

## Chromosome 3, 83cM

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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 from 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

P3-83F1: CCGGAAACATTTGTGTCTATTGCCCTG

P3-83R1: GAAGTATGTCCGGATAAAGCATCATG

Annealing temperature 53 °C

### Partial Sequence of G70 (resistant inbred) with p3-81 F1/R1

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1      TTTGTGTCTA TTGCCCTGGC GGCCCCGATT CTGATTTTGA GTACAGTACA CAGTCATACC
61     CGGGATATGA ACCTACTAGT ATGCGAGCTA TTCGAGCTAG GTGAGCATCA CATAACACAGG
121    TGTATTTGCA GTTTGATATT ATCTTTCCGT CAATTTGCAA TCAAATGGAA GTAGTTATCC
181    TGAATTATGC CTTAGGATTT CGGAATTTCA TCTATATACT TTAGTGATAA GTGAGAAGCT
241    CATCTATATG TTTCATTTT TATACCGGAG AAGTTTGTCT GTTATTACCG GAAAGTATCA
301    TATATCTGGA GAAAGATTAG GATTTGATGC TGGTTAATGC CTTTTGTCAT CCGAGATTTG
361    TTAACCTTC TATATACTTA TTAATTTTTT CTTGTTGGAA AAAAATGTGG CATTCCCTTAT
421    ATGTGGCTAA CTAGAAAGTT GTTATATCAC TTAGTCAAAA AAGTAAACTT TGGAAAGACA
481    AGATCAGGGC TGGTACTTAT GTGGTTCATT TTTCTAGATA CAATCCTTAT GTACAAGCTC
541    GAAGCCGGAT TGATCAACTT AAGAGATTGG GTCACAGTGT TGACAAGGTT TTTCTCCTTT
601    GGAAGTACTA CTAATTCCTT TCTGATTTTG GAAAATTGTT CTGAAATTGG CTGCTTTTCT
661    CATAGTTACG AATGACTAAT TGCAGGTTGA ATTTATCTTG ATGGGAGGTA CATTGATGTC
721    ATGCCTGCT GAATACCGTG ATTACTTCAC ACGGAA
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### Comparison of M82 (upper line) with G70 (lower line)

```
1      TCCGGAAACCATTTGTGTCTATTGCCCTGGCGGCCCGATTCTGATTTTGAGTACAGTAC
      |
1      .....TTTGTGTCTATTGCCCTGGCGGCCCGATTCTGATTTTGAGTACAGTAC
      |
61     ACAGTCATACACGGGATATGAACCTACTAGTATGCGAGCTATTTCGAGCTAGGTGAGCATC
      |
50     ACAGTCATACCCGGGATATGAACCTACTAGTATGCGAGCTATTTCGAGCTAGGTGAGCATC
      |
121    ACATACACAGGTGTATTTGCAGTTTGATATTATCTTTCCGTCAATTTGCAATCAAATGGA
      |
110    ACATACACAGGTGTATTTGCAGTTTGATATTATCTTTCCGTCAATTTGCAATCAAATGGA
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181  AGTAGTTATCCTGAATTATGCCTTAGGATTCGGAATTCATCTATATACTTTACTGATA
    |||
170  AGTAGTTATCCTGAATTATGCCTTAGGATTCGGAATTCATCTATATACTTTACTGATA

241  AGTGAGAAGCTCATCTATATGTTTCATTTTTTATACCGGAGAAGTTTGCTGTTATTACC
    |||
230  AGTGAGAAGCTCATCTATATGTTTCATTTTTTATACCGGAGAAGTTTGCTGTTATTACC

301  GGAAAGTATCATATATCTGGAGAAAGATTAGGATTTGATGCTGGTAAATGCCTTTTTGCA
    |||
290  GGAAAGTATCATATATCTGGAGAAAGATTAGGATTTGATGCTGGTAAATGCCTTTTTGCA

361  TCCGAGATTTGTTAAACCTTCTATATACTTATTAATTTTTTCTTGTTGGAAAAAATGTG
    |||
350  TCCGAGATTTGTTAAACCTTCTATATACTTATTAATTTTTTCTTGTTGGAAAAAATGTG

421  GCATTCCCTTATATGTGGCTAACTAGAAAGTTGTTATATCACTTACTCAAAAAAGTAACT
    |||
410  GCATTCCCTTATATGTGGCTAACTAGAAAGTTGTTATATCACTTACTCAAAAAAGTAACT

481  TTGGAAGACAAGATCAGGGCTGGTACTTATGTGGTTCATTTTTCTAGATACAATCCTTA
    |||
470  TTGGAAGACAAGATCAGGGCTGGTACTTATGTGGTTCATTTTTCTAGATACAATCCTTA

541  TGTACAAGCTCGAAGCCGGATTGATCAACTTAAGAGATTGGGTCACAGTGTGACAAGGT
    |||
530  TGTACAAGCTCGAAGCCGGATTGATCAACTTAAGAGATTGGGTCACAGTGTGACAAGGT

601  TTTTCTCCTTTGGAAGTACTACTAATTCTTTCTGATTTTGAAAATTGTTCTGAAATTG
    |||
590  TTTTCTCCTTTGGAAGTACTACTAATTCTTTCTGATTTTGAAAATTGTTCTGAAATTG

661  GCTGCTTTCCTCATAGTTACGAATGACTAATGCAGGTTGAATTTATCTTGATGGGAGGT
    |||
650  GCTGCTTTCCTCATAGTTACGAATGACTAATGCAGGTTGAATTTATCTTGATGGGAGGT

721  ACATTCATGTCATTGCCTGCTGAATACCGTGATTACTTCACACGGAATCTCCATGATGCT
    |||
710  ACATTCATGTCATTGCCTGCTGAATACCGTGATTACTTCACACGGAA

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**Comparison of W168 (upper line) with G70 (lower line)**

```

1      TCCGGAACATTTGTGTCTATTGCCCTGGCGGCCCGATTCTGATTTTGAGTACAGTACA
    |||
1      .....TTTGTGTCTATTGCCCTGGCGGCCCGATTCTGATTTTGAGTACAGTACA

61     CAGTCATACACGGGATATGAACCTACTAGTATGCGAGCTATTCGAGCTAGGTGAGCATCA
    |||
51     CAGTCATACCGGGATATGAACCTACTAGTATGCGAGCTATTCGAGCTAGGTGAGCATCA

121    CATAACAGGTGTATTTGCAGTTTGATATTATCTTTCCGTCAATTTGCAATCAAATGGAA
    |||
111    CATAACAGGTGTATTTGCAGTTTGATATTATCTTTCCGTCAATTTGCAATCAAATGGAA

181    GTAGTTATCCTGAATTATGCCTTAGGATTCGGAATTCATCTATATACTTTACTGATAA
    |||
171    GTAGTTATCCTGAATTATGCCTTAGGATTCGGAATTCATCTATATACTTTACTGATAA

241    GTGAGAAGCTCATCTATATGTTTCATTTTTTATACCGGAGAAGTTTGCTGTTATTACCG
    |||
231    GTGAGAAGCTCATCTATATGTTTCATTTTTTATACCGGAGAAGTTTGCTGTTATTACCG

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301  GAAAGTATCATATATCTGGAGAAAGATTAGGATTTGATGCTGGTTAATGCCTTTTTGCAT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
291  GAAAGTATCATATATCTGGAGAAAGATTAGGATTTGATGCTGGTTAATGCCTTTTTGCAT

361  CCGAGATTTGTTAAACCTTCTATATACTTATTAATTTTTTCTTGTGGAAAAAATGTGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
351  CCGAGATTTGTTAAACCTTCTATATACTTATTAATTTTTTCTTGTGGAAAAAATGTGG

421  CATTCCTTATATGTGGCTAACTAGAAAGTTGTTATATCACTTACTCAAAAAAGTAACTT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
411  CATTCCTTATATGTGGCTAACTAGAAAGTTGTTATATCACTTACTCAAAAAAGTAACTT

481  TGGAAAGACAAGATCAGGGCTGGTACTTATGTGGTTCATTTTTCTAGATACAATCCTTAT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
471  TGGAAAGACAAGATCAGGGCTGGTACTTATGTGGTTCATTTTTCTAGATACAATCCTTAT

541  GTACAAGCTCGAAGCCGGATTGATCAACTTAAGAGATTGGGTCACAGTGTGACAAGGTT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
531  GTACAAGCTCGAAGCCGGATTGATCAACTTAAGAGATTGGGTCACAGTGTGACAAGGTT

601  TTTCTCCTTTGGAAGTACTACTAATTCCTTTCTGATTTTGAAAATTGTTCTGAAATTGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
591  TTTCTCCTTTGGAAGTACTACTAATTCCTTTCTGATTTTGAAAATTGTTCTGAAATTGG


661  CTGCTTTCCTCATAGTTACGAATGACTAATTCAGGTTGAATTTATCTTGATGGGAGGTA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
651  CTGCTTTCCTCATAGTTACGAATGACTAATTCAGGTTGAATTTATCTTGATGGGAGGTA

721  CATTGATGTCATTGCCTGCTGAATACCGTGATTACTTCACACGGAATCTCCATGATGCTT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
711  CATTGATGTCATTGCCTGCTGAATACCGTGATTACTTCACACGGA

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**Blast Search**

Matched nothing on SOL genomics database greater than 90% full sequence on March 2, 2009. Matched with 90% accuracy to the following from NCBI database:

> [gb|BT012837.1](#)  Lycopersicon esculentum clone 113903F, mRNA sequence  
Length=1840

this subject sequence by: Sort alignments for  
E value [Score](#)  
[Percent identity](#) [Query start position](#)  
[Subject start position](#)

Score = 176 bits (194), Expect = 2e-40  
Identities = 99/100 (99%), Gaps = 0/100 (0%)  
Strand=Plus/Plus

```

Query 1   TTTGTGTCTATTGCCCTGGCGGCCCGATTCTGATTTTGAGTACAGTACACAGTCATACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 384  TTTGTGTCTATTGCCCTGGCGGCCCGATTCTGATTTTGAGTACAGTACACAGTCATACA 443

Query 61  CGGGATATGAACCTACTAGTATGCGAGCTATTCGAGCTAG 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 444  CGGGATATGAACCTACTAGTATGCGAGCTATTCGAGCTAG 483

```

Score = 134 bits (148), Expect = 5e-28  
Identities = 76/77 (98%), Gaps = 0/77 (0%)  
Strand=Plus/Plus

```
Query 514 CTAGATACAATCCTTATGTACAAGCTCGAAGCCGGATTGATCAACTTAAGAGATTGGGTC 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 480 CTAGATACAATCCTTATGTACAAGCTCGAAGCCGGATTGATCAACTAAAGAGATTGGGTC 539

Query 574 ACAGTGGTTGACAAGGTT 590
          ||||||||||||||||
Sbjct 540 ACAGTGGTTGACAAGGTT 556
```

Score = 132 bits (146), Expect = 2e-27  
Identities = 73/73 (100%), Gaps = 0/73 (0%)  
Strand=Plus/Plus

```
Query 684 AGGTTGAATTTATCTTGATGGGAGGTACATTCATGTCATTGCCTGCTGAATACCGTGATT 743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 552 AGGTTGAATTTATCTTGATGGGAGGTACATTCATGTCATTGCCTGCTGAATACCGTGATT 611

Query 744 ACTTCACACGGAA 756
          ||||||||||||
Sbjct 612 ACTTCACACGGAA 624
```

### Summary

The sequence data for G70 using p3-83 F1/R1 was very good. When a comparison was done between G70 (resistant inbred) and either susceptible plant (M82 or W168), the results showed there were no differences in over 700 bp. The above comparisons shows the comparison data and the results indicate that there is no introgression at 83 cM.