

2013 Breeding Progress for Rust Resistance in Confection Sunflower

Guojia Ma^{1,2}, Yunming Long^{1,3},
Sam Markell², Tom Gulya¹ and Lili Qi¹

¹USDA, ARS, NCSL, Fargo, ND

²NDSU – Plant Pathology, Fargo, ND

³NDSU – Plant Sciences, Fargo, ND





Objectives

- Re-location of rust resistance gene R_2
- Pyramiding of rust resistance genes in confection sunflower



Background knowledge

- Sunflower rust, incited by *Puccinia helianthi* Schwein
- Confection sunflower is more vulnerable to stresses than oilseed sunflower
- HA-R6 (R_{13a}) is the only highly resistant confection sunflower
- From our previous project, three rust resistance genes, R_2 , R_4 , and R_5 , have been introduced from oil type into confection sunflower
- Pyramiding multiple resistance genes is an effective way to overcome resistance ineffectiveness
- DNA markers closely linked to R-gene would assist selection of individuals carrying multi-R genes

Re-location of rust resistance gene R_2

Background

- R_2 gene was previously mapped to LG9 and co-segregated with SSR marker ORS333 (Lawson *et al.*, 2011)
- ORS333 was used to select homozygous BC_4F_3 families derived from the cross of CONFSCLB1*5/CM29 (carrying R_2 gene) and showed that it is not associated with rust resistance

R_2 gene was re-localized to LG14

- F_2 mapping population from HA 89 × CM29 (USDA-origin carrying the gene R_2)
- Rust phenotyping: A total of 117 F_2 -derived F_3 families (20 plants per family) were screened with rust race 336
- Genetic mapping
 - R_2 was localized to LG14 of sunflower with BSA
 - Genotyping of the 118 F_2 individuals with 13 polymorphic SSR markers from LG14 discovered one SSR (HT567) distal of R_2 at 4.1 cM

Further saturation of R_2 region with SNP markers

NSA SNP map

23 SNPs, 10.2 cM
covering R_2

Public SNP map

12 SNPs, 4.9 cM
covering R_2

- ❖ A total of 35 SNPs were screened between two parents
- ❖ Ten polymorphic SNP markers were genotyped in F_2 population, and integrated with SSR map
- ❖ Two SNPs flanking R_2 at 2.7 and 1.8 cM, respectively

Scheme for pyramiding of rust R-genes

Confection R-line ($R_2R_2r_{13a}r_{13a}$)
 Confection R-line ($R_4R_4r_{13a}r_{13a}$)
 Confection R-line ($R_5R_5r_{13a}r_{13a}$)

× Confection HA-R6 ($r_xr_xR_{13a}R_{13a}$)

↓
F₁S

$R_2r_2+R_{13a}r_{13a}$ $R_4r_4+R_{13a}r_{13a}$ $R_5r_5+R_{13a}r_{13a}$

Gamete	R_2R_{13a}	R_2r_{13a}	r_2R_{13a}	r_2r_{13a}
R_2R_{13a}	$R_2R_2R_{13a}R_{13a}$	$R_2R_2R_{13a}r_{13a}$	$R_2r_2R_{13a}R_{13a}$	$R_2r_2R_{13a}r_{13a}$
R_2r_{13a}	$R_2R_2R_{13a}r_{13a}$	$R_2R_2r_{13a}r_{13a}$	$R_2r_2R_{13a}r_{13a}$	$R_2r_2r_{13a}r_{13a}$
r_2R_{13a}	$R_2r_2R_{13a}R_{13a}$	$R_2r_2R_{13a}r_{13a}$	$r_2r_2R_{13a}R_{13a}$	$r_2r_2R_{13a}r_{13a}$
r_2r_{13a}	$R_2r_2R_{13a}r_{13a}$	$R_2r_2r_{13a}r_{13a}$	$r_2r_2R_{13a}r_{13a}$	$r_2r_2r_{13a}r_{13a}$



↓
F₂S

↓ Marker assisted selection

↓
F₃S homozygous double resistant lines

$R_2R_2+R_{13a}R_{13a}$ $R_4R_4+R_{13a}R_{13a}$ $R_5R_5+R_{13a}R_{13a}$

↓ Field performance test

↓
F₄S Germplasm release

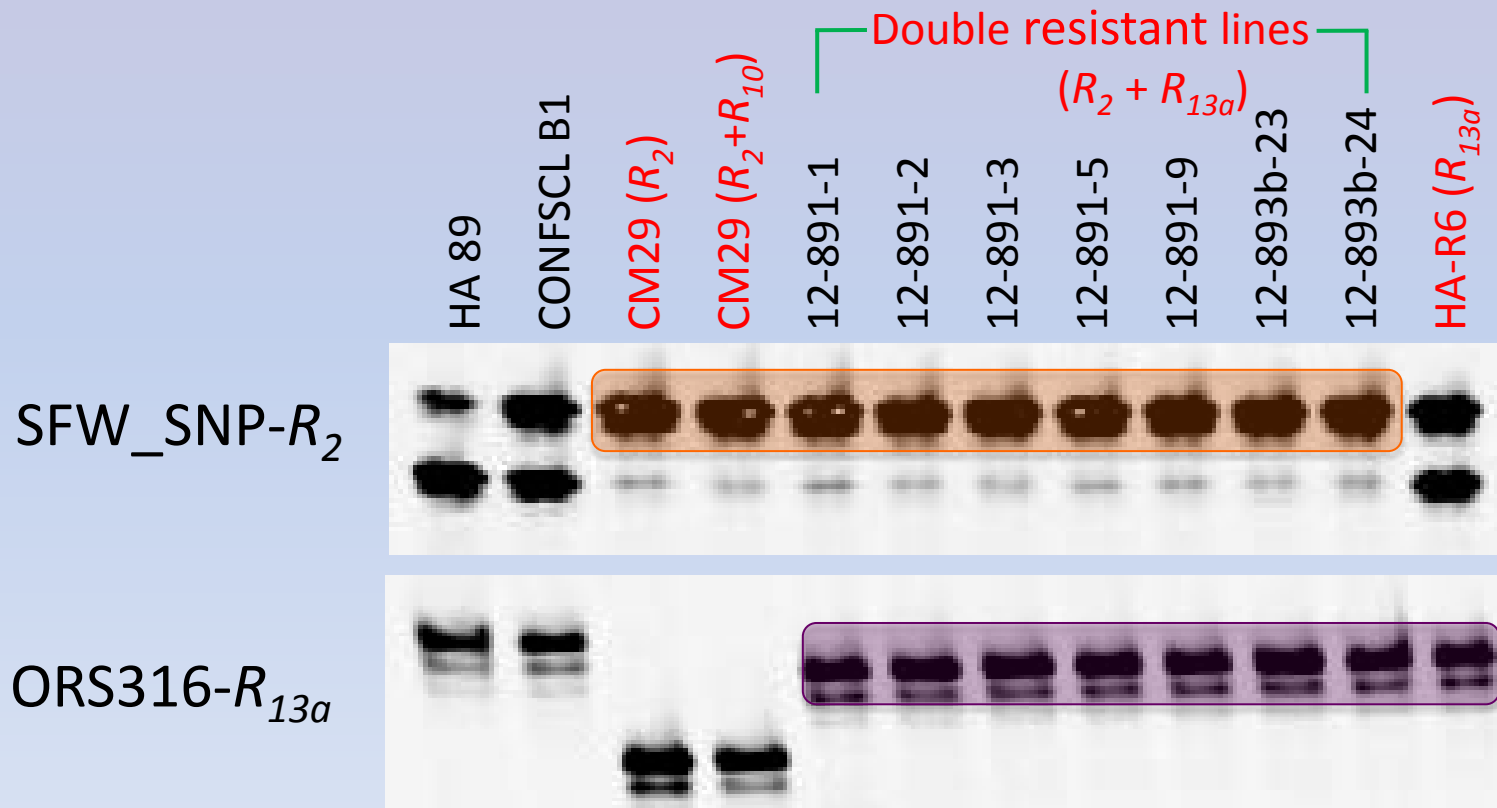
Table 1 The rust resistance genes and their linked DNA markers

R genes	Linkage group	Linked markers		References
		SSR	SNP*	
<i>R₂</i>	14	HT567	2 NSA-SNPs 2 SFW-SNPs	Current study
<i>R₅</i>	2	ORS1197 ORS653	2 SFW-SNPs	Qi <i>et al.</i> 2012, Long <i>et al.</i> unpublished data
<i>R₄</i>	13	ORS316, ZVG61, ORS581, HT382		Qi <i>et al.</i> 2011
<i>R_{13a}</i>	13	ORS316, ZVG61, ORS581, HT382		Gong & Qi <i>et al.</i> 2013

*NSA-SNP from NSA SNP Consortium; SFW-SNP from Bowers et al. 2012

Selection of the double R-line of R_2 and R_{13a}

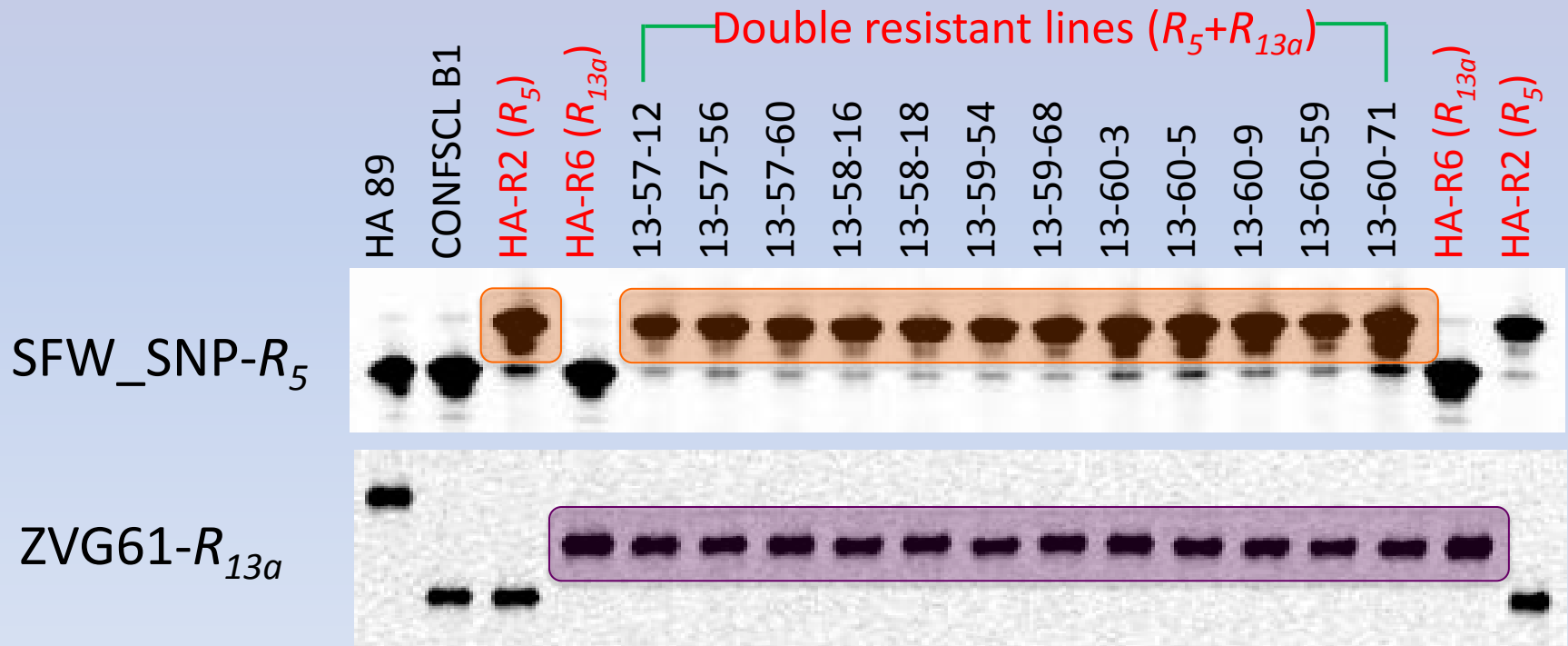
- A total of 524 F_2 plants from the cross between an R_2 line and an R_{13a} line were screened by DNA markers linked to R_2 and R_{13a}
- Eleven F_2 plants with the combination of R_2 and R_{13a} were obtained at the homozygous condition



HA 89: common parent in mapping of R_2 and R_{13a} ; CM29: R_2 donor; CONFSCLB1: confection recurrent parent to produce confection R_2 line; double resistant lines: selection from the cross of confection R_2 /HA-R6 (R_{13a})

Selection of the double R-line of R_5 and R_{13a}

- A total of 368 F_2 plants from the cross between an R_5 line and an R_{13a} line were screened by DNA markers linked to R_5 and R_{13a}
- Thirteen F_2 plants with the combination of R_5 and R_{13a} were obtained at the homozygous condition

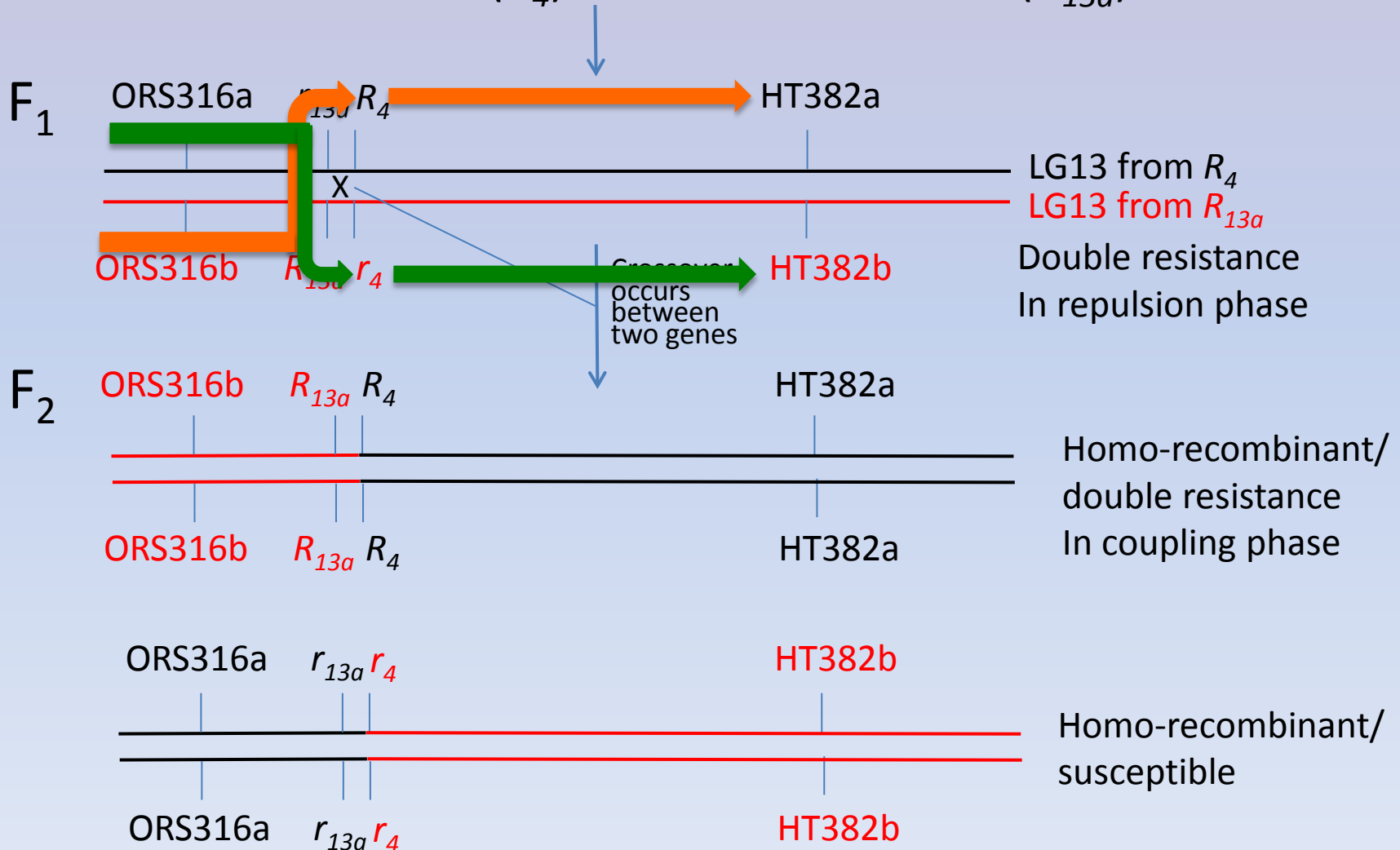


HA 89: common parent in mapping of R_5 and R_{13a} ; HA-R2: R_5 donor;
CONFSCLB1: confection recurrent parent to produce confection R_5 line;
double resistant lines: selection from the cross of confection R5/HA-R6

Progress in identifying double R-line of R_4+R_{13a}

Both R_4 and R_{13a} were mapped to LG13 and very tightly linked

Confection R-line (R_4) × Confection HA-R6 (R_{13a})



- A total of 1,147 F_2 plants from the cross between R_4 and R_{13a} were tested for rust resistance, and only one plant was found to be susceptible which was possibly derived from recombination
- Out of 1,116 F_2 plants screened with flanking markers, one was found to be expected recombinant with possible R_4 and R_{13a} in coupling phase
- Closer flanking SNP markers are needed for further confirmation

Field performance test for homozygous double resistant F_3 plants

- Eight homozygous R_5+R_{13a} resistant F_3 families and seven putative homozygous R_2+R_{13a} resistant F_3 families were planted and evaluated for their agronomic performance (height and flowering date) in Fargo field in summer 2013
- About 220 heads were bagged and harvested for germplasm release in the near future

Acknowledgments

- Angelia Hogness
- Cullen Walser
- Emily Wentzel

Financial support

Specialty Crop Block Grant, USDA-AMS
through ND Department of Agriculture

Thank you

Questions?