Mapping Domestication Traits in Soybean By Wild Soybean RIL Populations

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Introduction

In domesticating the soybean from the wild soybean, selection changed many traits including seed size, growth habit, plant height, and pod shattering (pod dehiscence). We hypothesize that the genomic regions in wild soybean that surround the genes controlling domestication traits may be sources of novel alleles for soybean improvement that were eliminated in selective sweeps during the domestication process.

Objective

To map the major agronomic QTL that differentiate domesticated and wild soybean.

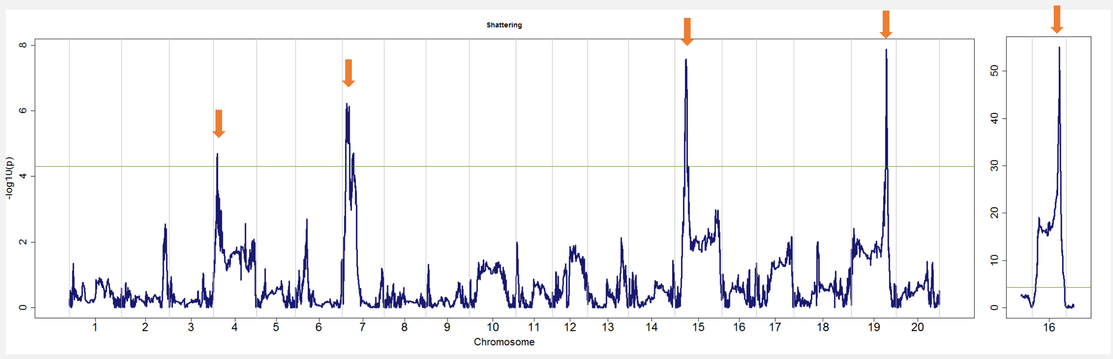

Fig 1: SNP associations with shattering susceptibility using SNP from chromosome 16 (right) as covariate. Green line indicates α=0.05 threshold.

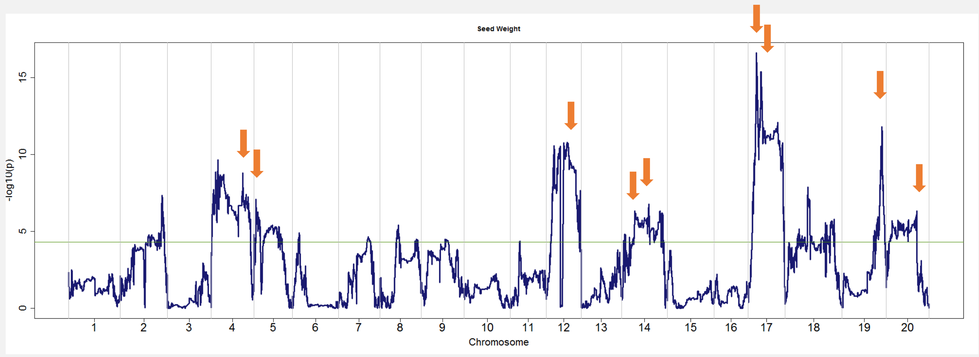

Fig 2: SNP associations with 100 seed weight. Green line indicates α=0.05 threshold.

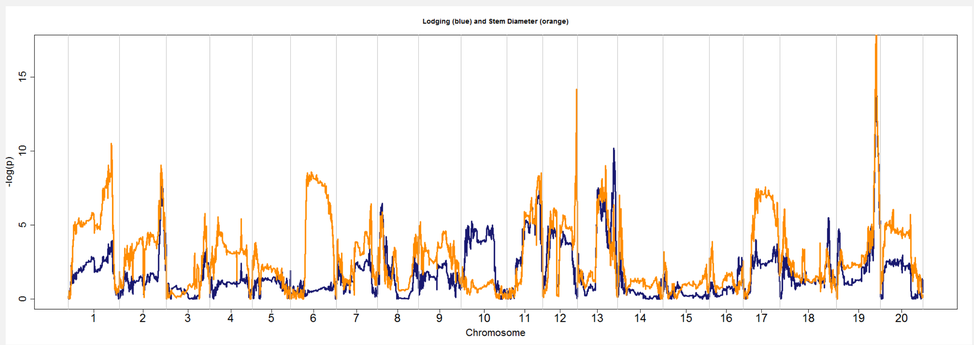

Fig 3: SNP associations with lodging (blue) and stem diameter (orange).

Materials and Methods

Recombinant inbred line (RIL) populations were derived from the interspecific crosses of Williams 82 and two wild soybean accessions (PI 468916 and PI 479752). 800 lines were selected for mapping from over 3000 F6 lines that were grown in 2012. The 800 RILs were selected to represent all possible combinations of extreme classes for six traits for the purpose of breaking linkages among these traits to improve the mapping process.

Experimental Design:
From 2013-2015, the lines were grown at Urbana, IL and W. Lafayette, IN in a randomized complete block design (RCBD) with two replications. Among 11 traits measured in the field, shattering, 100 seed weight, lodging, and stem diameter are described here. Lodging was rated on a 1 to 9 scale, and shattering was rated on a 1 to 6 scale (1: 0%, 2: 1-10%, 3: 11-25%, 4: 26-50%, 5: 51-80%, 6: >80%)

Genotyping:
Genotyping by sequencing (GBS) was used to produce nearly 28,000 SNP markers to use in QTL mapping. The protocol was a two enzyme (*HindIII-HinP1*) modification of the original protocol from Elshire *et al.* and Poland *et al.* GBS data was produced through the TASSEL GBS pipeline (Buckler lab) and tags were aligned to V1.0 of the *G. max* reference genome. Missing data was imputed using the FSFHap algorithm implemented in TASSEL5.

Results and Discussion

Five markers were significantly associated with shattering (pod dehiscence) (Fig 1). Single-marker analysis identified a highly significant region on chromosome 16 (at 29.6Mb), which appears to correspond to a QTL identified previously (Gao and Zhu 2013, Funatsuki *et al*. 2014). After including the SNP on chromosome 16 as a covariate in the model, four additional SNPs on chromosomes 4, 7, 15, and 19 were identified, which may be associated with smaller effect QTL.

CIM was used to detect nine SNP markers that were significantly associated with 100 seed weight (Fig 2). All but one marker were associated with a decrease in seed weight relative to the *G. max* parent, with the most significant SNP (8.98Mb on chromosome 17) accounting for a 0.6 g decrease (Table 1). However, the SNP at 13.89 Mb on chromosome 14 exhibits an unexpected 1.7 g increase in weight.

We observed a negative correlation (-0.55) between lodging and stem diameter, indicating that as stem diameter increases, lodging decreases. By comparing the plots of the two traits (Fig 3), commonalities and unique patterns can be identified. Chromosomes 11, 12, 13, and 19 show similar patterns of significance between the traits. Genes in these regions may be associated with characteristics related to both traits, which is not unexpected. The unique patterns on chromosomes 6 and 17 for stem diameter, and chromosome 10 for lodging indicate that there are genes that affect these traits independently.

Trait	Chromosome	Position (Mb)	-log10(p)	Effect*
Shattering	16	29.59	55.1	0.9
	19	37.69	7.9	0.3
	15	11.90	9.2	0.3
	7	4.90	6.4	0.2
	4	3.96	4.7	-0.2
Seed Weight	17	8.98	16.6	-0.6
	19	43.33	11.7	-0.5
	5	2.14	7.9	-0.4
	12	22.66	7.6	-0.3
	17	13.87	7.8	-0.4
	14	14.34	7.3	-0.3
	20	32.37	6.0	-0.3
	14	13.89	5.8	1.7
	4	40.18	4.2	-0.2

Table 1: SNPs associated with shattering and seed weight at α=0.05. *Effects expressed as change in score (shattering) and grams (seed weight)

Above: RIL field in 2013

Below: *G. soja* parent PI 479752

References

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