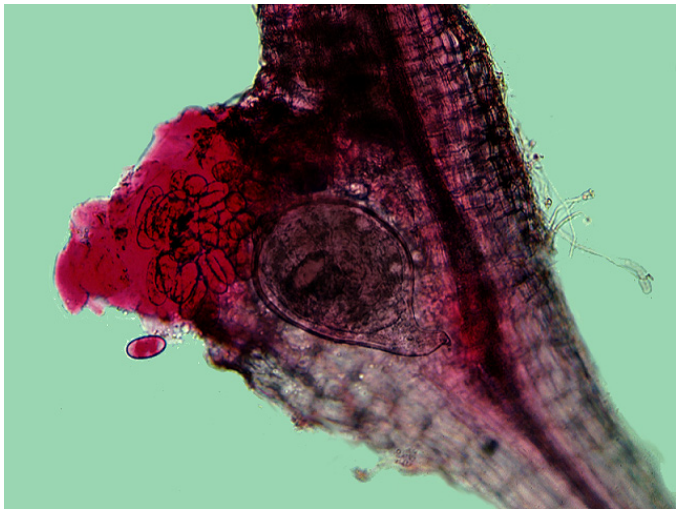
Root-knot Nematode Resistance in Upland cotton

Peng W. Chee

ICGI Conference

Raleigh, NC, Oct 10, 2012

The most important nematodes of cotton in the U.S.

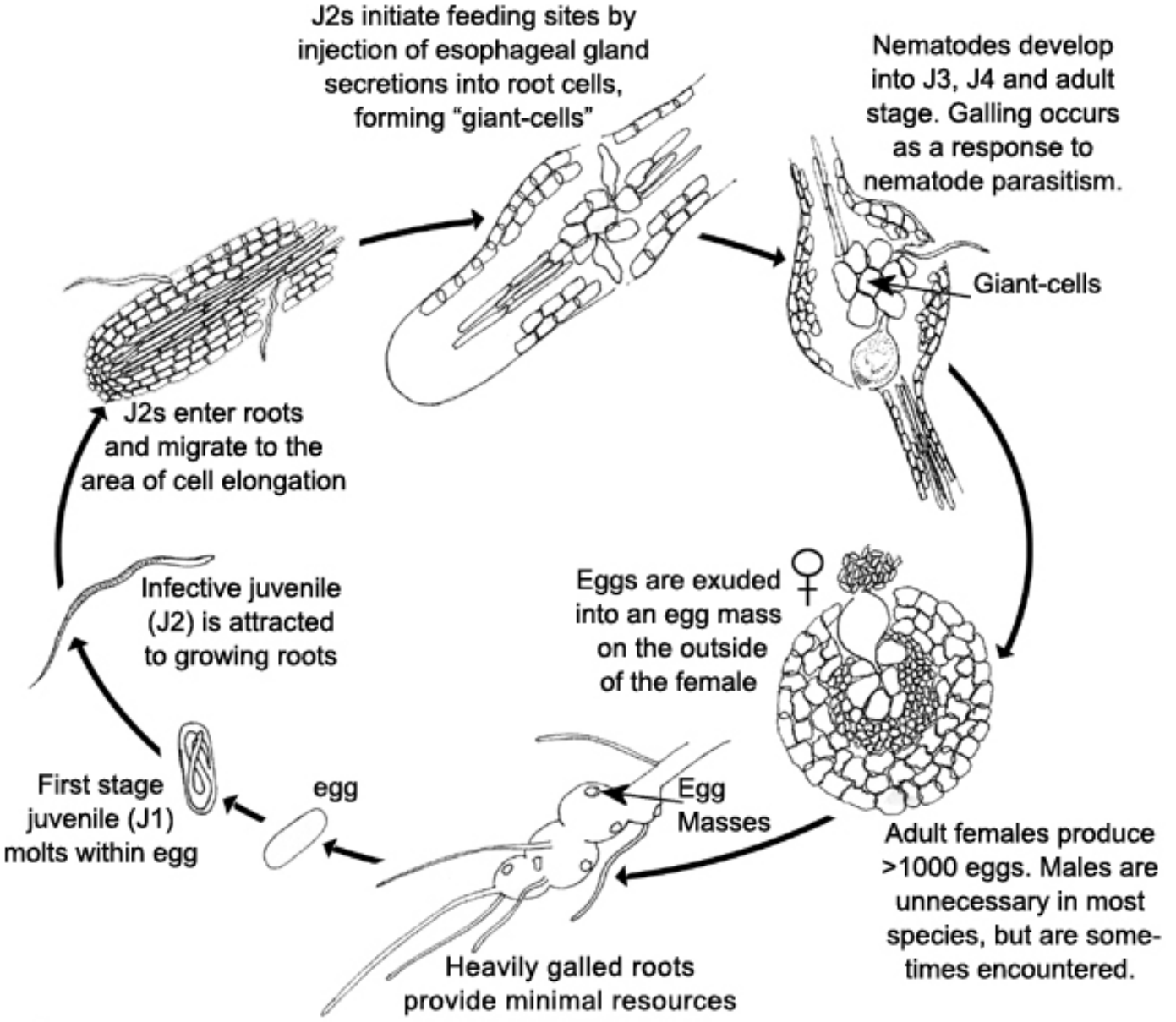


Southern root-knot
(Meloidogyne incognita)

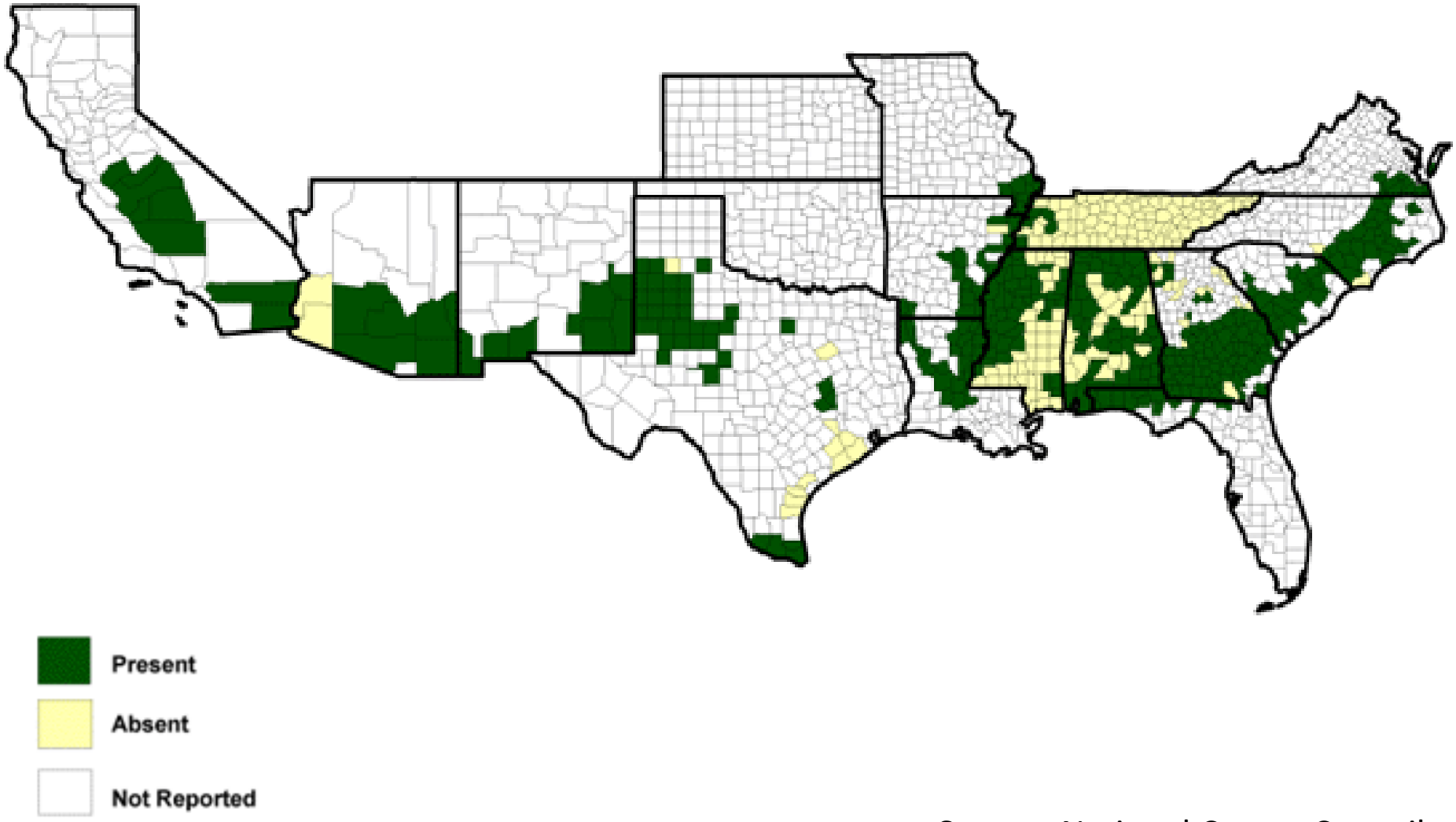
Reniform
(Rotylenchulus reniformis)

Columbia Lance
(*Hoplolaimus columbus*)

Disease Cycle and Epidemiology

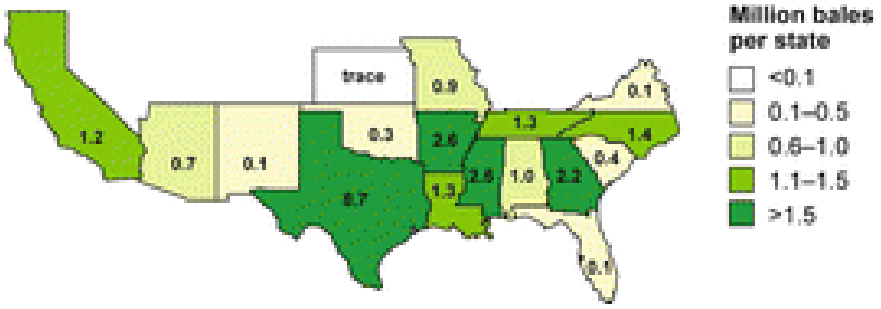


Population distributions and densities of root-knot nematodes in the cotton belt (2009)

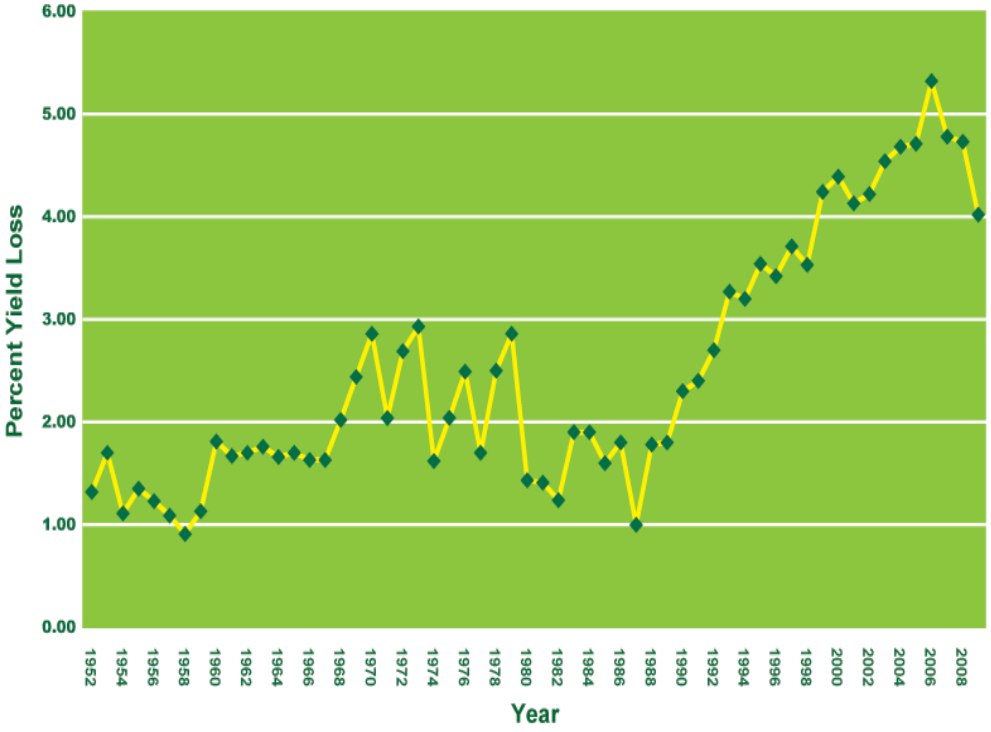


Source: National Cotton Council

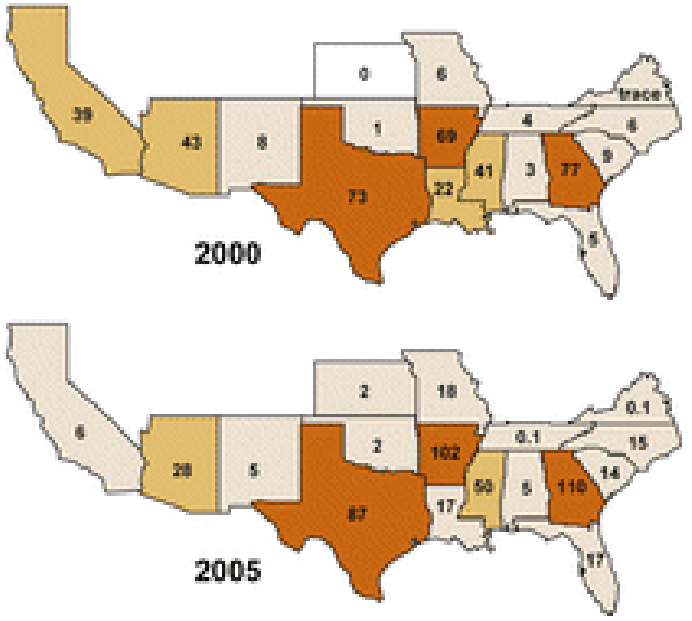
Cotton production, 2005



Nematode Yield Losses



Cotton losses due to *Meloidogyne incognita*



Robinson AF. 2007.
Annu. Rev. Phytopathol. 45:263–88


©2012 LSU AgCenter

Tools available for nematode management

- Crop Rotation
- Nematicides
- Plant-Host Resistance

Tools available for nematode management

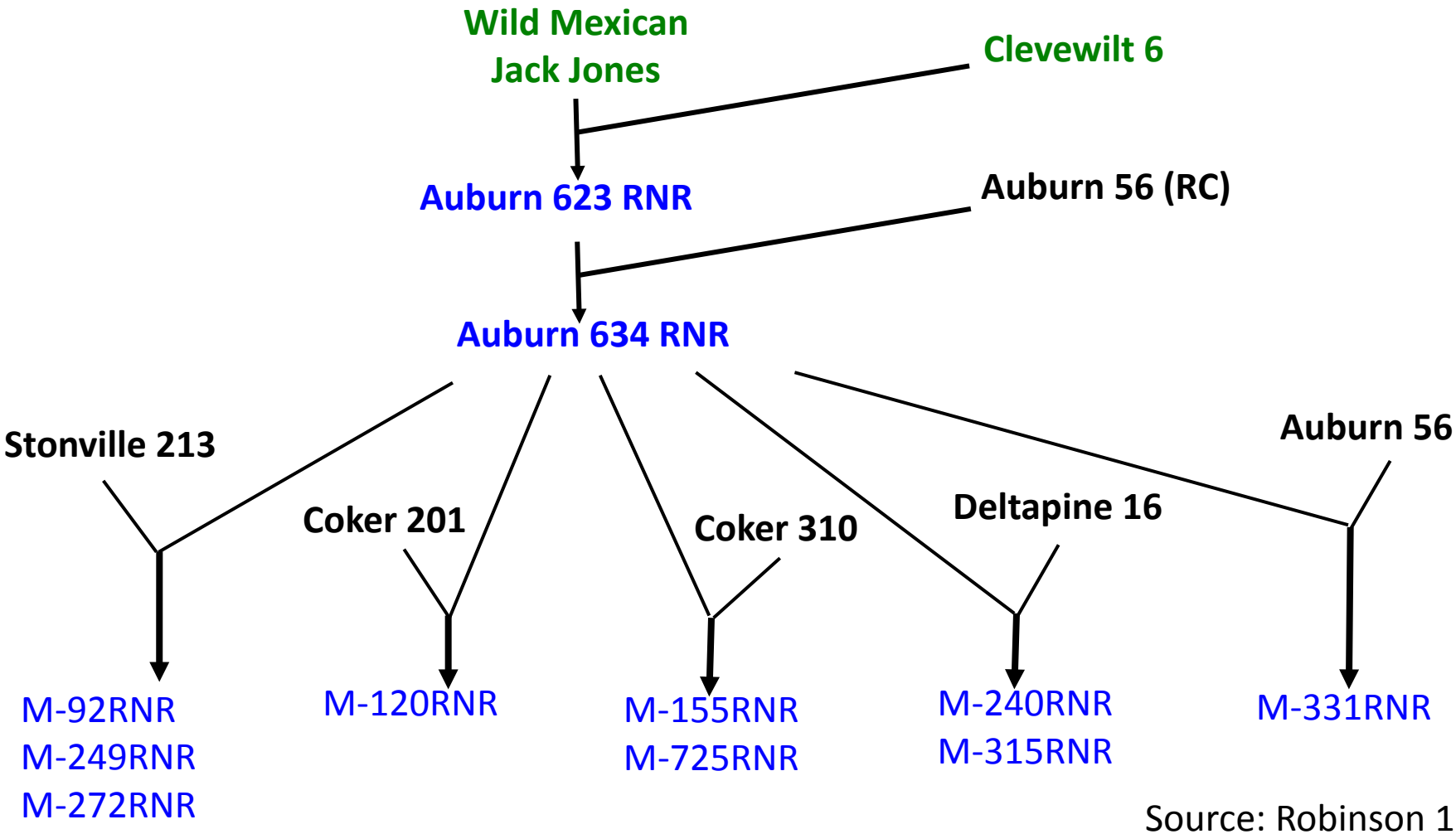
- Crop Rotation
- Nematicides
- Plant-Host Resistance

Tools available for nematode management

- Crop Rotation
- Nematicides
- Plant-Host Resistance

Sources of resistance to *M. incognita*

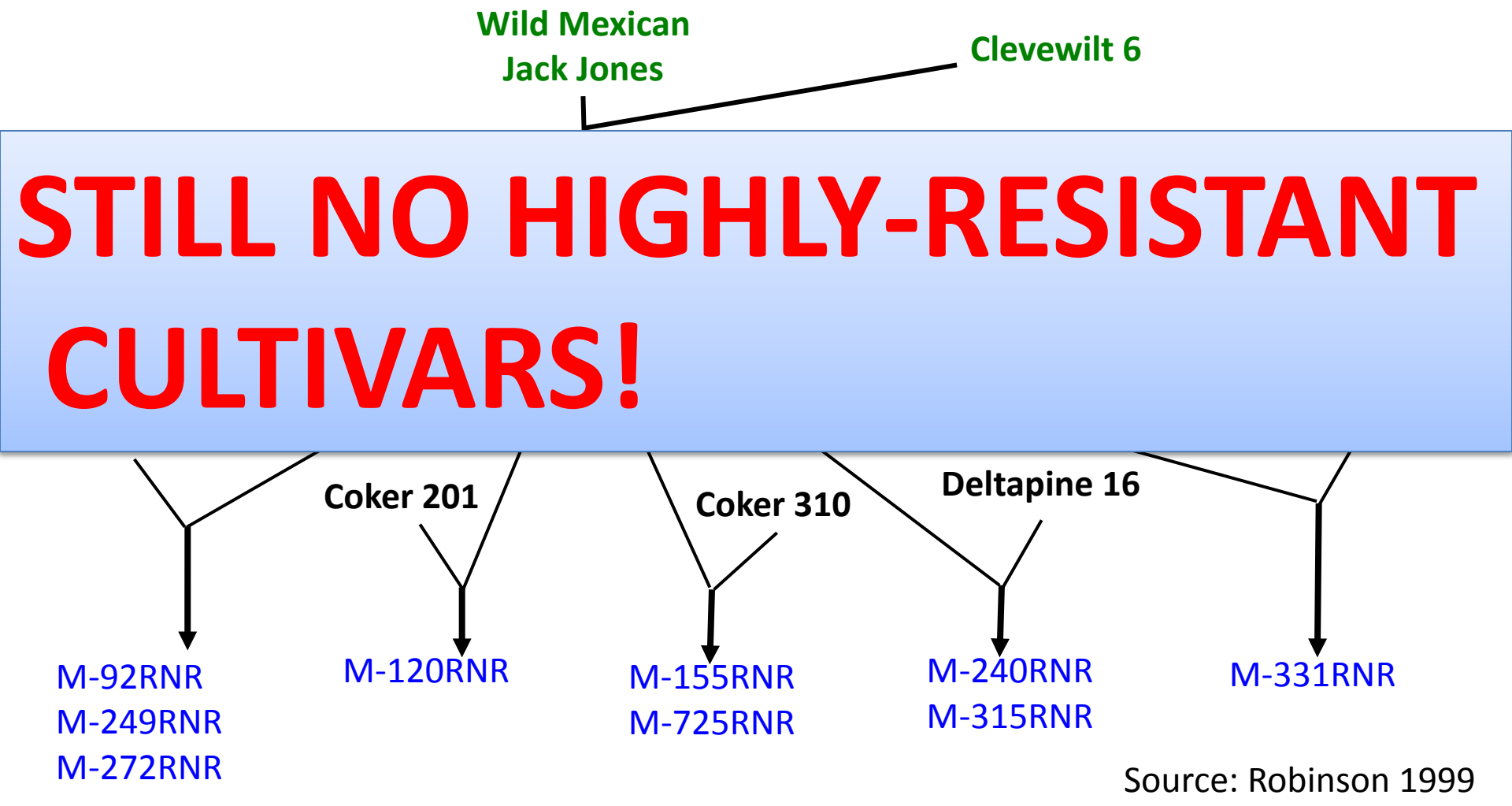
Auburn 623 – created by crossing Clevewilt 6-3-5 and Wild Mexico
Released to breeders in 1970



Source: Robinson 1999

Sources of resistance to *M. incognita*

Auburn 623 – created by crossing Clevewilt 6-3-5 and Wild Mexico
Released to breeders in 1970

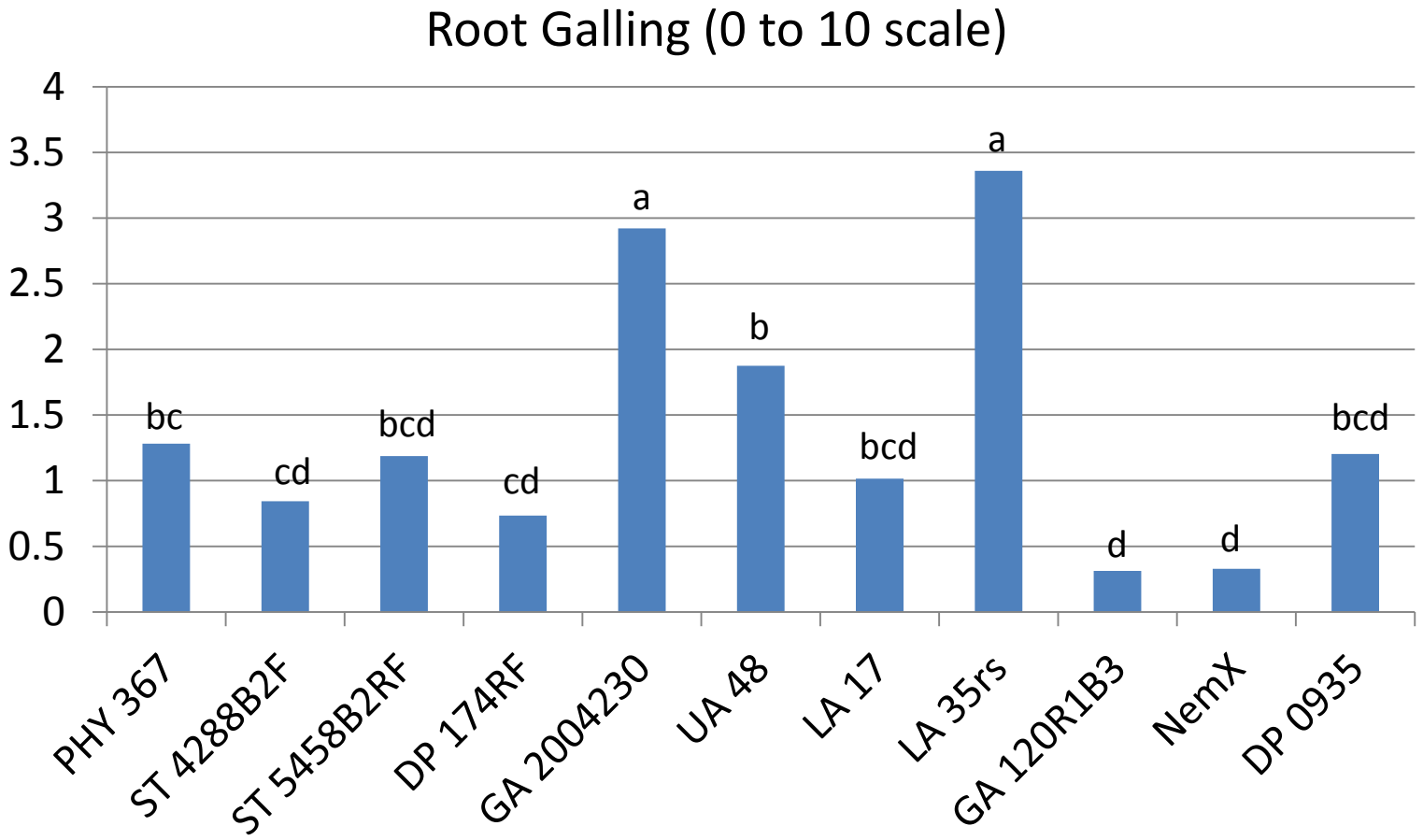


Source: Robinson 1999

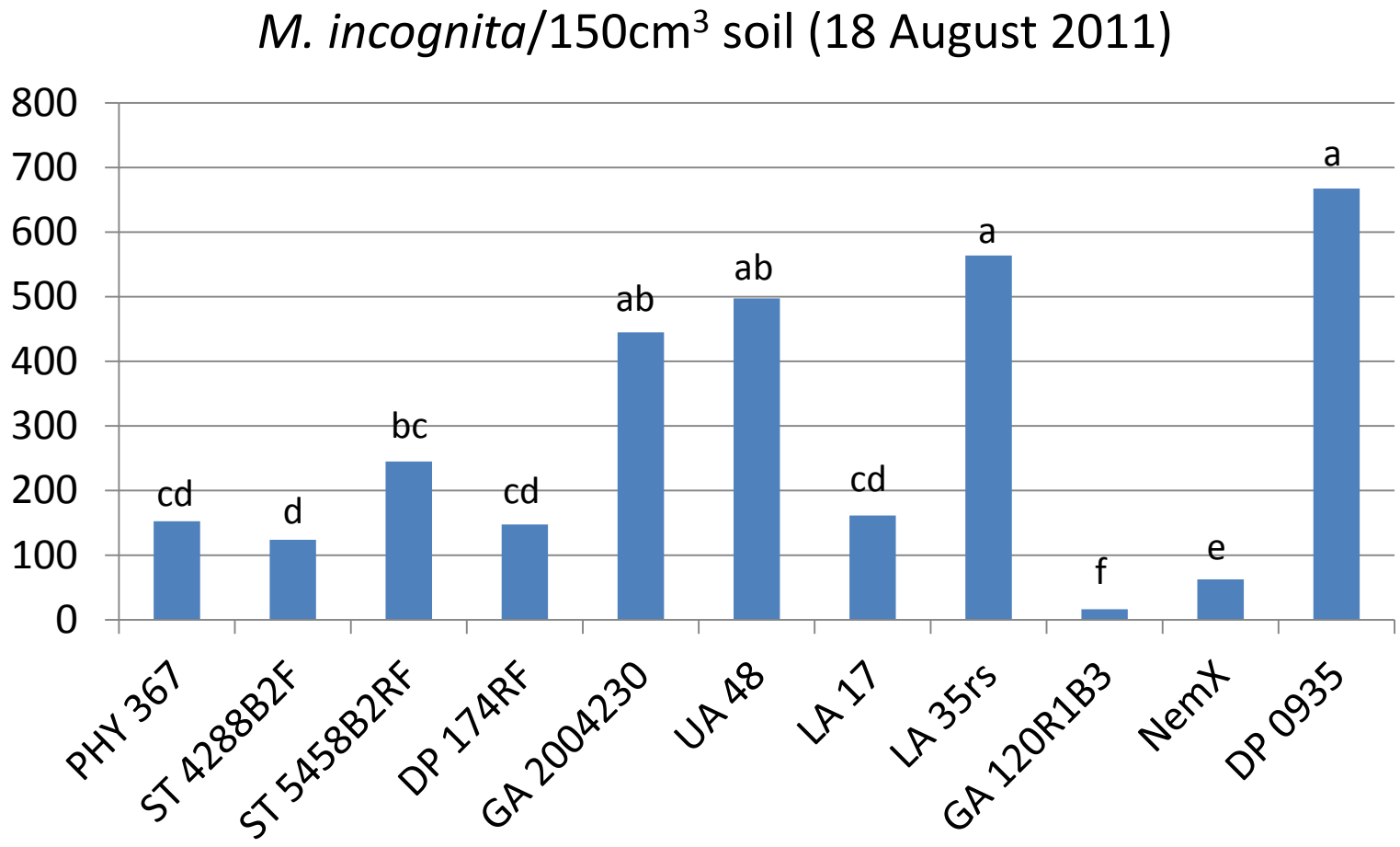
Development of GA 120R1B3 cotton germplasm line with a high level of resistance to *M. incognita*

Davis et al. 2011

- 2001 – crossed M120 RNR (resistant) with PD94042 (susceptible)
- Three generations of backcrossing into PD94042
- A single-seed descent – lowest galling and eggs count
- Eight generations of self-pollinations and individual plant selection



PHY 367, ST 4288, ST 5458, and DP 174 are moderately resistant and suppressed *M. incognita* levels by 63% to 82% vs. DP 0935 (or 45% to 74% vs. GA 2004230)



PHY 367, ST 4288, ST 5458, and DP 174 are moderately resistant and suppressed *M. incognita* levels by 63% to 82% vs. DP 0935

None of the currently grown commercial cotton cultivars expresses a high level of resistance to root-knot nematodes.

None of the currently grown commercial cotton cultivars expresses a high level of resistance to root-knot nematodes.

Why?

Genetic mapping populations

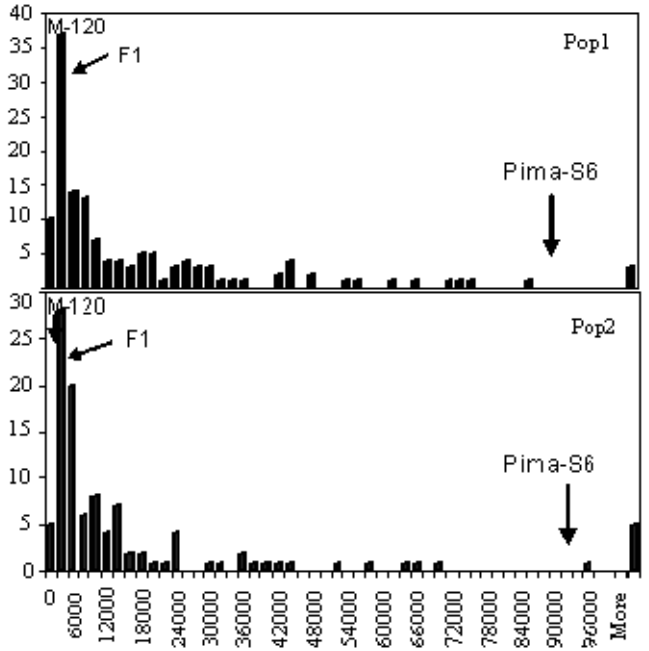
Pima S6 X M120 RNR

F1 Plant #1

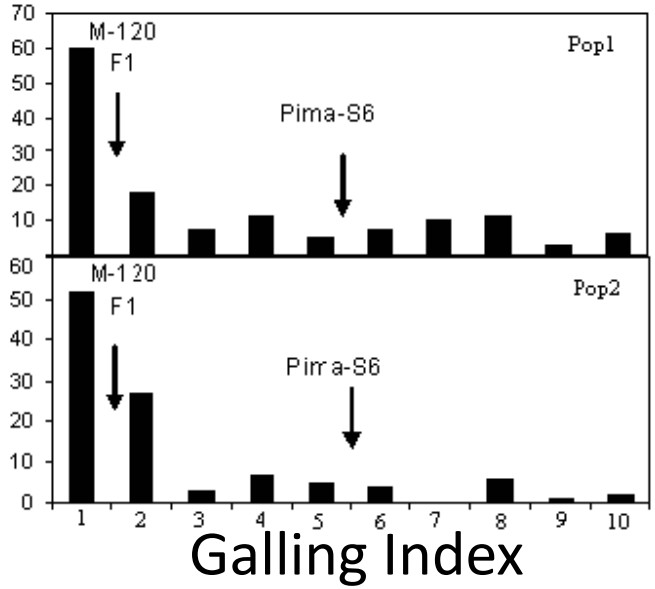
F1 Plant #2

107 F2 progeny

138 F2 progeny

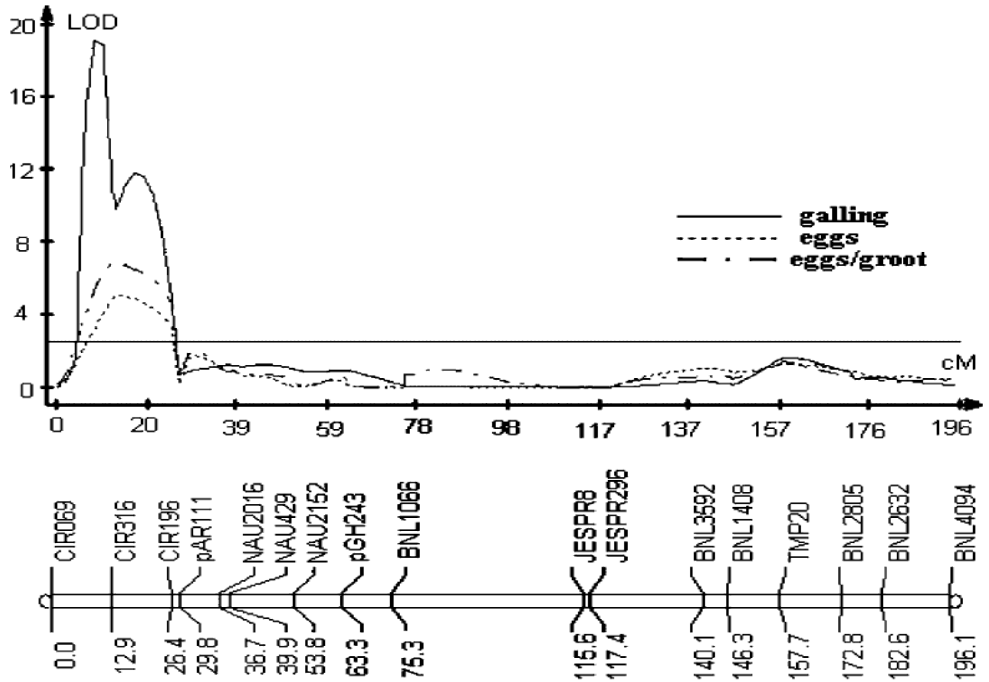


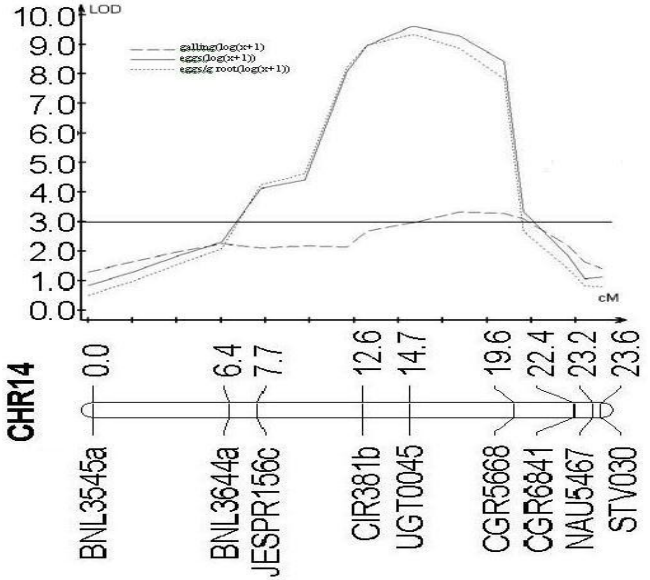
Egg counts



Galling Index

QTLs associated with galling - Chr. 11 and 14





PVA = 63%

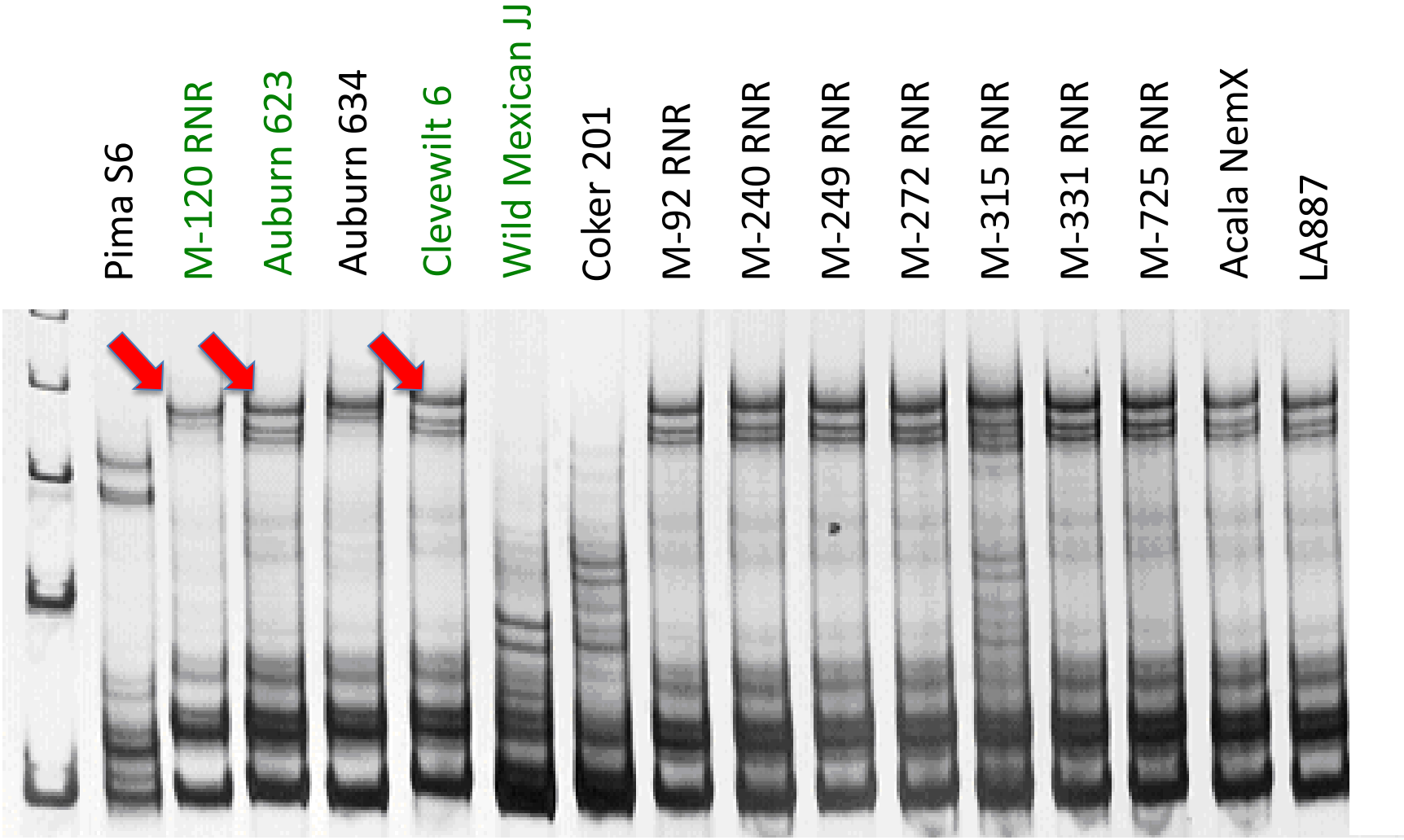
Add = -2.7

PVA = 32%

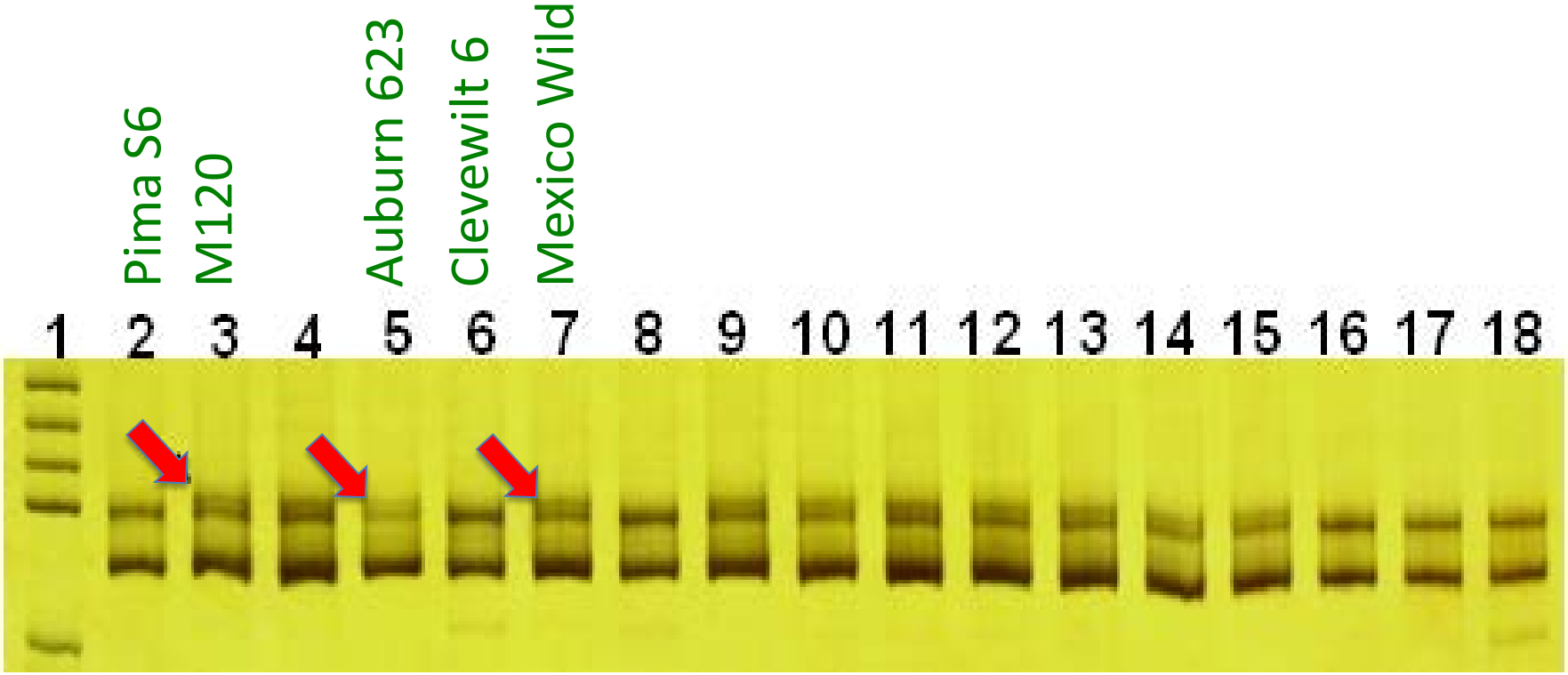
Add = -0.48

Shen et al. 2006

Origin of root-knot nematode resistance locus on Chromosome 11

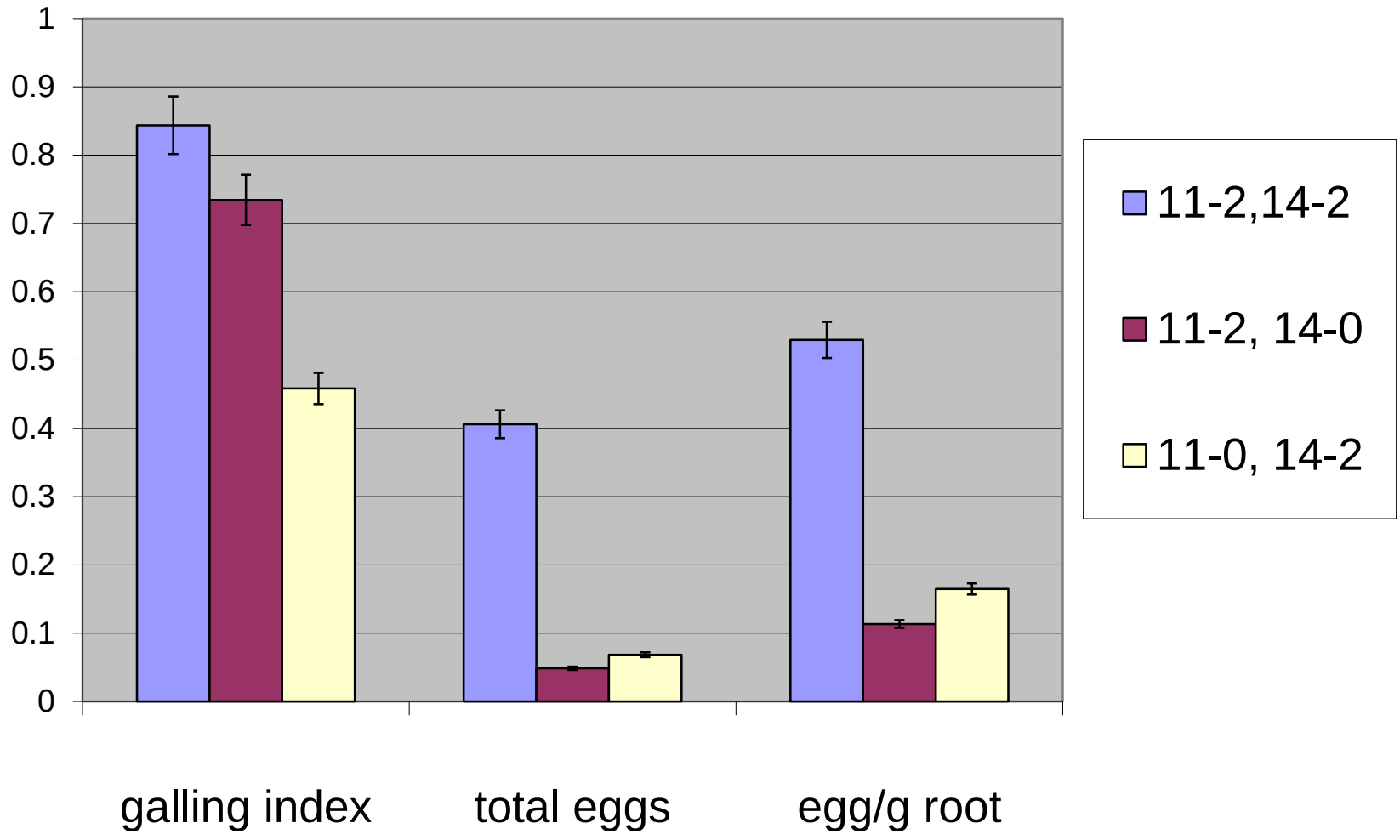


Origin of root-knot nematode resistance locus on Chromosome 14



1 Marker, 2 Pima S-6, 3 M-120 RNR, 4 Auburn 634 RNR, 5 Auburn 623 RNR, 6 Clevewilt 6, 7 Wild Mexican Jack Jones, 8 Coker 201, 9 M-92 RNR, 10 M-240 RNR, 11 M-249 RNR, 12 M-272 RNR, 13 M-315 RNR, 14 M-331 RNR, 15 M-725 RNR, 16 Auburn 56, 17 Acala NemX, 18 LA887.

Reduction in galling and eggs production among F2s carrying Chr 11 and Chr14 QTLs



Epistasis between Chr 11 and Chr14 QTLs (QTL Network)

Trait	QTLi	Interval-i	QTLj	Interval-j	AA	p-value	H^2(aa)
logeggs	1-6	UGT0045-CGR5668	2-1	CIR069-CIR316	-0.3007	0.001509	0.0494
logeggroot	1-5	CIR381-UGT0045	2-1	CIR069-CIR316	-0.3586	0.000016	0.0596

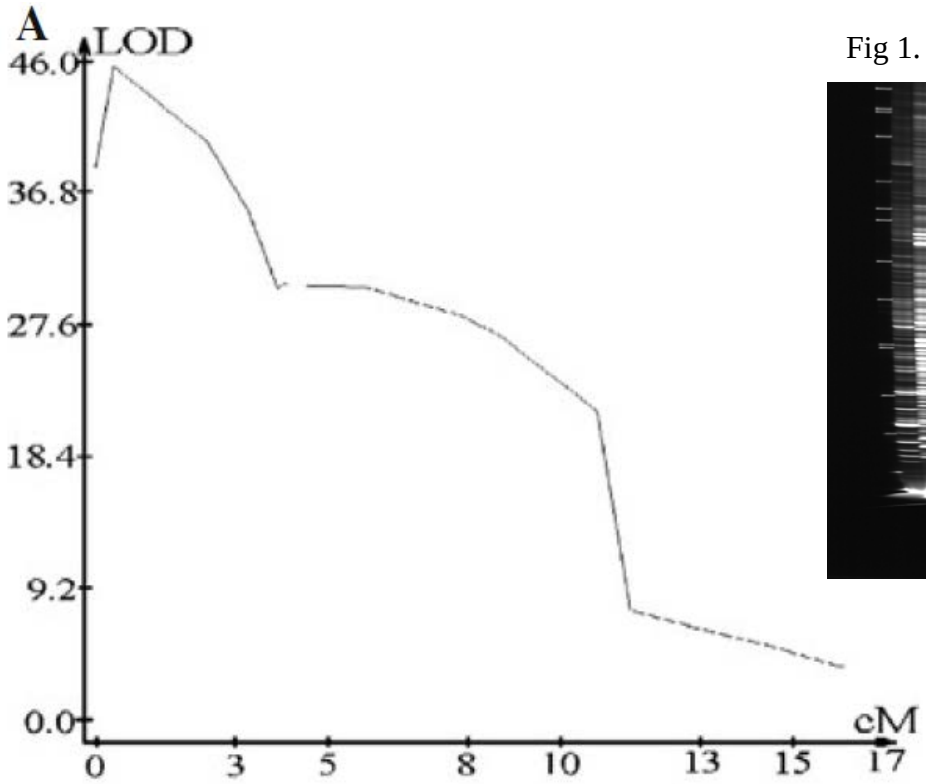
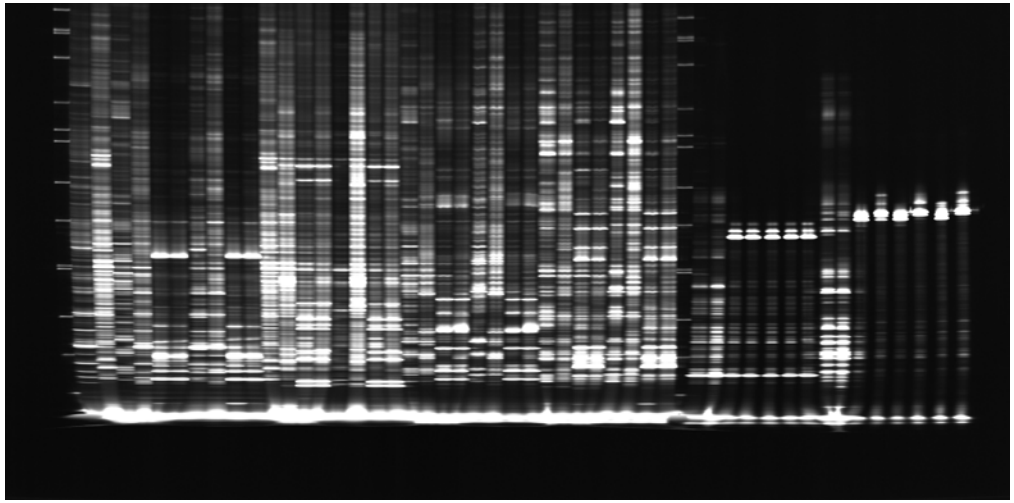
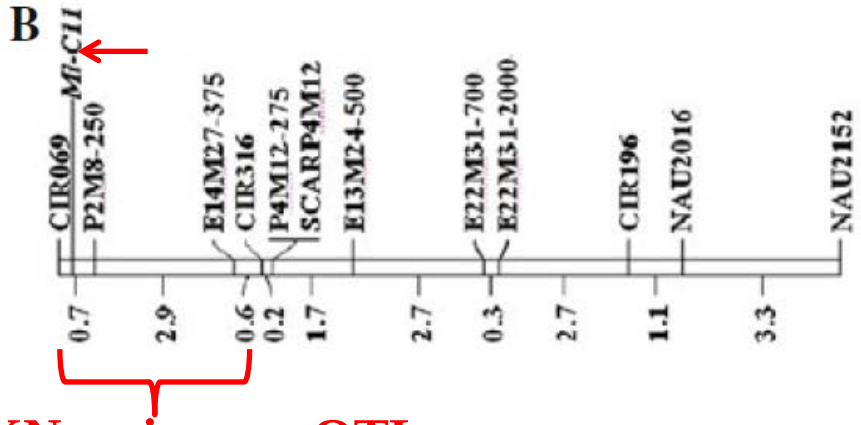


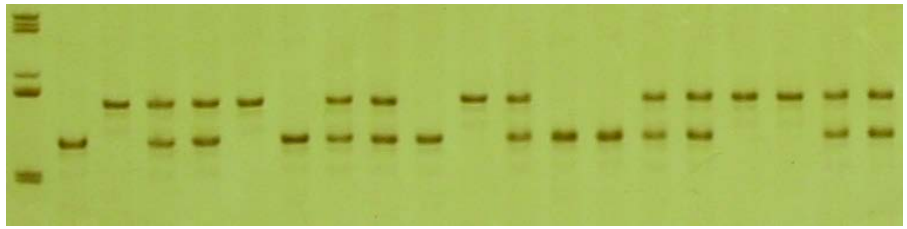
Fig 1. Polymorphisms analysis using AFLP markers





RKN resistance QTL

Fig 3. Polymorphisms analysis of SCAR marker P4M12 in mapping parents and individuals.



Shen et al 2010 TAG

Summary

- The root-knot nematode resistance in the Auburn 623RNR source is conferred by two major genes.
- The resistant allele on Chr. 11 is derived from Clevewilt-6, and the resistance allele on Chr. 14 is originated from Wild Mexican.
- The gene on Chr. 11 appears to mostly affect gall suppression while that on Chr.14 appears to reduce eggs production but has little effects on root galling.
- the transgressive segregation in Auburn 623RNR source could be due to the stacking of genes from two moderately resistant parents with different mechanisms for resistance.

Acknowledgements

Postdocs/Students

Dr. Guillermo Bacalaere
Nino Brown
Dr. Kedong Da
Aparna Desai
Dr. Yajun He
Dr. Naeem Iqbal
Pawan Kumar
Limei Liu
Dr. Edward Lubbers
Jinesh Patel
Dr. Hamidou Sakhanokho
Dr. Xinlian Shen
Dr. Baohua Wang

Technicians

Kippy Lewis
Jennifer McCurdy
Michael Jing
Jumin Zhuang
Stephen Walker

Collaborators

Dr. Richard Davis
Dr. Lloyd May
Dr. Andrew Paterson
Dr. C. Wayne Smith
Dr. Bob Nichols
Dr. Todd Campbell
Dr. Don Jones
Dr. Robert Wright

Funding source: COTTON INCORPORATED · CSREES USDA · NSF · GEORGIA COTTON COMMISSION

Thank you for your attention