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Introduction

Sucrose is a desirable sugar in soybean seed that affects the quality and taste of soyfoods and feed, while stachyose is a non-digestible sugar that induces flatulence in non-ruminant animals. Therefore, soybean cultivars with high sucrose and low stachyose would be valuable for soyfoods and meal markets. The objectives of this study were to identify QTL associated with seed sucrose and stachyose content using Simple Sequence Repeat (SSR) and Single Nucleotide Polymorphism (SNP) markers.

Materials and Methods

A low sucrose small-seeded line, MFS-553, was crossed with a high sucrose large-seeded plant introduction, PI 243545, to develop a sucrose QTL mapping population with 94 lines. A total of 5361 SNP markers covering 20 soybean chromosomes were used to screen the parental lines. Out of 5361, 2016 were polymorphic and used to screen the F_{3:4} population derived from MFS-553 x PI 243545. A normal stachyose cultivar, Osage, was crossed with a low stachyose line, V99-5089, and F₃ mapping population with 129 lines were developed for genetic study of stachyose content. A total of 34 SSR and 56 SNP markers on chromosome 10 and 11 were used to screen the parental lines. A total of 5 polymorphic SSR and 16 polymorphic SNP markers were used to screen the F_{3:4} lines derived from Osage x V99-5089. For phenotypic data, seed of F_{3:5} and F_{3:6} lines from MFS-553 x PI 243545 and Osage x V99-5089 were analyzed for sucrose and stachyose using high performance liquid chromatography (HPLC), respectively. Both populations were grown in Fayetteville in 2010, and in Argentina and Costa Rica winter nurseries in 2011.



MFS-553 PI 243545



Osage V99-5089

Results

Table 1. Summary of SNP markers used in screening F_{3:4} population from MFS-553 x PI 243545 for seed sucrose content.

Chr.	Length (cM)	No. SNP marker mapped	No. SNP locus located separately	Average distance between SNP loci (cM)
1	169.3	28	21	8.1
2	112.8	19	18	6.3
3	275.0	83	62	4.4
4	202.9	80	48	4.2
5	219.6	47	26	8.4
6	435.7	109	86	5.1
7	470.3	76	65	7.2
8	371.0	106	76	4.9
9	344.9	165	112	3.1
10	576.8	60	40	14.4
11	312.2	119	72	4.3
12	293.2	24	17	17.2
13	412.3	134	99	4.2
14	227.5	159	68	3.3
15	396.3	132	100	4.0
16	534.9	237	130	4.1
17	395.6	101	85	4.7
18	290.8	116	91	3.2
19	407.2	66	48	8.5
20	153.7	36	19	8.1
Average	330.1	95	64	5.1
Total	6602.0	1897	1283	

Table 2. Summary of SNP markers used in screening the F_{3:4} population from Osage x V99-5089 for seed stachyose content.

Chr.	Length (cM)	SSR markers	SNP markers	Polymorphic SSR	Polymorphic SNP	Coverage
10	111.8	33	37	9	13	5.3
11	23.4	1	19	1	5	3.9
Total	132.0	34	56	10	18	4.7

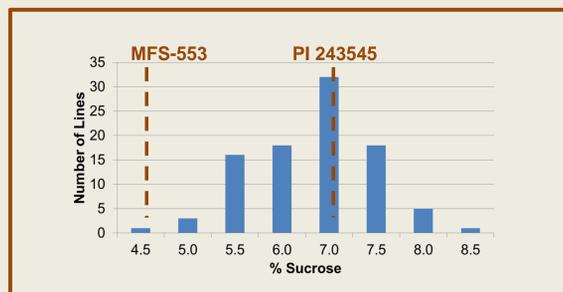


Figure 1. Sucrose distribution of F₃-derived lines from MFS-553 x PI 243545 (combined across locations and years)

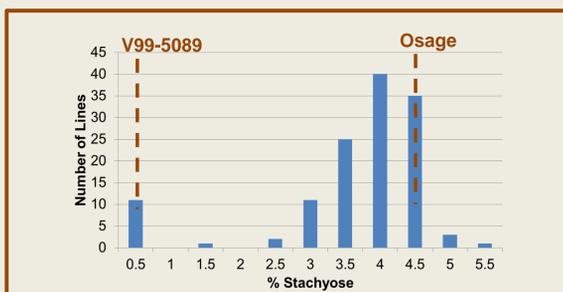


Figure 2. Stachyose distribution from F₃ lines from Osage x V99-5089 (combined across locations and years)

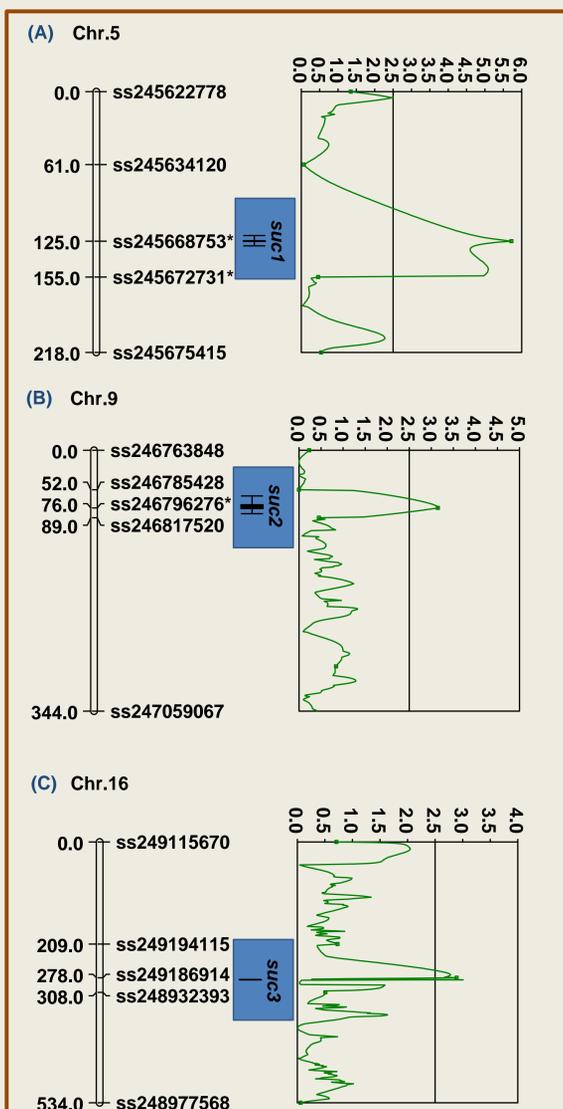


Figure 3. Composite interval mapping using SNP markers for seed sucrose QTL on Chr. 5, 9, and 16 in 94 F₃-derived lines from MFS-553 x PI 243545; (A) three locations and two years; (B) combined data across two locations in 2011; (C) in Fayetteville in 2010. *, **, *** represents significant association with seed sucrose content at P-value ≤ 0.05, 0.01, 0.001, respectively.

Table 3. Chi-square test for goodness-of-fit of stachyose content to a two-gene model in Osage x V99-5089 population for 2010, 2011, and two years combined.

	Range	No. normal stachyose lines	No. low stachyose lines	X ² (15:1)	P-Value
Fayetteville, 2010					
Osage	4.53 - 5.18	118	11	1.11	0.29
V99-5089	0.40 - 0.46				
F _{3:5} lines	0.19 - 5.08				
Argentina, 2011					
Osage	4.12 - 4.76	121	8	0.001	0.97
V99-5089	0.21 - 0.37				
F _{3:6} lines	0.23 - 5.38				
Costa Rica, 2011					
Osage	1.98 - 4.44	126	3	3.30	0.07
V99-5089	0.23 - 0.39				
F _{3:6} lines	0.20 - 4.77				
3 - Env. Combined					
Osage	1.98 - 5.18	126	3	3.30	0.07
V99-5089	0.21 - 0.46				
F ₃ -derived lines	0.22 - 5.05				

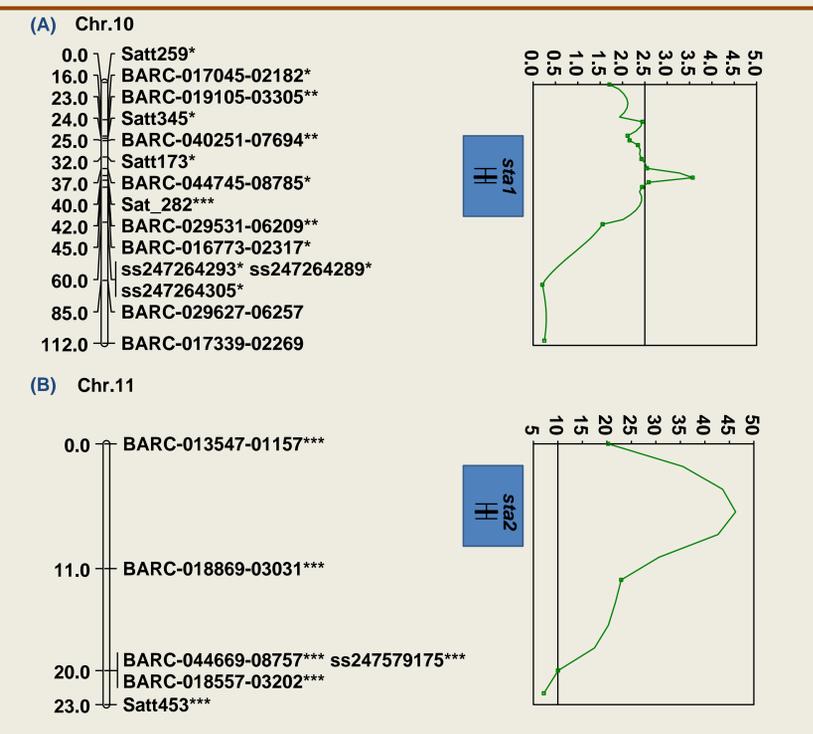


Figure 4. Composite interval mapping for seed stachyose QTL on chromosome 10 (A) and 11 (B) in 129 F₃-derived lines from Osage x V99-5089 evaluated across three environments. *, **, *** represents significant association with stachyose content at P-value ≤ 0.05, 0.01, 0.001, respectively.

Conclusions

- ❖ The sucrose content in the population from MFS-553 x PI 243545 showed a normal distribution as expected for multiple genes/QTL; whereas stachyose content in Osage x V99-5089 segregated in a digenic ratio of 15 normal : 1 low in the population.
- ❖ Three new sucrose QTL were found on Chr. 5, 9 and 16, explaining 46%, 10% and 8% of phenotypic variation for sucrose content, respectively.
- ❖ A new minor stachyose gene was identified on Chr. 10 which explained 11% of phenotypic variation for stachyose content.
- ❖ A stachyose gene on Chr. 11 was confirmed in present study that explained 81% of phenotypic variation for stachyose content.
- ❖ SSR/SNP markers and sugar QTL/genes identified from this study can be used for marker assisted selections in breeding soybean lines with desired sugar profile.

References

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