



**QTL analysis for resistance to root-knot nematodes in M-120 RNR
Upland cotton line**

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Genetics of Root-Knot Nematode Resistance in Cotton
Research Coordination Meeting
October 24, 2007 - Dallas, Texas

Objectives

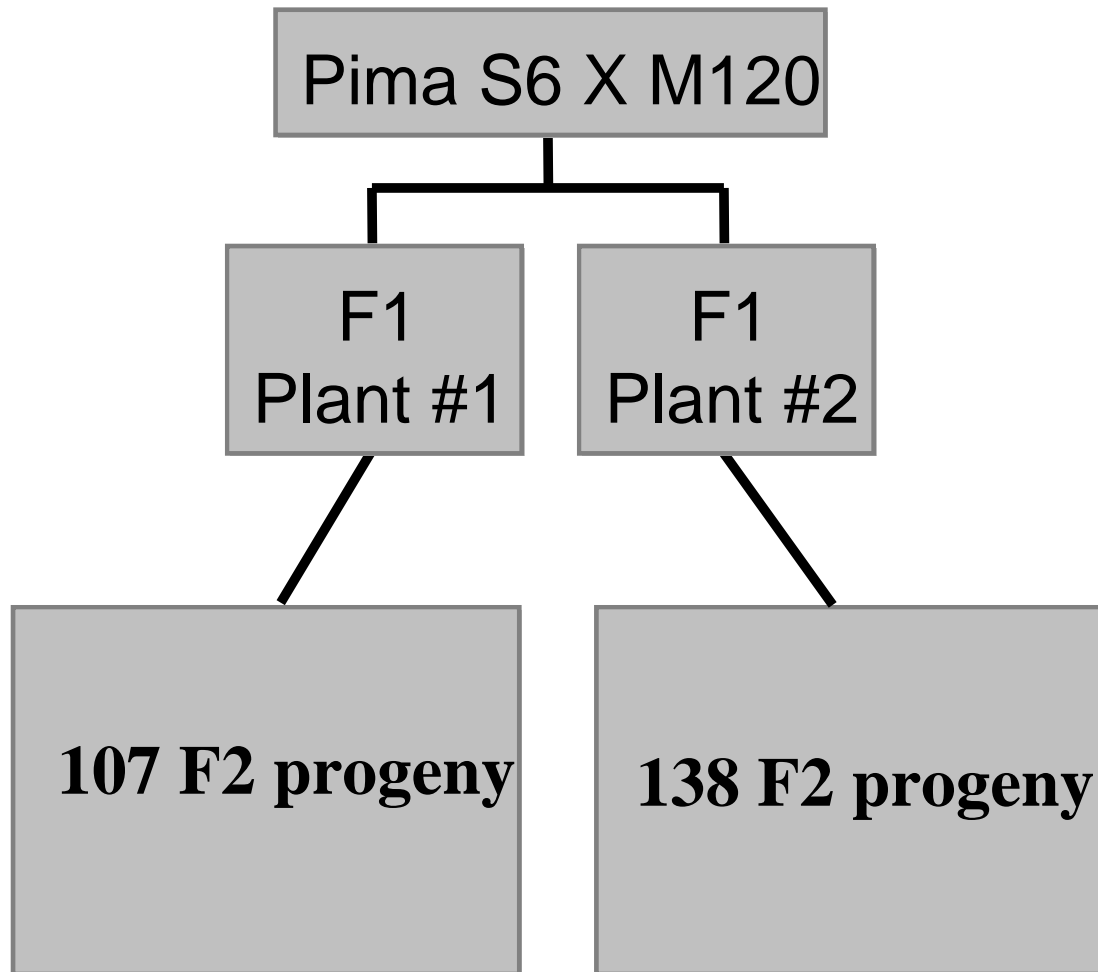
To identify DNA markers linked to genes conditioning resistance to RKN in cotton, and to develop a molecular marker-assisted selection strategy to improve breeding efficiency for resistance to RKN.

RKN - Root-Knot Nematodes (*Meloidogyne incognita*)

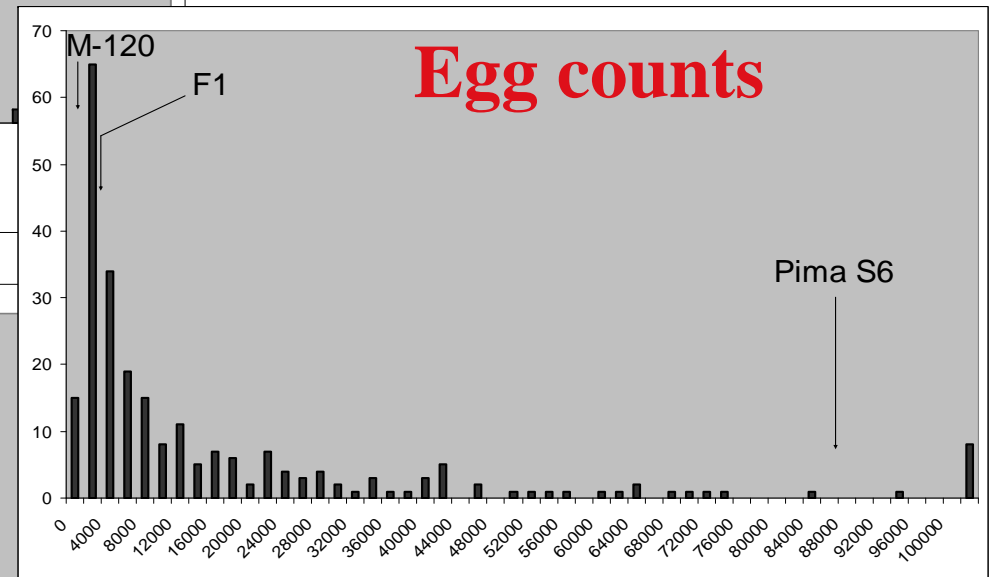
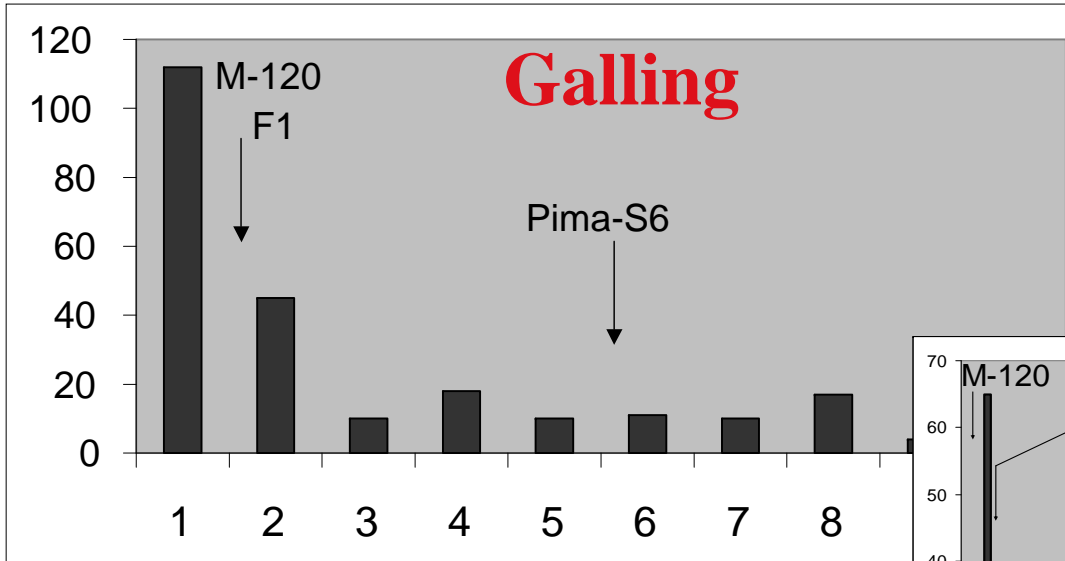
Approach

- Use ‘bulk segregation analysis’ method to quickly ‘scan’ the cotton genome with 200 mapped RFLP markers to identify the chromosomal location for RKN resistant gene(s).
- Develop PCR-based fingerprinting analysis (SSRs) near the root-knot resistance genes.

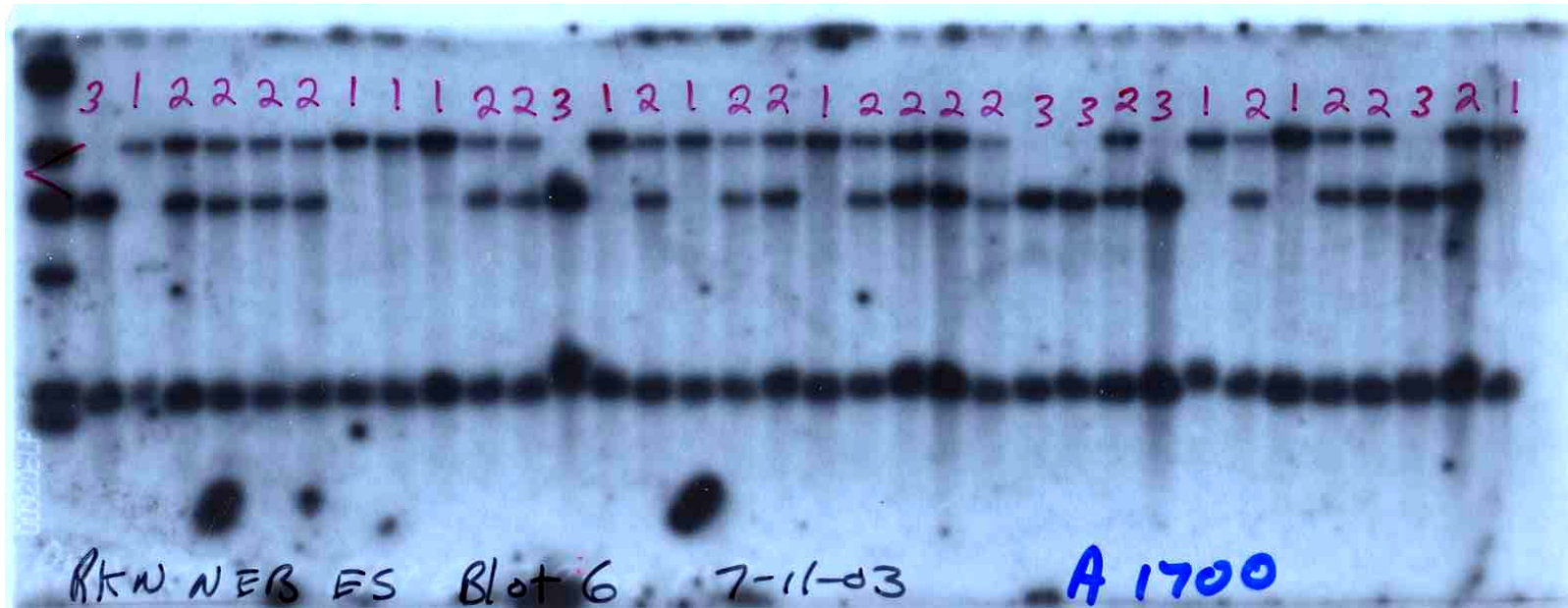
Genetic mapping population



Phenotypic distribution



RFLP markers linked to RKN resistance

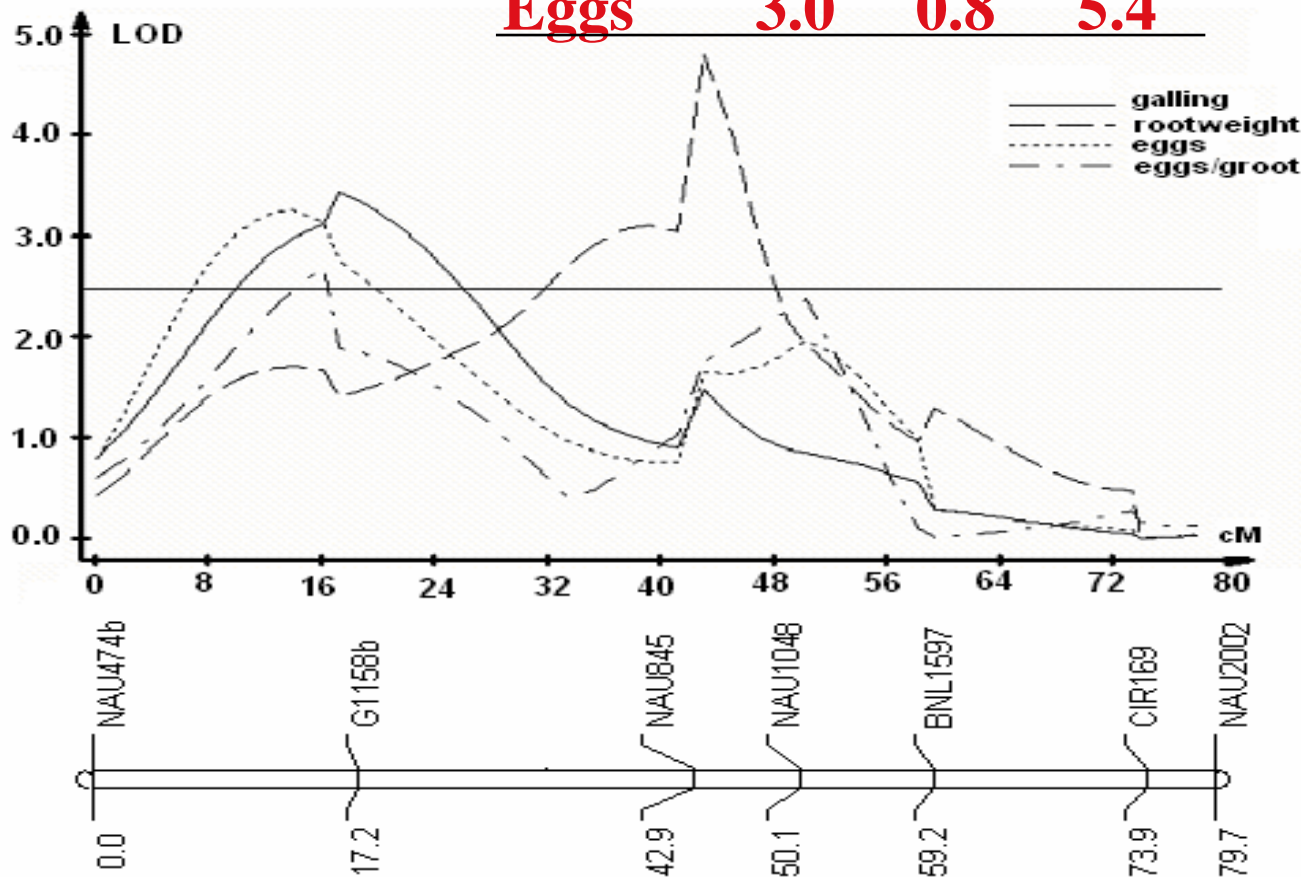


Marker	<i>n</i>	<i>P</i>	R ² (%)	Chr.
pAR111	130	< 0.0001	16.2	LG.A03
pGH243	209	<0.0001	8.1	LG.A03
G1158b	202	0.0009	5.3	Chr.07

QTL associated with resistance - Chr. 07

Mi-C07 locus (NAU474b - G1158b)

Trait	LOD	d/a	VAR
Galling	3.4	6.2	7.7
Eggs	3.0	0.8	5.4



Variation in root architecture

Pima-S6

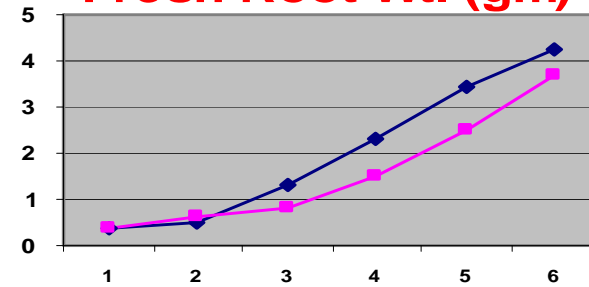
M-120



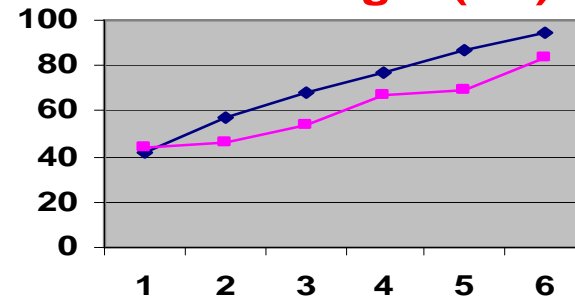
Pima S6 ———

M-120 ———

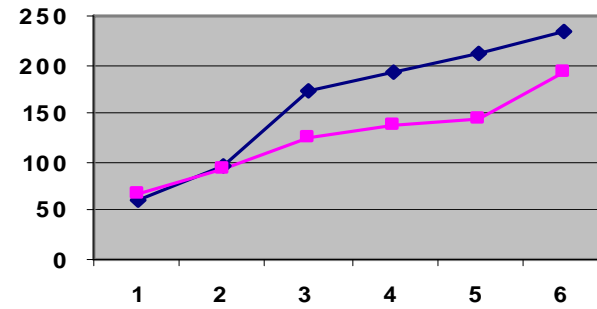
Fresh Root Wt. (gm)



Root Length (cm)



Lateral Root #s.

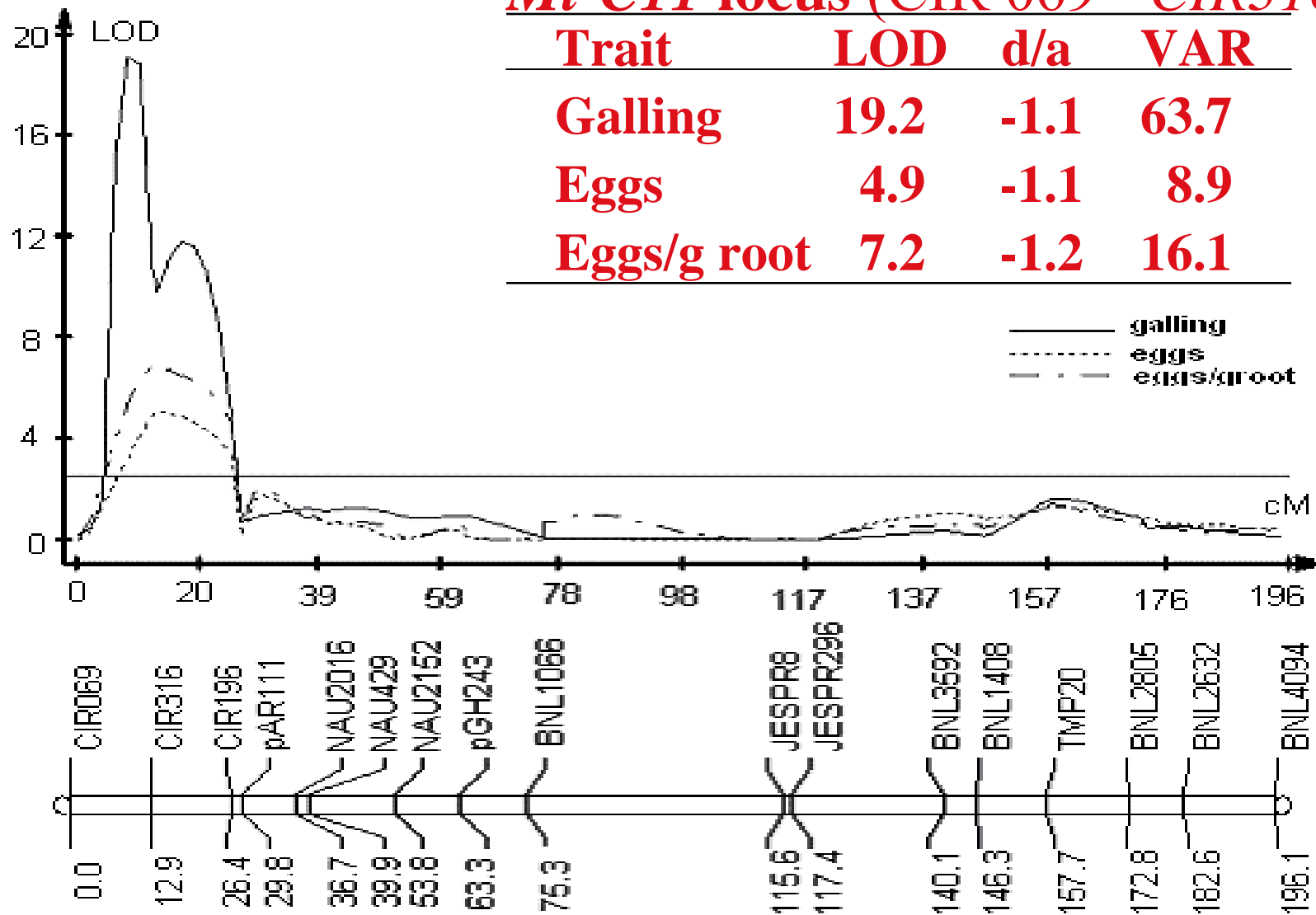


Week

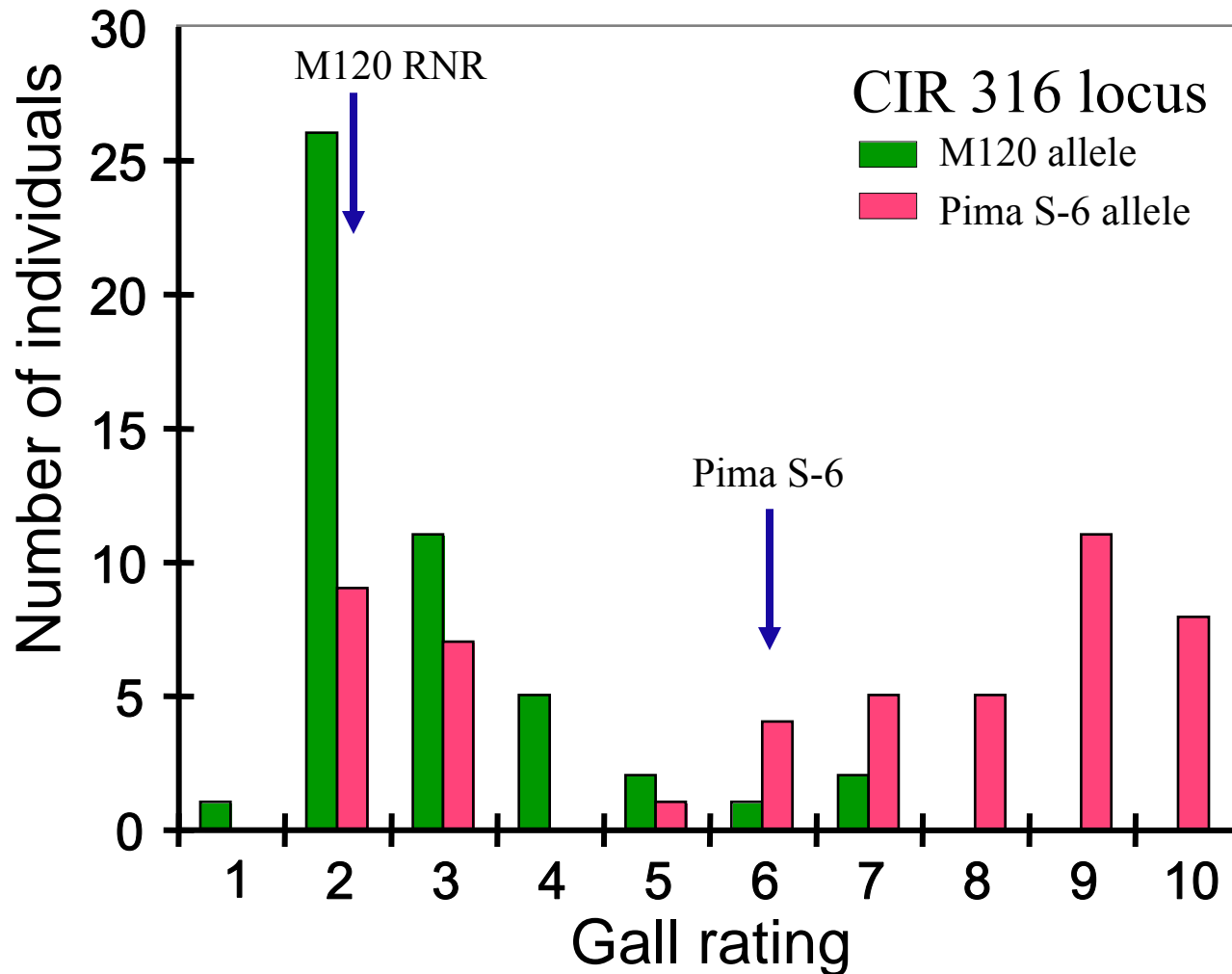
QTL associated with resistance - Chr. 11

Mi-C11 locus (CIR 069 - CIR316)

Trait	LOD	d/a	VAR
Galling	19.2	-1.1	63.7
Eggs	4.9	-1.1	8.9
Eggs/g root	7.2	-1.2	16.1

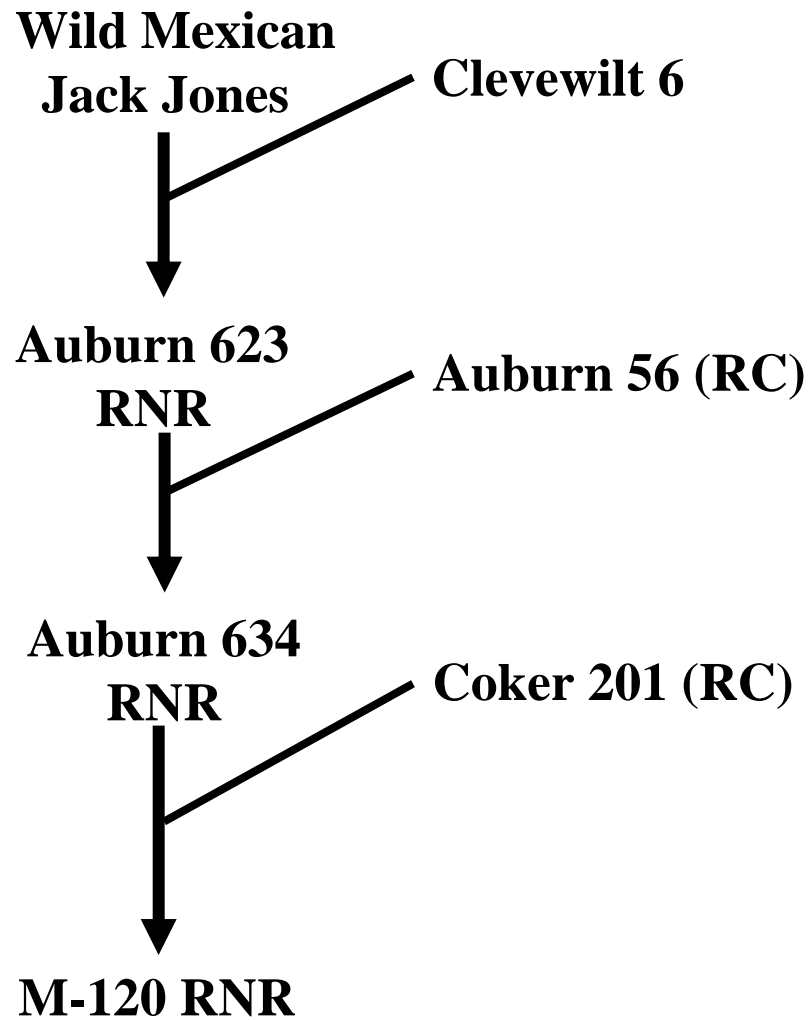


Selection efficiency using DNA markers



- If select only homozygote M120 progeny, we have 80% chance (33/41) of selecting a highly resistant individual (gall rating ≤ 3).

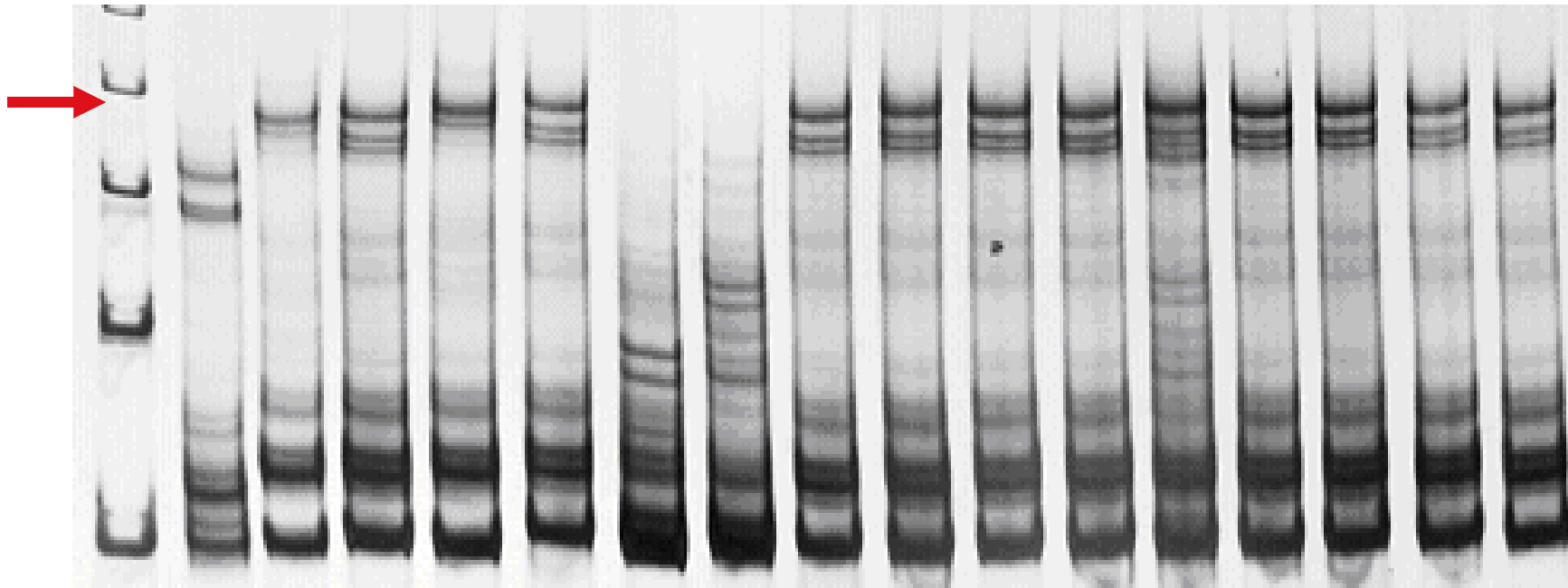
Pedigree of M120RNR



Source: Robinson 1999

Origin of root-knot nematode resistance locus on Chromosome 11

Pima S6
M-120 RNR
Auburn 623
Auburn 634
Clevewilt 6
Wild Mex. JJ
Coker 201
M-92 RNR
M-240 RNR
M-249 RNR
M-272 RNR
M-315 RNR
M-331 RNR
M-725 RNR
Acala NemX
LA887



SSR primer CIR316

Recap on progress

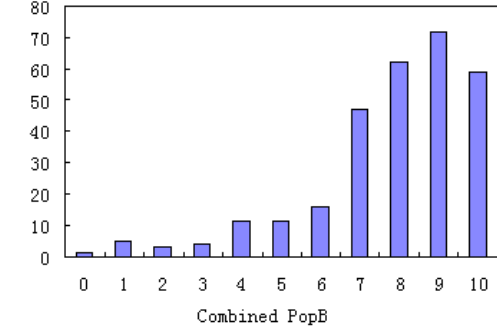
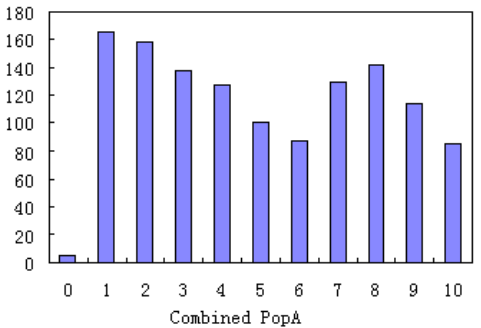
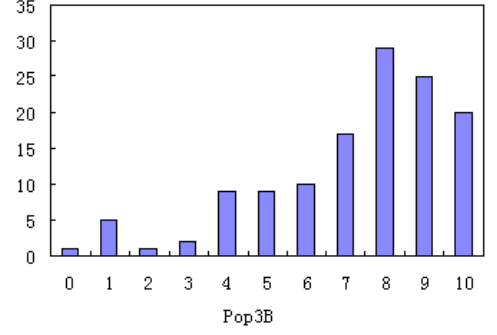
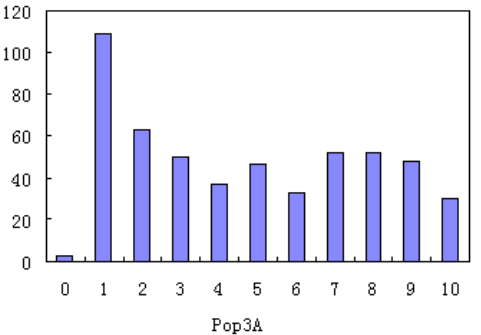
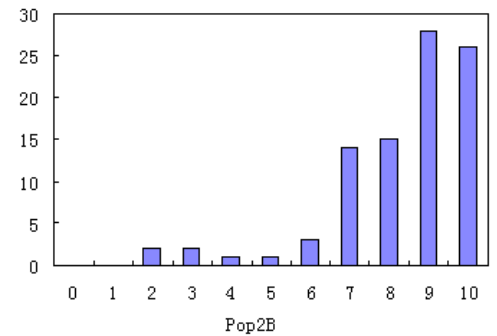
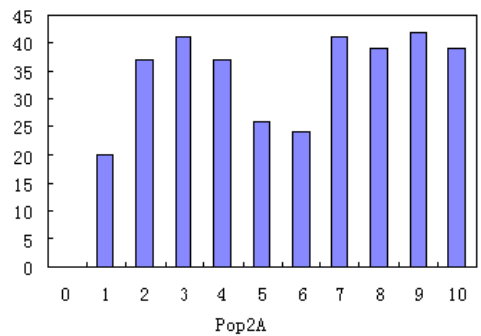
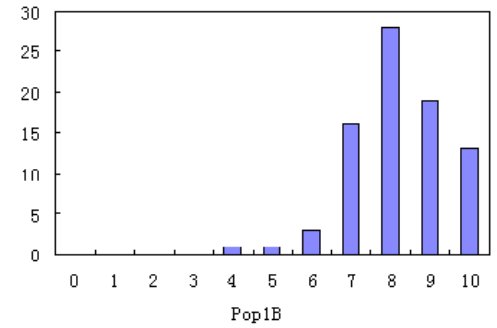
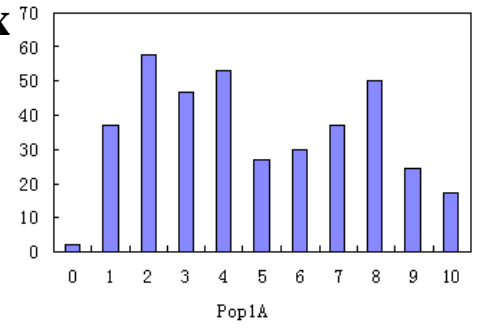
- 2002 Produced F1 from M120 x Pima S6 (funding from GA Cotton Commission)
- 2003 Screened F2 population for RKN resistance
- 2004 Completed genotyping F2 with RFLPs
- 2005 Reported linkage on LGA03 (Chr.11) during the CI sponsored meeting in Memphis, TN (received core funding from Cotton Inc.)
- 2006 Identified tightly linked SSR markers flanking the *Mi-C11* locus; reporting resistant locus in TAG
- 2007 Confirmation and fine-mapping

Towards fine mapping of the *Mi-C11* locus

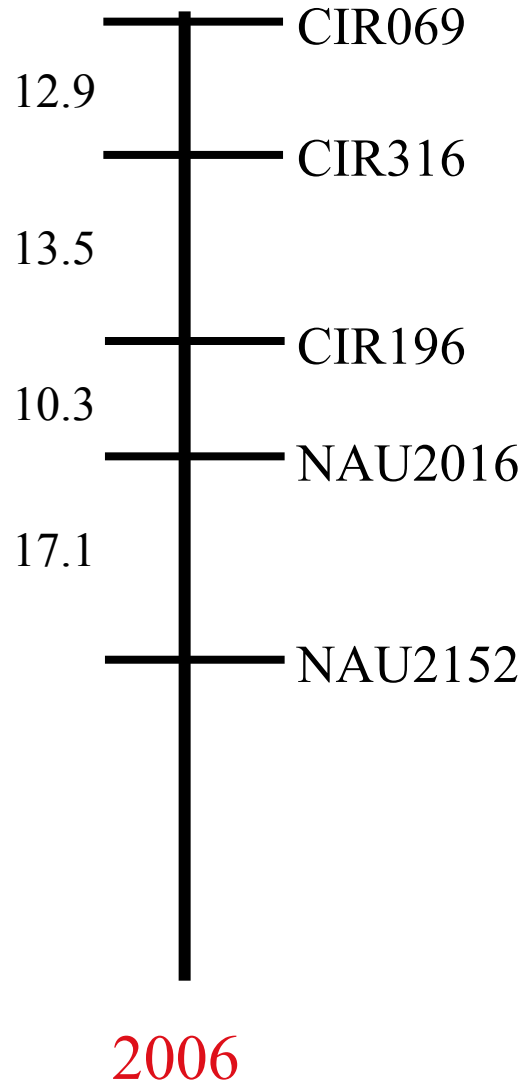
- Screened 1500 AFLP primer combinations
- An additional 1233 F₂ individuals were tested for resistance and genotyped to identify recombinants near the *Mi-C11* locus
- 326 of recombinants recovered
- Testing F3 families for resistance

Frequency distributions for galling index

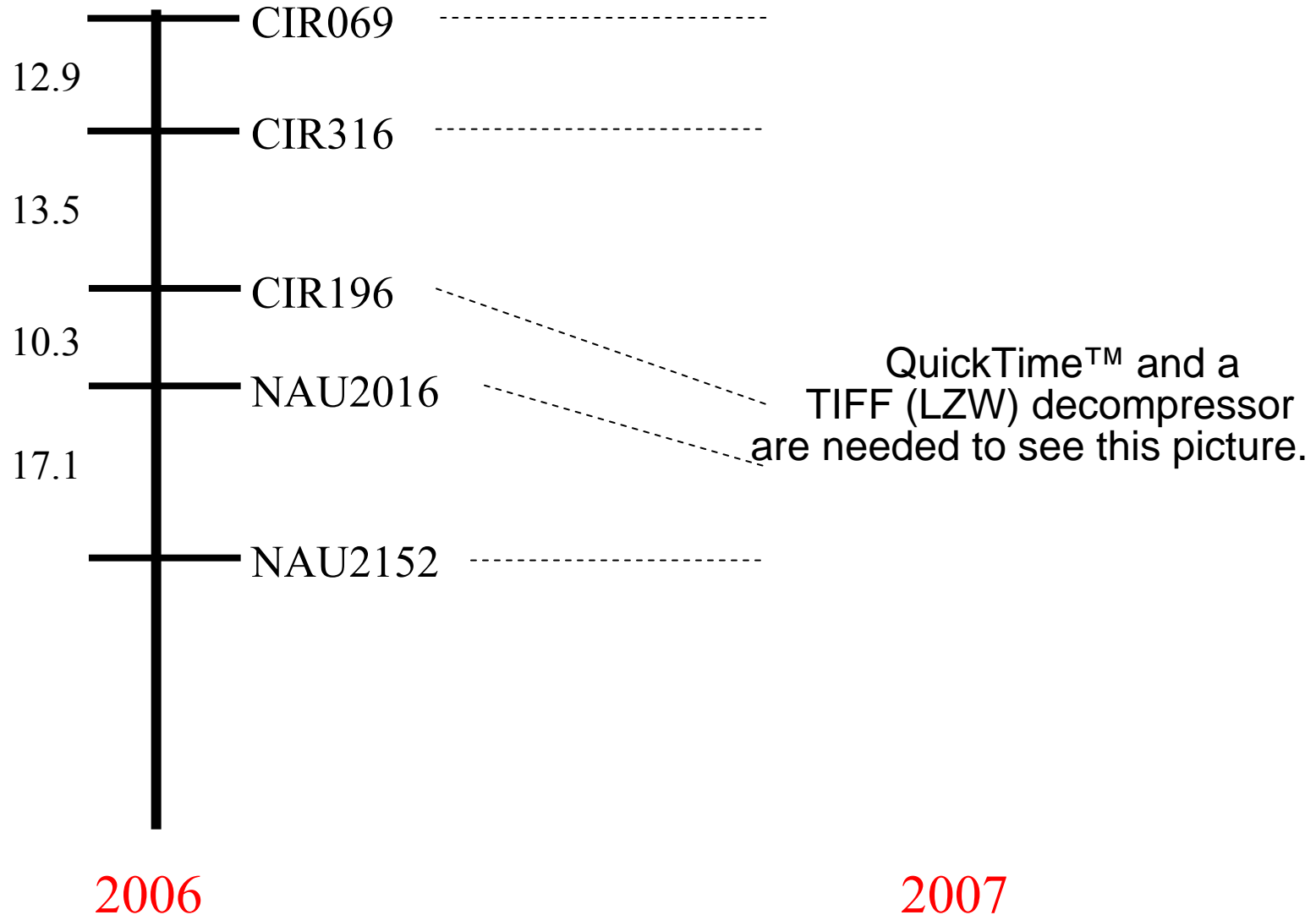
Population	n	Mean	VAR	Skew
Pop1A	382	4.88	7.44	0.22
Pop1B	71	8.23	1.72	8.54
Pop2A	347	5.80	8.14	-0.08
Pop2B	92	8.34	3.20	-1.69
Pop3A	523	4.74	9.17	0.211
Pop3B	128	7.27	5.57	-1.08
CombPopA	1252	5.08	8.56	0.122
CombPopB	291	7.84	4.14	-1.41



Current status of fine mapping



Current status of fine mapping



Graphical genotype of F2s with recombination near the *Mi-C11* locus

QuickTime™ and a
TIFF (LZW) decompressor
are needed to see this picture.

n

36

39

2

7

4

5

6

5

4

F2 recombinant plants



Summary

- Resistance to RKN in the M120 by Pima S6 population is conferred by one major gene on chromosome 11 and one or more minor genes.
- The major resistant locus in M120 RNR likely have originated from the Clewilt 6.
- The SSR markers flanking the *Mi-C11* locus could be effective in screening for nematode resistant progenies in breeding programs.

Acknowledgements

Collaborator

- Richard Davis
- Lloyd May

Postdoctoral Associate

- Guillermo Bacelaere
- Xinlian Shen

Funding Source

- Georgia Cotton Commission
- Cotton Incorporated

Thank you for your attention



Segregation ratios

Chi Square goodness of fit test

	n	segregation ratio			
		3:1	15:1	9:7	13:1
Pop1	382	0.05	<0.01	<0.01	0.025
Pop2	347	<0.01	<0.01	0.05	<0.01
Pop3	523	0.05	<0.01	<0.01	<0.01

Note:

1-7 resistance

8-10 susceptible

Genetic Models

3:1 single dominant gene

15:1 two dominant genes

9:7 two epistatic genes

13:1 one dominant and one recessive gene