

Chromosome 3, 69 cM

Adam Rasmussen and Douglas Maxwell
University of Wisconsin-Madison,
February 11, 2009

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 HUI-VF (lab code, W168, an inbred from Hebrew University of Jerusalem, F. Vidavski and H. Czosnek) and M82.

Primers

P3-69 F: CAGGATGTGCCTTATCTCTCAA

P3-69 R: AAGAGAGTGGTCAATGTCATCC

Annealing Temperature: 53 C.

Partial Sequence of G70 (Originate from Gc171, Resistant Inbred), p3-69

```
1      CAGGATGTGC CTTATCTCTT CAATTTGAAA TGGTCAATTA ACTCAAGACT GAAAGATGTT
61     ATCCAACAGT TTCAGAAGGT AATTGTGTAT TCTTTTATC ATGTTGCAGC TCTCCCCTCG
121    TTTGCATTG CATTGTAAC TATGATTAC TACTGATTAT TTCATCCACC AATGATATAT
181    GTGTAGTTA TCAACATTG TGAATTGTGA TTTTCTGCTA TAATTACCAT ATCTTTTCT
241    TAATGGATCC AGCATCTTGA GAAGCTTCAG GACTTTTGGA ATCTAATGGA TGACATTGAC
301    CACTCTCTTA
```

Partial Sequence of M82 (Susceptible), p3-69

```
1      CAGGATGTGC CTTATCTCTT CAATTTGAAA TGGTCAATTA ACTCAAGACT GAAAGATGTT
61     ATCCAACAGT TTCAGAAGGT AATTGTGTAT TCTTTTATC ATGTTGCAGC TCTCCCCTCG
121    TTTGCATTG CATTGTAAC TATGATTAC TACTGATTAT TTCATCCACC AATGATATAT
181    GTGTAGTTA TCAACATTG TGAATTGTGA TTTTCTGCTA TAATTACCAT ATCTTTTCT
241    TAATGGATCC AGCATCTTGA GAAGCTTCAG GACTTTTGGA ATCTAATGGA TGACATTGAC
301    CACTCTCTTA G
```

Partial Sequence of W168 (HUI-VF, Susceptible), p3-69

```
1      ASSEMLYFSE QUENCESINT GRUPCAGGAT GTGCCTTATC TCTTCAATTT GAAATGGTCA
61     ATTAACCTCAA GACTGAAAGA TGTATCCAA CAGTTTCAGA AGGTAATTGT GTATTCTTTT
121    TATCATGTTG CAGCTCTCCC CTCGTTTGCA TTTGCATTGT AACTTATGAT TTACTACTGA
181    TTATTTTCATC CACCAATGAT ATATGTGTAG TTTATCAACA TTTGTGAATT GTGATTTTCT
241    GCTATAATTA CCATATCTTT TTCTTAATGG ATCCAGCATC TTGAGAAGCT TCAGGACTTT
301    TGGAATCTAA TGGATGACAT TGACCACTCT CTTA
```

Comparison of G70 (upper line) with M82 (lower line)

```
1 CAGGATGTGCCTTATCTCTTCAATTTGAAATGGTCAATTAAGTCAAGACTGAAAGATGTT
  |||
1 CAGGATGTGCCTTATCTCTTCAATTTGAAATGGTCAATTAAGTCAAGACTGAAAGATGTT

61 ATCCAACAGTTTCAGAAGGTAATTGTGTATTCTTTTTATCATGTTGCAGCTCTCCCTCG
  |||
61 ATCCAACAGTTTCAGAAGGTAATTGTGTATTCTTTTTATCATGTTGCAGCTCTCCCTCG

121 TTTGCATTTGCATTGTAACCTTATGATTTACTACTGATTATTTTCATCCACCAATGATATAT
  |||
121 TTTGCATTTGCATTGTAACCTTATGATTTACTACTGATTATTTTCATCCACCAATGATATAT

181 GTGTAGTTTATCAACATTTGTGAATTGTGATTTTCTGCTATAATTACCATATCTTTTTCT
  |||
181 GTGTAGTTTATCAACATTTGTGAATTGTGATTTTCTGCTATAATTACCATATCTTTTTCT

241 TAATGGATCCAGCATCTTGAGAAGCTTCAGGACTTTTGGAACTAATGGATGACATTGAC
  |||
241 TAATGGATCCAGCATCTTGAGAAGCTTCAGGACTTTTGGAACTAATGGATGACATTGAC

301 CACTCTCTTA
  |||
301 CACTCTCTTAG
```

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

```
1 CAGGATGTGCCTTATCTCTTCAATTTGAAATGGTCAATTAAGTCAAGACTGAAAGATGTT
  |||
1 CAGGATGTGCCTTATCTCTTCAATTTGAAATGGTCAATTAAGTCAAGACTGAAAGATGTT

61 ATCCAACAGTTTCAGAAGGTAATTGTGTATTCTTTTTATCATGTTGCAGCTCTCCCTCG
  |||
61 ATCCAACAGTTTCAGAAGGTAATTGTGTATTCTTTTTATCATGTTGCAGCTCTCCCTCG

121 TTTGCATTTGCATTGTAACCTTATGATTTACTACTGATTATTTTCATCCACCAATGATATAT
  |||
121 TTTGCATTTGCATTGTAACCTTATGATTTACTACTGATTATTTTCATCCACCAATGATATAT

181 GTGTAGTTTATCAACATTTGTGAATTGTGATTTTCTGCTATAATTACCATATCTTTTTCT
  |||
181 GTGTAGTTTATCAACATTTGTGAATTGTGATTTTCTGCTATAATTACCATATCTTTTTCT

241 TAATGGATCCAGCATCTTGAGAAGCTTCAGGACTTTTGGAACTAATGGATGACATTGAC
  |||
241 TAATGGATCCAGCATCTTGAGAAGCTTCAGGACTTTTGGAACTAATGGATGACATTGAC

301 CACTCTCTTA
  |||
301 CACTCTCTTA
```

Blast Search

Data matched nothing in NCBI database greater than 90% accuracy. Data matched the following on SOL genomics website with greater than 90% identity:

[SGN-M2244](#) T1751 [cos_markers]

[SGN-M2244](#) T1751 [cos_markers]

Length = 532

Score = 151 bits (76), Expect = 5e-37
Identities = 76/76 (100%), Frame = +1 / +1

```
Query: 3   ggatgtgccttatctcttcaatttgaaatgggtcaattaactcaagactgaaagatggtat 62
          |||
Sbjct: 413 ggatgtgccttatctcttcaatttgaaatgggtcaattaactcaagactgaaagatggtat 472
```

```
Query: 63   ccaacagtttcagaag 78
          |||
Sbjct: 473   ccaacagtttcagaag 488
```

Score = 83.8 bits (42), Expect = 1e-16
Identities = 45/46 (97%), Frame = +1 / +1

```
Query: 251 agcatcttgagaagcttcaggacttttggaaatctaataatggatgacat 296
          |||
Sbjct: 487 agcatcttgagaagcttcaggacttttggaaatctaataatggatgacat 532
```

Summary

The data for p3-69 came out with good sequence, although very short. When a comparison was done between G70 (resistant inbred) and either susceptible plant (M82 or W168), the results showed no differences. Therefore it is concluded that there is no introgression at 69 cM.