Molecular mapping of the rust resistance genes in sunflower: results and prospects

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Sunflower production in North America has recently been threatened by the evolution of new virulent pathotypes of sunflower rust

- ♦ Thirty-nine different rust races were identified in 2008
- ♦ Rust races 334 and 336 were dominant over three years
- ♦ Race 777 is the most virulent and is able to infect all nine differentials
- ♦ Presently, race 777 remains at a low frequency in the rust populations, but can potentially cause serious epidemics if it becomes prevalent
- ♦ The majority of commercial hybrids are susceptible to the new predominant and virulent races

Rust resistance sources from USDA Sunflower unit

		Reaction to		
Sunflower line	**Type**	**race 336**	**race 777**	**Putative rust gene (s)**
Inbred lines				
CM 29*	**OB**	**R**	**S**	R_2
HA-R2	**OB**	**R**	**S**	R_5
HA-R3	**OB**	**R**	**MR**	R_4
HA-R6	**CB**	**R**	**R**	
HA-R8	**OR**	**R**	**R**	
RHA 397	**OR**	**R**	**R**	
RHA 464	**OR**	**R**	**R**	
Introgression lines				
PH3	**OB**	**R**	**R**	
PH4	**OB**	**R**	**R**	
PH5	**OB**	**R**	**R**	
PH6	**OB**	**R**	**S**	
TX16R	**OB**	**R**	**R**	
Rf ANN-1742	**OR**	**R**	**R**	

OB: oil-B line; OR: oil-R line; CB: confection-B line;
CR: confection-R line. * an old Canadian line

Qi et al. 2011 Phytopathol

Limited durability of single *R*-genes

- Race-specific *R*-genes can be overcome by new pathotypes
- There is an urgent need for strategies to develop inbred lines with durable resistance to the disease
- The concept of incorporating multiple *R*-genes into a single cultivar to achieve greater durability is referred to as '*gene pyramiding*'
- The selection of genotypes with gene combinations can be difficult using conventional methods
- Mapping rust resistance genes and developing robust molecular markers will facilitate this breeding approach and add precision to selection

Procedure for mapping of rust *R*-genes

I. Mapping population development

Parent 1 (Susc) × Parent 2 (Resist)

↓

F_1

↓

F_2 individuals

↓

F_3 families

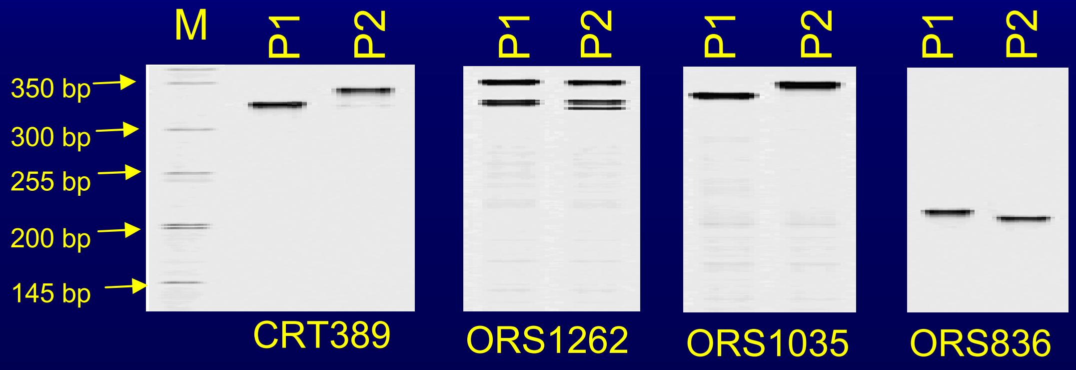
II. Rust screening of F_2 and F_3 populations

I. F_2 population: 150-200 plants

II. F_2-derived F_3 population: 150-200 families
20 plants/per family, a total of 3,000-4,000 plants

III. Marker screening (500-800 DNA markers)

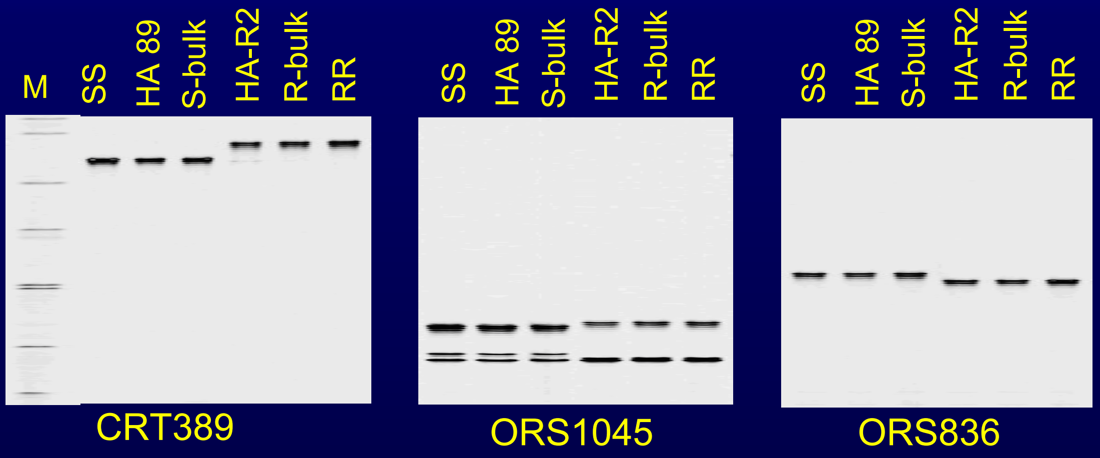
a. Identification of polymorphic markers for the two parental lines



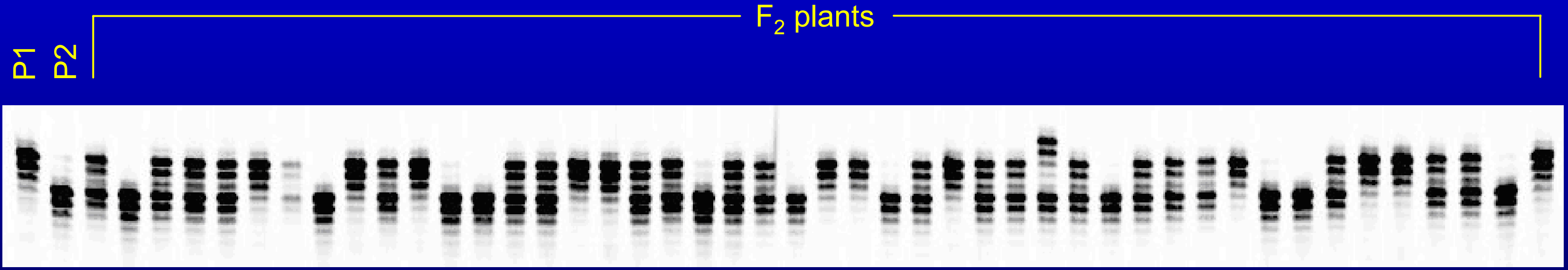
b. Bulked segregant analysis to determine genomic region associated with the rust resistance gene

S-bulk: DNA from ten homozygous susceptible F_2 plants

R-bulk: DNA from ten homozygous resistant F_2 plants



c. Scoring all individuals of a mapping population with polymorphic markers associated with rust resistance to determine their genotypes



IV. Genetic linkage analysis

Combine rust phenotypic and marker data to determine marker order and map distance

Progress of molecular mapping of the rust *R*-genes in sunflower

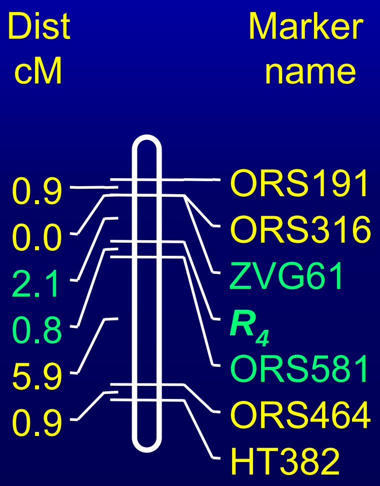
- Eight rust resistance genes, R_1-R_5, R_{10}, P_{u6}, and R_{adv}, were previously identified in sunflower
- R_1 gene in MC 69 and R_{adv} gene in P2 and RHA 340 lines were mapped to linkage groups (LGs) 8 and 13, respectively, and are no longer effective against the predominant and virulent rust races in U.S.
- R_2 gene in MC 29 was mapped to LG9 and is resistant to race 336

Lawson et al. 1998, Mol Breeding
Lawson et al. 2010, Mol Breeding
Yu et al. 2003, Crop Science

We have recently mapped four rust resistance genes in the different linkage groups of sunflower

R_4 **in HA-R3 resistant to race 336**

LG13



Dist cM

Marker name

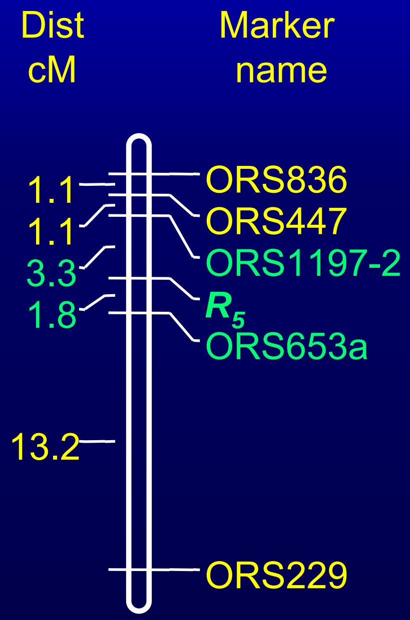
0.9
0.0
2.1
0.8
5.9
0.9

ORS191
ORS316
ZVG61
R_4
ORS581
ORS464
HT382

Qi et al. 2011
TAG 123:351-358

R_5 **in HA-R2 resistant to race 336**

LG2



Dist cM

Marker name

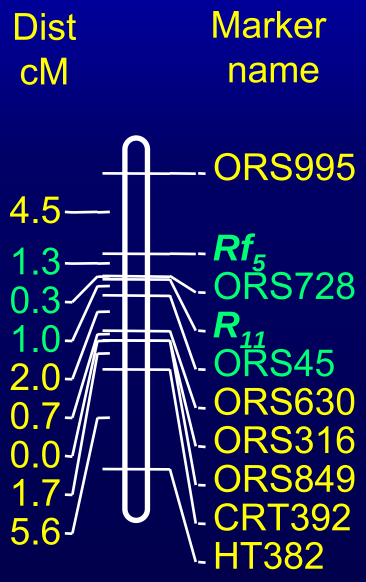
1.1
1.1
3.3
1.8
13.2

ORS836
ORS447
ORS1197-2
R_5
ORS653a
ORS229

Qi et al. 2011
Mol. Breeding DOI
10.1007

R_{11} in Rf ANN-1742 resistant to races 336 and 777

LG13



Dist cM

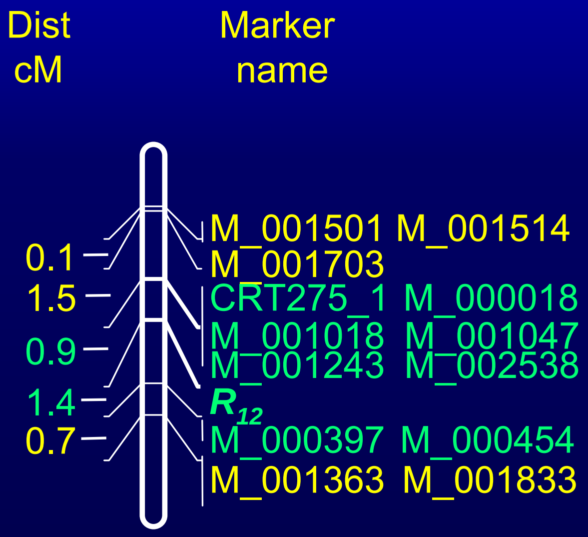
Marker name

4.5
1.3
0.3
1.0
2.0
0.7
0.0
1.7
5.6

ORS995
Rf_5
ORS728
R_{11}
ORS45
ORS630
ORS316
ORS849
CRT392
HT382

R_{12} in RHA 464 resistant to races 336 and 777

LG11



Dist cM

Marker name

0.1
1.5
0.9
1.4
0.7

M_001501 M_001514
M_001703
CRT275_1 M_000018
M_001018 M_001047
M_001243 M_002538
R_{12}
M_000397 M_000454
M_001363 M_001833

Future work

I. Integrate phenotypic and SSR data of the genes R_4, R_5, and R_{11} with SNP data to identify SNP markers linked to the *R*-genes

II. Continue mapping of the rust resistance genes in HA-R6, HA-R8, and RHA397

- ♦ HA-R6 is the only confection sunflower resistant to races 336 and 777, and the *R*-gene originated from a breeding line from France
- ♦ Rust resistance in HA-R8 is derived from a Native American (Havasupai) landrace from Arizona
- ♦ Rust resistance in RHA 397 originates from germplasm obtained from South Africa

III. Provide long-term durability of resistance to rust

a. Rust *R*-gene pyramiding in oil sunflower

HA-R2 × RHA464
(R_5+R_{12})

HA-R3 × RHA464
(R_4+R_{12})

HA-R3 × HA-R2
(R_4+R_5)

b. Rust *R*-gene pyramiding in confection sunflower

HA-R6
(new *R*-gene)

×

New confection line 1 (R_2)
New confection line 2 (R_4)
New confection line 3 (R_5)

A sample of gene pyramiding with marker-assisted selection

HA-R3 × RHA 464

$(R_4R_4r_{12}r_{12})$ $(r_4r_4R_{12}R_{12})$

↓

F_1

$(R_4r_4R_{12}r_{12})$

↓

F_2

Segregating

↓ Screen a large population with DNA markers

Select homozygous F_3

$(R_4R_4R_{12}R_{12})$

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