CFAES The Ohio State University-Horticulture and Crop Sciences

Soybean Breeding and *Rps* Gene Introgression for an Updated set of Differentials

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INTRODUCTION

- Diseases such as phytophthora stem and root rot account for the second largest yield-limiting factor for soybean [*Glycine max* (L.) Merr] in the US during a growing season [2] [4].
- In Ohio, this problematic oomycete has been present in the soils for the past 60 years [1].
- Long pathogen prevalence with long soybean productions comes with long-term disease management that needs to be approached efficiently.
- This prevalence combined with the oomycete rapid pace of evolution has resulted in more than 200 physiological races [3] [5].
- Currently, the most cost-effective and environmentally friendly management strategy is through host resistance.
- There are two mechanisms of host resistance, quantitative resistance which is conferred by multiple genes and single dominant resistant *Rps* genes which are specific to *Phytophthora sojae* effectors.
- To date, over 32 *Rps*-genes have been reported, and on-going research has identified up to 46 novel sources of *Rps*-mediated resistance.
- Ongoing research (unpublish data) has identified 46 potential novel sources of *Rps* genes which their specific pathotype response can be tested.
- Each *Rps* gene is only effective against specific races of the pathogen, making it important for breeders and producers to understand the race composition of the pathogen populations.
- Differentials, near-isogenic lines differing only for the presence of a *Rps* gene/allele, are used to characterize pathogen races and assess the diversity of *P. sojae* pathotype populations.
- These new genes could also potentially increase the available pool for single dominant combinations, supplement current breeding strategies and potential fine mapping studies.

OBJECTIVE

- Develop an updated set of differentials for each of the novel *Rps* genes as well as KASP-SNP markers for efficient marker assistant selection (MAS).

HYPOTHESIS

- The developed markers will be tightly linked to the region of interest so that a marker assistant selection (MAS) can be performed
- The use of background markers will speed the recovery of the recurrent parent genome
- Sets of differentials will present specific hypersensitive reaction to *P. sojae* isolates.

METHODS

1) In brief, recombinant inbred lines (RILs) were selected from numerous populations used to map novel *Rps* genes.
2) RILs act as the donor source of *Rps* genes and were crossed to cv. Williams to generate F1 and again to generate BC1.

METHODS (Cont.)

3) KASP or SSR forground markers will be used to select for each *Rps* gene in the BC1 individuals.
4) A set of KASP background markers distributed throughout the genome will be used to select for the Williams genetic background.
5) Selected lines will be backcrossed to Williams again and selection will proceed as described in 3) and 4) until progeny possess Wms allele at all background markers.
6) Hypocotyl test with appropriate isolates will be carried out to confirm the presence of single, novel *Rps* genes.

BACKCROSS TO WILLIAMS

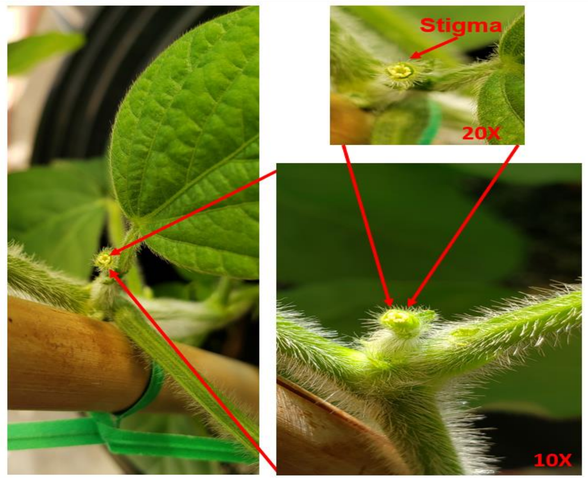
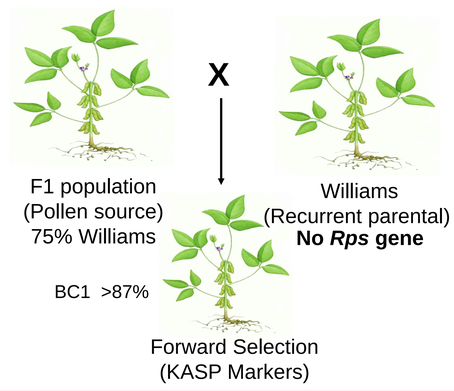
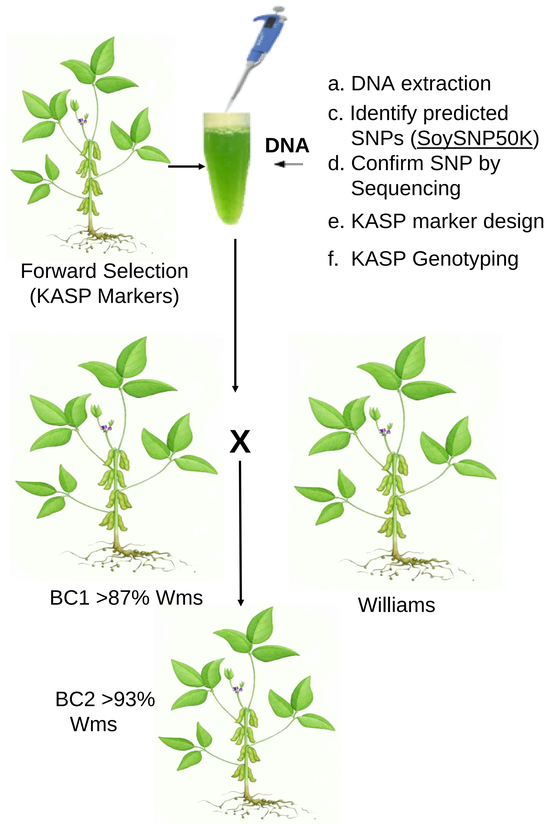


Figure 1. Backcrossing is currently being preform using the universal susceptible Williams. Williams lacks known *Rps* genes. The isoline, Williams 82 is the current soybean reference genome.

CROSSING WORKFLOW





HYPOCOTYL TEST

Figure 2. Laboratory phenotypic assay perform to evaluate specific compatibility and incompatibility of *P. sojae* pathotypes versus previously selected differentials.

Current Work

SNPs Marker Distribution

Chr	SNP	CentiMorgans (cM)	Chr	SNP	CentiMorgans (cM)
1	ss715579351	~31.86	11	ss715609325	~90.2
1	ss715579360	34.2	11	ss715610388	93.68
1	ss715580427	~40	11	ss715610308	~95
1	ss715580543	~100	11	ss715610384	~97
2	ss715581509	0.52	12	ss715613527	2.77
2	ss715583710	30.47	12	ss715612558	78.4
2	ss715582869	~98	12	ss715612708	88.33
2	ss715583528	~132	12	ss715612982	103.94
3	ss715584957	18.002	13	ss715581675	0.54
3	ss715585695	63.14	13	ss715614172	53.4
3	ss715585911	73.9	13	ss715615430	71.49
3	ss715585971	76.37	13	ss715616599	130.84
4	ss715587554	12.7	14	ss715618596	1.23
4	ss715588047	19.74	14	ss715619672	29.1
4	ss715588860	23.2	14	ss715615474	74.11
4	ss715588290	68.54	14	ss715619554	~105
5	ss715591525	~95	15	ss715623057	37.95
5	ss715591555	98.86	15	ss715623066	~40
5	ss715591599	100.13	15	ss715623072	~41
5	ss715592211	102.52	15	ss715622719	108.7
6	ss715592701	4.11	16	ss715623864	~49
6	ss715593275	~88	16	ss715624005	56.02
6	ss715593833	~116.6	16	ss715624379	66.53
6	ss715594465	124.58	16	ss715624612	79.58
7	ss715597358	~85	17	ss715628280	~30
7	ss715597544	91.98	17	ss715625805	~65
7	ss715597970	~109	17	ss715627477	~97
7	ss715598201	132.33	17	ss715627776	122.42
8	ss715599804	8.4	18	ss715631402	63.953
8	ss715602887	~57	18	ss715631601	71.38
8	ss715601091	120.81	18	ss715631769	~77
8	ss715602419	~169	18	ss715631762	~83
9	ss715602984	7.95	19	ss715635252	83.86
9	ss715605139	44.72	19	ss715635689	94.5
9	ss715604445	102.56	19	ss715635829	99.96
9	ss715604639	116.2	19	ss715635977	~107
10	ss715607172	~30	20	ss715636628	~15
10	ss715607597	37.41	20	ss715637432	41.1
10	ss715607398	~100	20	ss715637729	78.18
10	ss715607449	110.64	20	ss715638626	103.43

Table 1. Selected SNPs markers distributed through each chromosome haplotypes using SoySNP50K iSelect Bead Chip.

FUTURE DIRECTIONS

- Build KASP markers for forward selection using available *Rps* gene mapping data.
- Confirm background SNPs by performing sanger sequencing on Wms and selected plant introductions.
- Select BC2 individuals with the correct polymorphism for differential testing and perform a hypocotyl laboratory assay.

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