2016 Progress for Development of Super Confection Sunflower Effectively Resistant to Downy Mildew and Rust

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Outline

(Jan, 2014 — April, 2017)

- **Background knowledge**
- **Development of DM- and rust-*R* confection sunflower germplasm**
- **Mapping of DM *R*-gene in RHA 468**
- **Mapping of DM *R*-gene in PI 494578**
- **Future work**
- **Acknowledgements**

Background Knowledge

DM

- *Plasmopara halstedii*

Rust

- *Puccinia helianthi*

(Photo by Markell and Gong)

- **Serious sunflower diseases in the world**
- **Development of resistant hybrids is most economic tool for disease management**

Research Objectives in 2016

- **Selection of double homozygous BC_4F_2 individuals and advancement to BC_4F_3 generation**
- **Seed increase and evaluation of agronomic performance of BC_4F_3 generation in field**
- Molecular mapping of a new DM *R*-gene in RHA 468
- Molecular mapping of a new DM *R*-gene derived from *H. argophyllus* PI 494578

Research Strategy

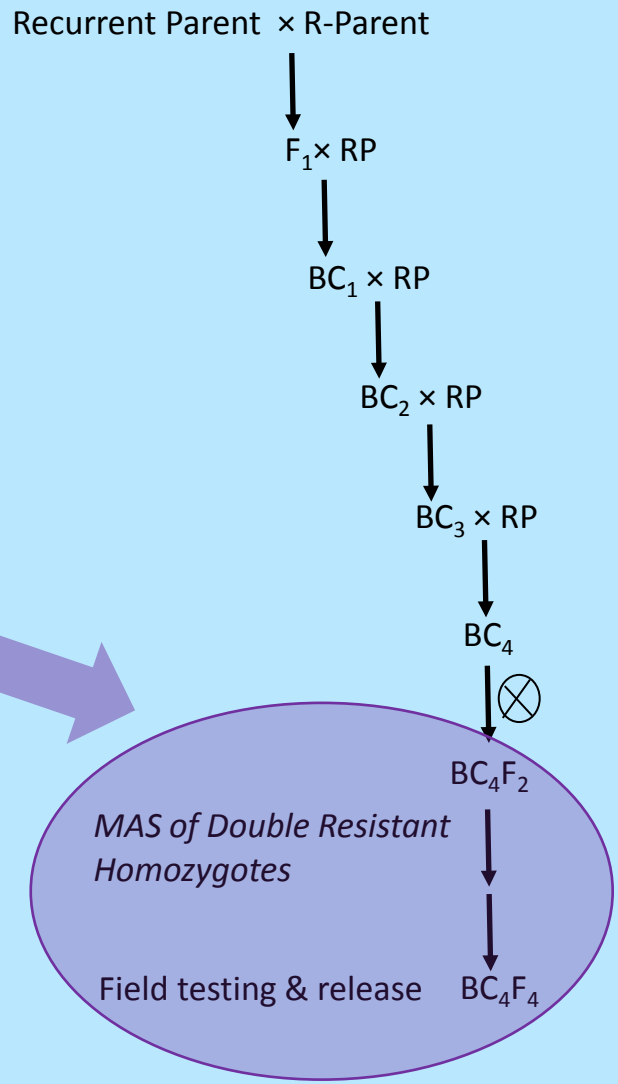
Initial crosses

- ✓ **CONFSCLR5 × RHA 464 (R_{12} + Pl_{ARG})**
- ✓ **HA-R6 (R_{13a}) × HA 458 (Pl_{17})**
- ✓ **HA-R6 (R_{13a}) × HA-DM1 (Pl_{18})**

Final products (BC_4F_4)

Confection line 1: R_{12} + Pl_{ARG}
Confection line 2: R_{13a} + Pl_{17}
Confection line 3: R_{13a} + Pl_{18}

Backcrosses



Cross-BC_1-BC_2-BC_3-BC_4F_1-BC_4F_2-BC_4F_3-BC_4F_4

- DM and rust resistant BC_4F_1 individuals were selfed for BC_4F_2 generation
- *R*-gene linked markers were used for double homozygotes selection
- Double homozygotes were advanced to BC_4F_3 generation

BC_4F_2	No. of seedlings tested	No. of double homozygotes
CONFSCLR5 × RHA 464 (R_{12} + Pl_{ARG})	214	6
HA-R6 (R_{13a}) × HA 458 (Pl_{17})	188	12
HA-R6 (R_{13a}) × HA-DM1 (Pl_{18})	376	32

Cross-BC_1-BC_2-BC_3-BC_4F_1-BC_4F_2-BC_4F_3-BC_4F_4

- **Spring 2016**
  - **DM and rust testing of the selected BC_4F_3 families to confirm marker selection results**
- **Summer 2016**
  - **Grow BC_4F_3 generation in field**
  - **Bagging heads for seed increase**
  - **Agronomic performance (plant height & flowering dates) evaluation and harvesting**

BC_4F_3	No. of double homozygotes	No. of families planted	No. of heads bagged
CONFSCLR5 × RHA 464 (R_{12} + Pl_{ARG})	6	4	240
HA-R6 (R_{13a}) × HA 458 (Pl_{17})	12	4	240
HA-R6 (R_{13a}) × HA-DM1 (Pl_{18})	32	5	41

Research Objectives in 2016

- Selection of double homozygous BC_4F_2 individuals and advancement to BC_4F_3 generation
- Seed increase and agronomic performance evaluation of BC_4F_3 generation in field
- **Molecular mapping of a new DM *R*-gene in RHA 468**
- Molecular mapping of a new DM *R*-gene derived from *H. argophyllus* PI 494578

Mapping of DM *R*-Gene in RHA 468

- Have been reported last year
- Finished all the experiments
- The new DM *R*-gene was mapped to LG1
- Working on manuscript

Research Objectives in 2016

- Selection of double homozygous BC_4F_2 individuals and advancement to BC_4F_3 generation
- Seed increase and agronomic performance evaluation of BC_4F_3 generation in field
- Molecular mapping of a new DM *R*-gene in RHA 468
- **Molecular mapping of a new DM *R*-gene derived from *H. argophyllus* PI 494578**

Mapping of DM *R*-Gene in PI 494578

- ***H. argophyllus*** **PI 494578**
  - **DM resistant line with unknown *R*-gene yet**
  - **Collected at Premont, TX**
- **HA 89: susceptible to DM**
- **Mapping populations**
  - **Genotyping on BC_1F_2 pop**
  - **Phenotyping on BC_1F_3 pop**

Phenotyping of DM Resistance

DM evaluation in $BC_1F_{2:3}$ population

- **114 $F_{2:3}$ families were inoculated with DM race 734**
- **27 S : 57 H : 30 R ($\chi^2 = 0.16$, $df = 2$, $P = 0.9231$), fitting 1:2:1 Mendelian ratio**
- **DM resistance in PI 494578 is controlled by single dominant gene**

Genotyping of BC_1F_2 population

114 BC_1F_2 and two parents were analyzed with GBS (genotyping-by-sequencing)

LGs	No. SNPs generated	No. polymorphic SNPs	No. SNPs fit 1:2:1 ratio
LG 1	5,701	970	17
LG 2	6,262	916	4
LG 3	5,833	866	8
LG 4	5,702	882	1
LG 5	7,987	1,239	1
LG 6	2,759	518	0
LG 7	2,693	452	0
LG 8	6,257	877	169
LG 9	7,859	1,299	2
LG 10	10,008	1,531	9
LG 11	5,684	885	3
LG 12	6,286	1,050	15
LG 13	7,449	1,103	44
LG 14	6,428	1,009	23
LG 15	5,861	912	1
LG 16	5,617	877	0
LG 17	7,389	1,210	1
Unassigned	12,802	1,795	16
Total	118,577	18,391	314

DM *R*-gene in PI 494578 Was on LG8

- **The DM resistance was linked with markers from LG8 of the sunflower genome**

- **DM *R*-gene from PI 494578 was mapped to an interval of 1.7 cM**

Broad Spectrum DM Resistance

- **Homozygous resistant line of BC_1F_3 (14-207-58) was tested with six DM races**
- **Immune to all six races tested**

Line	Downy mildew races											
	314		***700***		***710***		***714***		***734***		***774***	
	S	R	S	R	S	R	S	R	S	R	S	R
Cargill 270 (S-CK)	27	0	25	0	21	0	21	0	26	0	23	0
HA 89	15	0	16	0	16	0	17	0	17	0	22	0
HA-DM1 (R-CK)	0	15	0	17	0	14	0	14	0	14	0	9
14-207-58	0	35	0	33	0	34	0	34	0	33	0	40

New Germplasm Development

- **300 of BC_2F_2 seedlings were tested with DM race 734**
- **191 resistant individuals were recovered**
- **62 homozygous BC_2F_2 individuals were selected by SNP markers**
- **32 homozygotes were advanced to BC_2F_3 generation**

Ongoing Work (2017)

- **Super confection DM- and rust-R sunflower project**
  - **Threshing heads**
  - **DM, rust, and DNA marker tests of the finished BC_4F_4 lines for confirmation**
  - **Prepare documentations and seeds for germplasm release**

- **Complete the manuscript of molecular mapping of DM *R*-gene from *H. argophyllus* PI 494578**

- **Prepare the manuscript of molecular mapping of DM *R*-gene in the line RHA 468**

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Thank you

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Questions?