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
P3-72.2 F: GGTTGAATTAAGCTGAGTCG
P3-72.2 R: CCTCAAAGGCCCCAAACGTATTACCT

Annealing temperature: 53 C

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

```
1      AAGAGAAGAGA AGGGGACGGA AAATACAGAGA CTCCCAGACCT GTACTTATGG CACACAATCC
61     CGTTGCGCTC TTGCACTTNGA AAATTTATCC CCGGGAGGA AGTTGAAAGA GGGGAAGACC
121    GGATGTTCTCT TTGGTGTGG GGAACCAAGA AAAAGCAGGG CAGATAGTCT TACCTAAGAG
181    GTGGCCATAGAT GTGNNCNCAA GCCACAAGCT AGAAGACTTT ATCTGATTC GGGAAAGACC
241    AAGCAAGGATTTTTTATGAT TCAATAATCT CCAAAATAGC CAAAGGTGAG GAGGTATCA
301    CATTTAAACAA AACACTCACAC TAAATTACAA TACAAAGTATG ACTAGTTTTA TAACCACAG
361    TGTGATGCTCT TTAAGAAGAC ATGTCNCAA TTTATATTAT TCTCTNAAAG
421    GAGGATAAAGG TCTCAAAAGAAC GCAAAATCT TANNNGGTTGTTTTTGCTC TCCCGGGGN
481    CCGGAGCTCT TCCATAGGAG ATACGTTGGG GCTTTGAGCG
```

Partial Sequence of M82 (Susceptible), p3-72.2

```
1      TGAGTATTGC CACCGCAGGT GTTTGAGAGA ACATGGTNG GAANCCGACA NAGTTAACCA
61     CAGCTATTATGAGTCTTGGT TATGNTTGAAG CAAAGGAAGA GACGAGGTAT CAGGAAATCC
121    GGGACGCTATG GAAACTGAGA AAACCCGCTA CAGAATACAA ACTCTTCTGC TCTCTCCAG
181    GGGACGCTATG GAAACTGAGA AAACCCGCTA CAGAATACAA ACTCTTCTGC TCTCTCCAG
241    AAGCAGGCCAT ATGTCNCAA CAAAGATGGA GGCAGTCTCGC TCTGTTCTCG CAG
301    GACCTTTATTC GTGTCACCCTA CAAGAAGAGA CAAAGGTATG ATATAATTAC TAAATACAAG
361    GATACGGAAAC ATTTGAGTGAT GTACACTATT CAAACCAACAG ACTACCTTCTA ATTACATAC
421    AGTAAATAACG GTTTTTATAC TCTATGCTCA GTGTGTTCTGG ATGAGTACAT AAAAAATATC
481    GTGCAACATCT CAAATTATCCT CTAGAAAAAG CAAAGGATTG TTATAATTAC AACCCTCACG
541    TGTGAGTTTTG GTTTTCTTTT CGGGGGTGGG GAGCCTCTCTT TTAGGAAATA CTGGTGGG
```

Partial Sequence of W168 (Susceptible), p3-72.2

```
1      GTTGAAATTTAAGCTGAGTCG AGGGAGTTCTA GATATTAACCT ATGTGTTGTC ACTCTATCAG
61     TTGAGTATTGCC ACAGCAGGTAGTATGCTTA GATATTAACCT AGTGGTGTAGC ACTCTATCAG
```
Comparison of M82 (upper line) with G70 (lower line)

Comparison of G70 (upper line) with W168 (lower line)
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   aagagaagaaagggaacgggaatacaaggactccggagctgtacttatggcacacatccc 60
Sbjct: 666 aagacaagaaagggaacgggaatacaaggactccggagctgtactattgcacacatcct 725

Query: 61  ccgttgcctccttccntngaaattttatccccaggggaagctatgaaaacggaggaaccc 120
Sbjct: 726 ccgttgtcttcttcctttgaaattttgtctccaggggaagctatgaaaactgaggaaccc 785

Query: 121 ggtatgttctctttttggggtgggaaccaaagaaaaagcccccccattctactgactagqag 180
Sbjct: 786 ggtatgtttctctttttggtgaccaacagacaacagccccccgcatatgtctactcaagat 845

Query: 181 gtgcccacatgactgnccnccacaacagcagctcagaaagactttatattctgctcaccacaagaa 240
Sbjct: 846 gtgcccatctgctctcaagcacaacagctcagctctactttactgctcaccacaagaa 905

Query: 241 aagagaaagagttttttataattcaatctcttttcaaatagcaaacagttttgacccagg 295
Sbjct: 906 aagagaaagagttttttataattcaatctcttttcaaatagcaaacatttctcagg 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   aagagaagaaaggaacgggaatatcaagggactccggagctgtatgctatgccacactccc 60 |
| Sbjct: 592 aagacaagaaggaacaggaatcaagggactccggagctgtatgctatgccacacatcct 651 |

| Query: 61  ccgttgcctctctcntngaattatatcccccaggggaagctat 104 |
| Sbjct: 652 ccggttgtctctctctctgattatatatctccaggggaagctat 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.