Part 1:Progress on Rust Resistance Breeding of Confection Sunflowers and Part 2: Sunflower SNP Genetic Mapping

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Part 1: Progress on Rust Resistance Breeding of Confection Sunflowers

Objectives

1. Transfer rust resistance genes from oil sunflower to confection-type

    - Limited resistance in commercial confection hybrids
    - Confections are generally more susceptible to diseases

2. Molecularly mark the resistance genes

Rust resistance lines used in this project

Lines	Usage	Rust resistance		Origin of rust resistance
		Race 336	Race 777	
MC 29	**R-gene donors**	**R**	**S**	**Wild *H. annuus* in Texas**
HA-R2		**R**	**S**	**Wild *H. argophyllus***
HA-R3		**R**	**MR**	**Wild *H. annuus, H. argophyllus and H. petiolaris***
HA-R6	R-gene mapping	R	R	A breeding line from France
HA-R8		R	R	A landrace in Arizona, USA
RHA 397		R	R	South Africa
RHA 464		R	R	Wild *H. annuus* collected in California

Progress on the introgression of rust resistance genes to confectionary sunflower

Recurrent parent (RP) × R-gene donor

Recurrent parents(RP)

- CONFSCL B1
- CONFSCL R5
- Highly susceptible to race 336 and race 777

R-gene donors

MC 29, HA-R2, and HA-R3

CONFSCL B1 as the recurrent parent of MC 29 and HA-R2
CONFSCL R5 as the recurrent parent of HA-R3

RP × F_1

BC_4F_1 — **97% RP genome** — Summer 2011

BC_4F_2 — **MAS of homozygous resistant plants** — **In the end of seed ripening, Jan, 2012**

BC_4F_3 — **Obtain homozygous resistant F_3 families** — **Spring 2012**

BC_4F_4 — **Planting F_3 seeds in the field** — **Field performance test, Summer 2012**

Release new rust resistant confection lines — **2013**

Molecular mapping of new rust resistance genes

Evaluation of rust resistance in F_2 and $F_{2:3}$ families

F_2 Populations	Harvest of F_2 seeds	No. of F_2 plants	Harvest of F_3 seeds	Rust test for $F_{2:3}$ families
HA 89 × RHA 464	Spring, 2010	141	Fall, 2010	141 × 20
HA 89 × HA-R6	Fall, 2010	142	Spring/Summer2011	70 × 20
HA 89 × RHA 397	Fall, 2010	142	Spring/Summer2011	70 × 20
HA 89 × HA-R8	Fall, 2010	142	Spring/Summer2011	Will start in Feb

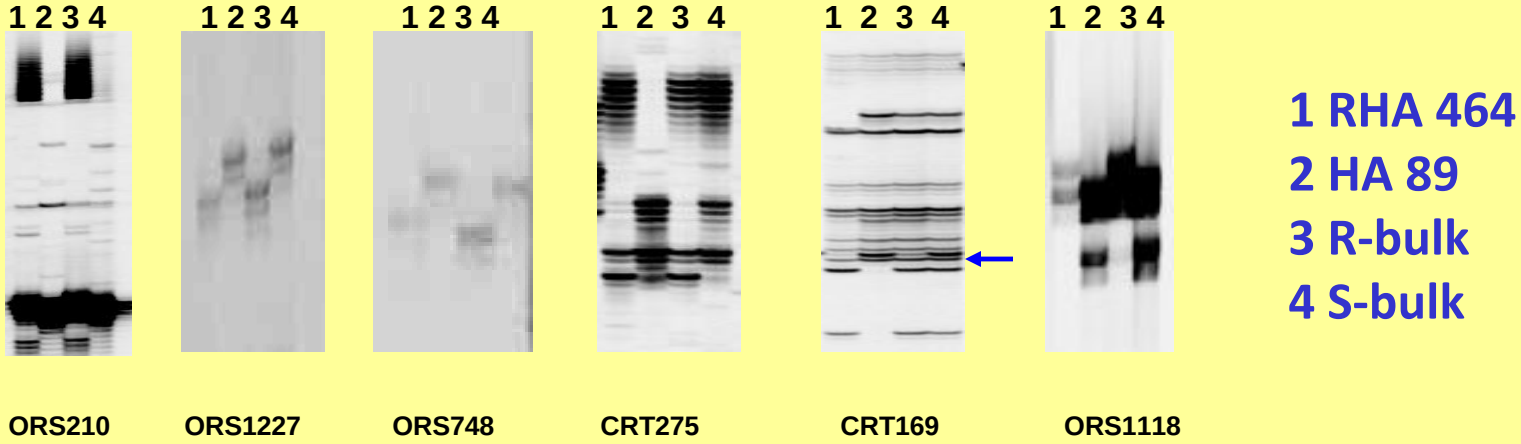
20 seedlings was rust inoculated in each F_3 faimily

Mapping of rust resistance gene in RHA 464

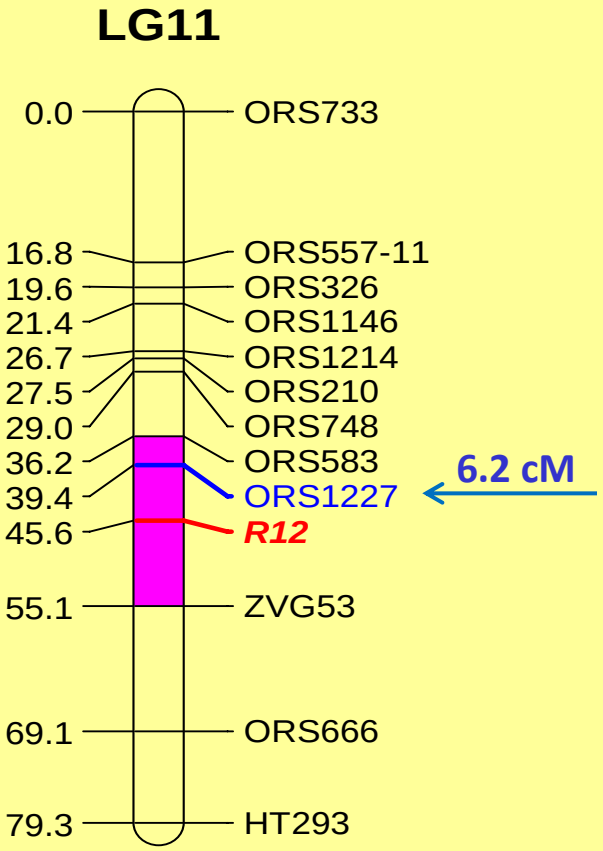
Polymorphism screening
- •870 mapped SSR markers
- •398 showed polymorphism

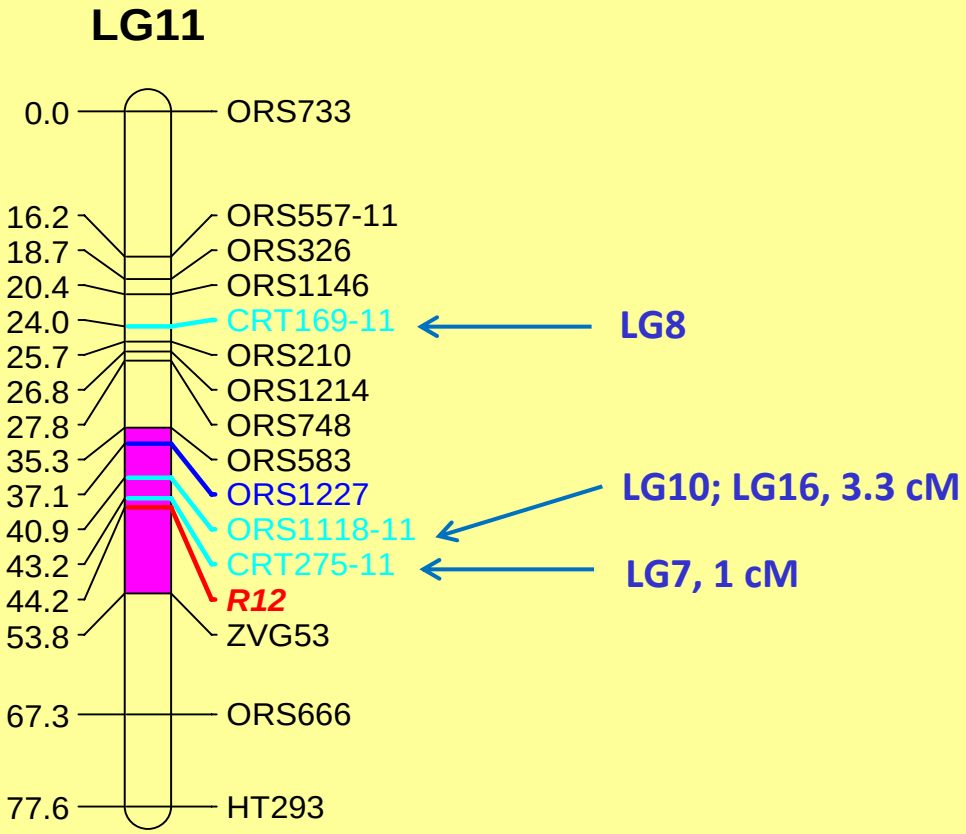
Bulked segregant analysis
- •R-bulk: 10 homozygous resistant F_2 plants
- •S-bulk: 10 homozygous susceptible F_2 plants

- •Designated as R_{12}
- •20 markers previously mapped in LG11 showed polymorphism
- •7 polymorphic between R and S-bulk
- •Genotyped in 141 F_2 individuals of HA 89 and RHA 464



Mapping R_{12} using SSR markers

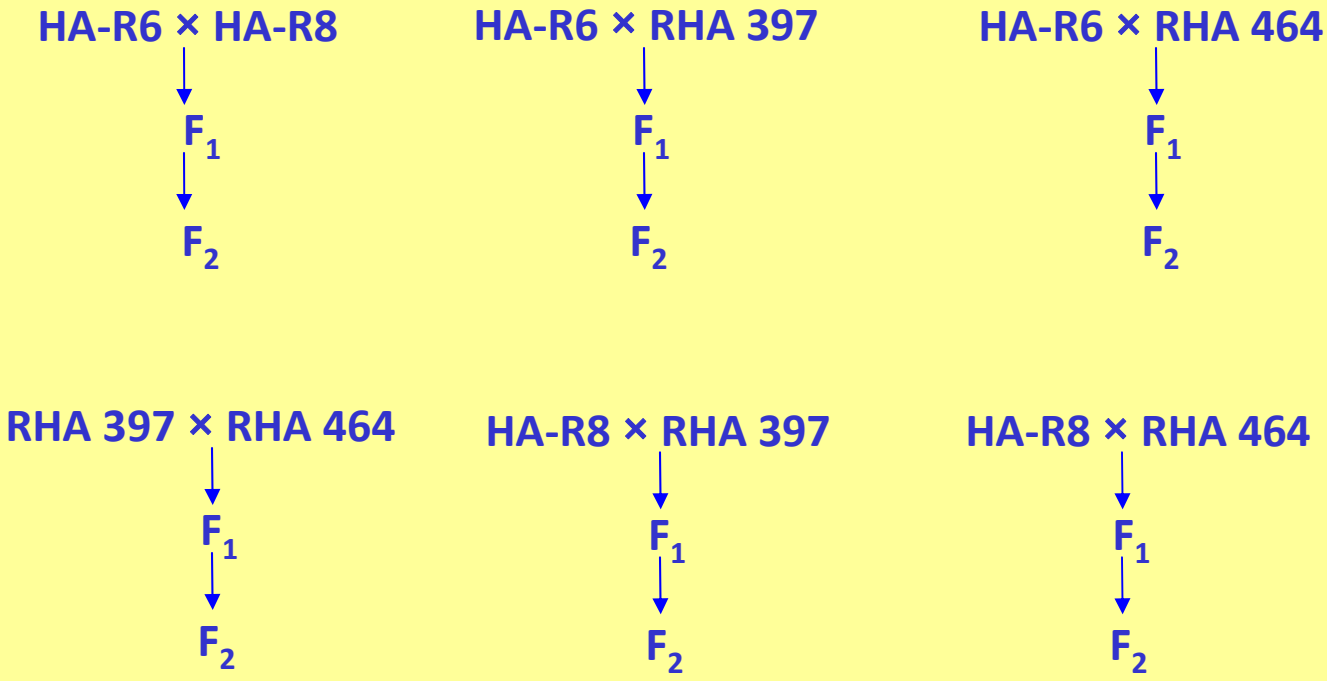




- After BSA, genotyping only focus on those markers mapped in LG11 in the published maps
- 12 SSR markers associated with R_{12} were mapped in this population

- In the SNP mapping project, all polymorphic SSR markers were genotyped, then CRT169-11, ORS1118-11 and CRT275-11 previously mapped in other LGs were mapped in LG11
- 15 SSR markers associated with R_{12} were mapped

Allelic analysis of rust resistance genes in HA-R6, HA-R8, RHA 397 and RHA 464



200 plants / F_2 population evaluated for rust resistance

Part 2: Sunflower SNP Genetic Mapping

Mapping population

- F_2 from HA 89 and RHA 464
- HA 89 is susceptible to rust and downy mildew.
- RHA 464 is resistant to rust and downy mildew.
- 141 individuals

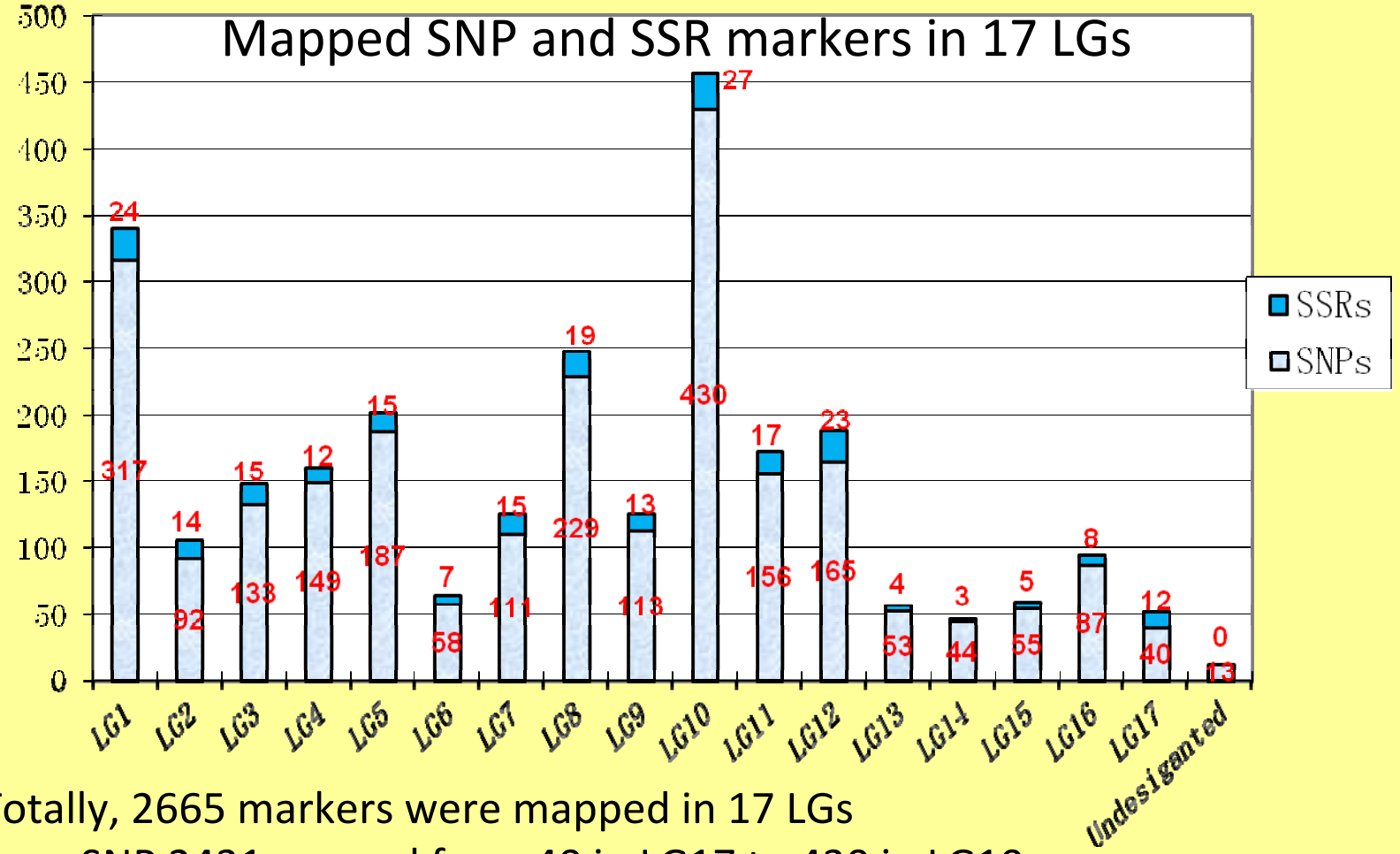
Available markers

- **SNP**
  2797→ 2446
- **SSR, as bridge/anchor markers**
  291 → 238
- **Genes: *R_{12}* and *PI_{ARG}***

Mapping construction

- **JoinMap 4.1**
- **Mapping algorithm: Regression Mapping**
- **Mapping function: Kosambi**
- **Mapping parameters**
  Lod threshold: 1.00
  Rec threshold: 0.4000
  Jump threshold: 5.000
  Ripple value: 1

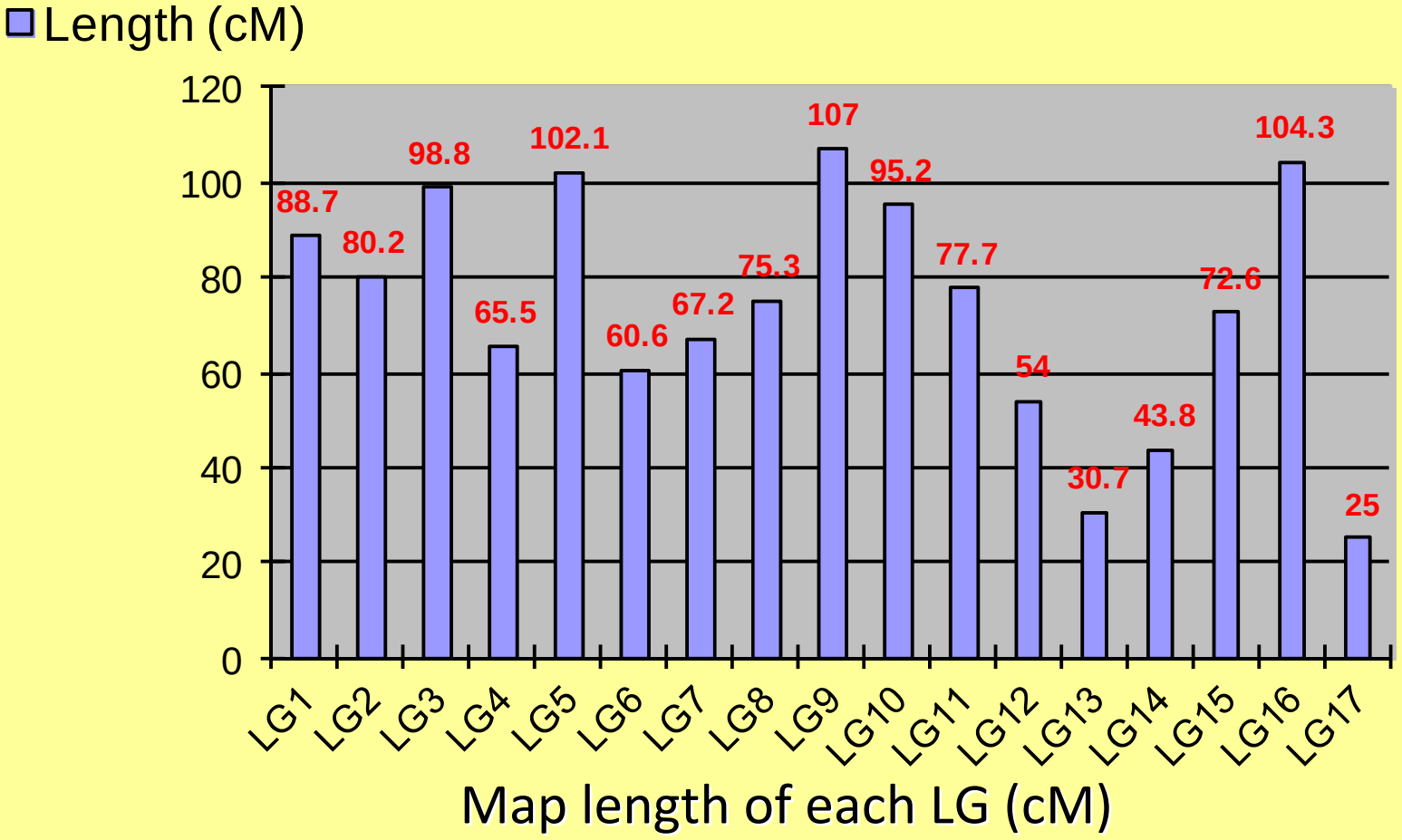
SNP mapping results of HA89× RHA464



Totally, 2665 markers were mapped in 17 LGs

- SNP 2431, ranged from 40 in LG17 to 430 in LG10
- SSR 233, ranged from 3 in LG13 to 27 in LG10
- R_{12}
- LG1, LG8 and LG10 with a larger amount of markers

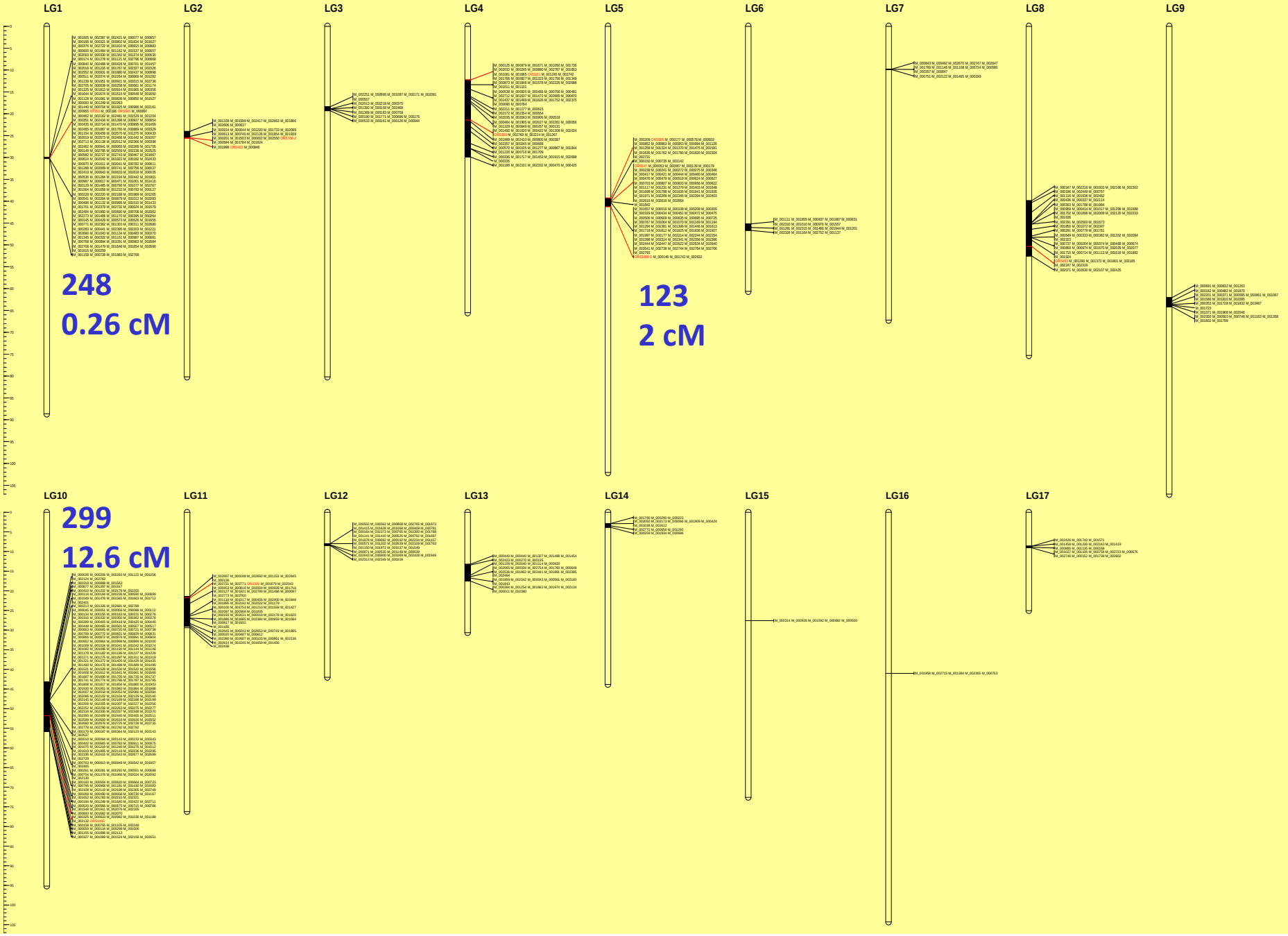
SNP mapping results of HA89× RHA464



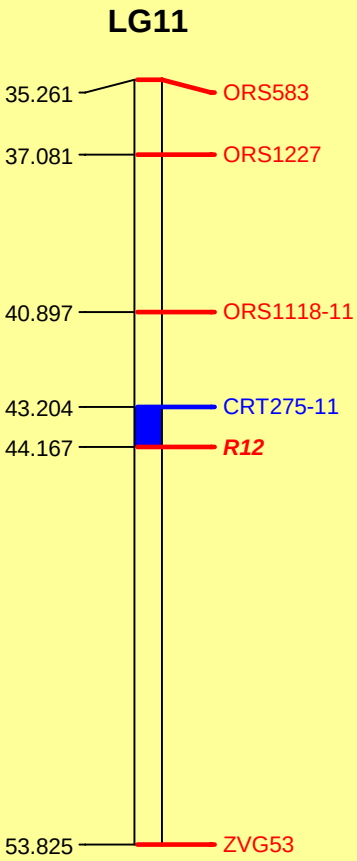
Totally, this map covered 1251.3 cM

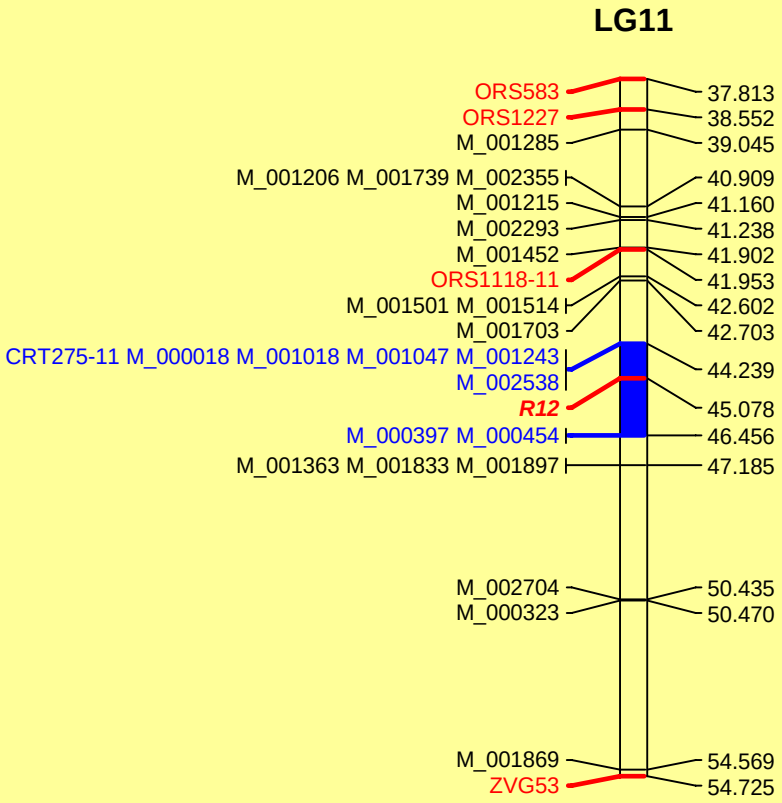
- Ranged from 25 cM in LG17 to 107 cM in LG9
- LG13, LG14 and LG17 with a shorter map coverage

Co-segregated SNP markers clustered and distributed in all 17 LGs



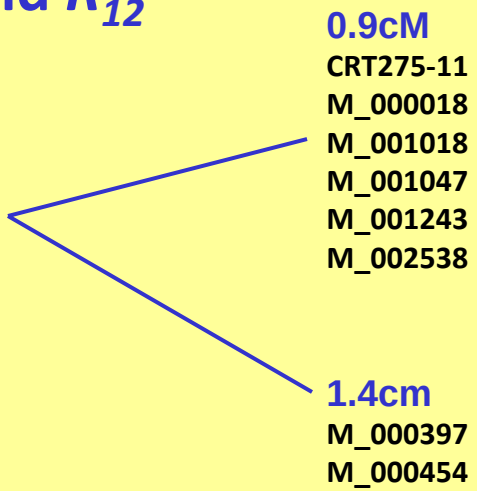
SNP markers linked to rust resistance gene R_{12}





Summary of SNP mapping results

- 2665 markers located in ~1250 loci
- composed of 2431 SNP, 233 SSR and R_{12}
- 1251.3 cM,
- ~1 cM per locus
- R_{12} was flanked by two groups of co-segregated markers



Special for this population

- Lower map coverage of LG13, LG14, and LG17
- Co-segregated SNP markers, totally 1415 SNPs (58.3%), clustered and distributed in all LGs

Future work

- MAS of homozygous BC_4F_2 individuals, obtain rust resistant homozygous BC_4F_3 families before growing season this year. The confection breeding lines resistant to the predominant race will be released in 2013
- Continue identifying molecular markers linked to new rust resistance genes in HA-R6, HA-R8 and RHA 397
- Continue investigating the allelic relationships among new rust resistance genes in this project.
- Finalize the SNP mapping in F_2 population of HA 89 and RHA 464
- Map integration of all mapped rust genes in this project

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