

Genetic and Molecular Characterization of Host-Plant Resistance to Root-knot Nematodes and Fusarium Wilt in Cotton



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Project Objectives

- 1 Determine the genetic basis of resistance to root-knot nematode (RKN) and Fusarium wilt (FW); uniqueness of NemX v. other *R* genes
- 2 Develop linked molecular markers to RKN and FW resistance genes;
- 3 Localize RKN *R* genes to chromosome genome of cotton;
- 4 Develop a high resolution linkage map around the *R* genes.

The Phenotype of Parents for Reaction to RKN and to FOV

Genotype	<i>M.</i> <i>incognita</i> (RKN)*	<i>F.o.</i> <i>vasinfectum</i> (FOV)**	RKN +FOV*
SJ-2	S	S	S
NemX	R	S	R
Pima S-7	S	R	MR

*I. Seedling inoculation method

**II. Cut-root-dip method

SJ-2

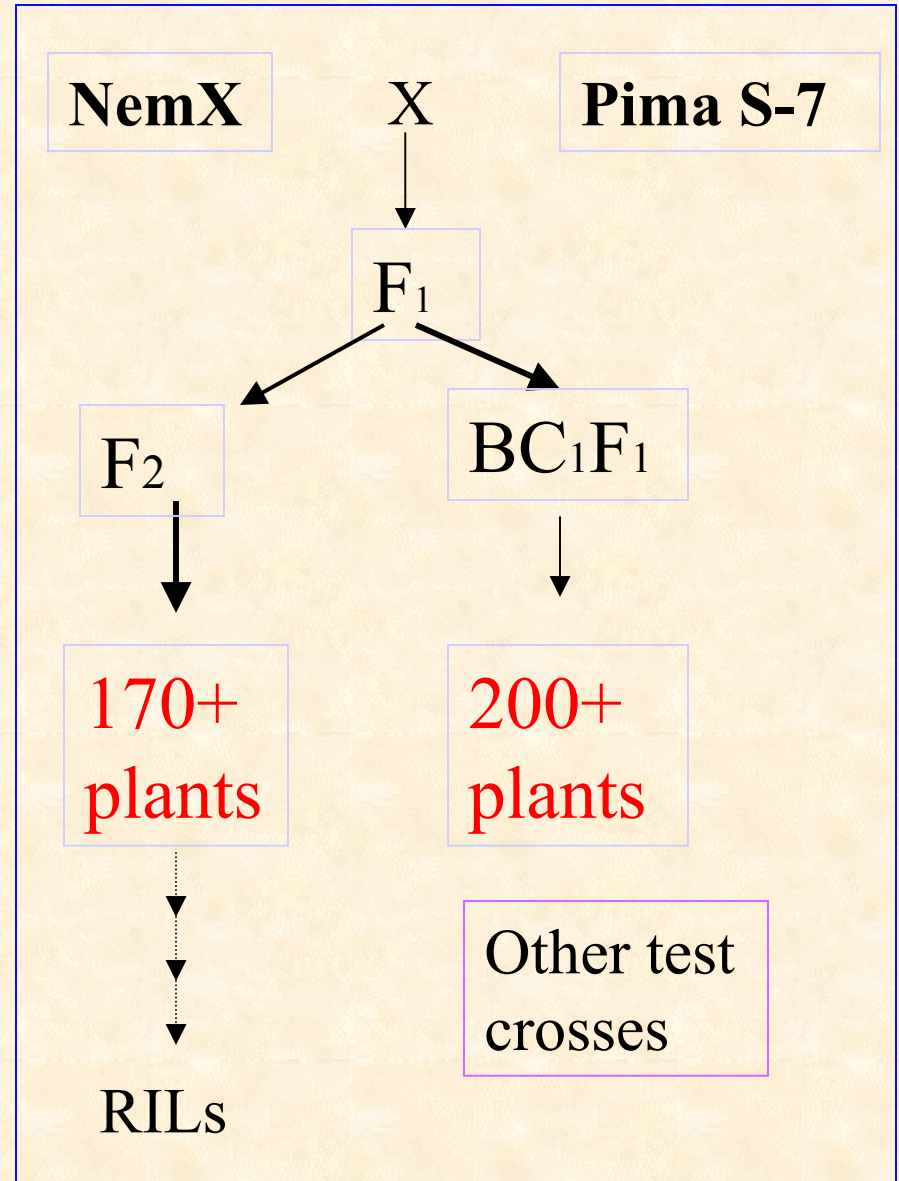
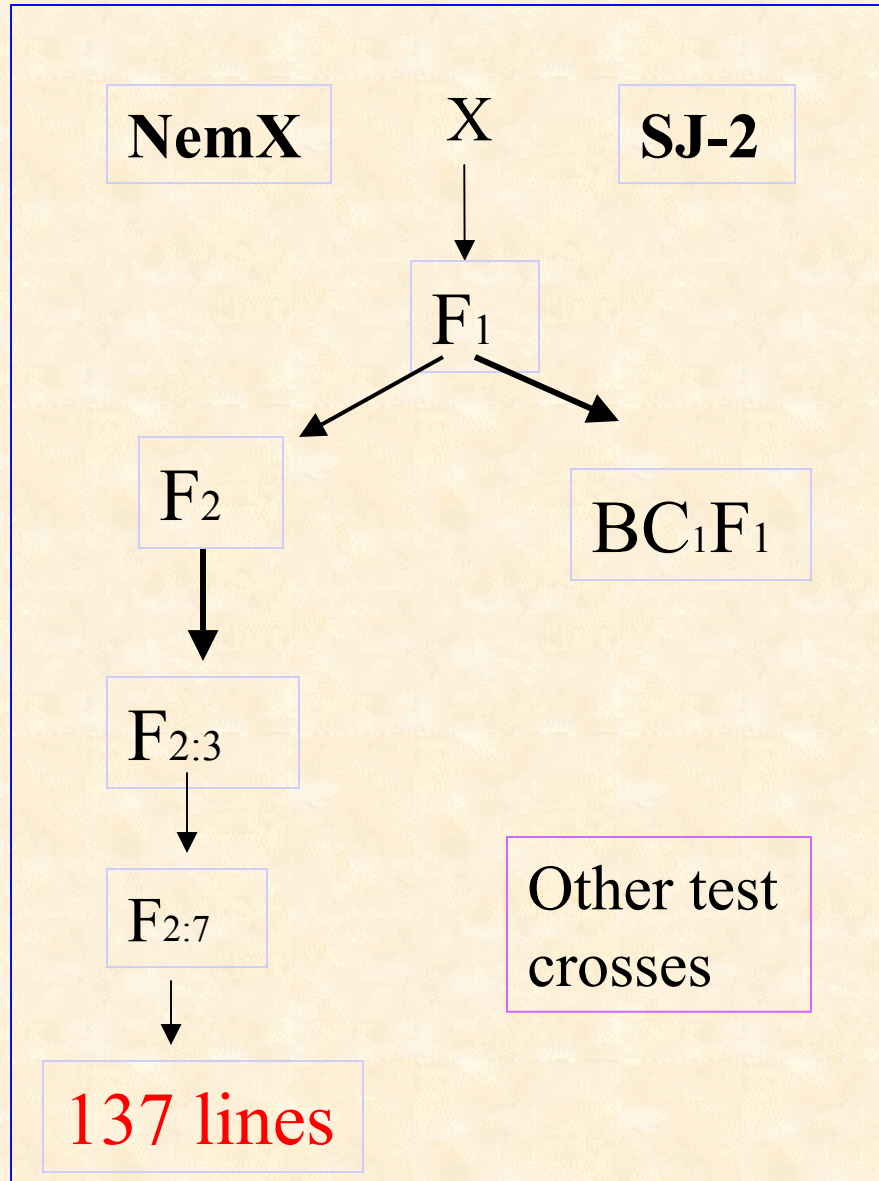
Root-knot Nematode

Pima S-7

NemX



Plant Populations



F_2 and BCF_1 plants

F_2



BCF_1



NemX x Pima S-7

The Phenotype of Parents and F1 for Reaction to *M. incognita*

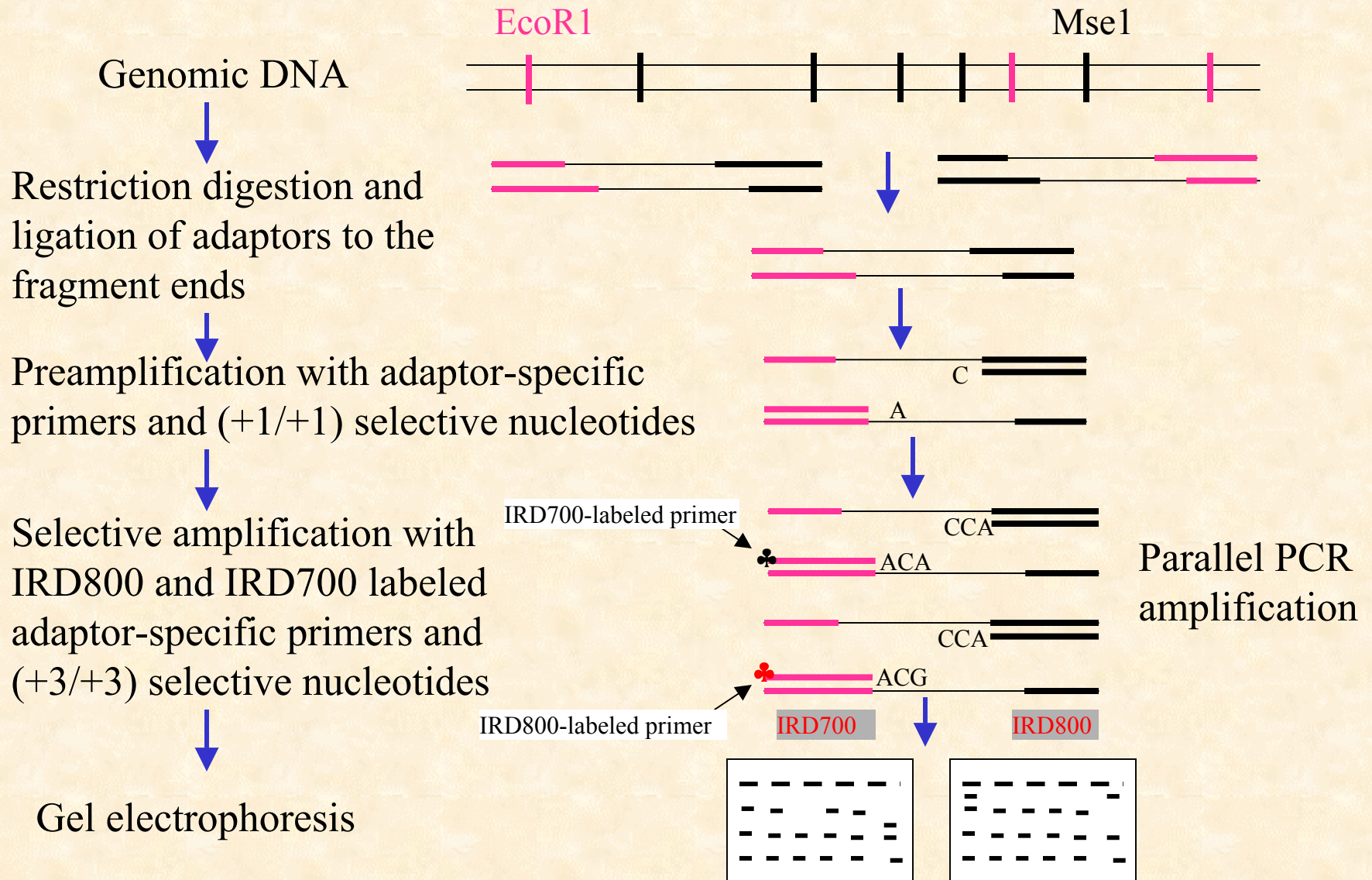
Genotype	Gall rating	Total eggs (in 1000s)	Eggs/g root
SJ-2	5.58a	259.4a	4,129a
NemX	1.17b	14.8c	291b
N901	1.35b	8.0c	175b
F1			
SJ-2 x NemX	5.37a	186.9ab	2,295a
Sj-2 x N901	5.06a	147.4b	2,487a

Summary of Segregation Data for *Meloidogyne incognita* Resistance in Cotton Cultivar Acala NemX

Parent or generation	Total plants or families	Observed R: I: S ratio	Expected R: I: S ratio	χ^2	P value
SJ-2	10	0 : 0:10	All S	0	>0.995
NemX	10	10 : 0: 0	All R	0	>0.995
F ₁	10	0 : 0: 10	All S	0	>0.995
BC ₁	346	91 : 172: 83	86.5 : 173: 86.5 (1:2:1)	0.382	0.75-0.90
		Observed R: Seg: S ratio	Expected R: Seg: S ratio		
F _{2:3}	84 (families)	7 : 45: 32	5.3 : 42: 36.8	1.386	0.50-0.75
F _{2:3}	132 (families)	9 : 71: 52	8.3 : 66: 57.7	1.001	0.50-0.75

R - Resistant; S - Susceptible; I – Intermediate ; Seg – Segregating.

Multiplexed AFLP Protocol

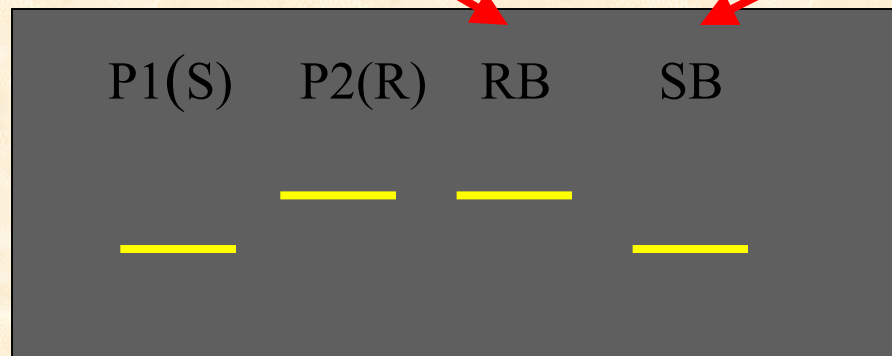


Bulked Segregant Analysis (BSA)

- BSA is used to make resistant plant DNA pools and susceptible DNA pools to obtain markers that correlate with each resistance trait.
- BSA has proved to be a powerful technique to identify markers linked to resistance genes.

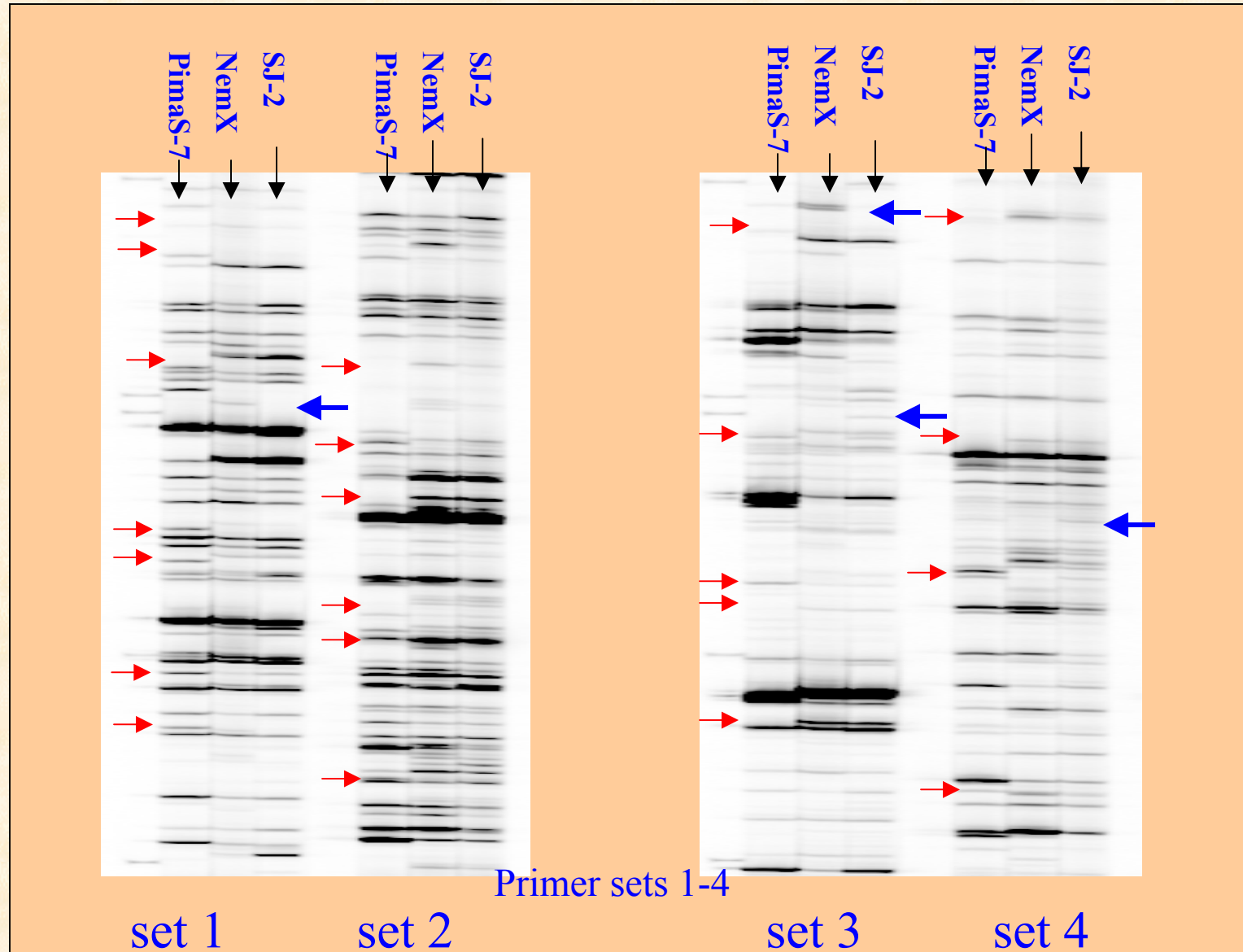
Individual homozygous F_2
or $F_{2:3}$ resistant plants (7-10)

Individual homozygous F_2 or
 $F_{2:3}$ susceptible plants (7-10)

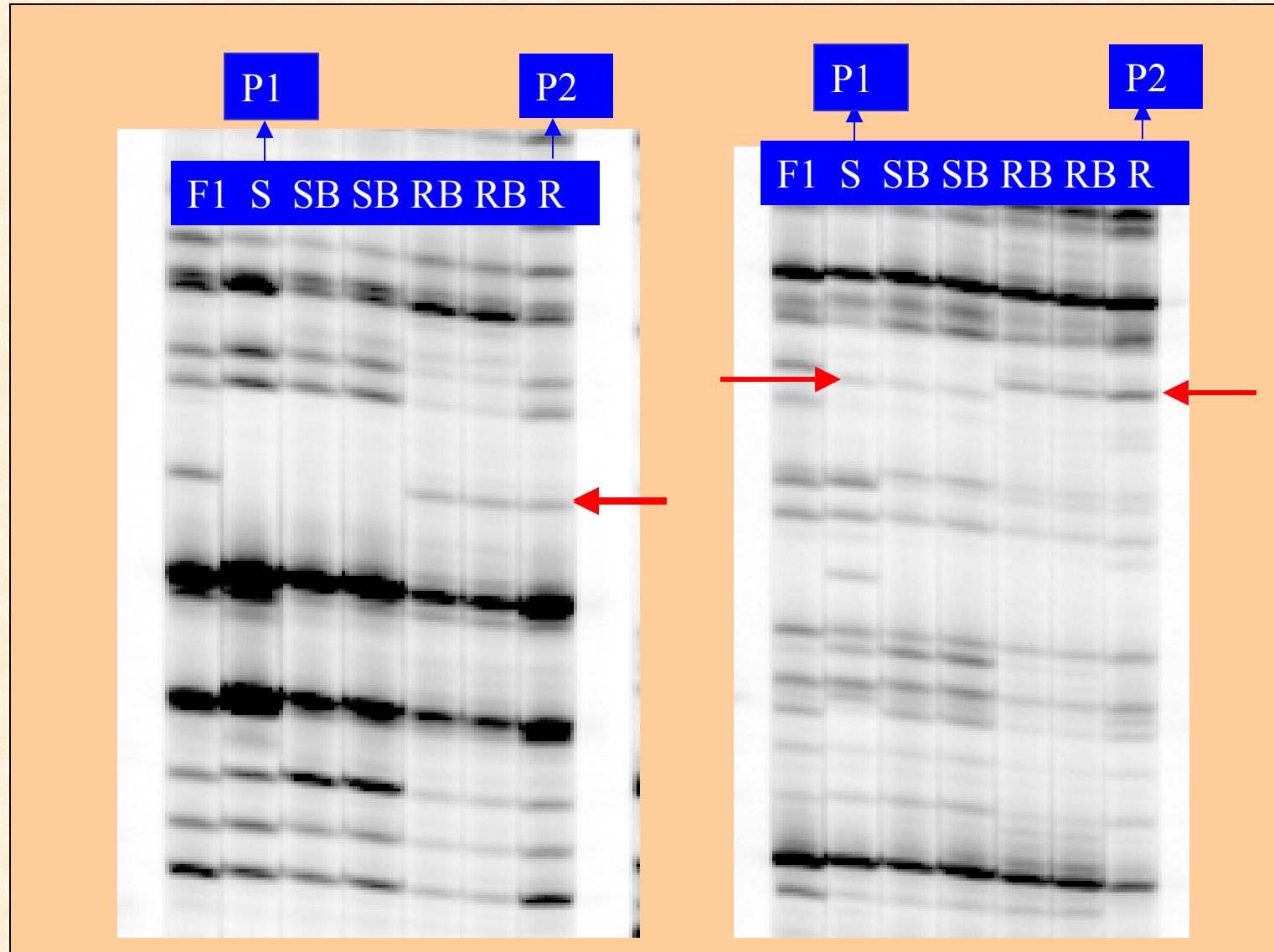


AFLP (amplified fragment length polymorphism)

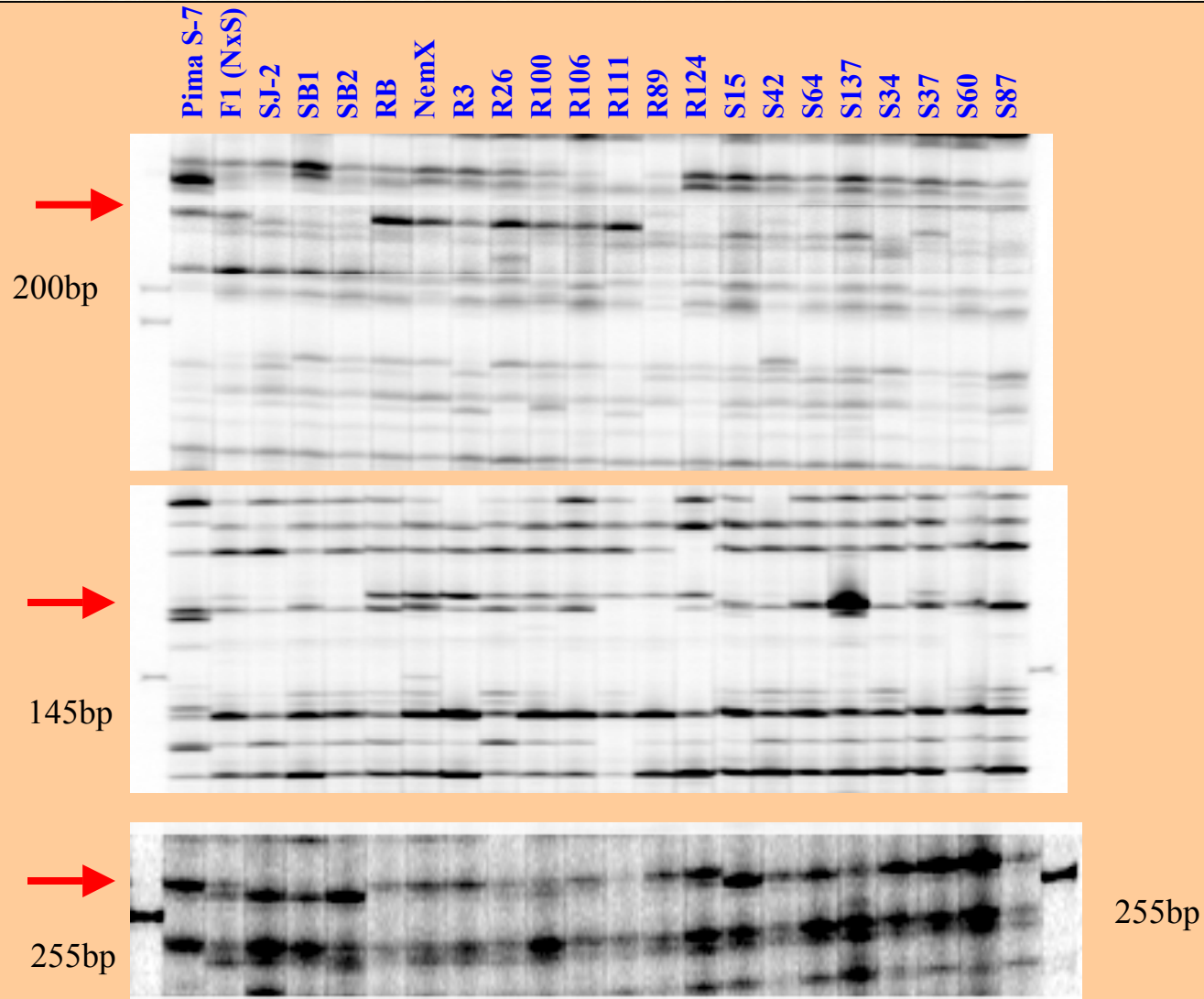
Screening of Parental Polymorphism



AFLP and Bulked Segregant Analysis (BSA)

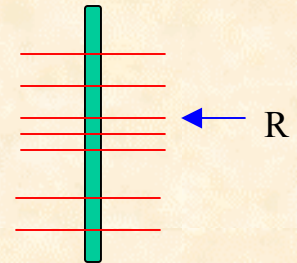


Potential Markers

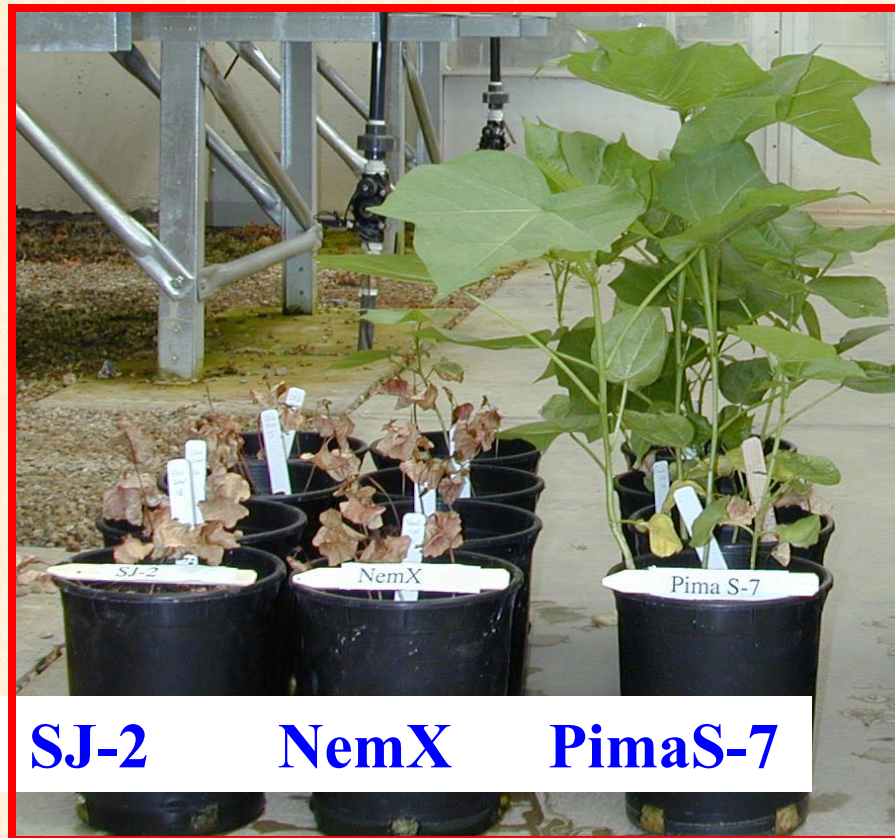


Future Work

- 1 Screen potential markers for linkage to nematode and wilt resistance traits;
- 2 Use markers to confirm gene interactions that determine resistance phenotype;
- 3 Convert markers to STS/SCAR forms;
- 4 Localize resistance genes to the chromosomes;
- 5 Fine mapping of resistance genes



Reaction to FOV



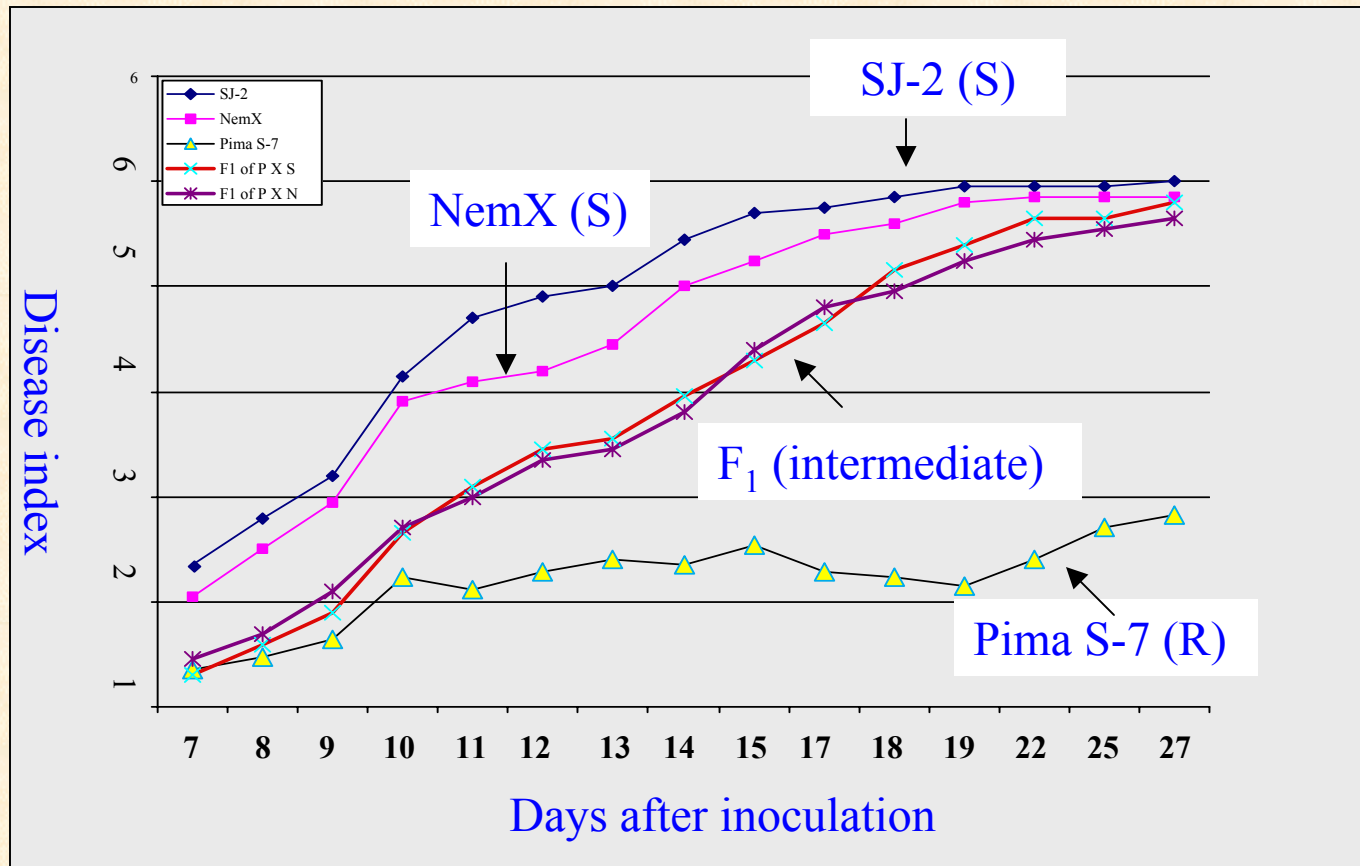
SJ-2

NemX

PimaS-7

Cut-root-dip method
4 weeks after inoculation

The development of Fusarium wilt Disease in Parents and F₁ plants



F₁ Pima S-7 x NemX
Pima S-7 x SJ-2

Cut-root-dip method