

# Chromosome 3, 72 cM

Adam Rasmussen and Douglas Maxwell  
University of Wisconsin-Madison  
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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 HUI-VF (lab code, W168, an inbred from Hebrew University of Jerusalem, F. Vidavski and H. Czosnek) and M82.

## Primers

P3-72.2 F: GGTTGAATTAAGCTGCAGTCGAG

P3-72.2 R: CCTCAAAGCCCAAACGTATTACCT

Annealing temperature: 53 C

## Partial Sequence of G70 (Resistant Inbred), p3-72.2

```
1      AAGAGAAGAA AGGGAACGGG AATACAAGGA CTCCGGAGCT GTACTTATGG CACACATCCC
61     CCGTTGCCTC CTCCNTNGA AATTTTATCC CCAGGGGAAG CTATGAAAAC GGAGGAACCC
121    GGTATGTTCT CTTTTGGTGG GGAACCAAAG AAAAAGCCCG GCATATGGTC TACTCAAGAG
181    GTGCCCATGA CTGNCCNCAA GCACAAGCTC AGAAGACTTT ATTCTGTTCC ACCACAAGAA
241    AAAGCAAAGG ATTTTATATA TTCAATACCT TCAAAATACG AACAGTTGA GCAGGTATCA
301    CATTAAAAAC AAACACTCAC CTAAATTACA TACAAGTAAT ACTTGTTTTA TAATCATAG
361    TGTAGTGTCC CTTTAGCATC TAAAGAACAA ATTCNCACAA CTTTAATTAT TCTCTNAAGA
421    GAGCATAAAG TTCANAAACA GCANAAACT TANNGNGTTG TTTTGTTCG TTCCNNGGGN
481    CGGGAGCTCT TCTTCAGNA ATACGTNGGG GCTTGAGG
```

## Partial Sequence of M82 (Susceptible), p3-72.2

```
1      TGAGTATTGC CACCGCAGTT GTTCTGAAGA ACAATGGTNG GAANCCCGTC NAGTTAACCA
61     CAGCTATATT AAGCCCTTTG ATGTNTAAGA CAAGAAAGGG AACGGGAATA CAAGGACTCC
121    GGAGCTGTAC TTATTGCACA CATCCTCCGT TGTCTTCTTC CTTTGAAATT TTGTCTCCAG
181    GGAAGCTAT  GAAAACTGAG GAACCCGGTA TGTCTCTTT TGGGTGGGAA CCAGAGAACA
241    AGCCCGGCAT ATGGTCTACT CAAGATGTGC CCATTACTGT CCTCAAGCAC AAGCTCCGTA
301    GACTTTATTC TGTTCCACCA CAAGAAAAAG CAAAGGATTT TTATAATTCA ATACCTTCAA
361    AATACGAAAC AATTGATGAG GTATCACATT CAAAACAAAC ACTCTCCTAA ATTACATACA
421    AGTAATACTT GTTTTATAAC TCATAGTGTA GTGTTCCTTT AGCATCTTAA GAACAAATTT
481    GTCACAACCT CAATTATCTT CTTAAGAGAG CATAAAGTTC AAAACCAGCC GAAAACCTTA
541    TGTGTTGTTT TGTTTCNTTT CCGGGGNCGG GAGCTCTTCT TTAGGAAATA CGTTTGGGC
```

## Partial Sequence of W168 (Susceptible), p3-72.2

```
1      GTTGAATTAA GCTGCAGTCG AGGGAGTCTA GATATTAAC ATGTGGTGTC ACTCTATCCA
61     TTGAGTATTG CAACAGCAGT TATACTGAAG AACAATGGTN GAAAGCCTGT CAAGTTAACC
```



```

181 GTGCCCATGACTGNCCNCAAGCACAAGCTCAGAAGACTTTATTCTGTTCCACCACAAGAA
    ||||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
328 GTGCCATTACTGTCTCAAGCACAAGCTCAGTAGACTTTATTCTGTTCCACCACAAGAA

241 AAAGCAAAGGATTTTTATAATTCAATACCTTCAAATACGAAACAGTTGAGCAGGTATCA
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
388 AAAGCAAAGGATTTTTATAATTCAATACCTTCAAATACGAAACAATTGATCAGGTATCA

301 CATTAAAAACAAACACTCACCTAAATTACATACAAGTAATACTTGTTTTATAACTCATAG
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
448 CATTCAAACAAACACTCTCCTAAATTACATACAAGTAATACTTGTTTTATAACTCATAG

361 TGTAGTGTCCCTTTAGCATCTAAAGAACAAA . TTCNCACAACCTTAATTATTCTCTNAAG
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
508 TGTAGTGTCTCTTTAGCATCTTAAGAACAATTTGTCCACAACCTCAATTATTCTCTTAAG

420 AGAGCATAAAGTTCANAAACAGCANAAAACCTTANNGNGTTGTTTTGTTTCGTTCCCGGG
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
568 AGAGCATAAAGTTCAGAAACAGCCGAAAACCTTAAGGTGTGTTTTGTTTCGTT

```

**Blast Search**

Data did not match greater than 90% accuracy to anything on NCBI database.  
 Data did match greater than 90% to the following from SOL genomics database:

[SGN-M6951](#) C2\_At1g64770

Length = 1,379

Score = 426 bits (215), Expect = 1e-119  
 Identities = 274/295 (92%), Frame = +1 / +1

```

Query: 1 aagagaagaaagggaaacgggaatacaaggactccggagctgtacttatggcacacatccc 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 666 aagacaagaaagggaaacgggaatacaaggactccggagctgtacttattgcacacatcct 725

Query: 61 ccgttgccctccttcctntngaaatTTTatccccaggggaagctatgaaaacggaggaaccc 120
    ||||| || ||||| | ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 726 ccgttgcttcttcttcttngaaatTTTgtctccaggggaagctatgaaaactgaggaaccc 785

Query: 121 ggtatgttctcttttgggtggggaaccaagaaaaagcccggcatatggtctactcaagag 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 786 ggtatgttctcttttgggtggggaaccagagaaacagcccggcatatggtctactcaagat 845

Query: 181 gtgcccattactgtcctcaagcacaagctcagtagactTTTattctgttccaccacaagaa 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 846 gtgcccattactgtcctcaagcacaagctcagtagactTTTattctgttccaccacaagaa 905

Query: 241 aaagcaaaggatTTTTATAATTCAATACCTTCAAATACGAAACAGTTGAGCAGG 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 906 aaagcaaaggatTTTTATAATTCAATACCTTCAAATACGAAACAATTGATCAGG 960

```

>[SGN-M6951](#) C2\_At1g64770-2 [cosii\_markers]  
 Length = 695

Score = 131 bits (66), Expect = 9e-31  
Identities = 94/104 (90%), Frame = +1 / +1

```
Query: 1 aagagaagaaagggaaacgggaatacaaggactccggagctgtacttatggcacacatccc 60
      ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 592 aagacaagaaagggaaacaggaatacaaggactccggagctgtacttattgcacacatcct 651
```

```
Query: 61 ccgttgcctccttcctntngaaatcttcccccaggggaagctat 104
      |||||| | | ||||| | |||||| |||| | ||||||| |||||||
Sbjct: 652 ccgttgtcttctcctttgaaattatatctccaggggaagctat 695
```

### Summary

The sequence data for p3-72.2 was satisfactory. For G70 (resistant inbred) especially, it was hard to determine a consensus sequence because the sequence from the reverse primer was not good. For this set of primers, the comparison was made between a consensus sequence of both M82 and W168 (susceptible) with just the forward sequence from G70 (resistant inbred). Despite this, there was still a significant number of differences, enough for us to conclude that there is an introgression.