2014 Progress for Molecular Mapping of the Downy Mildew Resistance Genes in Sunflower

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Project Objectives (April 2012 - March 2015)

1. Develop SNP markers linked to the gene Pl_{Arg} in RHA 464
2. Investigate inheritance of DM resistance genes in RHA 428, HA 458, and 803-1, and a putative new gene from *H. argophyllus* PI494573
3. Identify SSR markers linked to DM resistance genes in RHA 428, HA 458, and 803-1, and to a putative new gene from *H. argophyllus*
4. Use SNP markers to saturate the regions where the new DM resistance genes reside

Project Progress (2012-2013)

1. Identified SNP markers linked to the gene Pl_{Arg} in RHA 464

2. Mapped a novel DM R-gene, Pl_{17}, from HA 458 to LG4 and identified SSR and SNP markers linked to Pl_{17}

3. Introgressed and mapped a novel DM R-gene, Pl_{18}, derived from wild species *H. argophyllus* to LG2 and identified SSR markers linked to Pl_{18}

The Goals for 2014

1. Develop SNP markers linked to the gene Pl_{18}

2. Complete mapping of DM resistance genes in 803-1 and RHA 428, respectively

Develop SNP markers linked to *Pl*$_{18}$

- A total of 46 SNPs (25 NSA and 21 SFW SNPs) from LG2 were selected covering the *Pl*$_{18}$ region and screened between the two the parents.

- 13 SNPs that showed polymorphism were genotyped in the F_2 population, and integrated with the SSR map

- The 10 SNPs flank *Pl*$_{18}$ at 1.2 and 0.9 cM, respectively

Mapping DM resistance gene in 803-1

Background

- The line 803-1 has been used as one of the nine standard differential lines to identify DM races, and is resistant to the most of DM races. The DM resistance in 803-1 originated from *H. tuberosus.*

- An F_2 population was developed from the cross of HA 89 with 803-1.

DM phenotyping

- A total of 140 F_3 families (30 seedlings per family) were phenotyped with DM hot race 734.
  - 39 homozygous susceptible
  - 68 heterozygous resistant
  - 33 homozygous resistant

- The DM resistance derived from 803-1 is controlled by a single dominant gene tentatively named as Pl_{803}.

Marker development

- SSR marker screening of parents
  Among 849 SSR markers screened, 283 (33%) showed polymorphism between the two parents

- Bulk segregant analysis was conducted with polymorphic SSRs, and *PI_{803}* was located on LG13

- Genotyping of the 140 F_2 individuals with 12 polymorphic SSR markers from LG13 revealed two SSRs flanking *PI_{803}* at 0.5 and 4.7 cM, respectively

Marker development cont.

- A total of 44 SNPs (14 NSA and 30 SFW SNPs) from LG13 were selected covering the *PI_{803}* region and screened between the two parents.

- 15 SNPs that showed polymorphism were genotyped in the F_2 population, and integrated with the SSR map.

- Four SNPs cosegregated with *PI_{803}*.

Mapping DM resistance gene in RHA 428

Background

- RHA 428 is an oilseed male-fertility restorer line resistant to downy mildew. The source of resistance for RHA 428 is derived from wild *H. annuus* collected from New Mexico.

- An F_2 population was developed from the cross of RHA 428 with HA 274.

Association of a male fertility restoration gene with downy mildew resistance gene in RHA 428

- The F_2 population derived from RHA 428/HA 234 was segregated for male fertility.
- All fertile F_2 plants were advanced to the F_3 generation.
- Interestedly, very few DM susceptible F_3 families were detected in the F_3 population, indicating that the male fertility restorer gene is linked to the DM R-gene.

DM phenotyping

- A total of 173 fertile F_3 families (30 seedlings per family) were phenotyped with DM hot race 734.
  - 3 homozygous susceptible
  - 112 heterozygous resistant
  - 58 homozygous resistant

- The DM resistance in HA 428 is controlled by a single dominant gene tentatively named as Pl_{428}.

Fertility test in the field

- A total of 173 fertile F_3 families (30 plants per family) were grown in the field and evaluated male fertility at the flowering stage.

  1 homozygous male sterile
  115 heterozygous male fertile
  57 homozygous male fertile

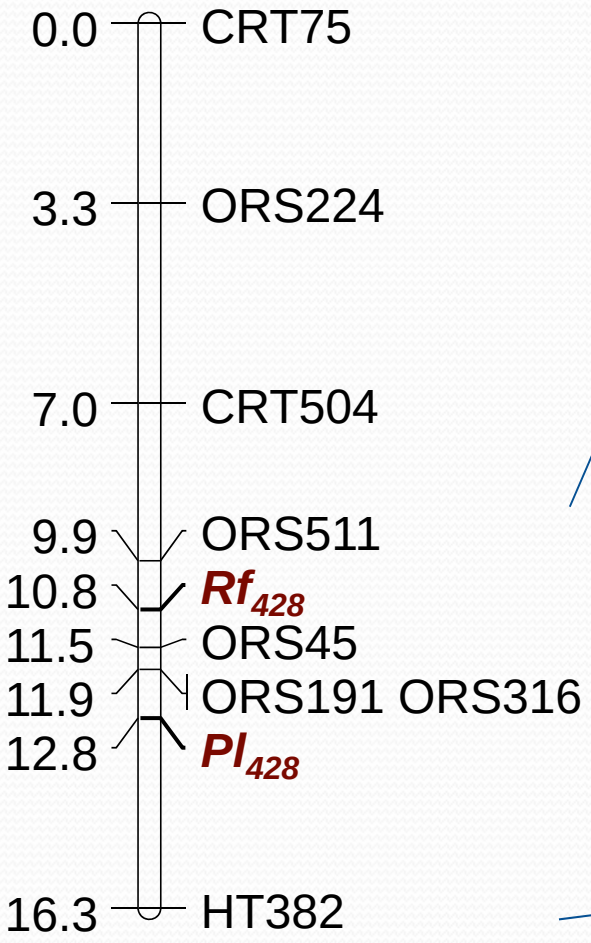
- The male fertility restoration in HA 428 also is controlled by a single dominant gene tentatively named as Rf_{428}.

Marker development

- SSR marker screening of parents
  Among 860 SSR markers screened, 293 (34%) showed polymorphism between two parents.
- Bulk segregant analysis was conducted with polymorphic SSRs, and *Pl_{428}* was located on LG13.
- Genotyping of the 173 F_2 individuals with 8 polymorphic SSR markers from LG13 revealed that *Rf_{428}* linked to *Pl_{428}* at a genetic distance of 2.0 cM.

Marker development cont.

SSR map of Rf_{428} and Pl_{428} in LG13



SNP marker saturation

- 23 NSA SNPs and 30 SFW SNPs were selected.
- Genotyping of the F2 population will be done by March 2015.

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