTTTCAGAATCCTCTTGTTTTAAT
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Blast Search

No match

SGN BAC Clone Search

The sequence matches with 99% accuracy to the following:

SGN-U203492
Organism Capsicum annuum
SGN-U221249
Organism: Lycopersicon Combined
SGN-U267031
Organism: Solanum tuberosum
At1g73820 on TAIR
Organism: Arabidopsis

Summary

The sequence results from Gc171 were very good. When the sequence of Gc171 was compared with HUJ, the results showed that there were numerous differences between the two sequences (see red nucleotides). There were a total of 17 differences between these two.