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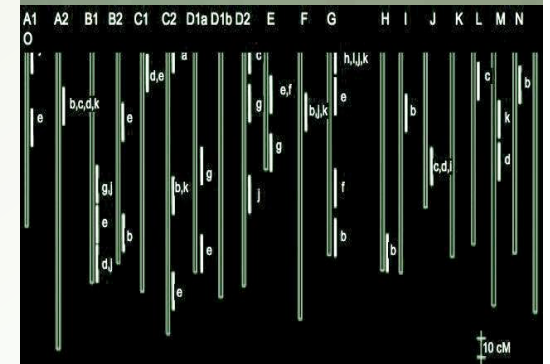
# QTL mapping for SCN resistance in *Glycine soja*: What have we learned?

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# 1. Introduction

## Resistant cultivars

- 1970s: release of resistant cultivars
- Resistance sources: Peking, PI88788
- 93% of 760 Cultivars derive from Peking / PI 88788  
Concibido *et al.* (2004)
- Narrow genetic base of SCN resistance in *G. max*
  - pathogen overcomes resistance due to “race shifts”



# 1. Introduction

## SCN resistance

» **Resistant cultivars**



» **Hypersensitive response**



» **Syncytium degeneration**



» **Extensin, catalase, cyclin,  
aldolase, GTP-binding protein.**

Peking 8d (Resistant)



Thinner Juveniles



Juveniles more developed

Kent 8d (Susceptible)



## 1. Introduction

# Genetics of SCN resistance

- Polygenic trait, many QTL
- Major genes: *rhg 1*, *rhg 2*, *rgh 3*, *Rhg 4*, *rhg5*

**Need to identify NEW resistance genes**



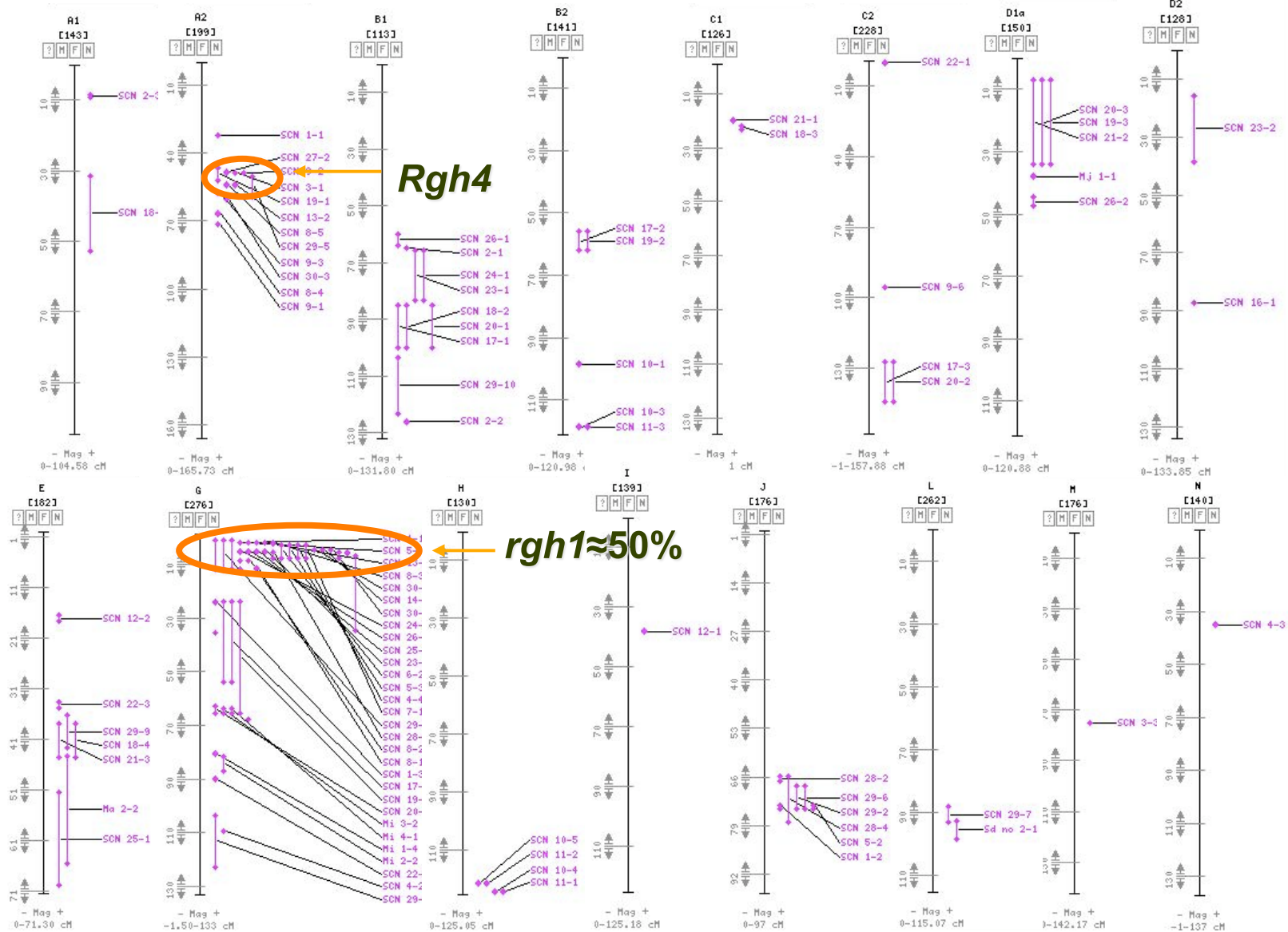
Potential source of NEW  
SCN resistance genes

Durable resistance against  
multiple HG Types

# 1. Introduction

## SCN-resistance QTL

SoyBase, 2009



## 1. Introduction

# SCN-resistance QTL (Winter *et al.* 2007)

- QTL effects
- QTL stability across genetic backgrounds

## 2. Objectives

- 1) To determine if the loci at the resistant QTL from the original *G. soja* parent, PI 464925B harbor alleles with similar effects in other *G. soja* germplasm.

**121 F<sub>6</sub>: *G. max* NK S08-80 X *G. soja* PI 458536**

- 2) To determine if the QTL for SCN resistance derived from *G. soja* PI 464925B, have the same effect when combined in a different *G. max* background.

**209 F<sub>4</sub>: *G. max* OAC Shire X *G. soja* PI 464925B**

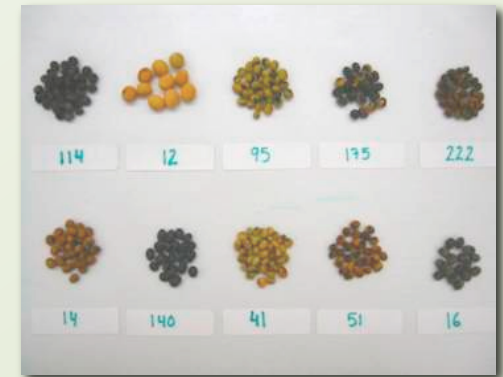
### 3. Materials and Methods

## Plant materials – 1<sup>st</sup> Challenge

- » 'Westag 97': Susceptible cultivar used in nematode culture
- » Chatham isolate HG Type 7 (Race 3) --> 50x
- » *G. max* x *G. soja* populations advanced by SSD:

**Pop2:** 121 F<sub>6</sub> RILs --> **'NK S08-80'** X PI 458536

**Pop4:** 209 F<sub>4</sub> RILs --> 'OAC Shire' X **PI 464925B**



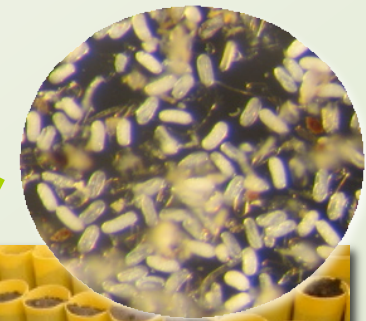
#### Controls:

- » 'Lee 74'--> Susceptible (S) to all SCN races (HG Types)
- » 'Ina' --> resistant (R) to races 1, 2, 3, 5 and MR to 14, S to 4
- » 'Jack'--> R to races 3 and 4
- » 'RCAT Ruthven' --> MR to race 3 (HG Type 7)



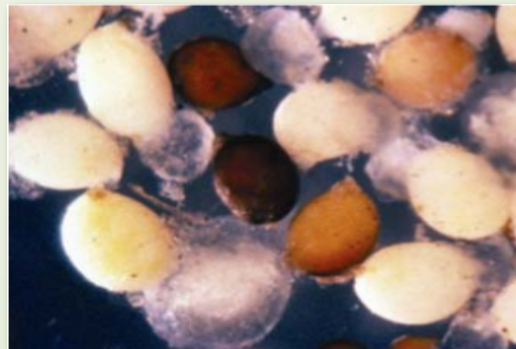
### 3. Materials and Methods

## Nematode Bioassay



### 3. Materials and Methods

## Nematode Bioassay



**Female Index (FI):**

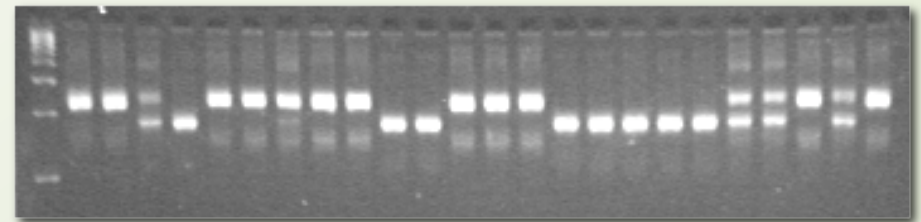
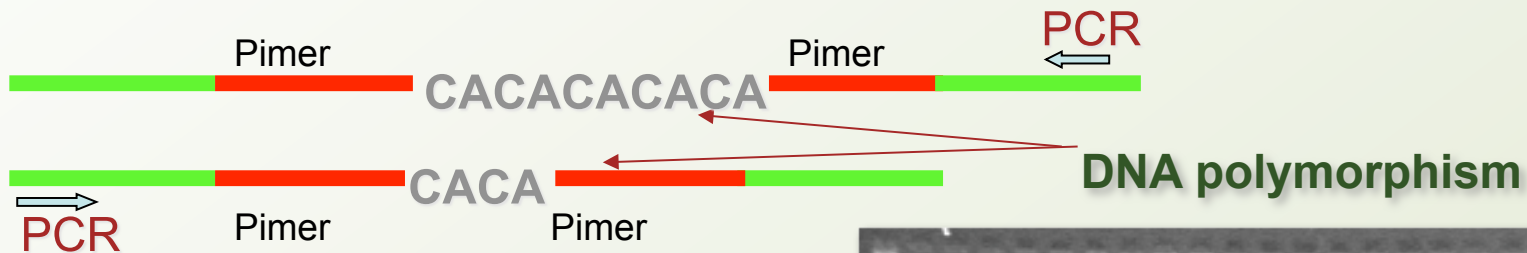
**FI= (# Cyst on RIL/**

**# Cyst on Lee 74)\*100**

### 3. Materials and Methods

## SSR Genotyping

Simple Sequence Repeat Markers



» 20 SSRs (Winter *et al.* 2007).



» 100 SSRs (Soybase, 2008) LGs O, K, I, G, C1, M, A2, E, F



49 polymorphic SSRs selected for mapping Pop2

50 polymorphic SSRs selected for mapping Pop4



## 4. Results

### Root weight analysis (Pop2) – 2<sup>nd</sup> challenge

- Entry F-value = 7.11,  $p < 0.0001$
- Root weight F-value = 40.42,  $p < 0.0001$

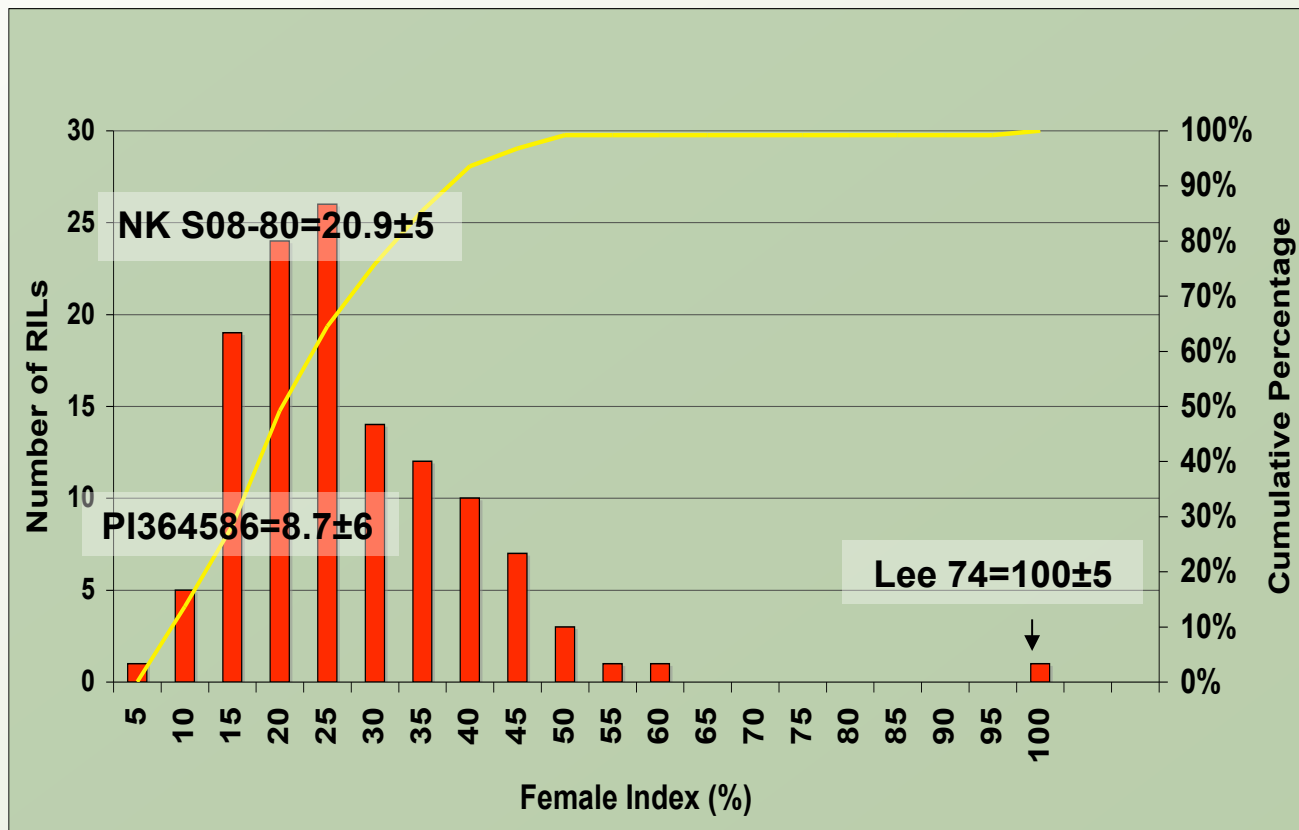
**Root wt significant covariate ( $r = 0.26$ ) → Adjust cyst count**



## 4. Results

# Segregation of Female Index (FI)

Pop2: 'NK S08-80' x PI 458536



FI calculated with adjusted Cyst count

HR= Highly Resistant

MS= Moderately Resistant

MS= Moderately Susceptible

S= Susceptible

**Broad Sense Heritability: 84.2%**

## 4. Results

# SSRs associated with SCN resistance

Pop2. Data based on single factor ANOVA

SSR	Linkage Group	P > F	R <sup>2</sup> (%)	Allelic Means		
				A	B	H
Satt345	O	0.0004	12.6	19.7 ±1.0	14.3 ±0.9	18.7 ±2.5
Satt466	O	0.0012	11	19.1 ±1.0	14.5 ±0.9	21.5 ±2.9
Satt173	O	0.0088	7.8	18.8 ±1.0	14.8 ±1.0	19.7 ±2.3
Satt578	C1	0.0123	7.2	18.8 ±0.9	14.8 ±1.0	18.7 ±2.4
Satt326	K	0.0162	6.8	14.9 ±1.0	18.9 ±0.9	16.4 ±2.7
Satt185	E	0.0236	6.2	16.1 ±1.0	17.0 ±0.9	23.8 ±2.6
Sat_167	K	0.0315	5.7	16.0 ±0.9	17.9 ±1.0	33.6 ±7.3
Satt349	K	0.0380	5.5	15.2 ±1.0	18.5 ±0.9	20.7 ±3.7

$\mu=0.05$

A= 'NK S08-80' allele

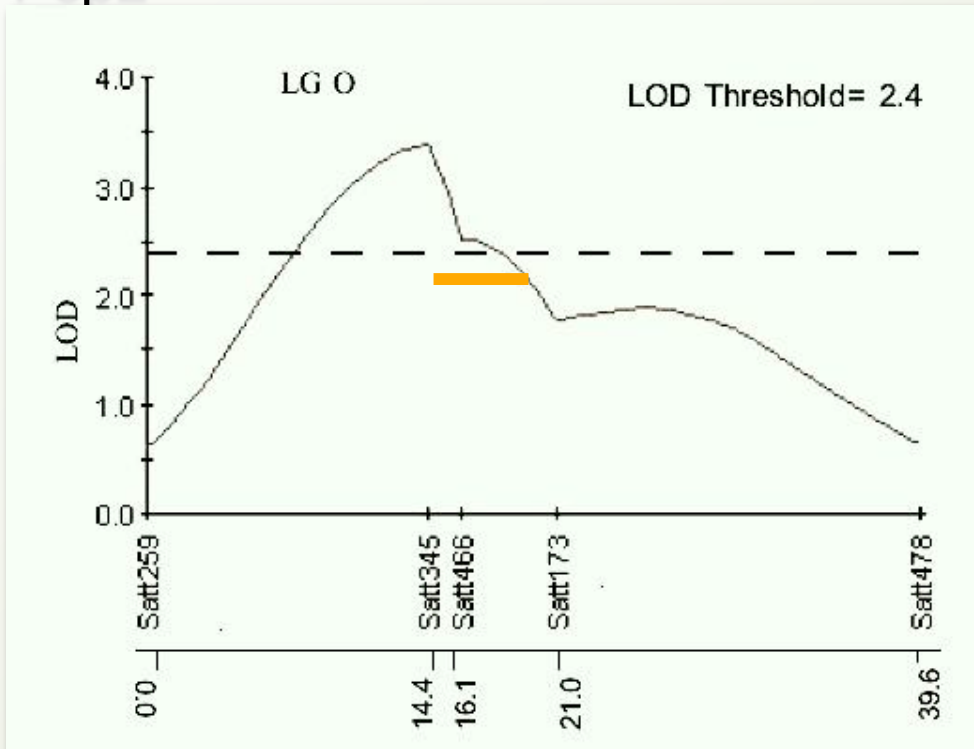
B= PI 458536 allele

H= Heterozygous allele

## 4. Results

# QTL associated with SCN resistance

Pop2



— LOD= 2.02,  $R^2= 5.1$   
(Winter *et al.* 2007)

### VALIDATION OF QTL

#### Objective 1:

alleles at the resistant QTL on LG O from PI 464925B have similar allelic effects in other *G. soja* germplasm

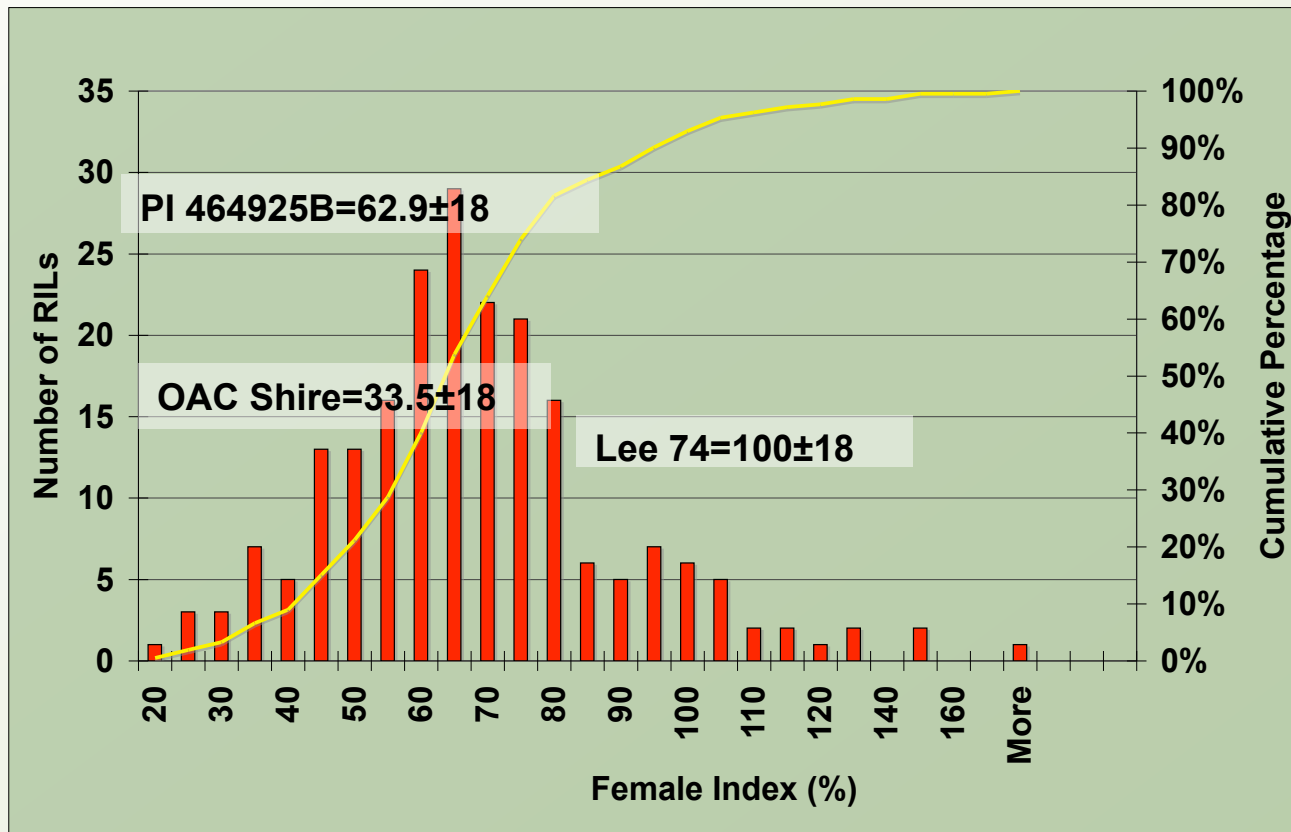
LG	Interval	Length (cM)	Position (cM) <sup>a</sup>	$R^2$ (%)	LOD
O	Satt345-Satt466	4.9	14.43	12.20	3.39

<sup>a</sup> expressed as the distance from the first marker

## 4. Results

# Segregation of Female Index (FI)

Pop4: 'OAC Shire' x PI 464925B



**FI** calculated with adjusted Cyst count

**HR**= Highly Resistant

**MS**= Moderately Resistant

**MS**= Moderately Susceptible

**S**= Susceptible

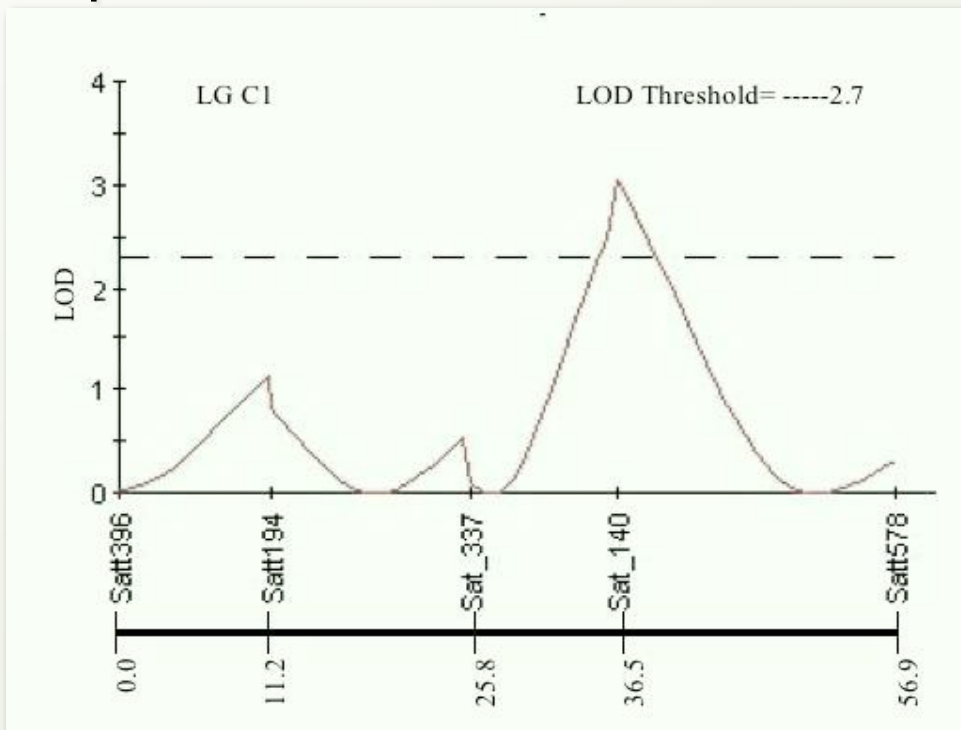
**Broad Sense Heritability: 41.4 %**



## 4. Results

# QTL associated with SCN resistance

### Pop4 NOVEL QTL on LG C1



- Single factor ANOVA confirmed some individual marker/QTL but interval mapping did not

LG	Interval	Length (cM)	Position (cM) <sup>a</sup>	R <sup>2</sup> (%)	LOD
C1	Sat_140-Satt578	20.3	36.50	6.90	3.04

<sup>a</sup> expressed as the distance from the first marker

## 4. Results

# Epistatic interactions – 3<sup>rd</sup> challenge

Locus 1		Locus 2		F-Value	P>F	R <sup>2</sup> (%)	Two-locus Genotypic Means				Additive effect	
LG	SSR	LG	SSR				AA	AB	BA	BB	L1/A	L1/B
<b>'NK 08-80' x PI 458536</b>												
C1	Satt139	O	Satt466	14.56	0.000235	<b>11</b>	22.7	13.6	15.3	16	3.38	-1.21
<b>'OAC Shire' x PI 464925B</b>												
C1	Sat_337	E	Satt185	15.6	0.00012	<b>9</b>	22.1	31.4	26.2	24.4	-2.13	3.54
C1	Satt194	E	Satt369	17.1	5.88E-05	<b>10</b>	23.5	31.4	26.9	23.3	-1.72	4.04
O	Satt445	G	Satt533	15.7	0.00011	<b>9</b>	22.5	27.7	30.1	24.5	-3.81	1.6

**A** allele from *Glycine max*

**B** allele from *Glycine soja*

**L1/A** additive effect of locus 1 in combination with the *G. max* allele at locus 2, calculated as (AA-BA)/2

**L1/B** additive effect of locus 1 in combination with the *G. soja* allele at locus 2, calculated as (AB-BB)/2

## 5. Conclusions

1. Segregation for FI showed continuous variation in both populations - quantitative SCN resistance.
2. Root weight - a significant covariate and should be considered when analyzing SCN data from *G. soja*.
3. High polymorphism confirmed genetic variability between *G. max* and *G. soja*
4. Confirmation of SCN-resistant QTL on LG O derived from different *G. soja* backgrounds

## 5. Conclusions

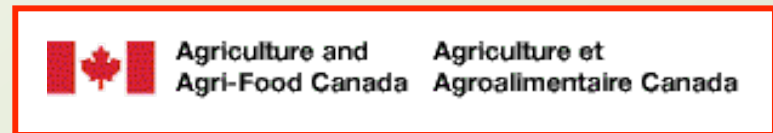
5. Previously reported QTL intervals were not confirmed in the population derived from 'OAC Shire' x PI 464925B indicating that the effect of resistance alleles from PI 464925B is dependent of the background of the *G. max* parent.
6. New QTL on C1 identified in cross OAC Shire x PI 464925B
7. Epistatic interactions between loci play a significant role in the expression of SCN resistance
8. **Opportunity:** a vast array of untapped and often unknown trait variation exists in *G. soja*, particularly for disease resistance including SCN



## 7. Acknowledgements



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**Thank you**

