

# Genotypic and Phenotypic Evaluation of Soybean Lines from *Glycine max* by *Glycine soja* Backcrosses

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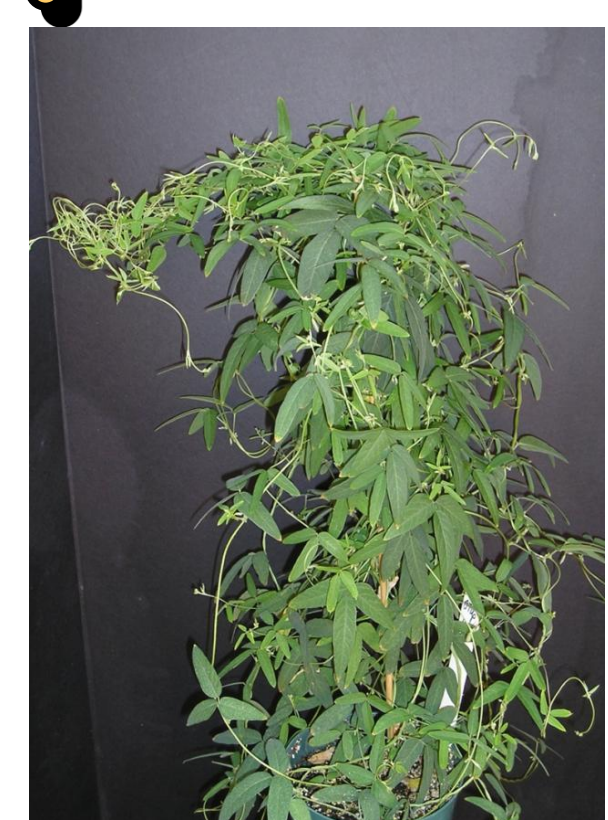
## Introduction

By pedigree more than half of the genetic contribution to current soybean production in the U.S. comes from only 5 ancestral lines (Gizlice et al., 1994). Although wild soybean is genetically much more diverse than soybean (Hyten et al., 2006), very little effort has been devoted to utilizing wild soybean in soybean breeding.

## Objectives

- To identify high yielding lines derived from backcrosses between five *G. soja* accessions and Williams 82.
- To determine the genetic contribution from each *G. soja* parent.

## Materials and Methods



*Glycine soja*

Field of *G. max* x *G. soja* backcross lines



## Population development

The *G. soja* × *G. max* backcross lines were developed using the wild soybean parents, PI 65549, PI 479767, PI 483461, PI 549046 and PI 507807 and the cultivar Williams 82. The first four *G. soja* lines were crossed to Williams 82 and the F1 plants backcrossed to Williams 82. The BC2 parent lines were developed through intensive family selection and backcrossed to Williams 82. Lines from PI 507807 (BC1) and PI 549046 (BC2) were developed by family selection beginning in the F2 generation. The BC2 lines from PI 479767 and PI 483461 were selected by early generation testing through yield testing F2 lines in the F3 and F4 generation to identify the best F6 lines. The BC2 lines derived from PI 65549 were developed from an SSD population that was inbred to the F5 generation.

## Field procedures

- The derived lines and checks were evaluated in two replications at three locations in Illinois and a location each at Ohio, Missouri and Nebraska in 2011 and two locations in Illinois and a location in Missouri in 2012.

## Genotyping procedures

- All entries were genotyped with 1536 SNP markers using the Universal Soy Linkage Panel 1.0 using the Illumina GoldenGate assay.

## Statistical analysis

The data were analyzed using the PROC GLM function in SAS (SAS 9.1, SAS Institute, Cary NC). Genotypic (SNP) data was analyzed using genome studio (v 1.0) and Microsoft Excel to identify regions of introgression in the backcross-derived lines.

## Results and Discussion

Table 1. Data for the highest yielding line from each donor parent and the recurrent parent, Williams 82 from 8 locations in Nebraska, Missouri, Illinois, Ohio in 2011 and 2012

Donor	# of BC <sup>†</sup>	Total lines	Yield kg/ha	Mat. days	Ldg. (1 to 5)	Hgt. cm
PI 65549	2	4	3162	5	2.0	98
PI 479767	2	8	3505	-3	2.2	106
PI 483461	2	3	3387	-6	1.9	107
PI 507807	1	4	3239	3	2.2	113
PI 549046	2	5	3327	4	2.0	103
Williams 82			3312	Oct. 2	2.0	111
LSD (0.05)			260	1.3	0.3	5.5

<sup>†</sup> Backcrosses

Table 2. Location in cM of SNPs introgressed into all derived lines from three of the *G. soja* parents

Donor	Chromosome							
	1	2	3	4	7	14	18	20
PI 65569	41,42	133		51,52	73			
PI 479767							12	17
PI 483461	97		28		73	63,64		85

Table 3. Frequency of SNPs (position in cM) that were commonly introgressed into derived lines from multiple *G. soja* parents

Donor	Chromosome	
	3	7
	27.6 cM	72.6 cM
PI 65569	0.8	1.0
PI 479767	0.8	
PI 483461	1.0	1.0
PI 507807		0.8

Figure 1. Frequency of PI 483461 alleles on chromosome 7 in derived lines

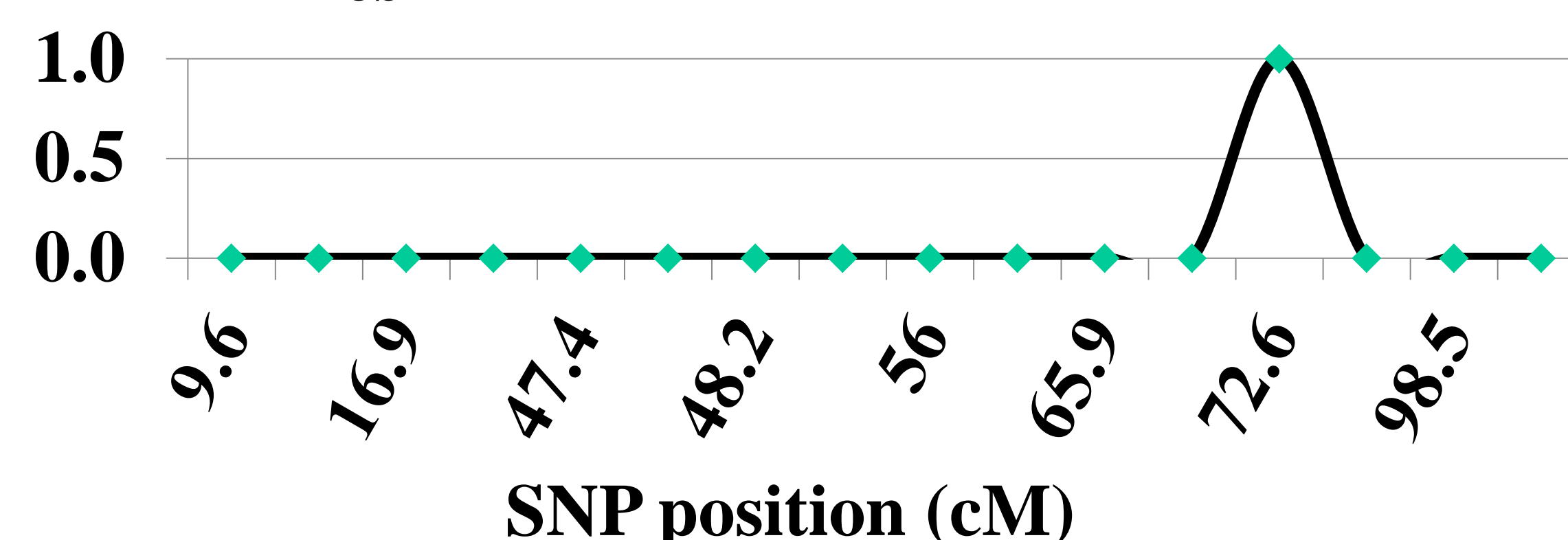
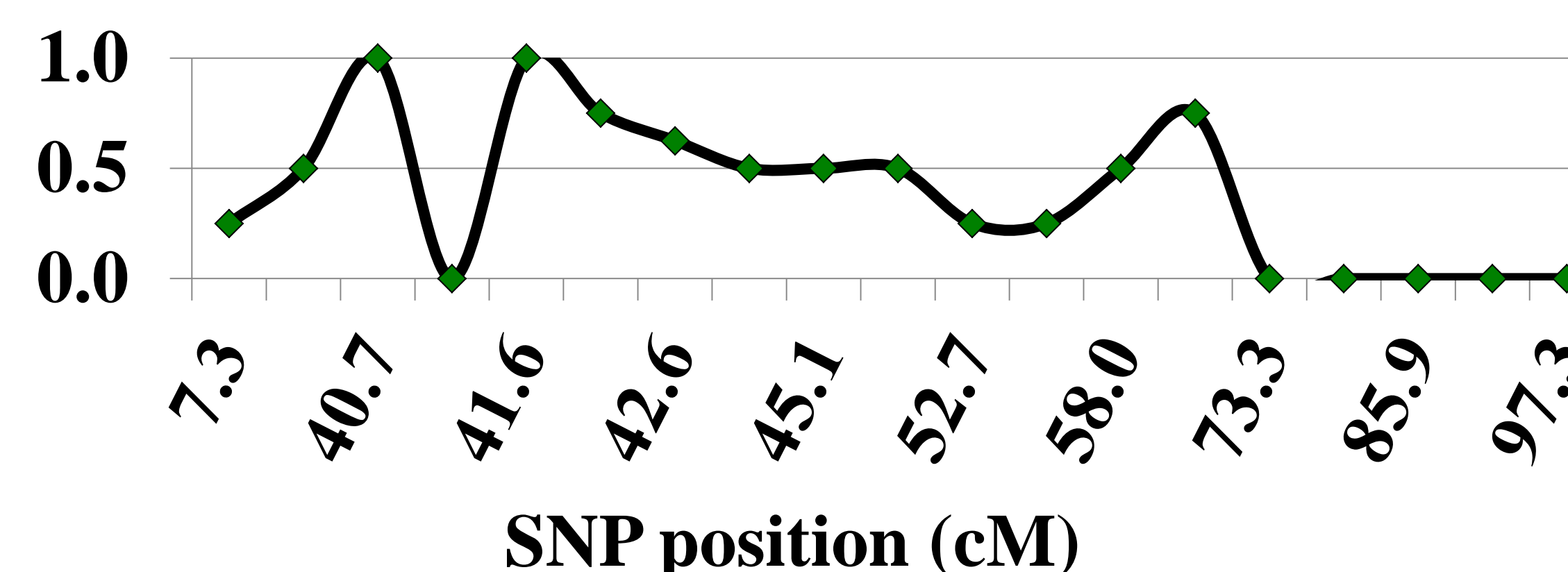


Figure 2. Frequency of PI 65549 alleles on chromosome 1 in derived lines



For every *G. soja* parent, we identified lines that were not significantly different from Williams 82 in seed yield (Table 1). The best line yielded 193 kg/ha more than Williams 82. Time to maturity was not related to seed yield among these lines. All of the lines were similar to Williams 82 in lodging and some lines were significantly shorter than the recurrent parent.

Despite intense selection pressure to recover good agronomic types, 14% of SNP alleles in the derived lines came from the *G. soja* parents. This is what would be expected from a random set of BC2 lines. Some alleles in the derived lines were exclusively from the *G. soja* parent (Table 2). The consistency of these alleles in every line indicates that they may be linked to the selected agronomic traits and the diversity of these loci among the *G. soja* lines shows that each *G. soja* parent is likely making a unique genetic contribution. There are two loci for which the *G. soja* allele was frequently introgressed from three *G. soja* parents (Table 3). Although the *G. soja* allele was not in every line, the allele on chromosome 3 occurred in 12 of 15 lines and the allele on chromosome 7 was in 10 of 11 lines.

Fig. 1 illustrates an introgression pattern for the alleles in Table 2. In some cases, additional alleles from the chromosome were introgressed at low frequencies or two closely linked alleles were introgressed in all lines. Fig. 2 shows the rare occurrence where two alleles just over a cM apart occurred in all four lines derived from PI 65549 and a third allele, between them, that was consistently maintained as the *G. max* allele. This was observed twice in lines derived from PI 65549.

All lines derived from PI 483461 had alleles on five chromosomes that were exclusively from *G. soja* but there were also six chromosomes that had no *G. soja* alleles. All other lines had some alleles from *G. soja* on every chromosome.

## Conclusions

- Alleles consistently introgressed from *G. soja* indicate linkage to agronomically important genes.
- Diversity of introgressed alleles from *G. soja* lines indicates unique contributions from each parent.
- The yield and genotypic diversity of derived lines supports the use of *G. soja* in soybean improvement.

## References

- Gizlice, Z., et al. 1994. Crop Sci. 34:1143-1151.
- Hyten, D.L., et al. Proc. Natl. Acad. Sci. U. S. A. 103:16666-16671.

