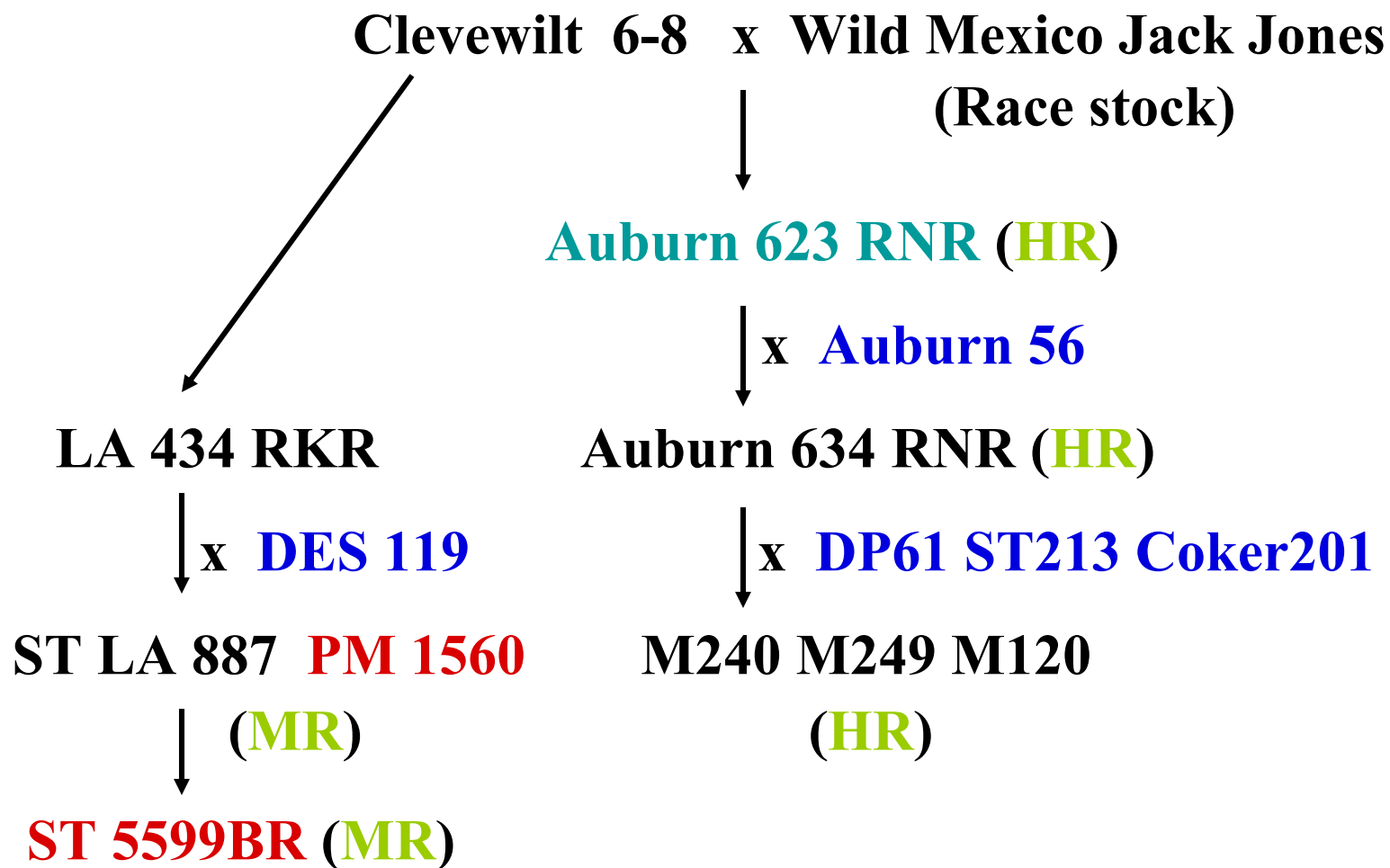


# **Root-Knot Nematode Resistance in Cotton: Research Progress at NMSU**

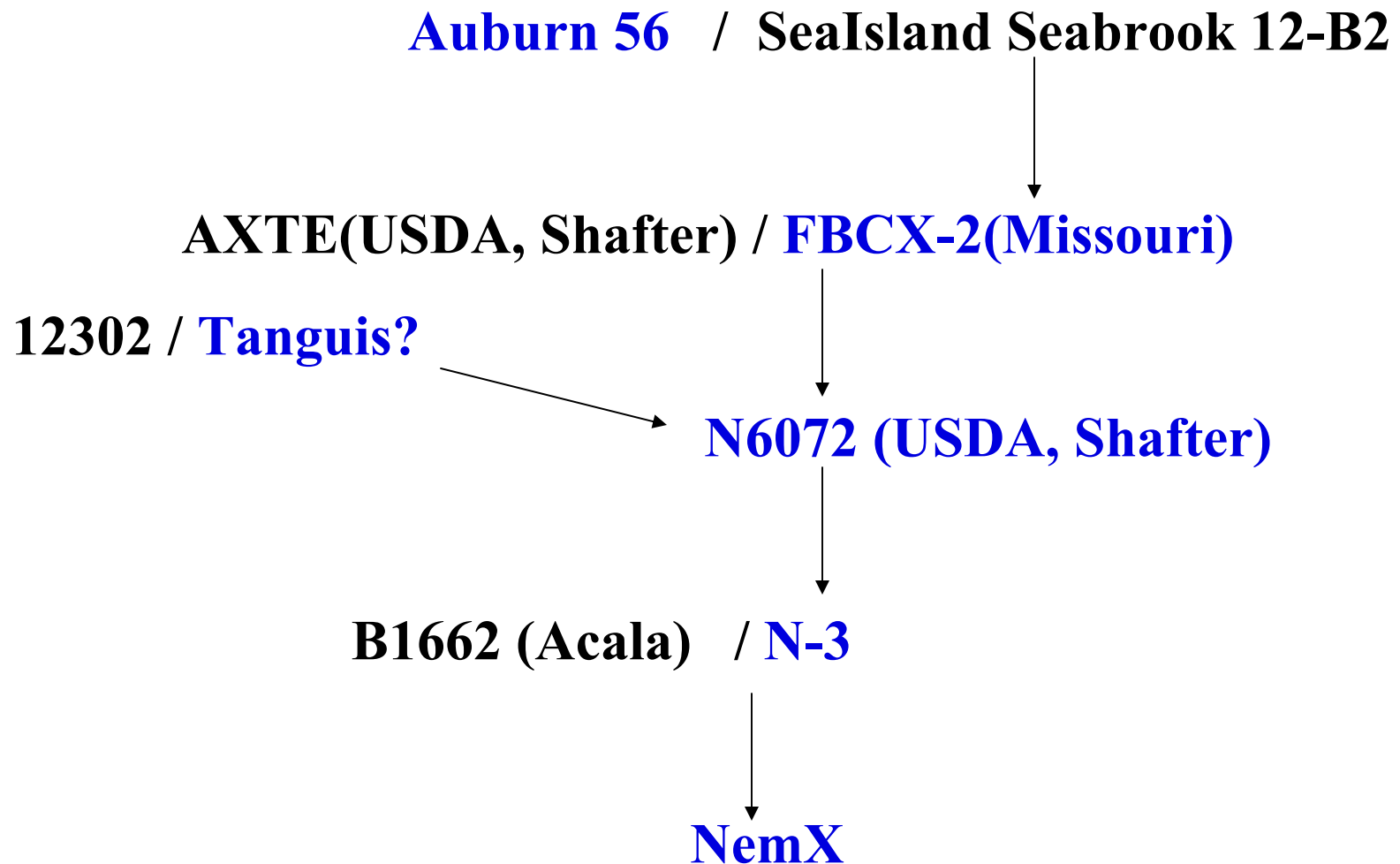
**Jinfa Zhang**

**New Mexico State University**

# Major Cotton Germplasm Sources for RKN Resistance: Auburn 623

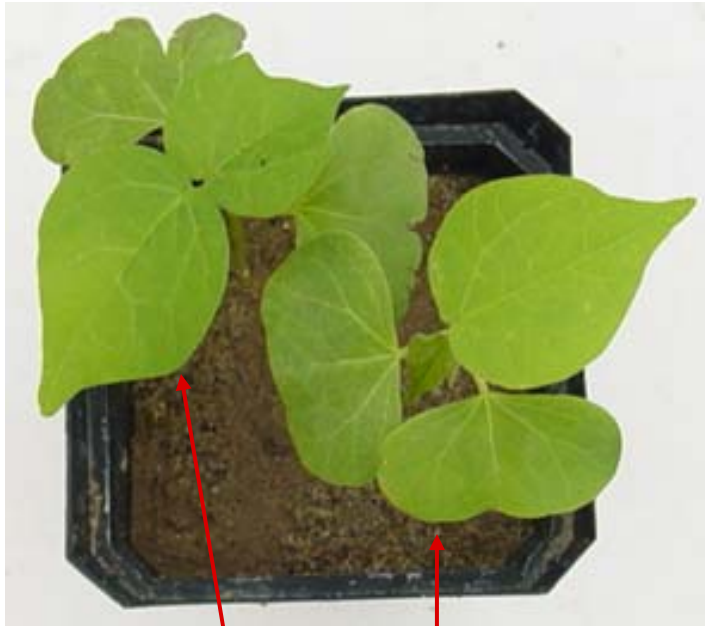


# Major Cotton Germplasm Sources for RKN Resistance: Acala NemX



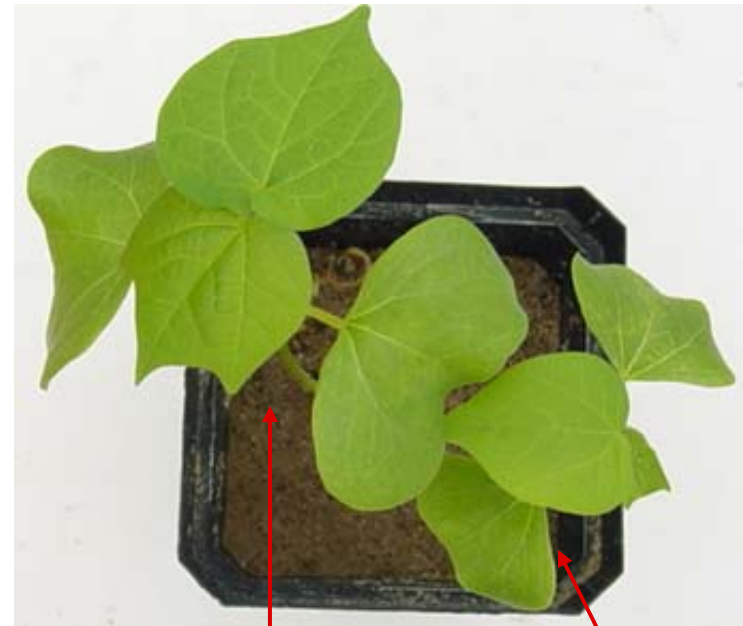
# Galling Index

- |          |  |
|----------|--|
| <b>0</b> | <b>No galls</b>                                  |
| <b>1</b> | <b>Light galling (&lt;25% roots with galls)</b>  |
| <b>2</b> | <b>Moderate galling (20-50% root galling)</b>    |
| <b>3</b> | <b>Heavy galling (50-75% root galling)</b>       |
| <b>4</b> | <b>Very heavy galling (&gt;75% root galling)</b> |



**ST 474**

**1517-99 (CK)**



**Auburn 634**

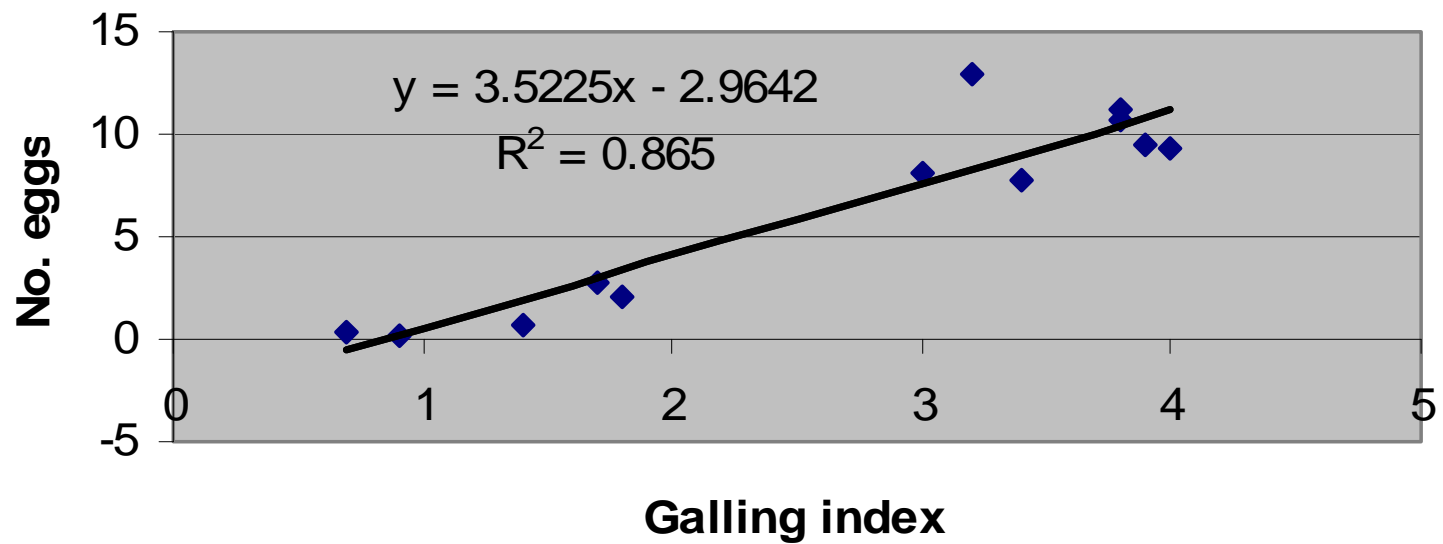
**1517-99 (CK)**



## Genotypic Differences in RKN Resistance

<b>Cultivar</b>	<b>Galling</b>	<b>Galling</b>	<b>Eggs x10<sup>5</sup>/g root</b>
<b>33B</b>	<b>S</b>	<b>3.8</b>	<b>11.18</b>
<b>ST 474</b>	<b>S</b>	<b>3.9</b>	<b>9.49</b>
<b>SG 747</b>	<b>S</b>	<b>4.0</b>	<b>9.27</b>
<b>PM 1560BG</b>	<b>S</b>	<b>3.8</b>	<b>10.71</b>
<b>SG 125</b>	<b>S</b>	<b>3.2</b>	<b>12.97</b>
<b>DP 428BG</b>	<b>S</b>	<b>3.0</b>	<b>8.08</b>
<b>Maxxa</b>	<b>S</b>	<b>3.4</b>	<b>7.81</b>
<b>A 634</b>	<b>R</b>	<b>0.7</b>	<b>0.39</b>
<b>M 240</b>	<b>R</b>	<b>1.4</b>	<b>0.76</b>
<b>M 315</b>	<b>R</b>	<b>0.9</b>	<b>0.24</b>
<b>33B x A 634 F1</b>	<b>MR</b>	<b>1.8</b>	<b>2.14</b>
<b>NemX</b>	<b>MR</b>	<b>1.7</b>	<b>2.70</b>
<b>1517-99 (CK)</b>	<b>S</b>	<b>3.8</b>	

## Relationship between galling index and no. eggs



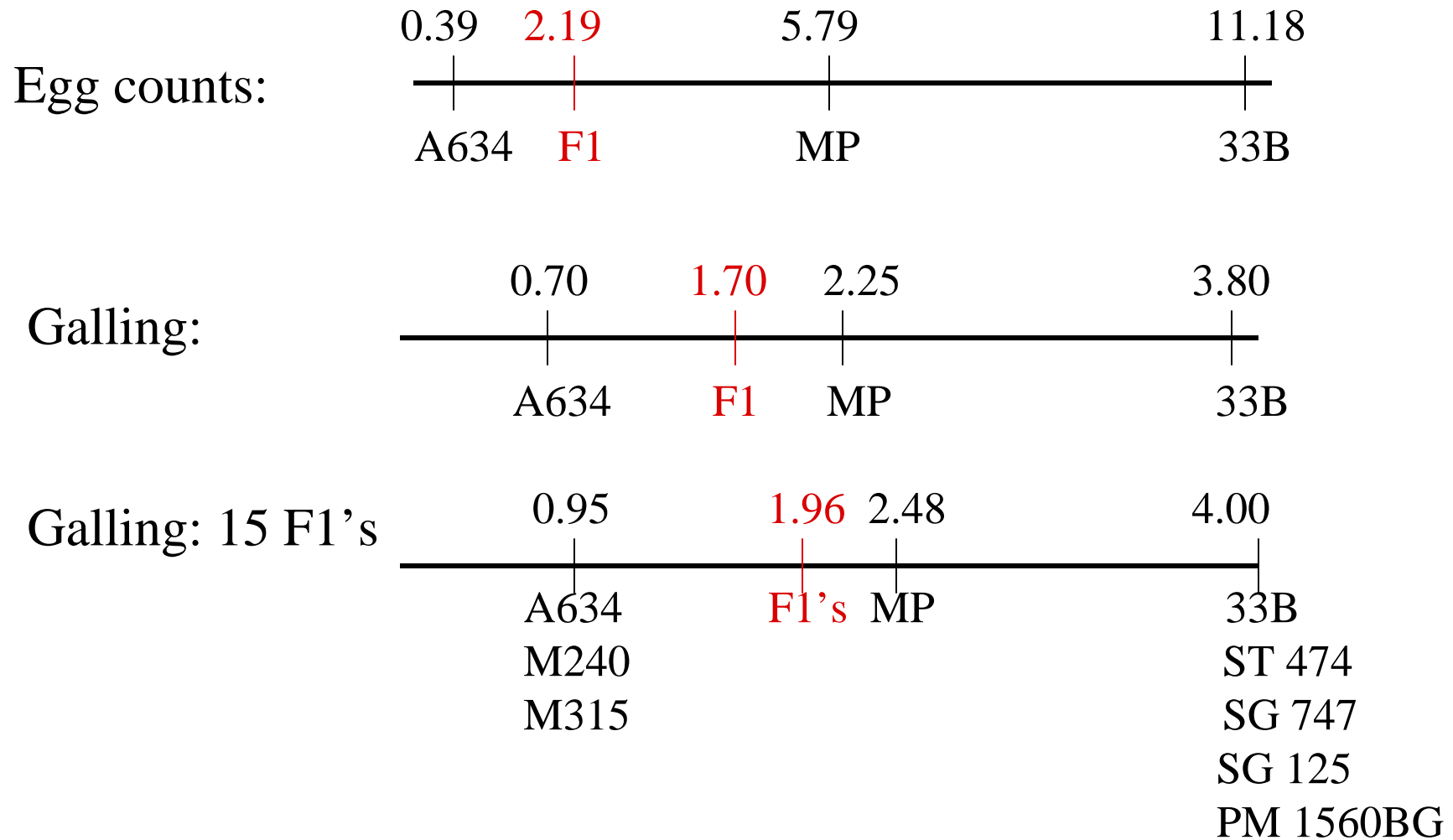
## Correlation between Plant Growth and RKN Resistance

	Plant height	No. Leaves	Plant weight	Galling index	No. eggs/g
Plant height	<b>1</b>				
No. leaves	<b>0.754*</b>	<b>1</b>			
Plant weight	<b>0.704*</b>	<b>0.549</b>	<b>1</b>		
Galling index	<b>-0.712*</b>	<b>-0.797*</b>	<b>-0.664*</b>	<b>1</b>	
No. eggs/g	<b>-0.755*</b>	<b>-0.817**</b>	<b>-0.683*</b>	<b>0.925**</b>	<b>1</b>

N = 12



# The Resistance in Auburn Source: Incomplete Dominance



## Estimates of Genetic Parameters

<b>Genetic parameter</b>	<b>Estimator</b>
<b>Broad-sense heritability: Hb</b>	<b>0.82</b>
<b>Narrow-sense heritability: Hn</b>	<b>0.65</b>
<b>Number of effective factors: K1</b>	<b>0.30</b>
<b>Number of effective factors: K2</b>	<b>1.17</b>

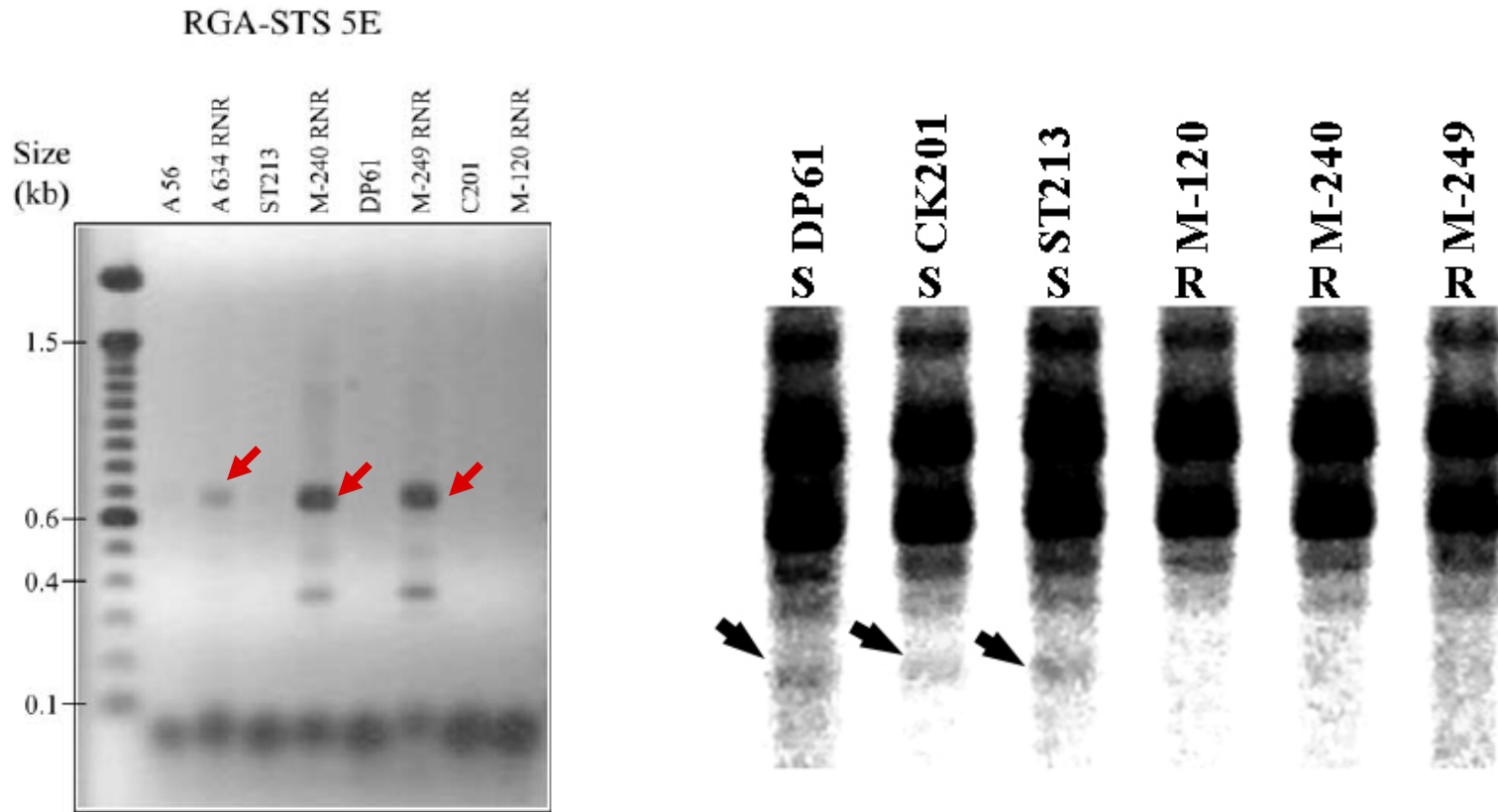
# Segregation Data

<b>Population</b>	<b>No. R</b>	<b>No. S.</b>	<b>Exp. ratio</b>	<b><math>\chi^2</math></b>
<b>1517-99 x ST 5599 F3</b>	<b>60</b>	<b>22</b>	<b>3:1</b>	<b>0.15</b>
<b>Nem-X x Auburn 634 F3</b>	<b>168</b>	<b>0</b>	<b>15:1</b>	<b>11.2**</b>

# Controversial but Clearer Picture

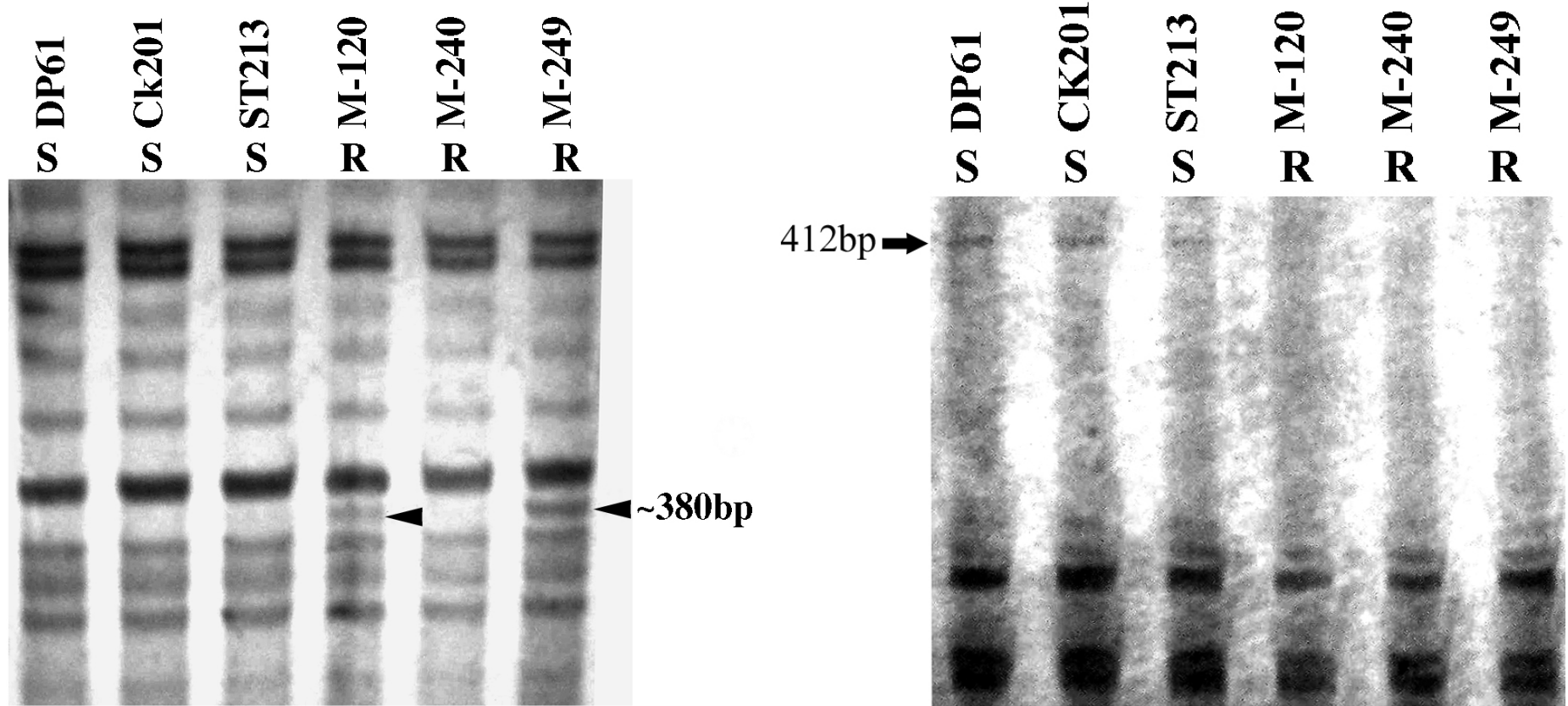
- **Auburn source: WM Jack Jones x Clevewilt → Auburn 623**
  - Shepherd (1974): polygenic and partially dominant
  - Jenkins's lab (McPherson, 1993): 1 dominant & 1 additive
  - Starr's lab (Zhou, 1999): 2 dominant genes
  - McPherson et al. (2004): two genes, *Mi-1* & *Mi-2*
  - **G.h. race stocks and conversions:**
    - McPherson (1993) & M 19-- 1 additive
    - McPherson et al. (2004): M 78-- 1 dominant, *Mi-1*  
M 75-- 1 dominant & 1 additive
  - **Clevewilt: *Mi-2*?**
    - Benzawada et al. (2003): 1 recessive gene
    - Zhou (1999): LA 887 (derived from Clevewilt) - 1 recessive gene = Nem-X, *rkn1*
    - Present study: ST 5599BG (same as LA 887) - 1 incomplete dominant gene
- **Nem-X:**
  - Starr's lab (Zhou, 1999): 1 recessive gene
  - Roberts' lab: single gene, *rkn1* mapped to LG A03
  - Present study: possible one of the two genes in the Auburn source, *Mi-2*

# Auburn 623 Source

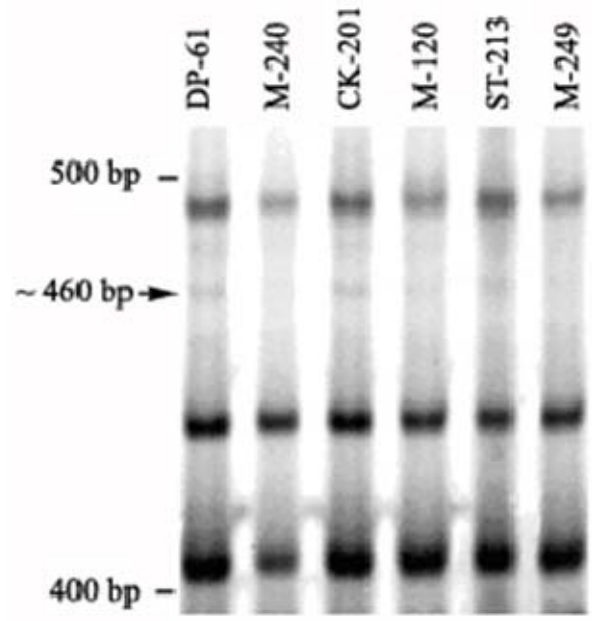
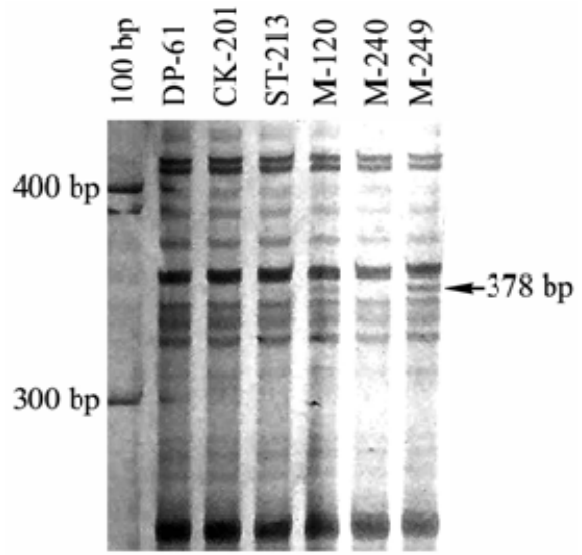


**Genomic DNA from three pairs of NILs amplified with resistance gene analog (RGA) primers RGA-STS 5E and RLK.**

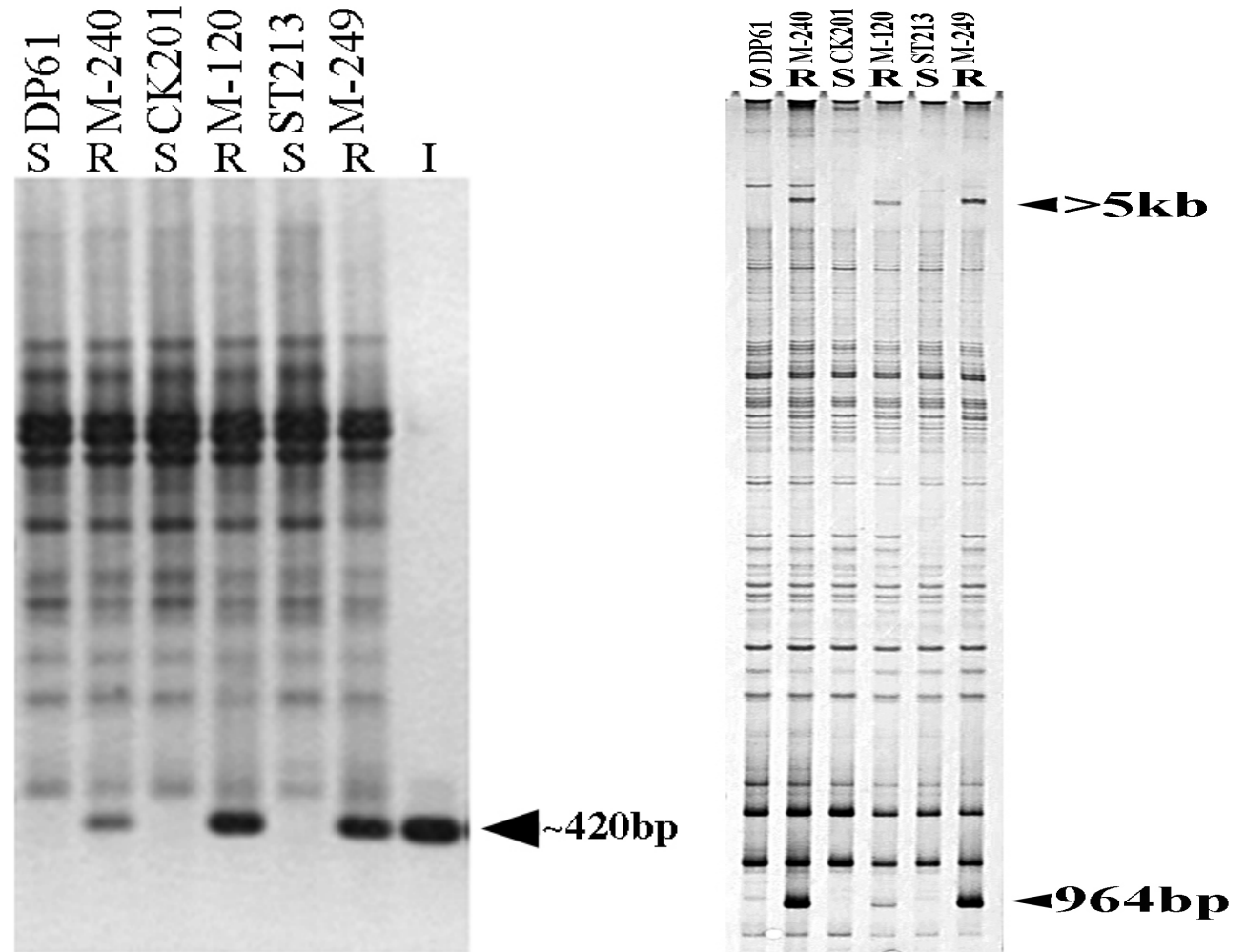
# Auburn 623 Source



**Two AFLP polymorphic markers amplified by primer pair B1 and C3 from genomic DNA isolated from near-isogenic lines resistant or susceptible to RKN.**



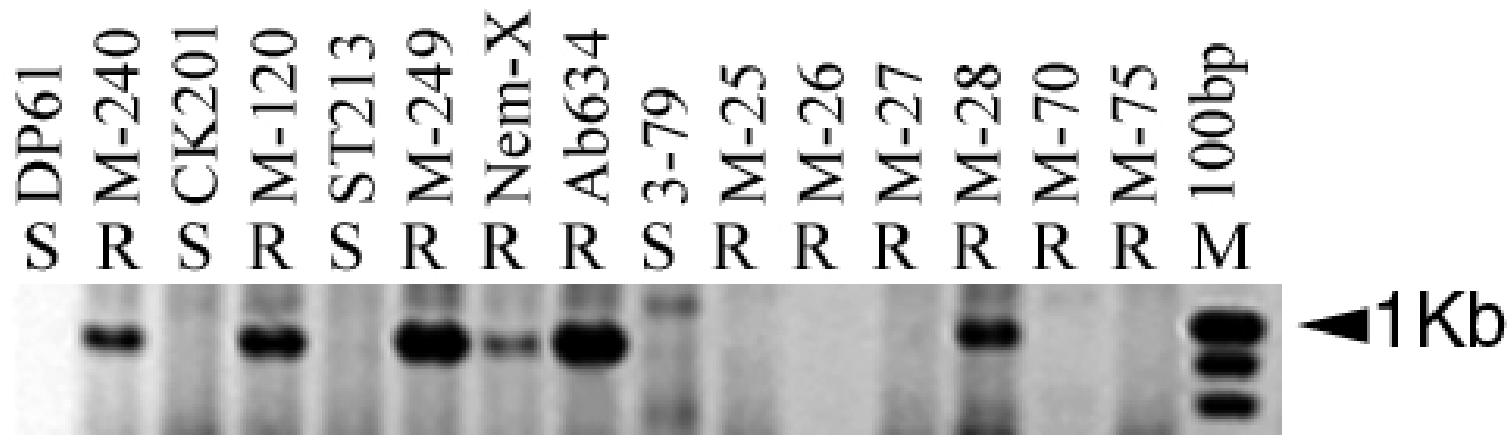
# Auburn 623 Source



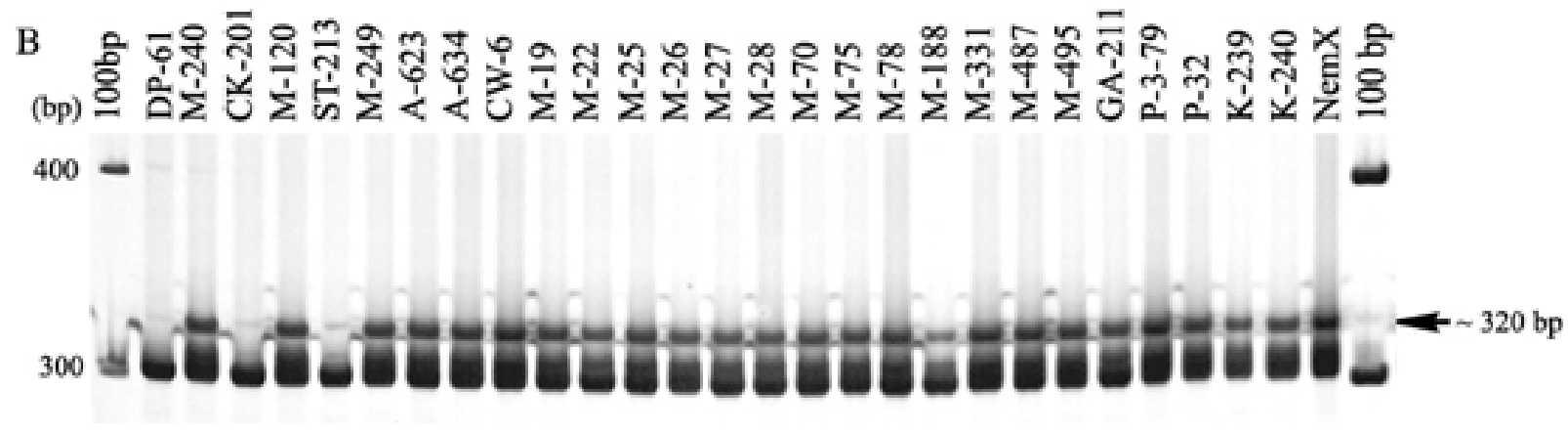
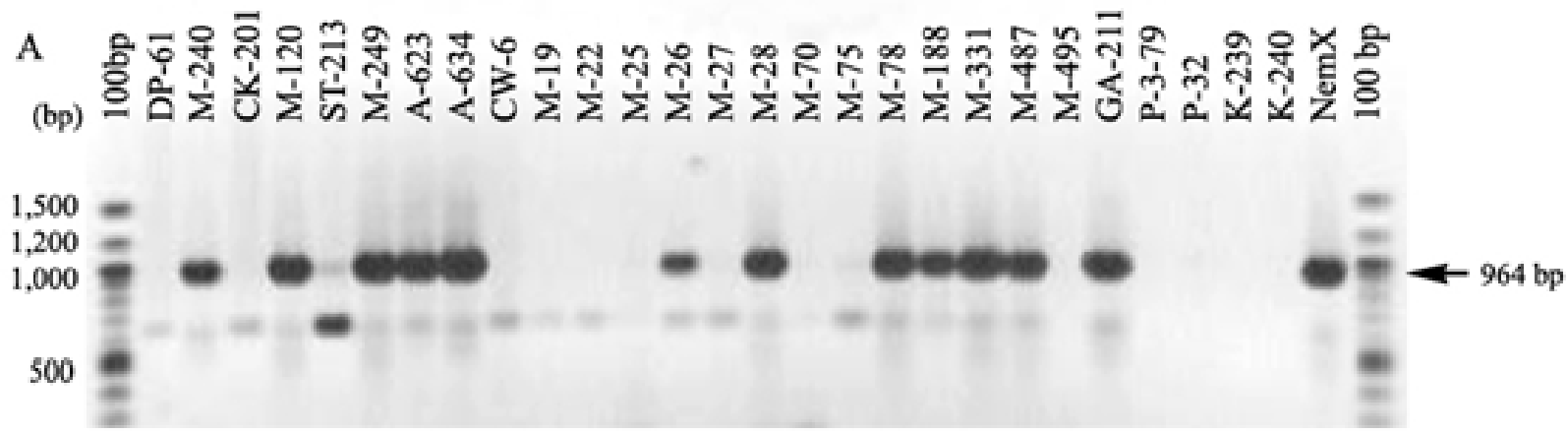
**Three RAPD markers (NMRKN6931-420, NMRKN7811-1000, and NMRKN7811-5000) associated with cotton resistance to RKN.**

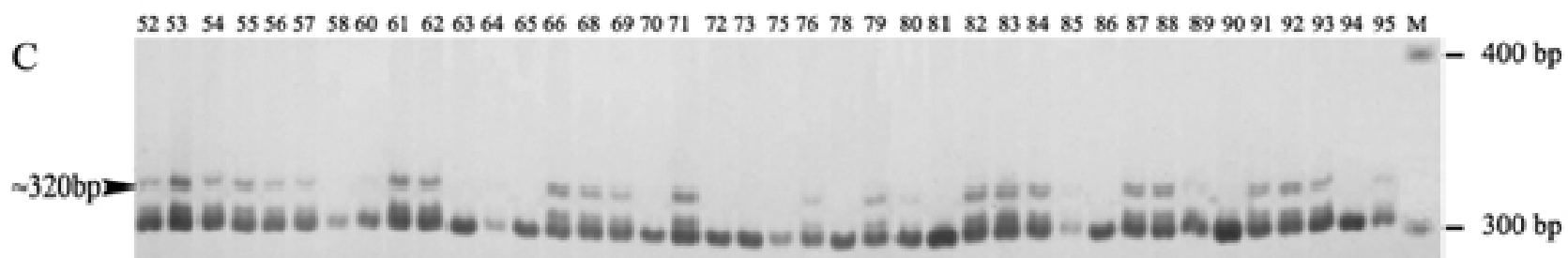
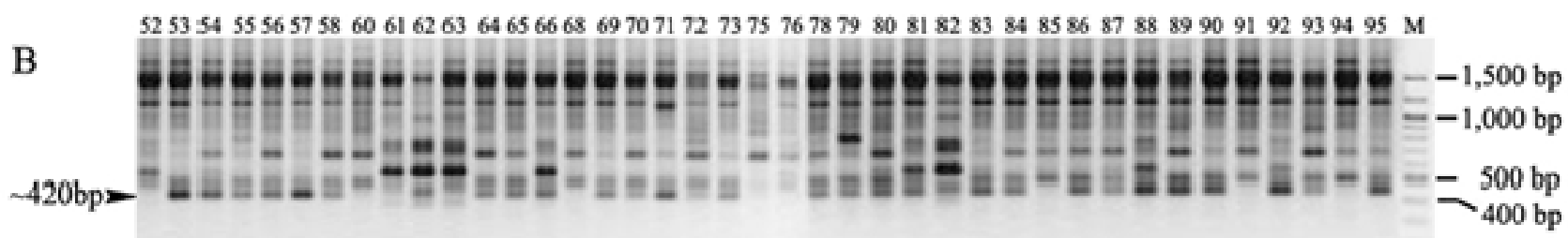


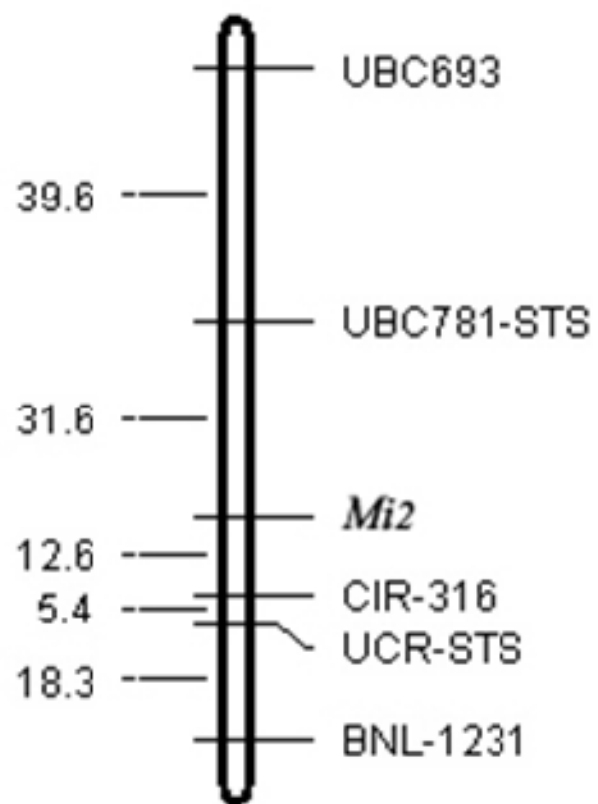
## Auburn 623 Source



**A sequence tagged site (STS) marker (NMRKNR7811-1000 STS) amplified by STS primers designed from the NMRKN7811-1000 fragment. It is absent in all the susceptible lines and present in all the Auburn lines, Nem-X, and some converted race stocks.**







# Germplasm Screening

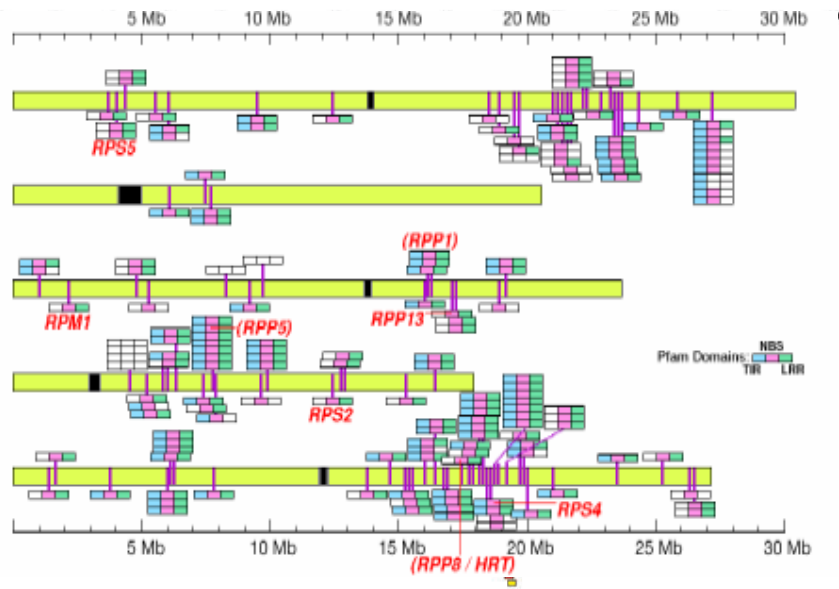
Genotype	PI No.	Pedigree	Reaction to RKN	UBC 693-420	UBC 781-1000	UBC 781-964 STS	UCR-STS	CIR 316	Group
DP 61			S	-	-	-	-	-	3
M-240	592511	AB 634 RNR / DP61	R	+	+	+	+	+	1
CK 201			S	-	-	-	-	-	3
M-120	592509	AB 634 RNR / CK201	R	+	+	+	+	+	1
ST 213			S	-	-	-	-	-	3
M-249	592512	AB 634 RNR / ST213	R	+	+	+	+	+	1
AB 623 RNR	SA 1492		R	+	+	+	+	+	1
AB 634 RNR	GP 166	AB 623 RNR / AB 56	R	+	+	+	+	+	1
Clewe wilt 6	SA 245		?	-	-	-	+	+	3
M-19 RNR	517931	<i>Richmondii</i> / DP 16	R	+	-	-	+	+	2
M-22 RNR	517932	<i>Latifolium</i> / DP 16	R	+	-	-	+	-	2
M-25 RNR	517933	<i>Punctatum</i> / DP 16	R	+	-	-	+	-	2
M-26 RNR	517934	<i>Punctatum</i> / DP 16	R	+	-	-	+	-	2
M-27 RNR	517927	<i>Punctatum</i> / DP 16	R	+	-	-	+	-	2
M-28 RNR	517928	<i>Punctatum</i> / DP 16	R	+	+	+	+	-	1
M-70 RNR	517930	<i>Latifolium</i> / DP 16	R	+	-	-	+	+	2
M-75 RNR	517929	<i>Latifolium</i> / DP 16	R	+	-	-	+	+	2
M-78 RNR	517930	<i>Latifolium</i> / DP 16	R	+	+	+	+	+	1
M-188 RNR	517936	<i>Latifolium</i> / DP 16	R	+	+	+	+	-	1
M-331 RNR	592515	AB 634 RNR / AB56	R	+	+	+	+	+	1
M-487 RNR	517937	<i>Punctatum</i> / DP 16	R	+	+	+	+	+	1
M-495 RNR	517938	<i>Punctatum</i> / DP 16	R	+	-	-	+	-	2
M-725 RNR	592516	AB 634 RNR / CK310	R	+	-	-	+	+	2
GA 96-211	633019	GA77-27/'PD-3'//GA88-92/3/M-240-RNR/4/M-120-RNR/5/'LA887'	R	+	+	+	+	+	1
Wild Mexican	TX 2516		?	+	-	-	+	-	2
Jack Jones									
Pima 3-79			S	-	-	-	+	-	3
NM 24016			S	-	-	-			3
Pima 32			S	-	-	-	+	-	3
SxP			S	-	-	-	+	-	3
Amsak			S	-	-	-	+	-	3
Acala NemX			R	+	+	+	+	+	1

# What Do We Know About Plant Genomes?

- **Coding sequences: gene families (~25%)**
  - **Arabidopsis**
    - ~26,000 genes
    - 867 gene families
    - 6457 genes (~ 1/4 of total number of genes)



## NBS-LRR Genes in Arabidopsis (Meyers et al., 2003)



## NBS Genes in Rice (Monosi et al., 2004)



# RGA-AFLP Analysis





Genomic DNA is **digested** with a frequent and a rare cutting enzyme (*MseI* and *EcoRI*)



Three types of restriction fragments are generated: ones with *EcoRI* cut at both ends, ones with *EcoRI* cut at one end and *MseI* cut at other end, and ones with *MseI* cuts at both ends.

*EcoRI* adapter  
*MseI* adapter



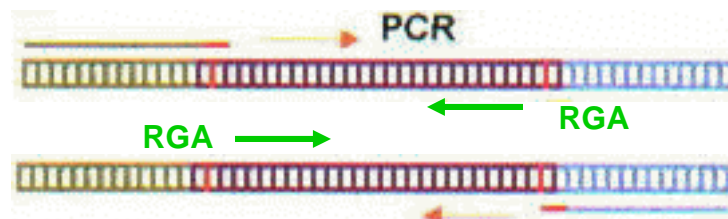
Specific adapters to restriction sites are then **ligated** to generated fragments.



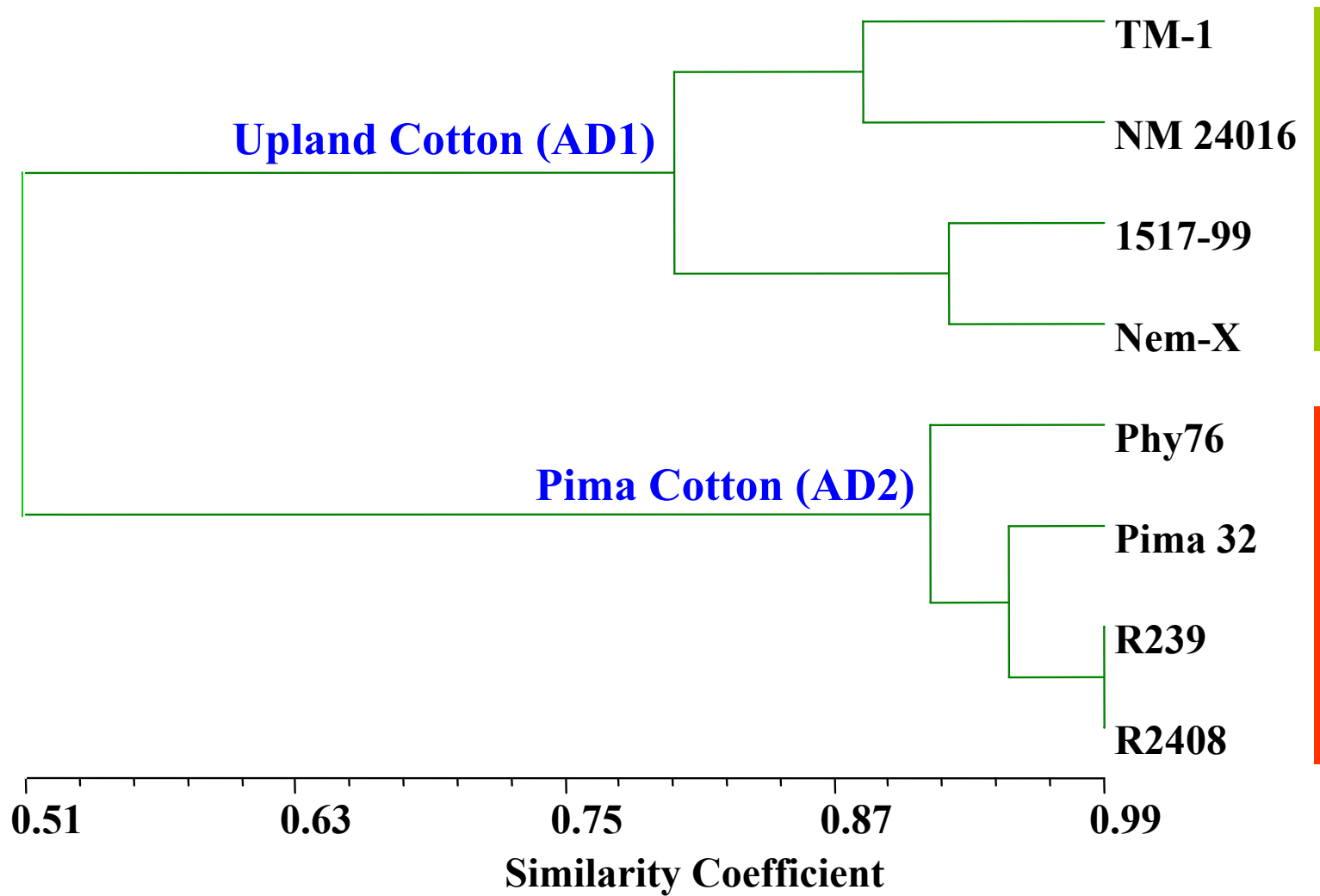
+1 Selective primers  
(*EcoRI* adapter + selective base A)  
(*MseI* adapter + selective base C)



**Preselective amplification** step achieves a 16-fold reduction of the complexity of the restriction-ligation products

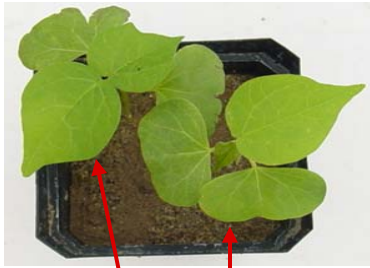


## RGA-AFLP Analysis

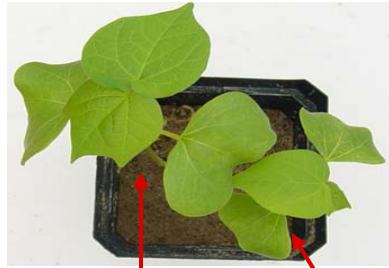


**Cluster analysis based on RGA-AFLP**

# Root-knot Nematode Resistance



ST 474 1517-99 (CK)



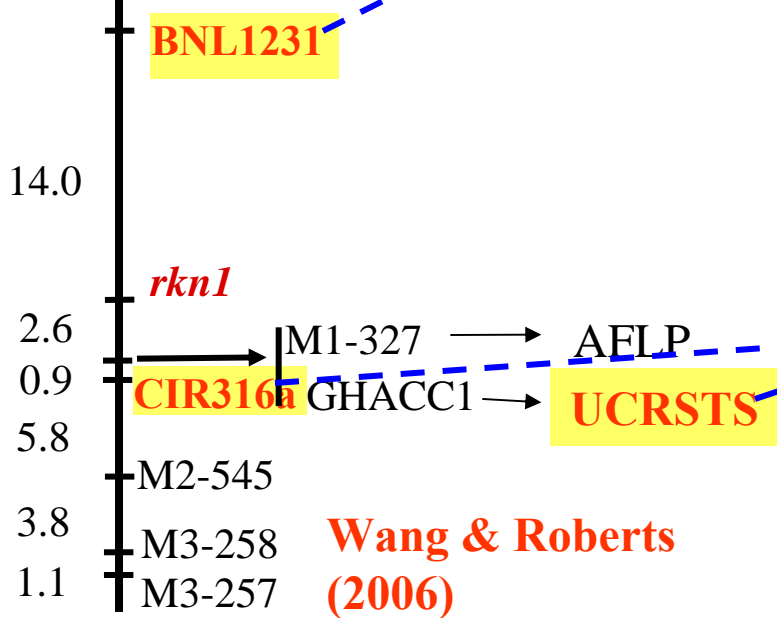
Auburn 634 1517-99 (CK)



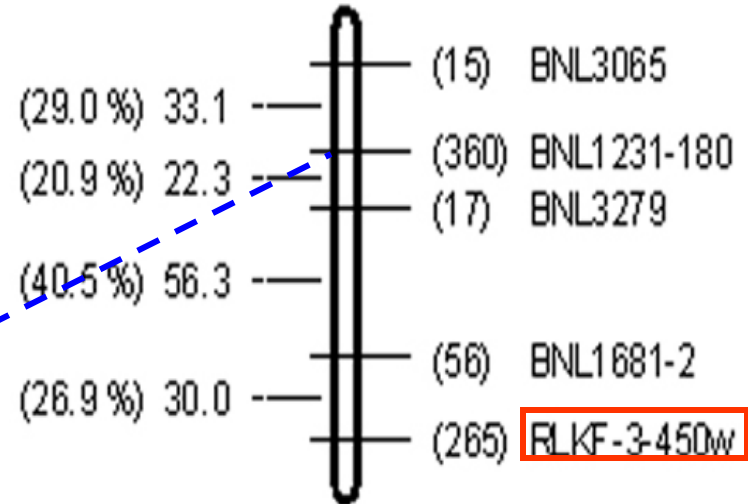
## Chromosome 11

Dis (cM)

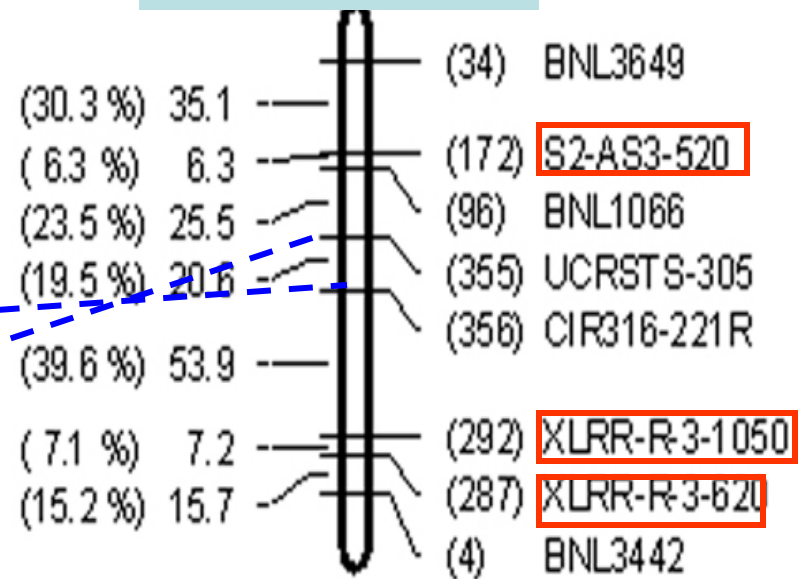
Markers

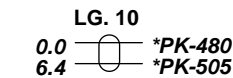
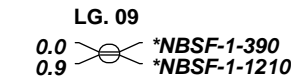
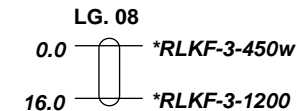
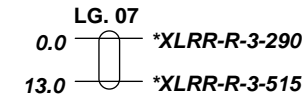
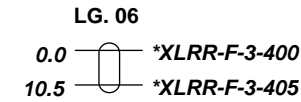
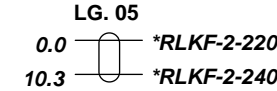
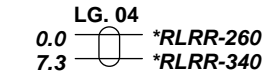
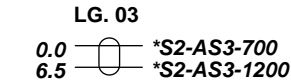
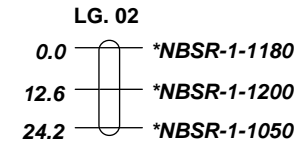
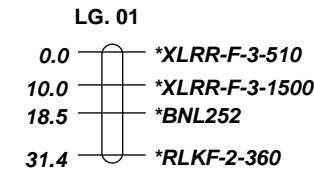
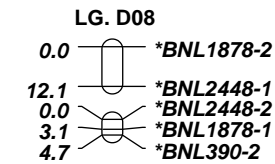
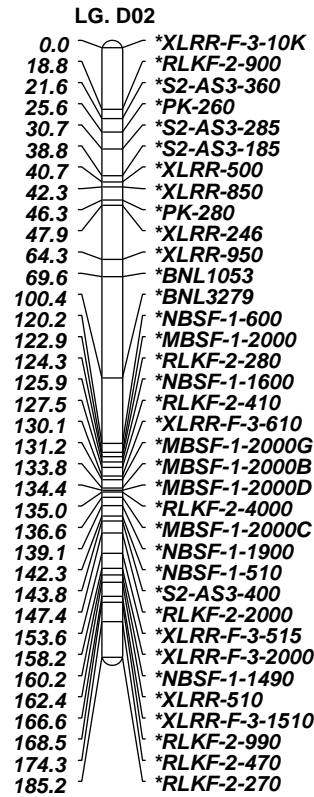
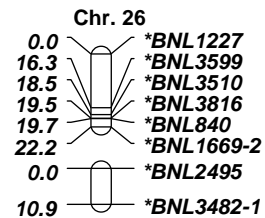
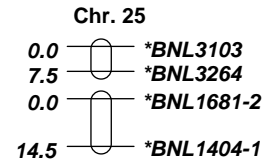
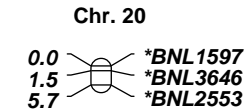
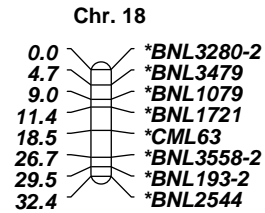
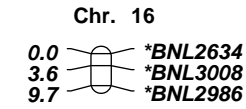
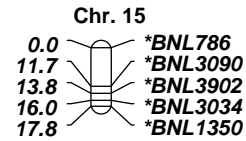
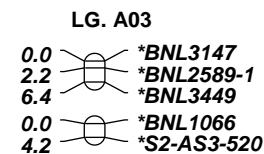
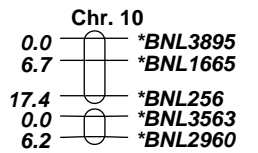
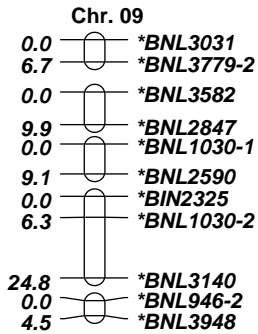
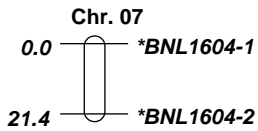
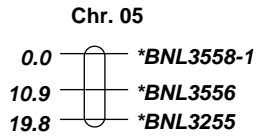
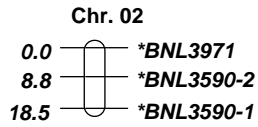


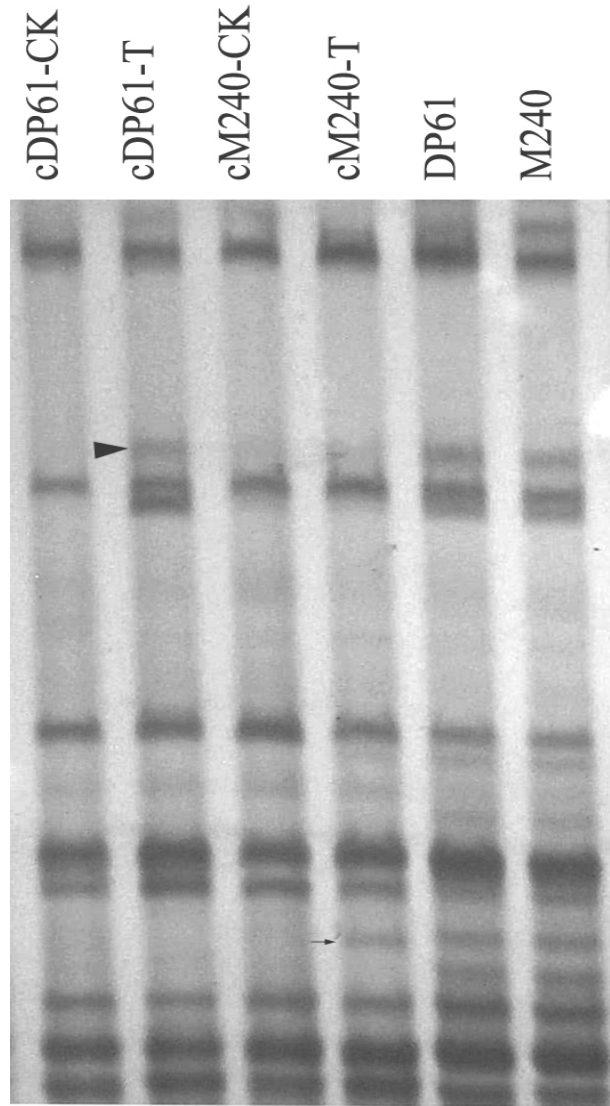
## Chromosome 22



## Chromosome 11







**cDNA-AFLP analysis**

# Marker Screening

<b>Line</b>	<b>RAPD 6911</b>	<b>RAPD 7811</b>	<b>STS 7811- 1000</b>	<b>UC- CAP</b>	<b>CIR 316a</b>
<b>Auburn source</b> <i>Mi-1, Mi-2</i>	+	+	+	+	+
<b>Most race stocks</b> <i>Mi-1?</i>	+	-	-	-	-
<b>W M Jack Jones</b> <i>Mi-1?</i>	+	-	-	+	-
<b>Clevewilt 6</b> <i>Mi-2?</i>	-	+	+	+	+
<b>La lines</b> <i>Mi-2?</i>	?	?	?	+	+
<b>NemX</b> <i>rkn1=Mi-2?</i>	+	+	+	+	+
<b>Susceptible lines</b>	-	-	-	-	-