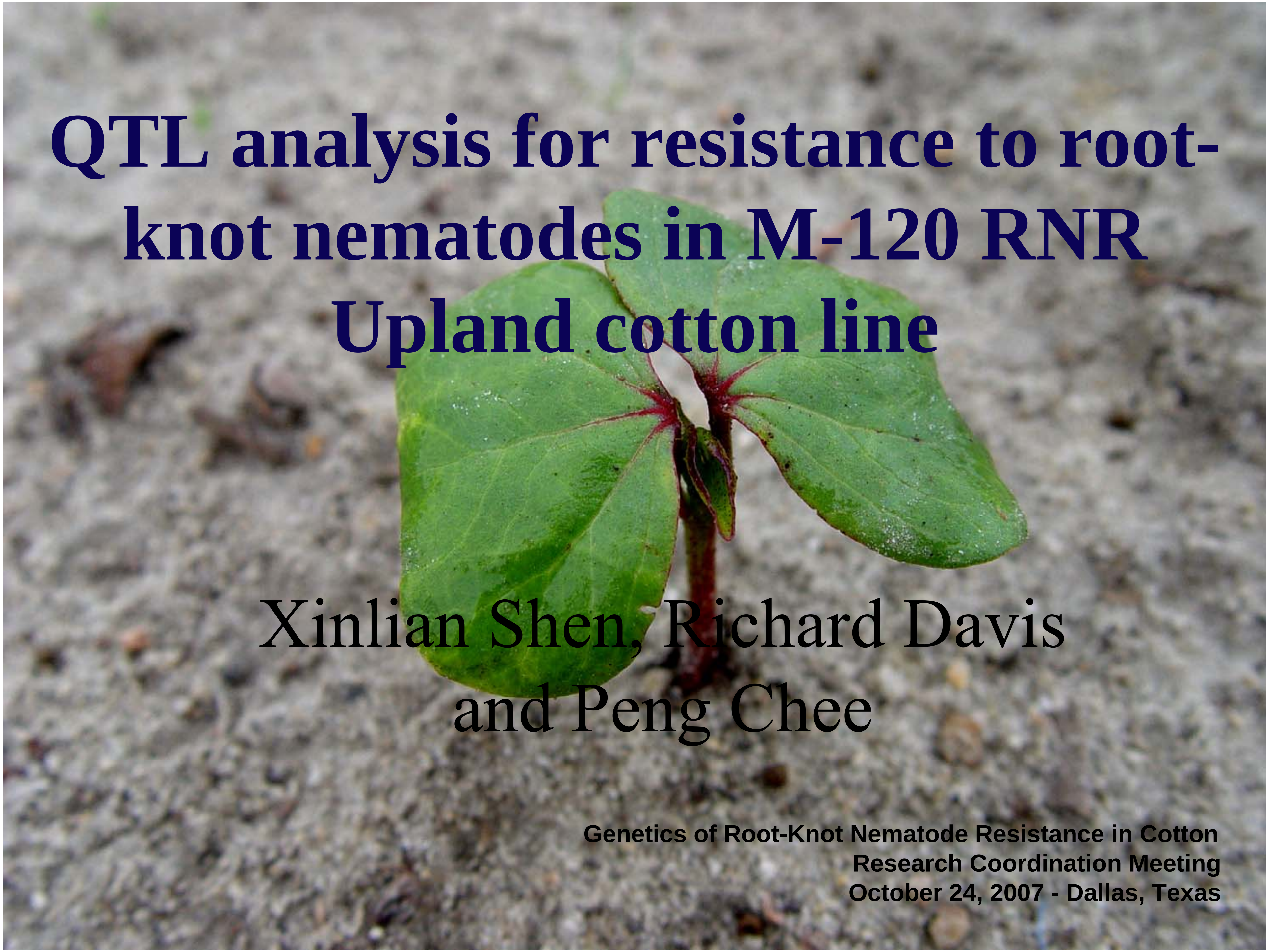

QTL analysis for resistance to root-knot nematodes in M-120 RNR Upland cotton line

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and Peng Chee

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

Objectives

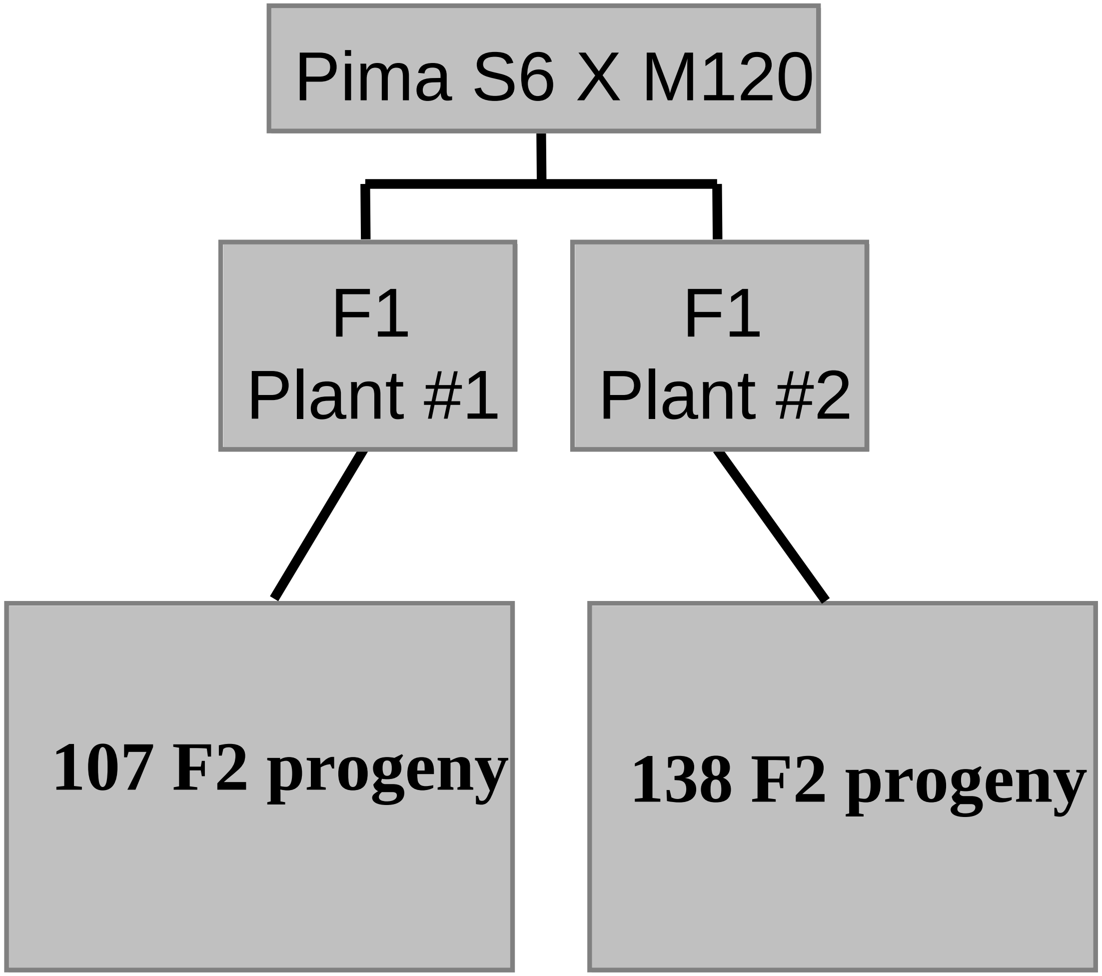
To identify DNA markers linked to genes conditioning resistance to RKN in cotton, and to develop a molecular marker-assisted selection strategy to improve breeding efficiency for resistance to RKN.

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



Pima S6 X M120

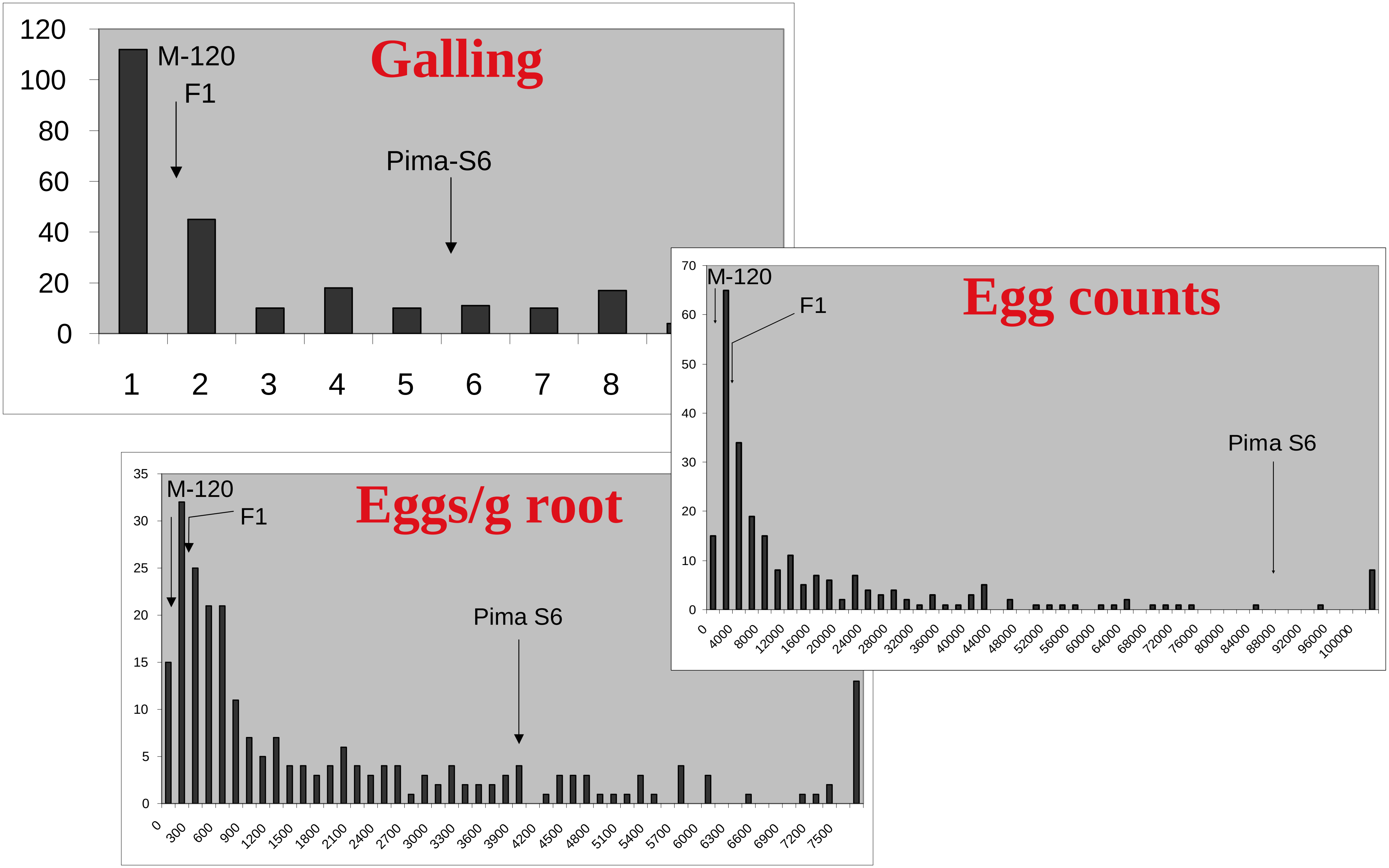
F1
Plant #1

F1
Plant #2

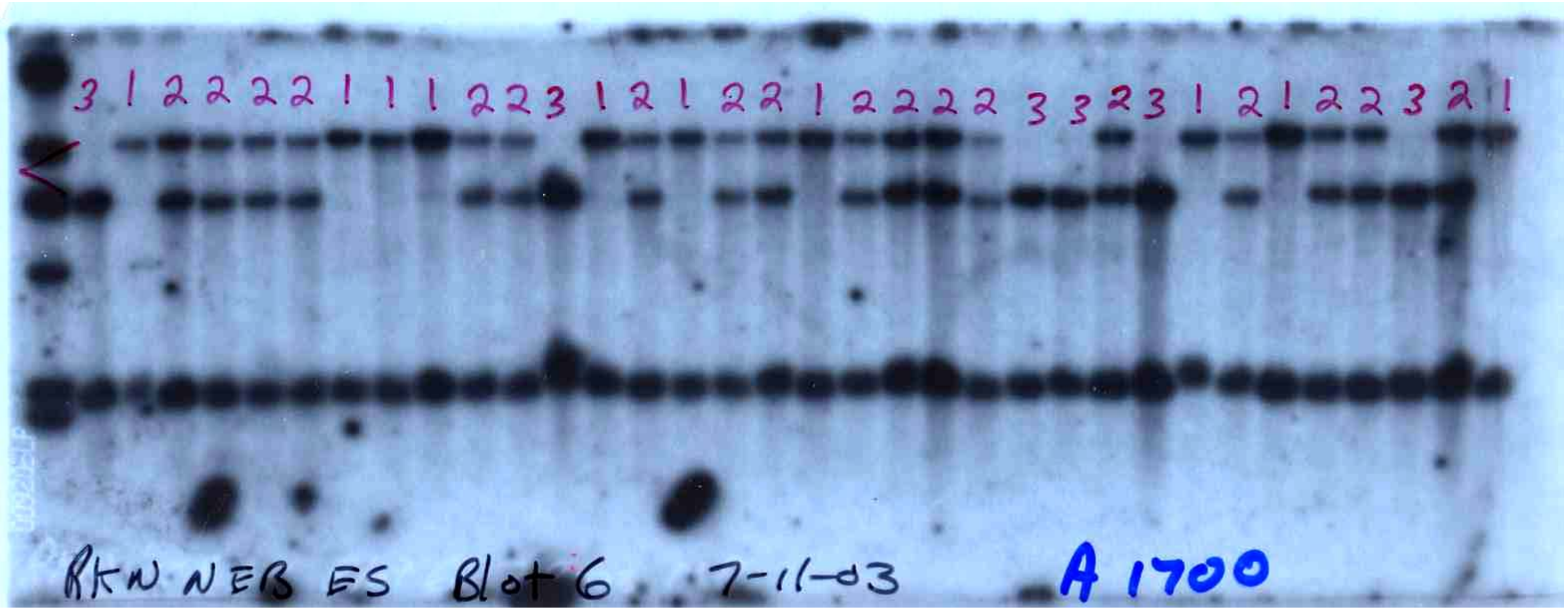
107 F2 progeny

138 F2 progeny

Phenotypic distribution



RFLP markers linked to RKN resistance

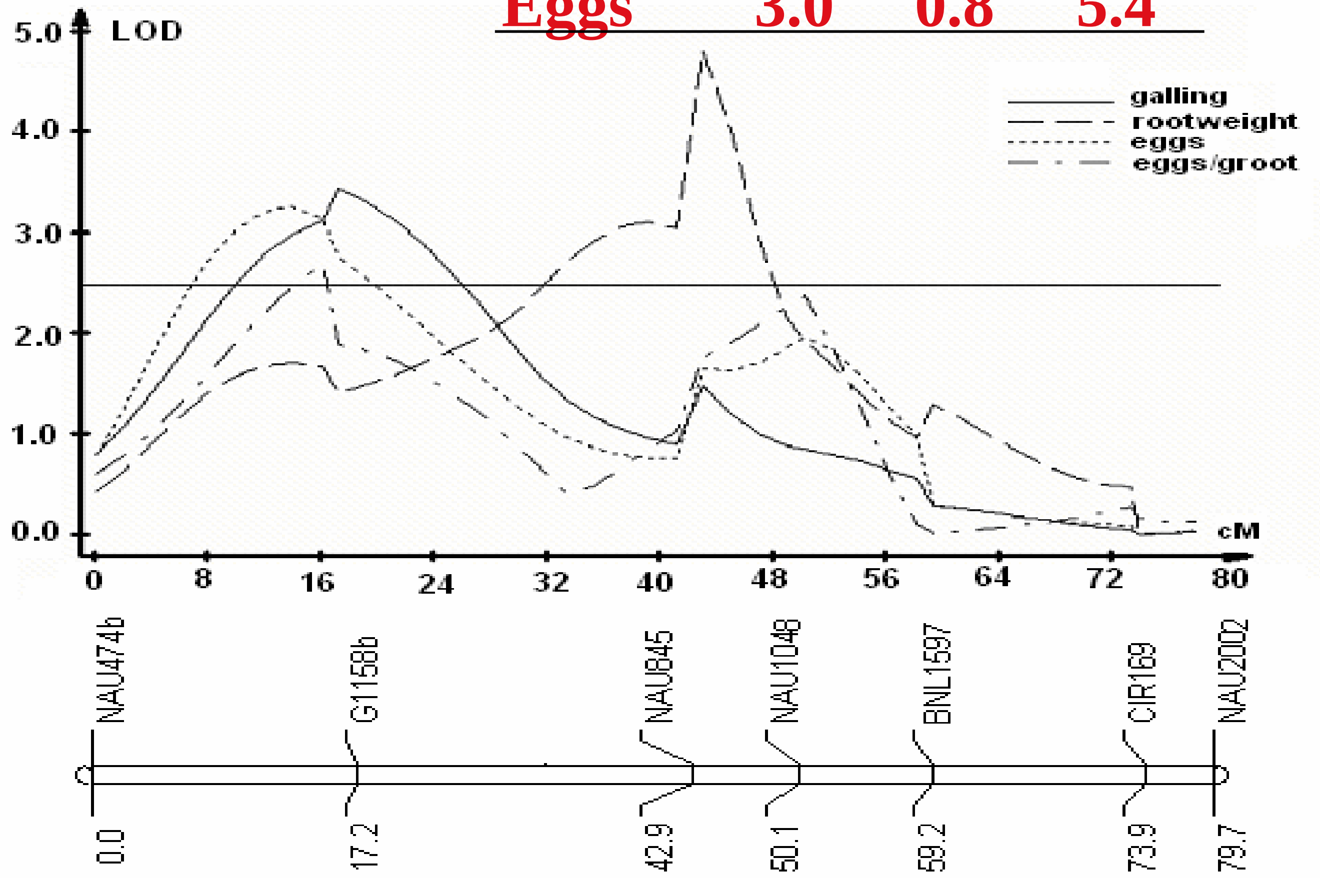


Marker	*n*	*P*	R^2(%)	Chr.
pAR111	130	< 0.0001	16.2	LG.A03
pGH243	209	<0.0001	8.1	LG.A03
G1158b	202	0.0009	5.3	Chr.07

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



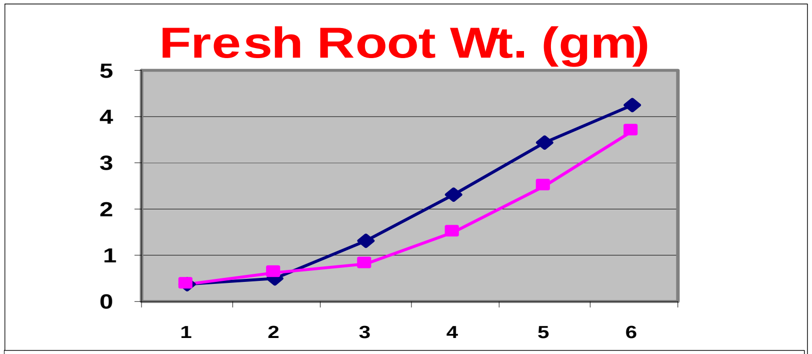
Shen et al. 2006

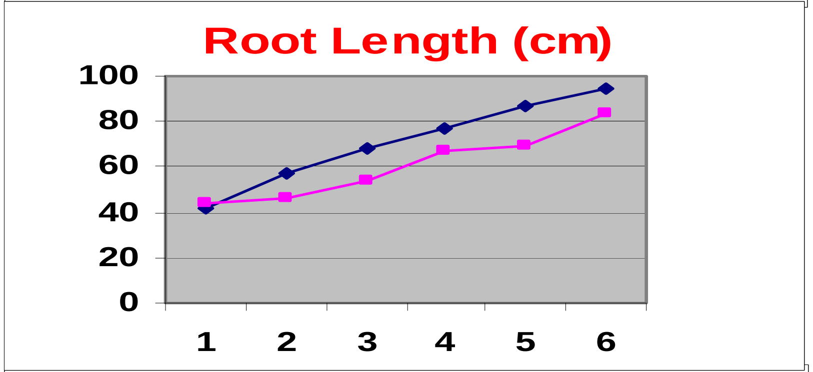
Variation in root architecture

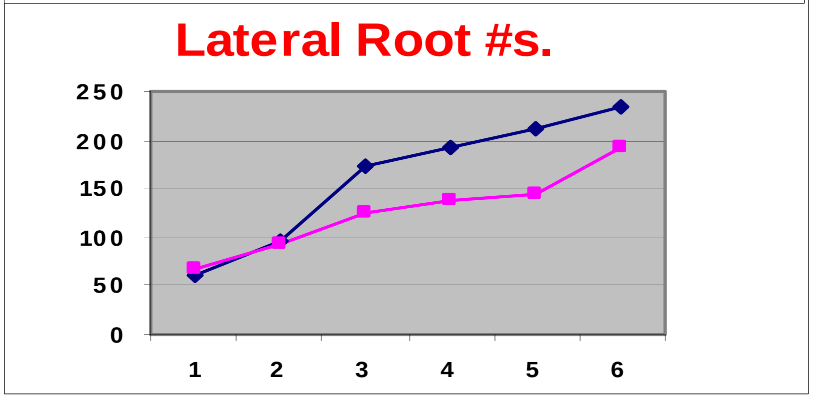
Pima-S6 **M-120**

Pima S6 ——

M-120 ——





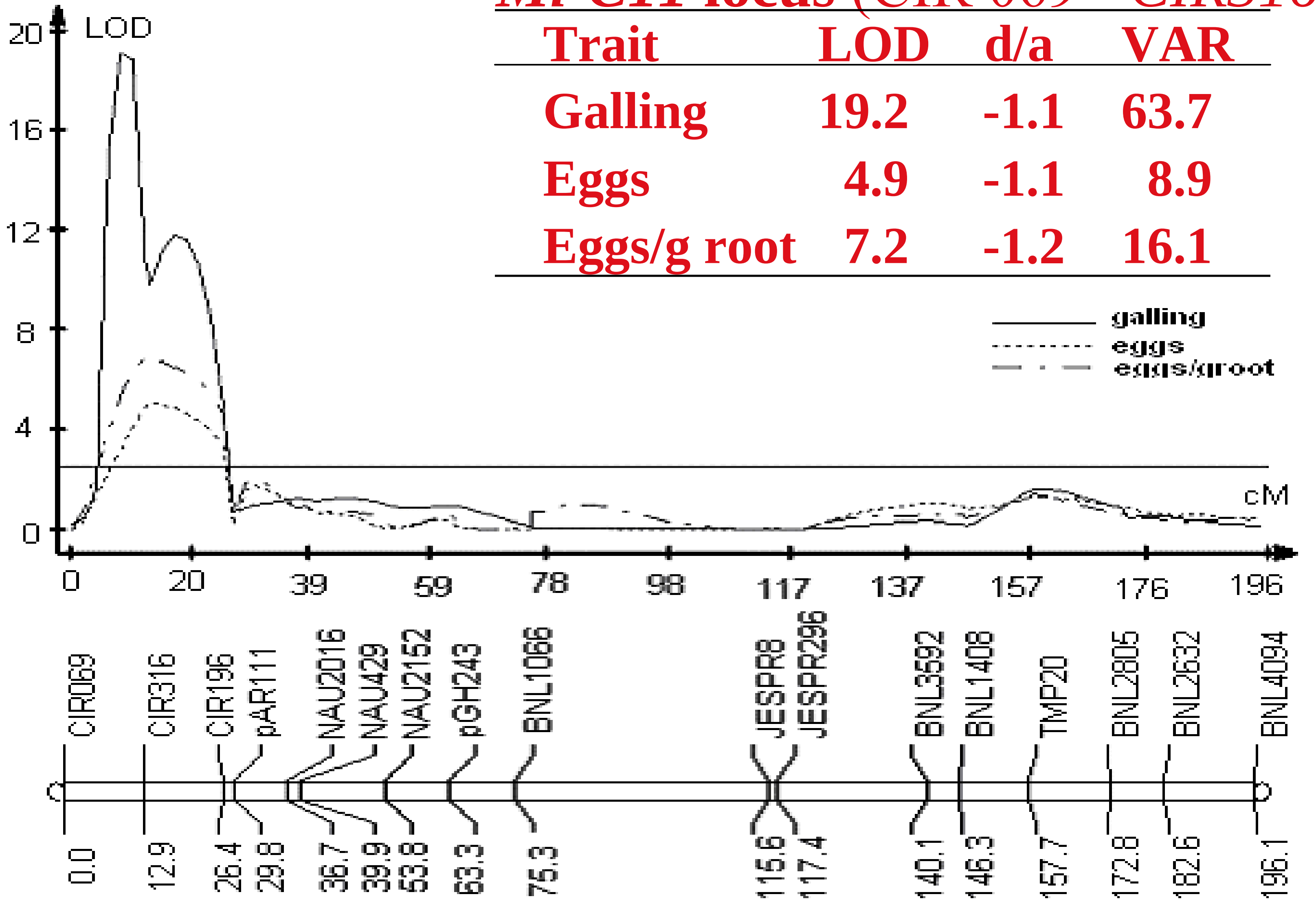


Week

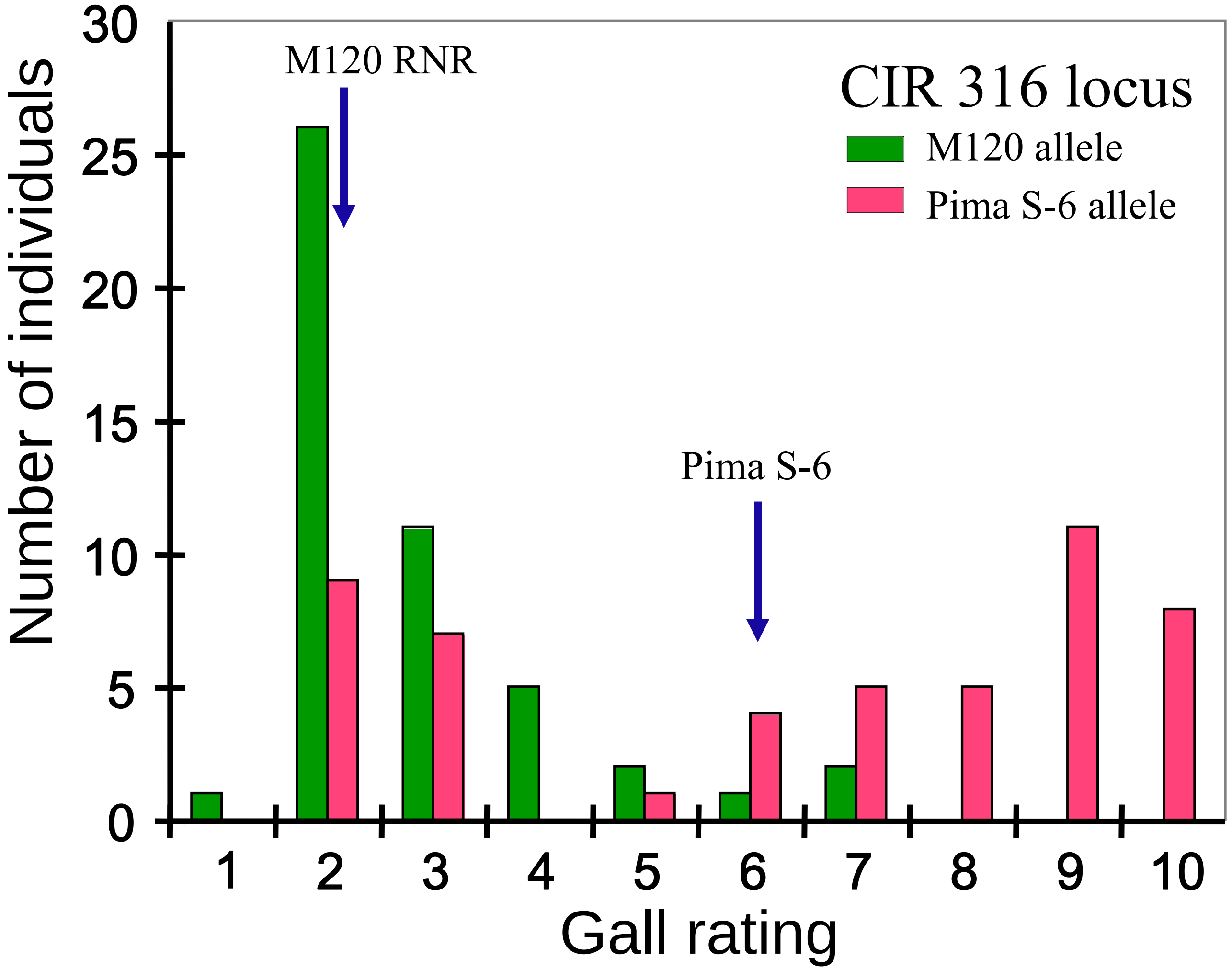
QTL associated with resistance - Chr. 11

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

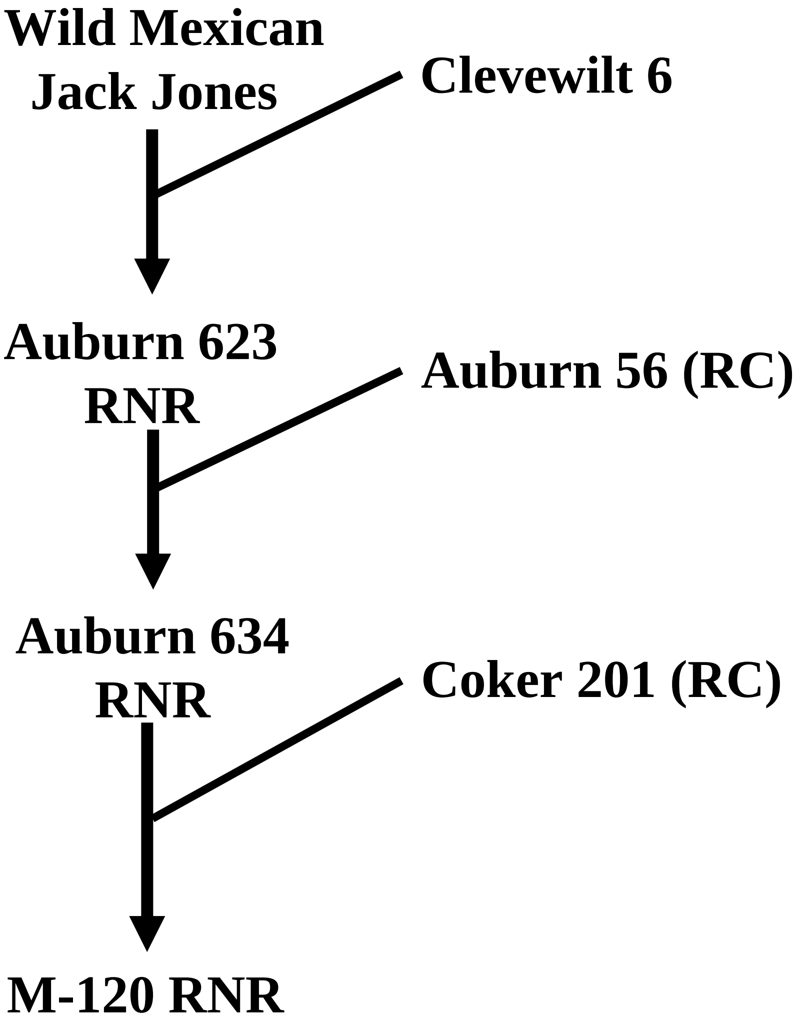


Selection efficiency using DNA markers



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

Pedigree of M120RNR



Wild Mexican
Jack Jones

Clevewilt 6

Auburn 623
RNR

Auburn 56 (RC)

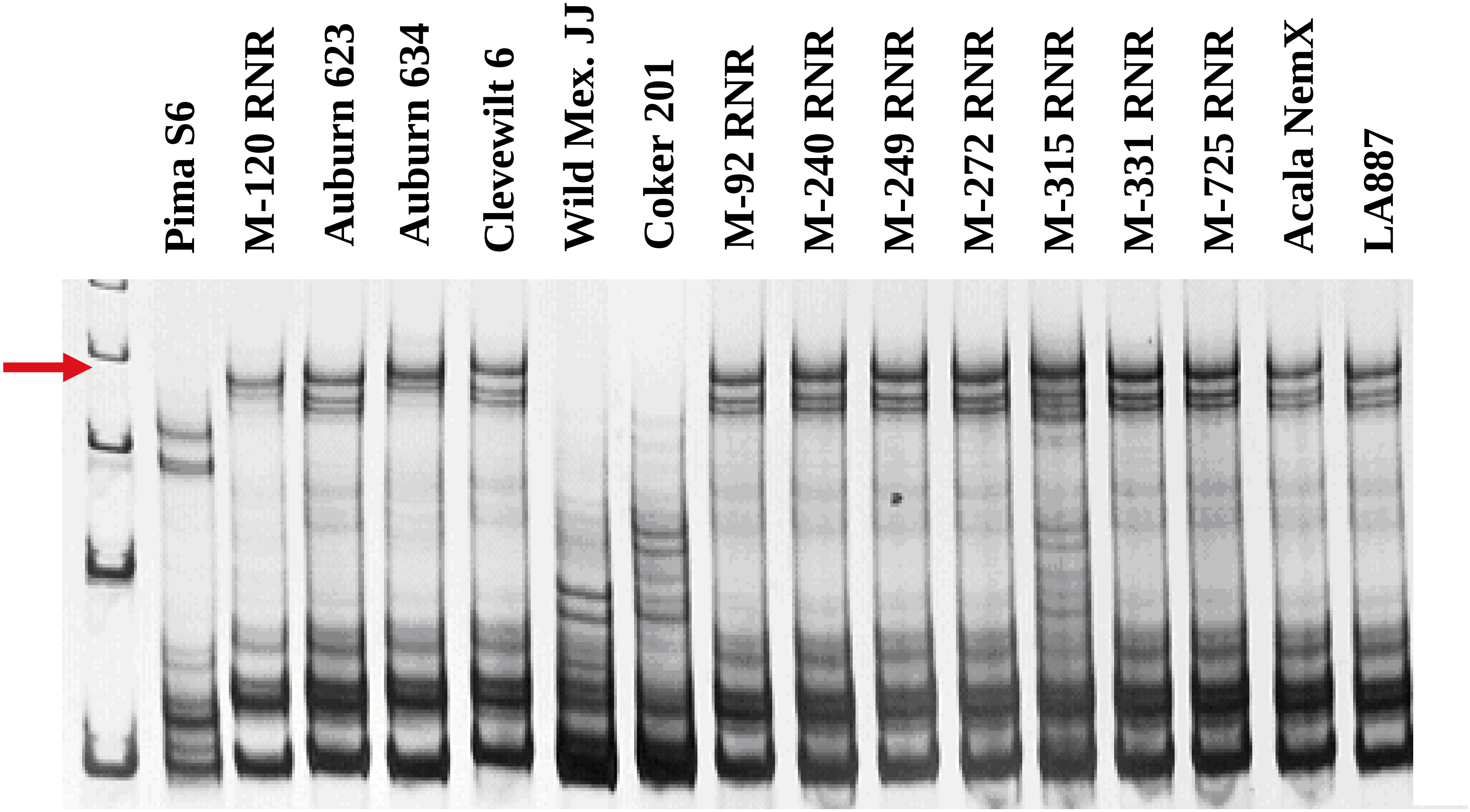
Auburn 634
RNR

Coker 201 (RC)

M-120 RNR

Source: Robinson 1999

Origin of root-knot nematode resistance locus on Chromosome 11



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

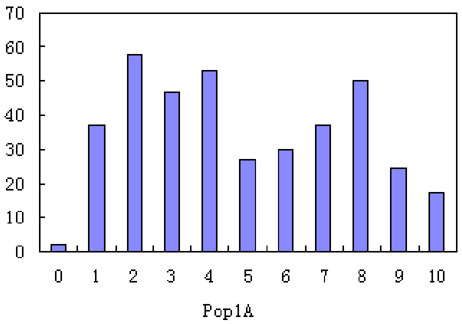
- An additional 1233 F_2 individuals were tested for resistance and genotyped to identify recombinants near the *Mi-C11* locus

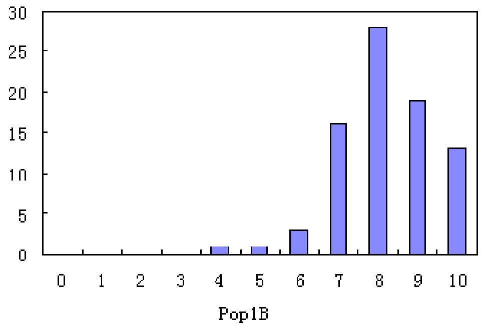
- 326 of recombinants recovered

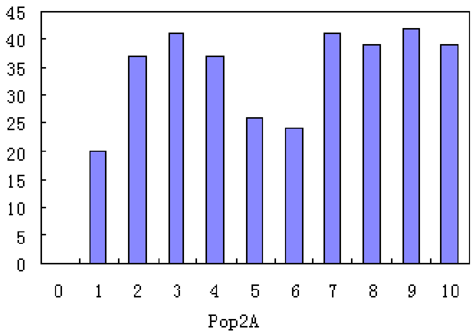
- Testing F3 families for resistance

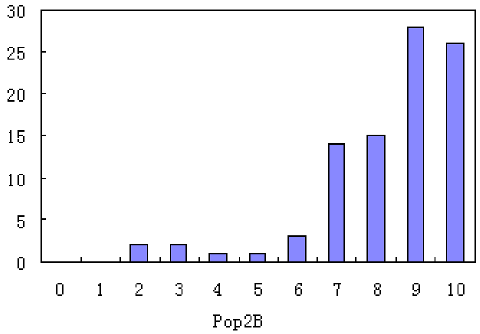
Frequency distributions for galling index

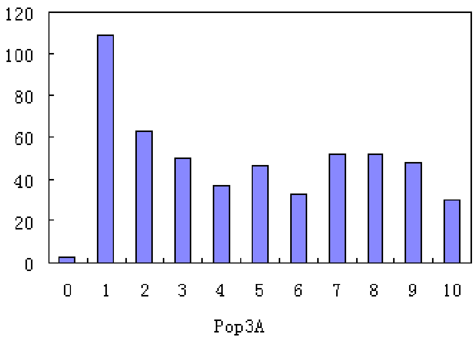
Population	n	Mean	VAR	Skew
Pop1A	382	4.88	7.44	0.22
Pop1B	71	8.23	1.72	8.54
Pop2A	347	5.80	8.14	-0.08
Pop2B	92	8.34	3.20	-1.69
Pop3A	523	4.74	9.17	0.211
Pop3B	128	7.27	5.57	-1.08
CombPopA	1252	5.08	8.56	0.122
CombPopB	291	7.84	4.14	-1.41

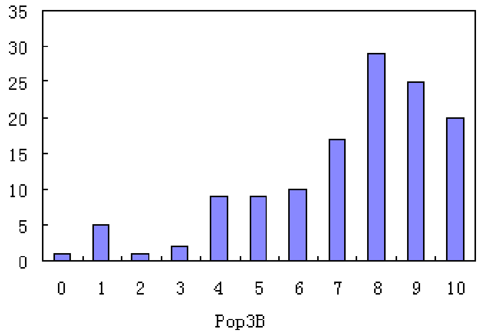


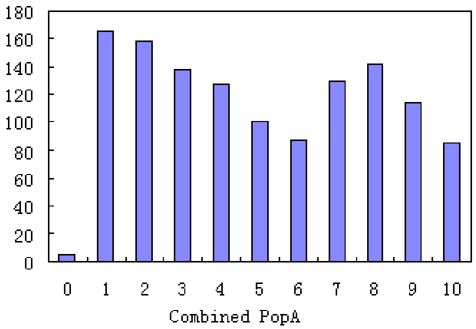


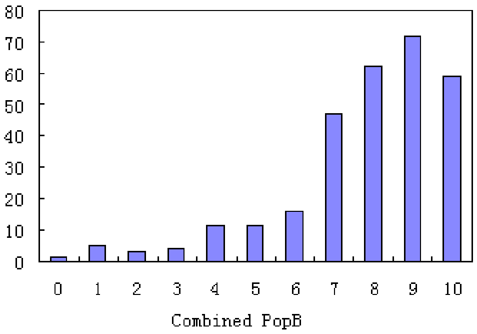




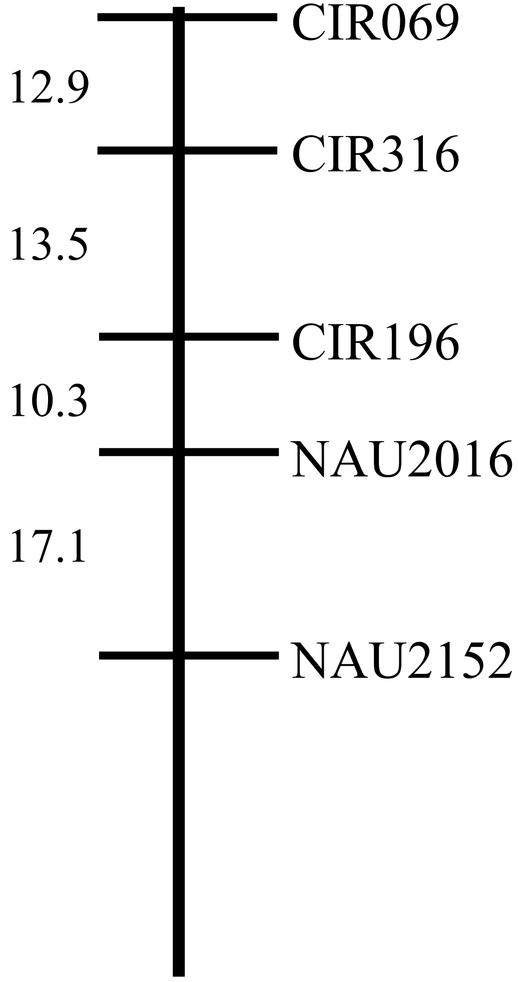






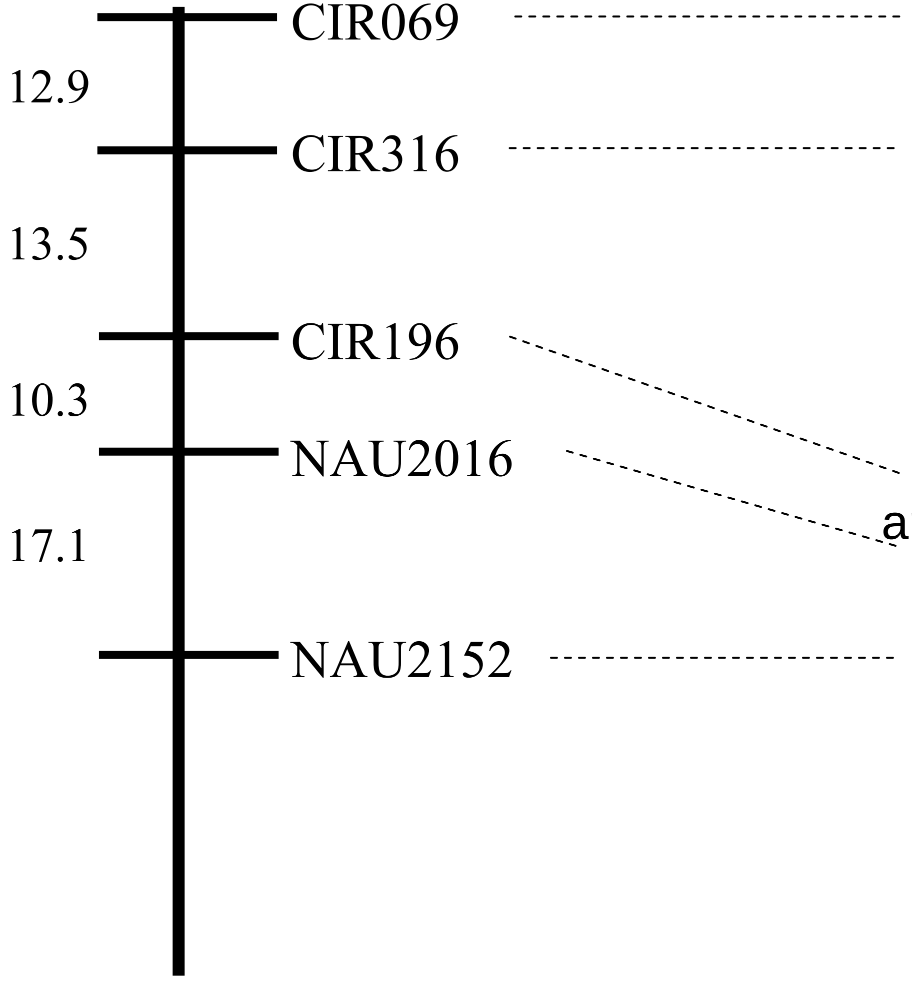


Current status of fine mapping



2006

Current status of fine mapping



CIR069

12.9

CIR316

13.5

CIR196

10.3

NAU2016

17.1

NAU2152

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

2006

2007

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

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 Clevewilt 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