

# **Molecular Markers and Mapping of Root-knot Nematode Resistance in Cotton**



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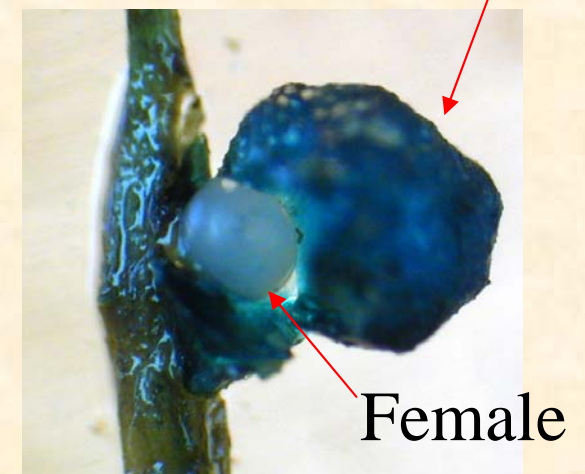
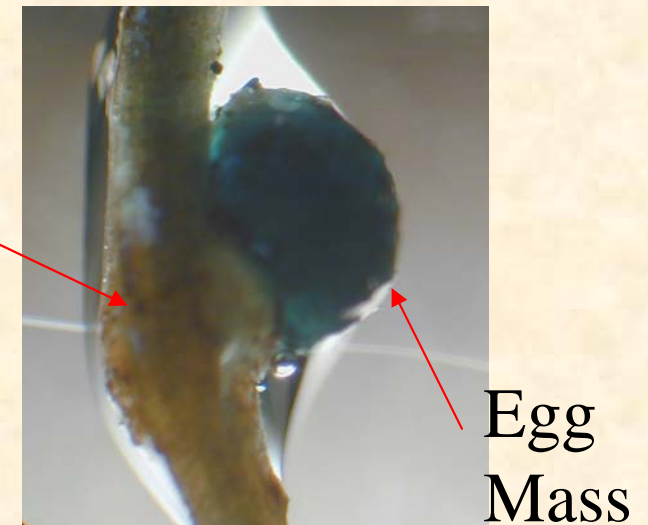
**USDA-ARS, WICS, Res Unit, Shafter**

# Outline

1. Background
2. Markers & Mapping of RKN R genes in *G. hirsutum*  
Acala NemX and Auburn 634 sources
3. Transgressive segregation for enhanced resistance
4. Mapping TS genes in *G. barbadense*
5. Search for gene origins in *Gossypium*

# Root-knot Nematodes are one of the Most Economically Important Pests in Cotton

- Occur in every cotton-producing area in United States.



# Parental Reaction to Root-knot Nematode

**NemX**

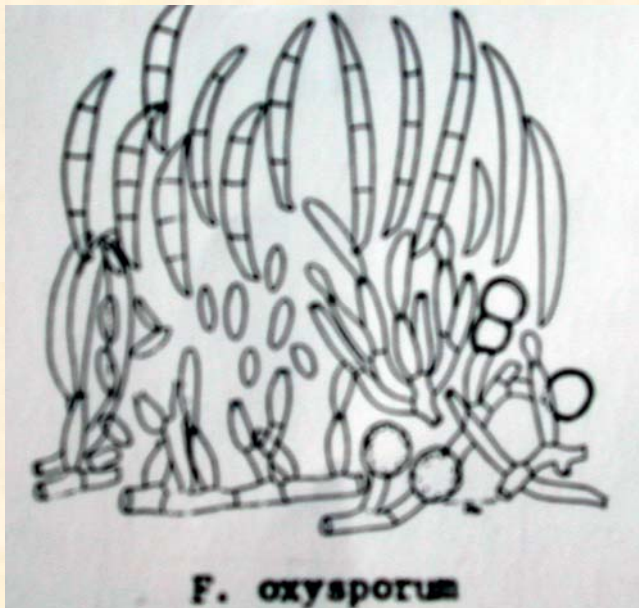
**Pima S-7**

**SJ-2**



# Fusarium wilt of Cotton

Vascular disease caused by  
the soilborne Fungus  
Pathogen: *Fusarium*  
*oxysporum* f. s.p.  
*vasinfectum* (FOV)



**Pima S-7**

**SJ-2**

**NemX**

**FOV**

**R**

**S**

**S**

**RKN**

**S**

**S**

**R**



FOV R4

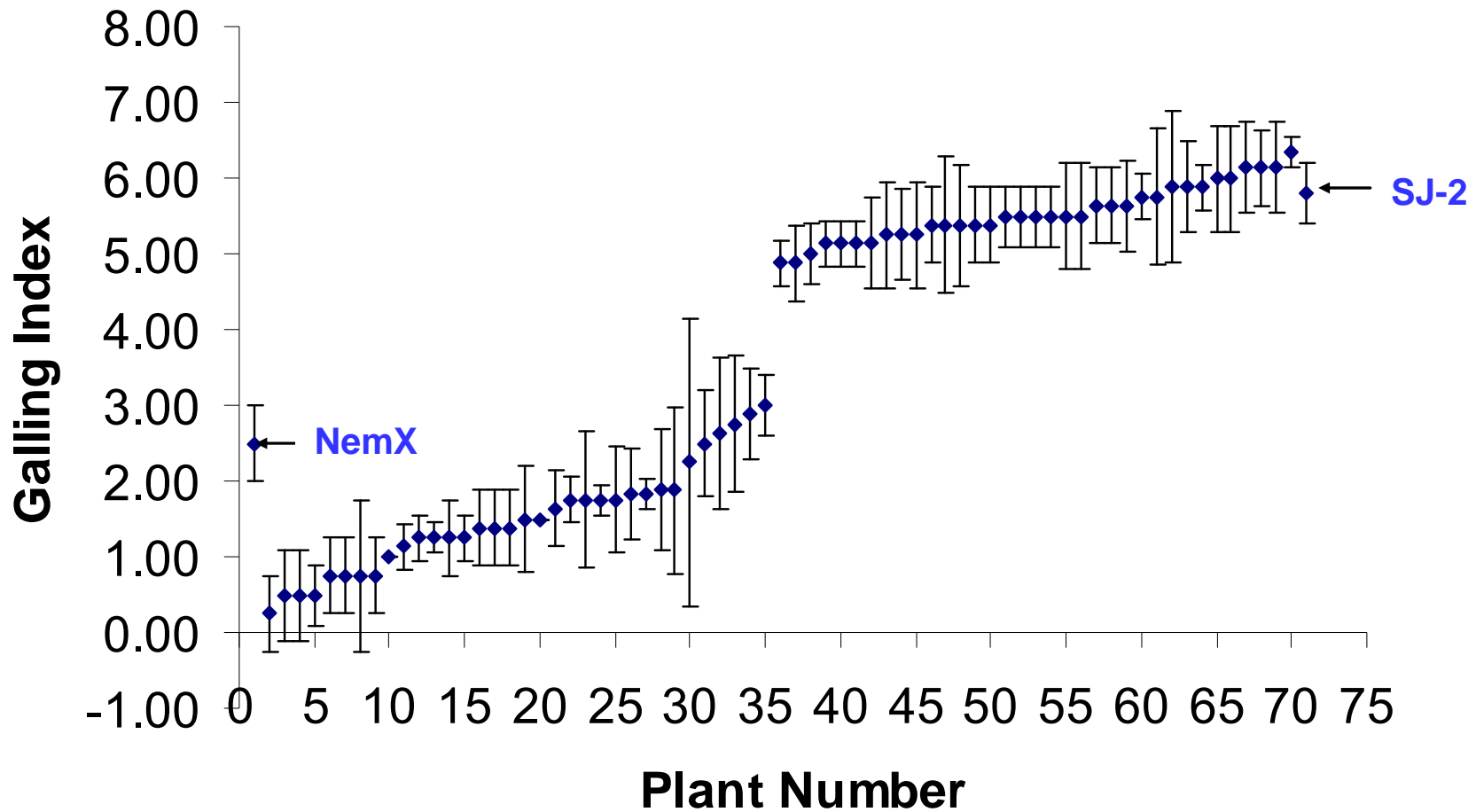
FOV R4

+RKN

NemX



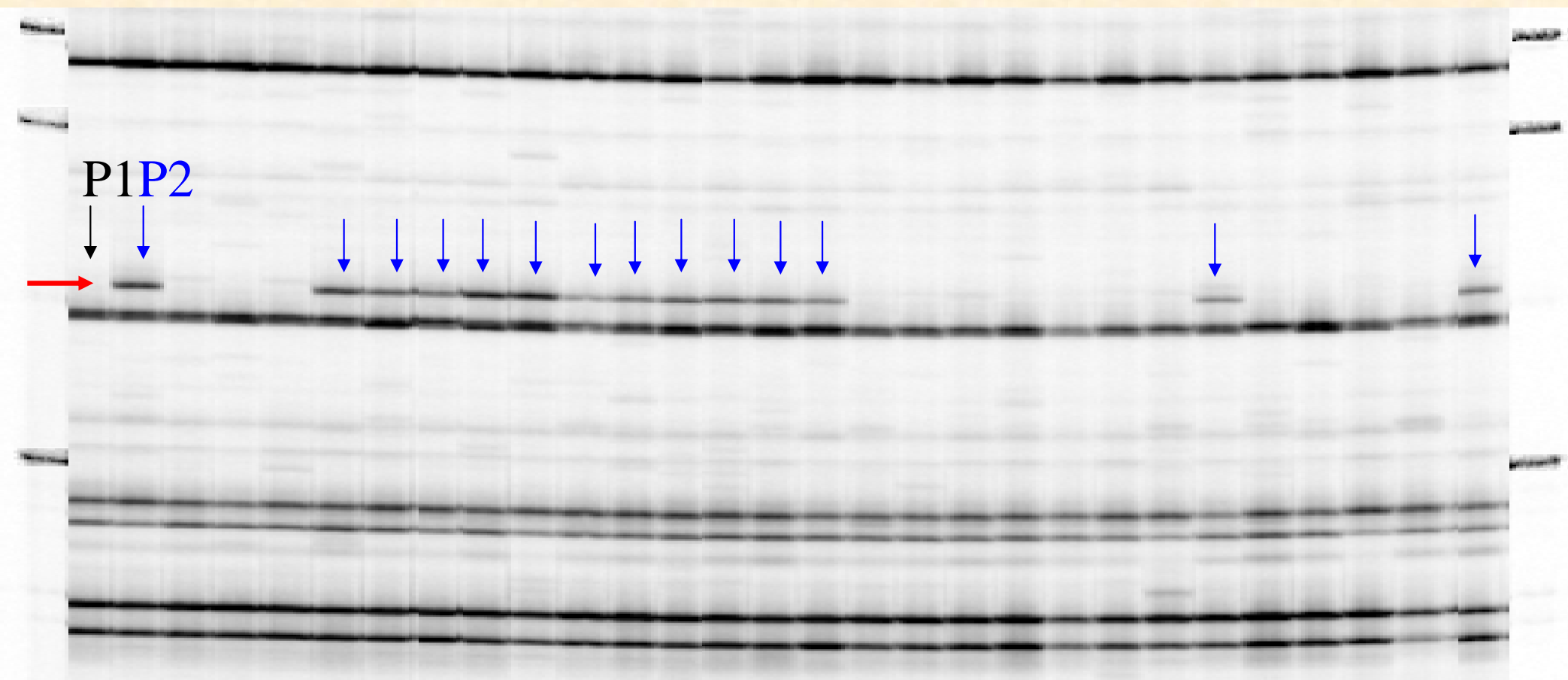
# F<sub>2:7</sub> RIL Gallling Index





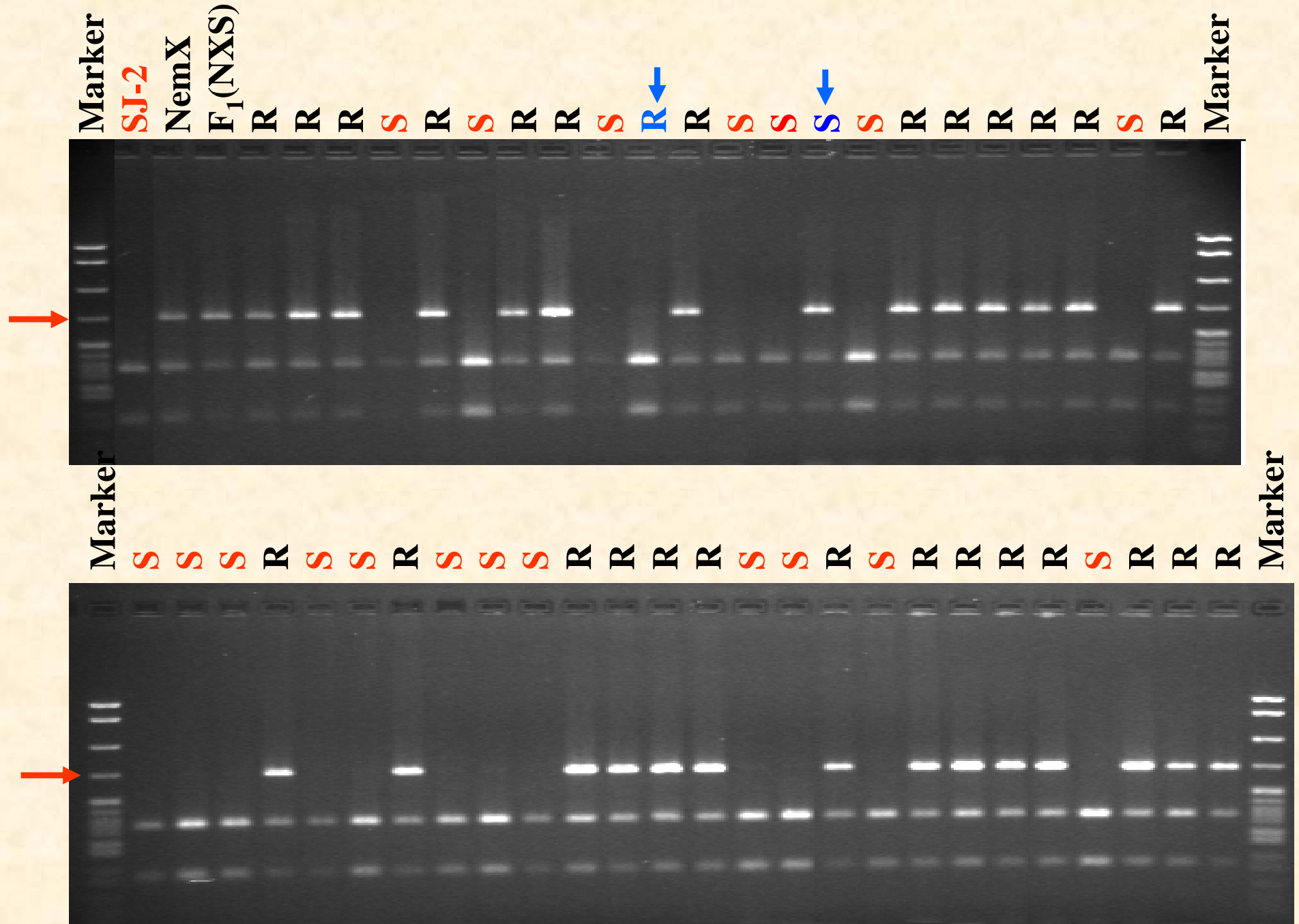
# AFLP marker and RIL F<sub>2:7</sub> (NemX x SJ-2)

M S R S S S R R R R R R R R R R S S S S S S S S R S S S S R M



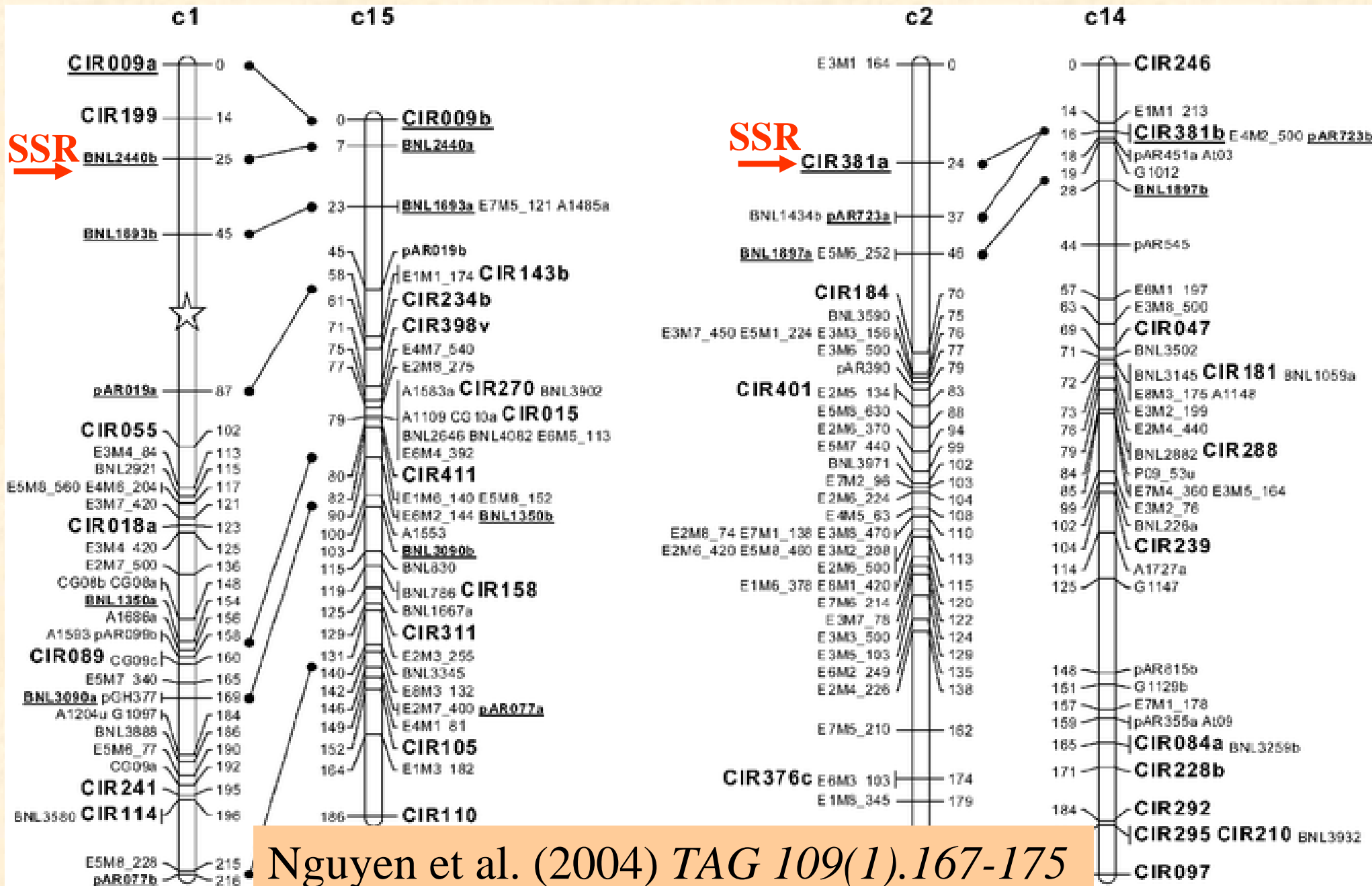
4/128 EcoR1/Mse1

# CAPS marker (*Nla*III) RIL<sub>7</sub> (NemX x SJ-2)

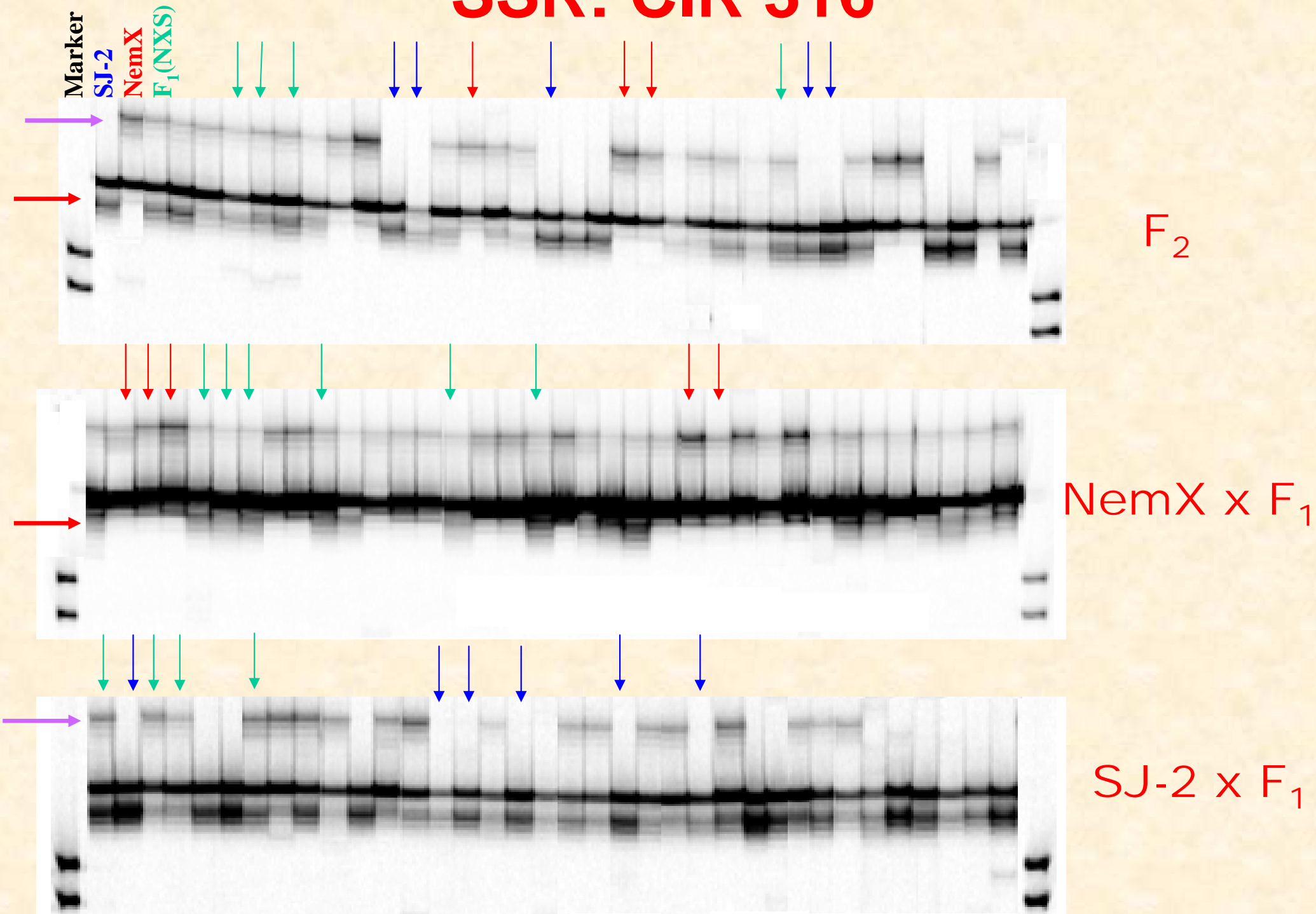


# Cotton Linkage map

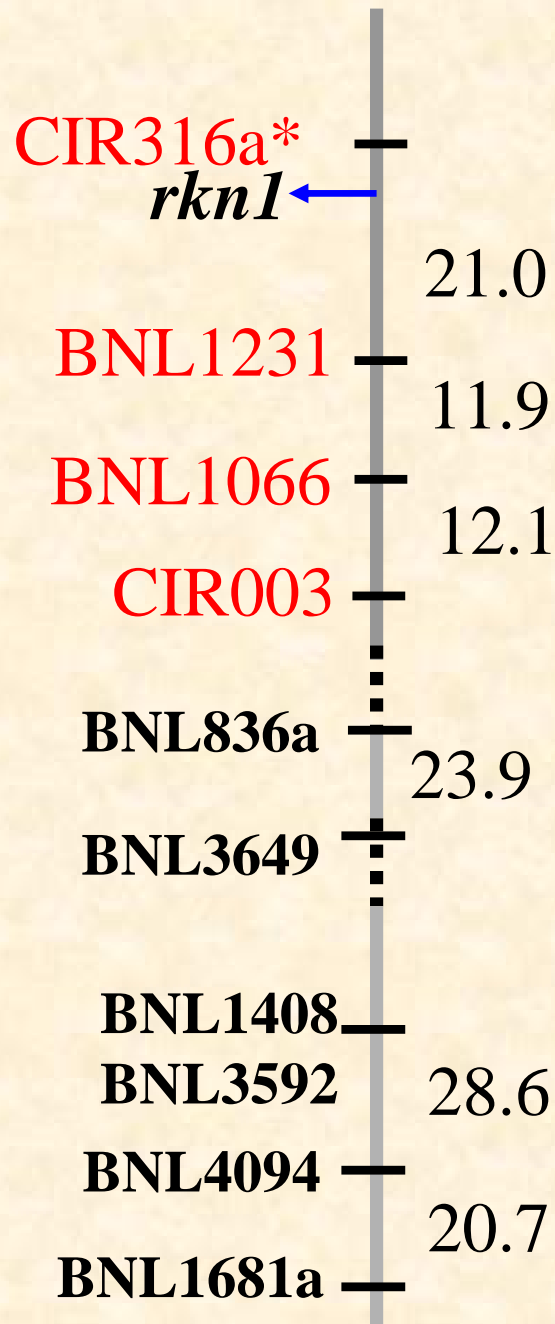
284 primers



# SSR: CIR 316



F<sub>2</sub> (Pima S-7 x NemX)



**Chr.11**

## Localization of NemX R gene

Published data:

- Nguyen et al. (2004) TAG
- Rong et al. (2004) Genetics
- <http://cottondb.tamu.edu>
- Frelichowski, Ulloa (2006) MGG
- Unpubl. data Mauricio Ulloa

# Other RKN resistance mapping studies in Auburn 634 sources

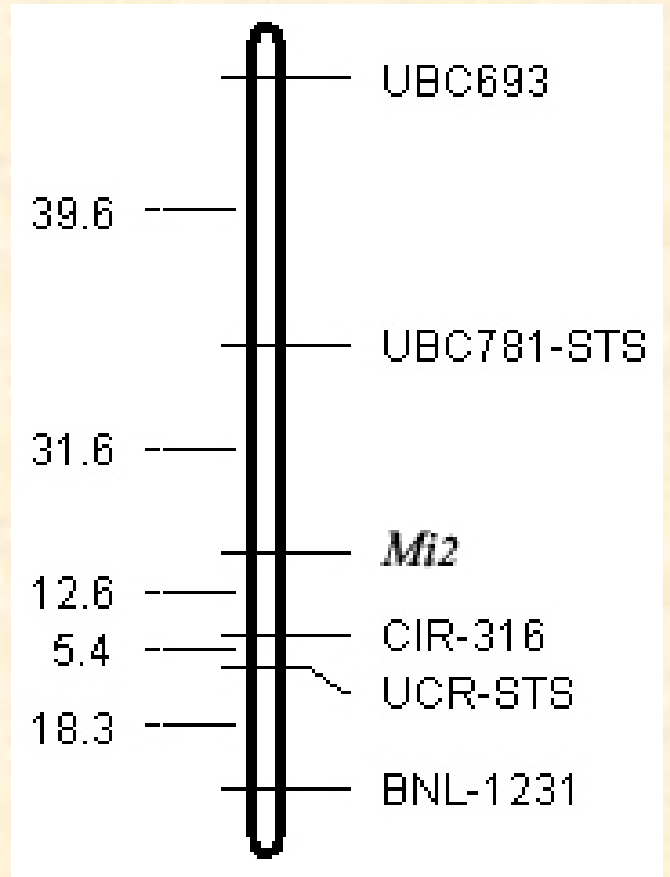
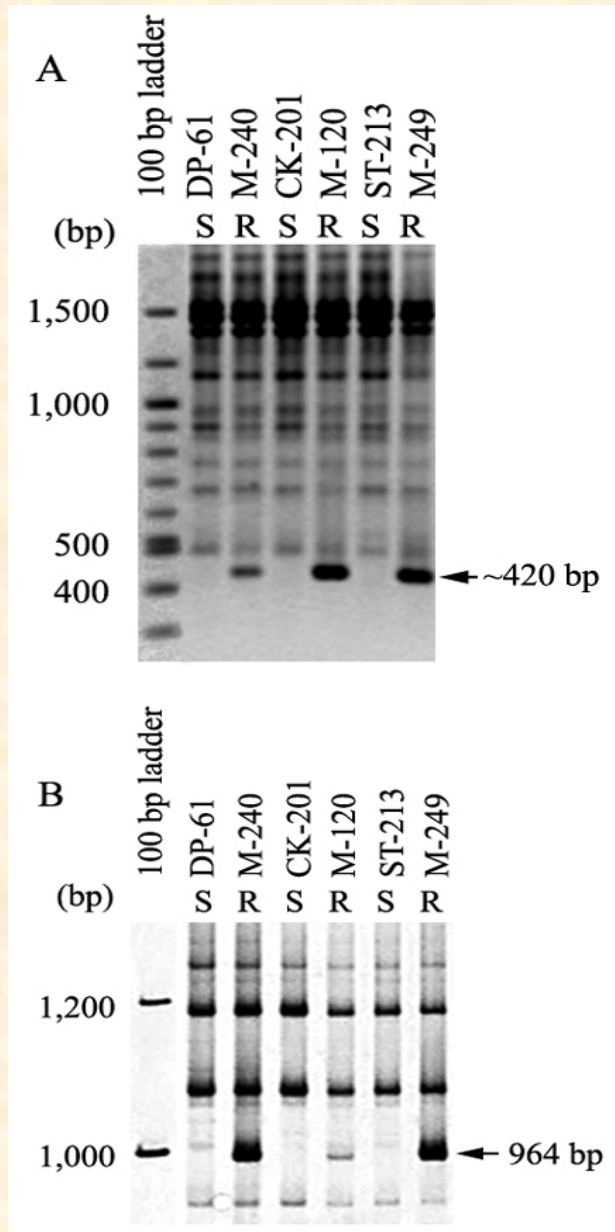
- 1 Shen, Davis, May, Chee et al. TAG, 2006
  - 2 QTL Chr. 11 and Chr. 7 ( $F_2$  with M120)
- 2 Ynturi, Jenkins et al. Crop Sci., 2006
  - 2 SSRs, Chr. 11 and 14 (NIL from A634)
- 3 Nui, Zhang, Wang, Roberts et al. Crop Sci. 2007
  - Major gene in A634 (*Mi2*) on Chr. 11 ( $F_2$  with A634)

# Localization of A634 R gene

Nui et al Crop Sci 2007

Chr.11

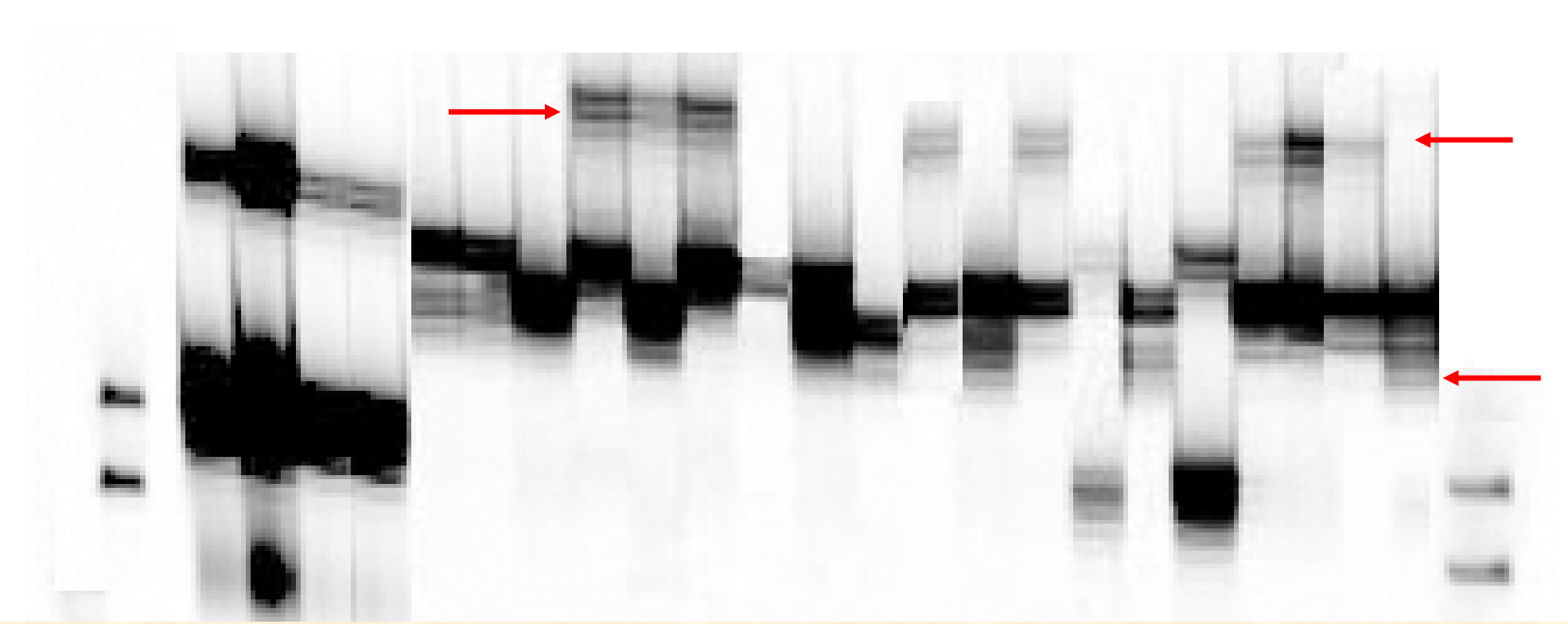
ST 474 x A 634 F<sub>2</sub>



# Cotton germplasm: Marker Screening

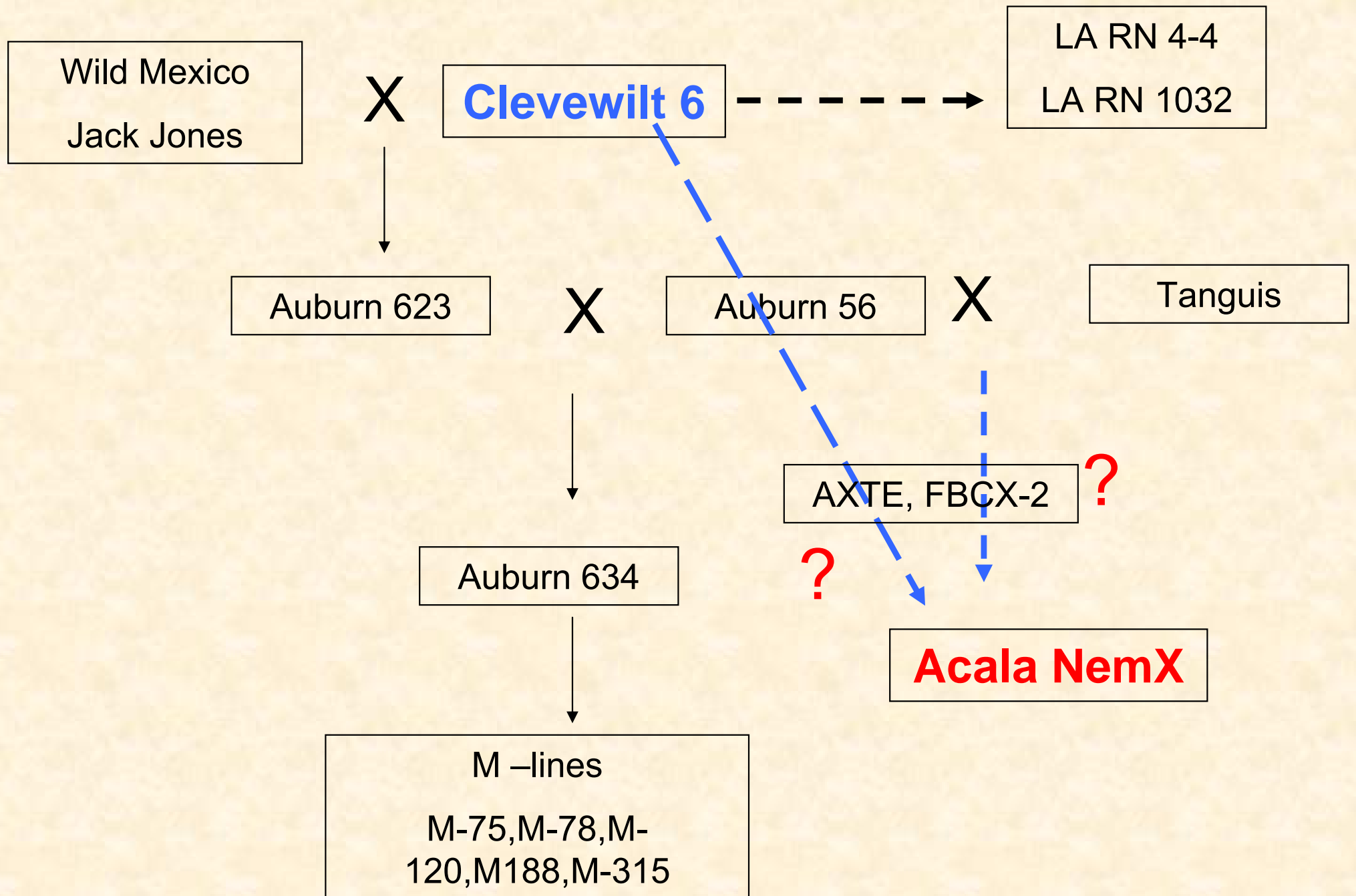
SSR: CIR 316

Marker  
PimaS-2  
PimaS-3  
PimaS-4  
PimaS-7  
Coker100  
Coker307-6  
Wild Mexico  
Clevewilt 6  
Auburn 623  
Auburn 634  
Auburn56  
M-75  
M-78  
M-120  
M-188  
M-315  
TX 110  
Acala442  
Tanguis  
LARN 4-4  
LA RN 1032  
NemX  
SJ-2  
Marker





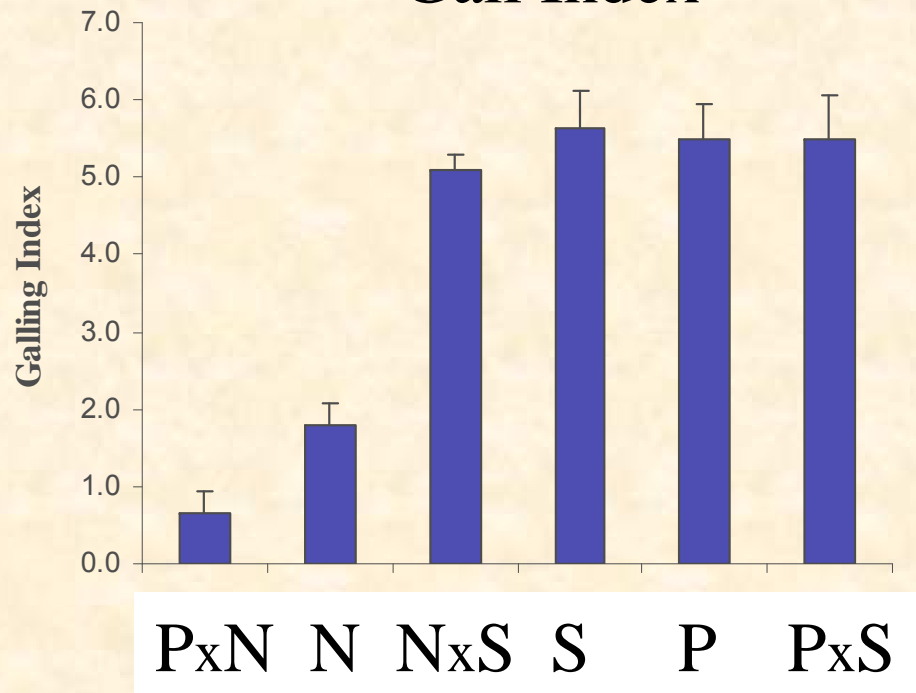
# Root-knot Nematode Resistance Sources



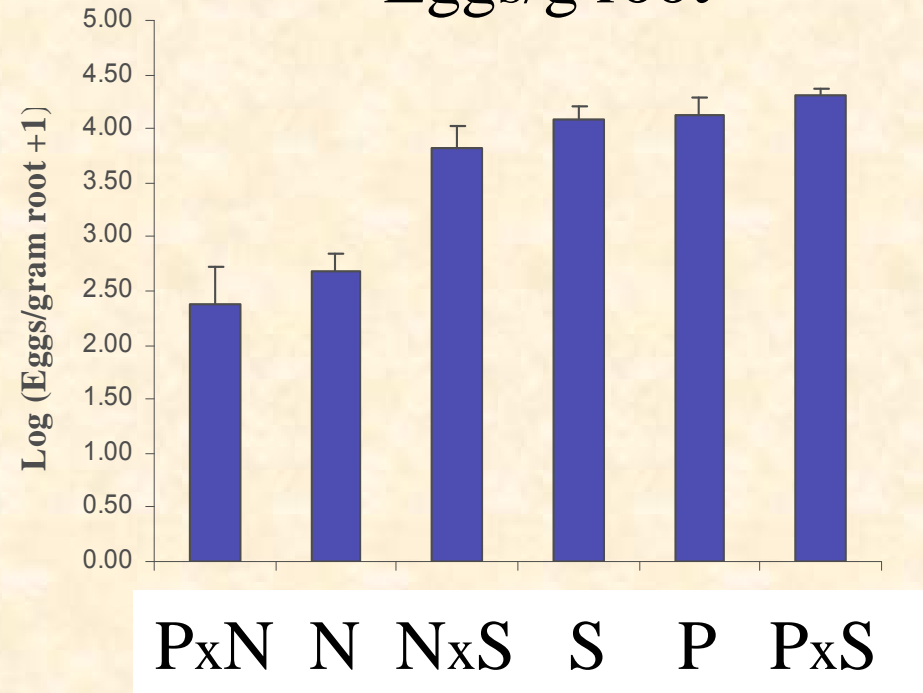
<b>F<sub>2</sub></b>	<b>SJ-2</b>	<b>NemX</b>	<b>Pima S-7</b>	<b>Clewevilt 6</b>	<b>Auburn 634</b>	<b>Auburn 623</b>	<b>Tanguis</b>
Clewevilt 6	✓	✓	✓				
WildMexico	✓	✓					
Auburn 56	✓	✓	✓	✓	✓		✓
Auburn 634	✓	✓	✓	✓			
Auburn 623	✓	✓					
M-75	✓	✓	✓		✓		
M7-78	✓	✓	✓		✓		
M-120	✓	✓					
M-188	✓	✓	✓			✓	
M315	✓	✓	✓			✓	
LA RN 4-4	✓	✓	✓		✓		
LA RN 1032	✓				✓		
Pima S-3		✓					
Pima S-2					✓		
Pima S-1				✓			

# F<sub>1</sub> and Parent Resistance phenotypes for NemX, Pima S-7, SJ-2

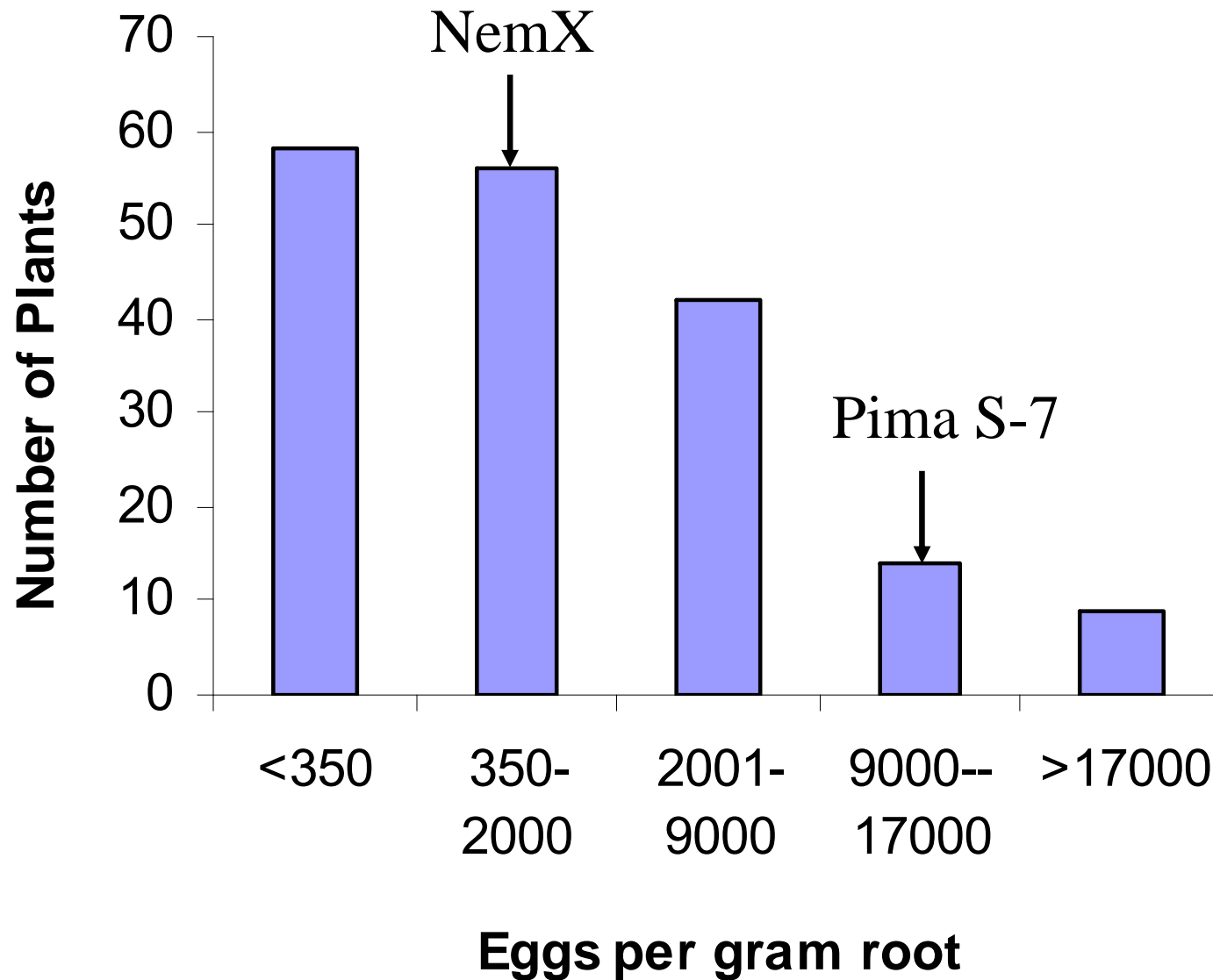
## Gall Index



## Eggs/g root

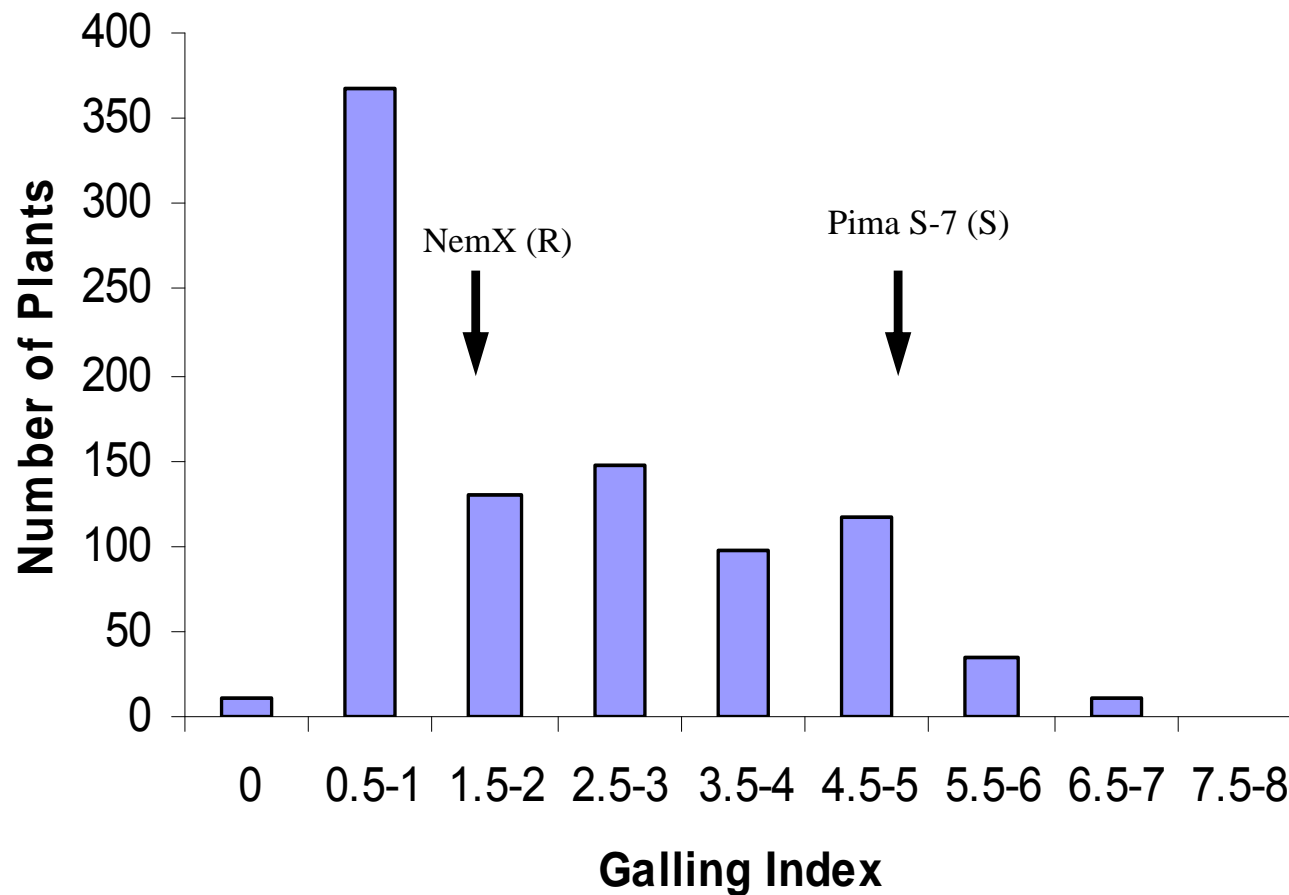


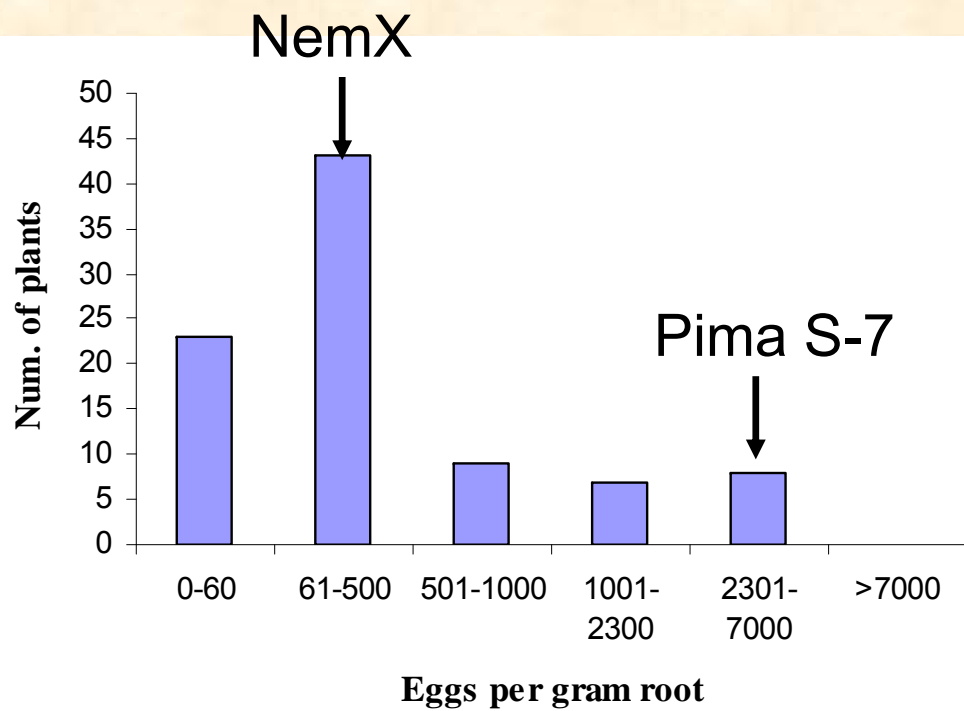
# F<sub>2</sub> (Pima S-7 x NemX) 179 plants



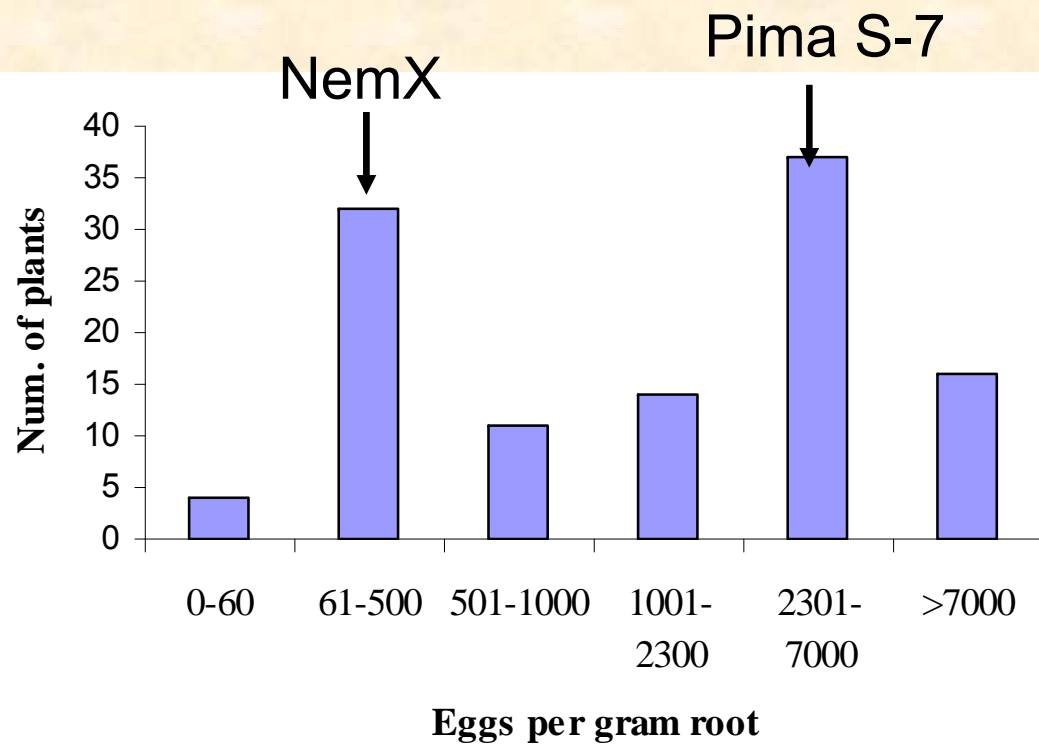
# Galling response of plants from 64 F<sub>2:3</sub> families of Pima S-7 x NemX

Extreme phenotypes of transgressive segregants outside parent range





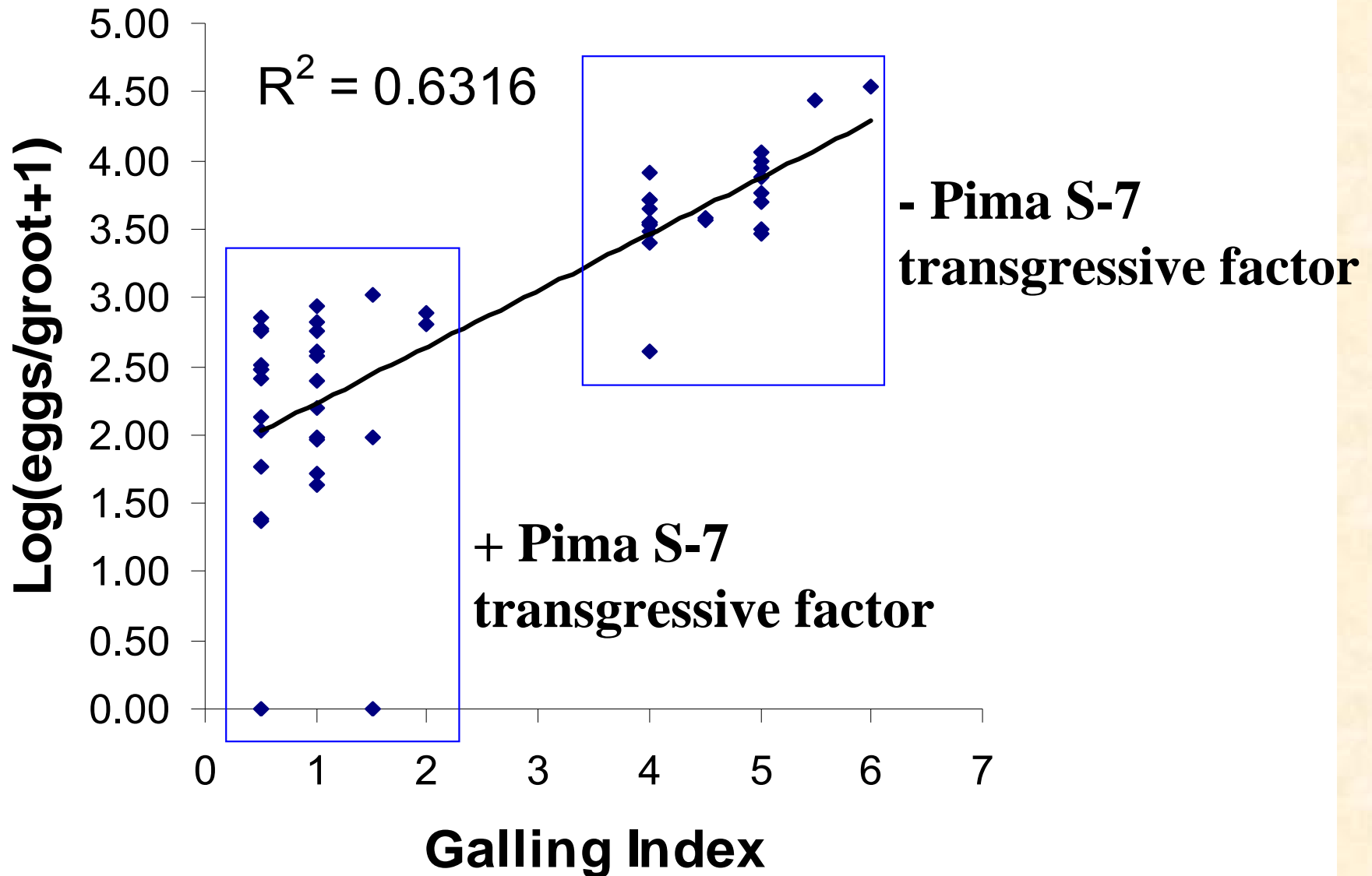
**BC<sub>1</sub>F<sub>1</sub> (NemX x F<sub>1</sub>)**  
**(90 plants)**



**BC<sub>1</sub>F<sub>1</sub> (Pima S-7 x F<sub>1</sub>)**  
**(114 plants)**

# Testcross NemX x F<sub>1</sub> (PimaS-7 x SJ-2)

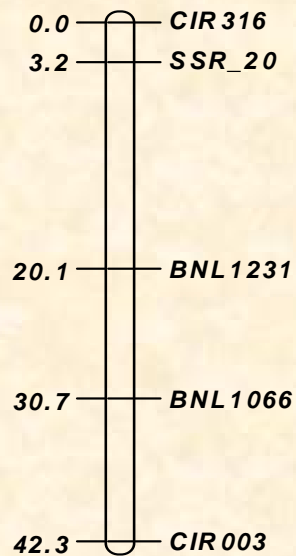
All plants Het for *rkn1*; ½ have PS7 factor



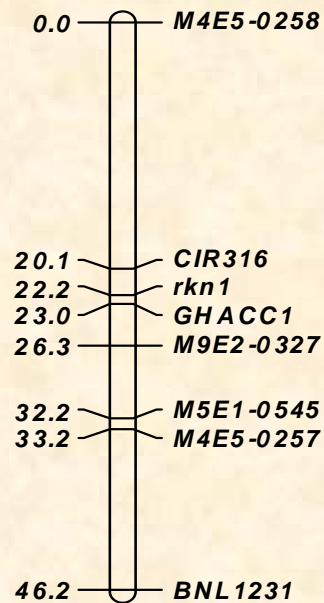




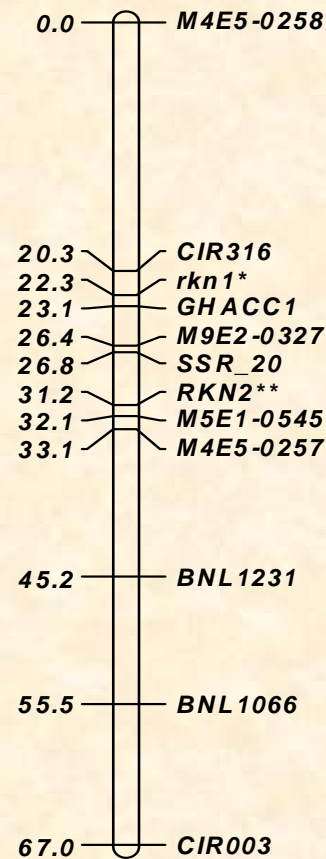
# Linkage groups and Joint-group representing Chr 11 showing the distance and position relationships between SSR markers and the nematode resistance genes *rkn1*\* and *RKN2*\*\*.



**Pop 1**  
**Chromosome 11**  
**F2 interspecific**  
**(Pima S-7 x**  
**NemX) LOD = 4.0**



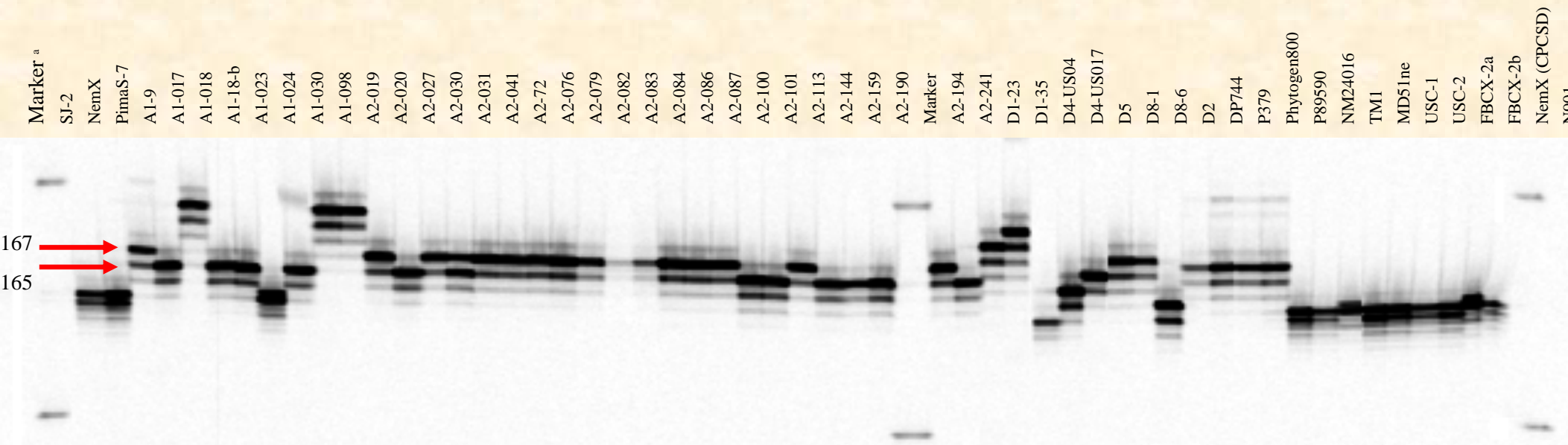
**Pop 2**  
**Chromosome 11**  
**F2 intraspecific**  
**(NemX x SJ-2)**  
**LOD = 6.0**

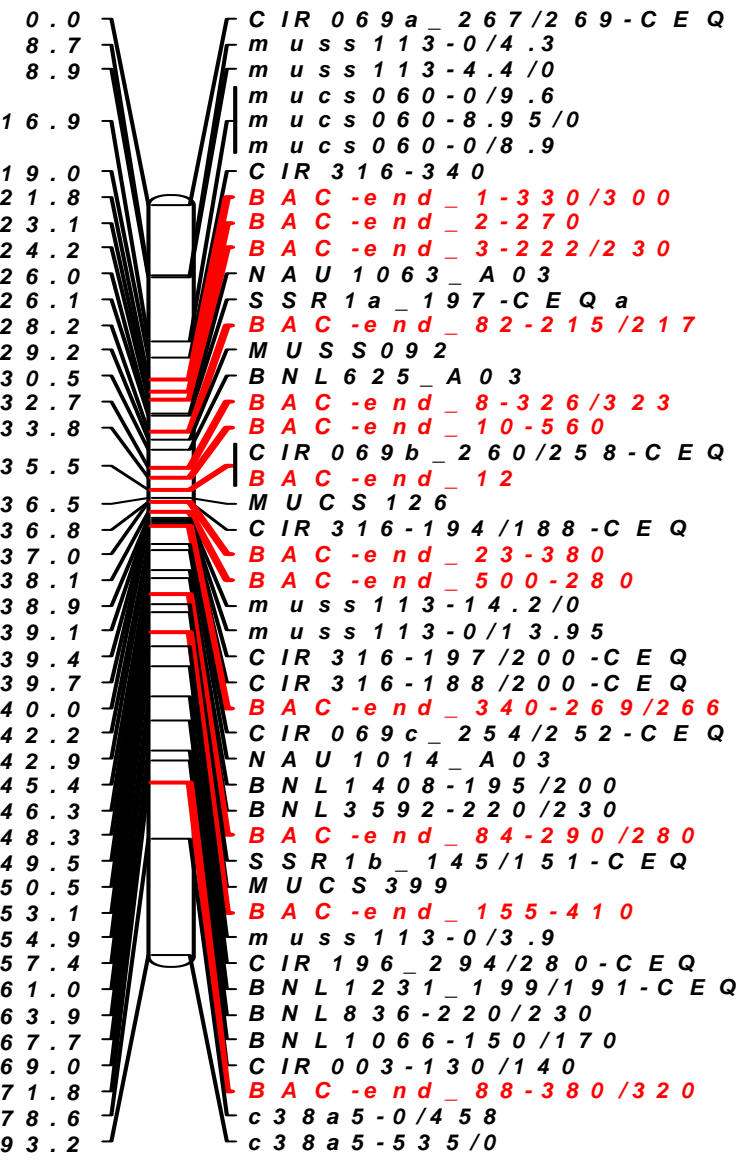


**Joint-LG**  
**Chromosome 11**

# Cotton marker/R gene origin Screening A and D genome donors

*RKN2* SSR marker – MUCS-088





Current working map of Chr 11, with BAC-end derived SSRs in the CIR316/BNL1231 region.

# Summary

- Chromosome 11 important RKN R gene region: *rkn1*, A634 source, *RKN2*
- Excellent markers linked to *rkn1* and *RKN2* for MAS (SSR, CAPs, SNP)
- Transgressive segregation for enhanced resistance phenotypes
- Marker screening of diverse germplasm - test for unique R genes and origins
- Saturation mapping tied to physical mapping

# Acknowledgements

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**Bob Nichols (Cotton Inc)**

**Jim Starr (Texas A&M)**

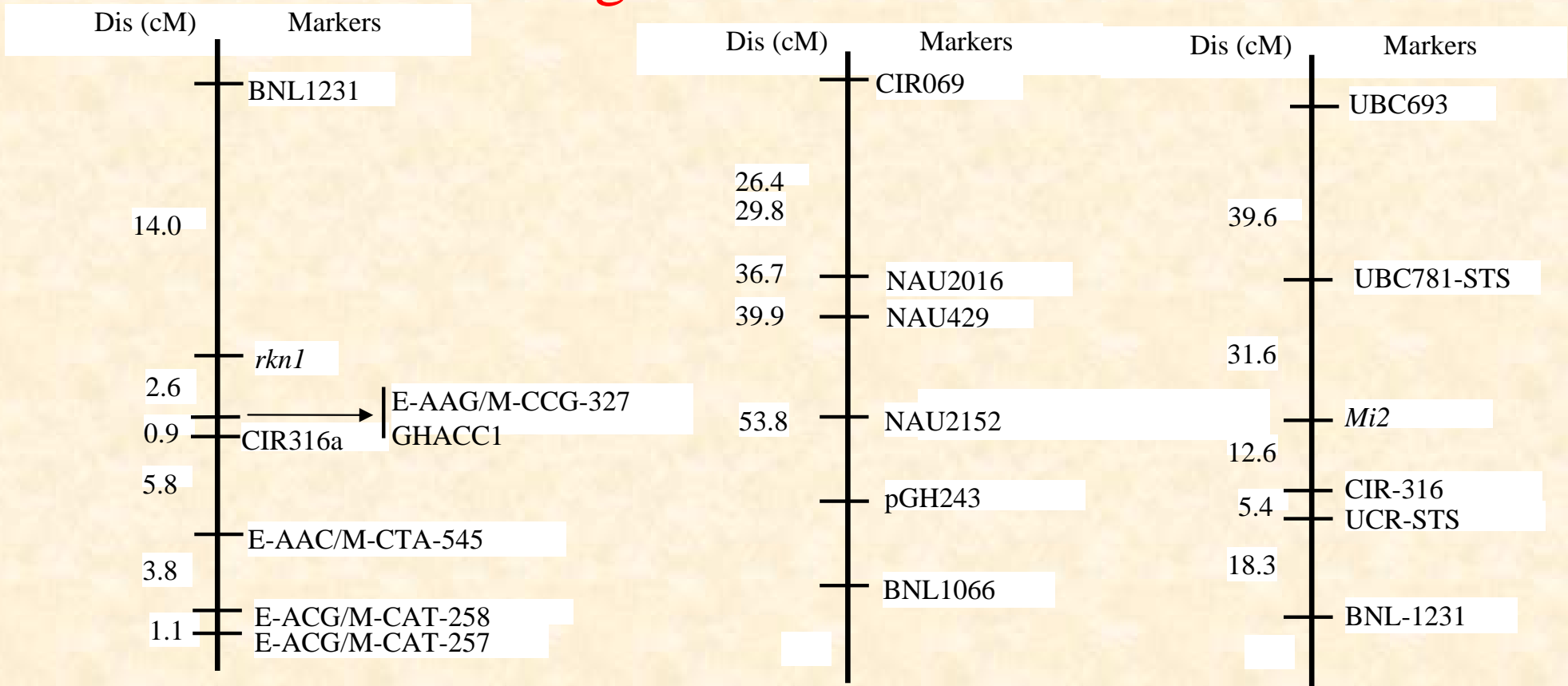
**Richard Davis and Peng Chee  
(U. Georgia)**

**Johnnie Jenkins (USDA, MS)**

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UC Discovery Grant Program

# Linkage groups representing Chr 11 showing the distance and position relationships between SSR markers and the nematode resistance genes



Wang et al  
Rkn1-NemX

Shen et al  
M120-Au 634

Nui et al  
Au 634