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Introduction

- Soybean (*Glycine max*) meal provides a high-protein feed ingredient that is used predominantly in poultry and swine production.
- Incorporating exotic germplasm could help breeders to achieve the elusive breeding goal of developing a high yielding soybean cultivar with above average protein content.

Research Objectives

- Identify high protein QTL in a line derived from the high protein germplasm N6202 (Carter et al., 2010).
- Incorporate this trait into a high yielding genetic background.
- Determine the feasibility of developing high protein germplasm with marketable oil content.

Materials and Methods

Plant Materials

Pro 5	Pro 16
G03-3385 × N06-10035	G03-3621 × N06-10011
132 lines	133 lines

Parents

- G03-3385 and G03-3621 are high protein selections from the cross: cv. 'Benning' (Boerma et al., 1982) x Korean PI 'Danbaekong' ('Danbaekong' carries high protein locus on chromosome 20 previously identified by Warrington et al. 2011).
- N06-10035 and N06-10011 are high protein selections from the cross cv. 'Young' (Burton et al., 1987) x 'N6202' (Carter et al., 2010) (N6202 has two Japanese varieties in its pedigree: Nakasennari and Fukuyataka).

Phenotypic Evaluations

- 2011 and 2012: F₄ and F_{4.5} populations grown in Clayton, NC and evaluated for total protein and oil content.
- 2013: Pro 5 evaluated for yield: 2 env, 3 reps per location.



Pro 5 population at maturity in Clayton, NC Genotyping procedures for Pro 5 population

Molecular Marker Analysis

- DNA was extracted from each F_{4.5} line in Pro 5 and Pro 16.
- Lines from Pro 5 were genotyped using the 1536 SNPs of the Illumina GoldenGate Universal Soy Linkage Panel.
- Composite interval mapping analysis was conducted by Windows QTL Cartographer.

Statistical Analysis

- ANOVA and genotypic means for percent seed protein and percent oil content were calculated for Pro 5 and Pro 16.

Results

Protein Analysis

- High protein lines with acceptable oil levels were identified in the progeny of both crosses (Table 1).
- The statistical analysis for protein within both Pro 5 and Pro 16 populations showed statistically significant differences between genotypes and also between years (p-value <0.0001).
- Transgressive segregation indicates that the QTL from N06-10035 and N06-10011 parents are different than those from the G03-3385 and G03-3621 parents (Figure 1).
- Identified 418 polymorphic markers in Pro 5.

Table 1. Lines with the highest and lowest values for percent seed protein and oil, and lines with highest values for the sum of protein and oil concentration.

Line	Pro 5		Average Yield		Pro 16		
	Protein % (DW)	Oil % (DW)	(bu/A) Clayton, NC	(bu/A) Plymouth, NC	Line	Protein % (DW)	Oil % (DW)
Pro5-15	49.863*	19.226	53.86	43.94	Pro16-96‡	47.086*	21.047
Pro5-138	42.072^	22.437	52.00	41.98	Pro16-37	41.403^	22.578
Pro5-84	42.571	22.576*	58.74	34.17	Pro16-105	44.745	19.967^
Pro5-111	48.898	18.069^	51.85	47.41	Pro16-112	43.154	22.633*
Pro5-148‡	48.333	20.776	57.33	35.76	G03-3621	44.449	22.053
G03-3385	44.045	21.531	56.68	41.13	N06-10011	44.631	20.859
N06-10035	45.018	21.232	53.97	46.67	Pro16 mean	44.363	21.503
Pro5 mean	45.712	20.599					

‡ Indicates the line with the highest values for the sum of % protein and oil

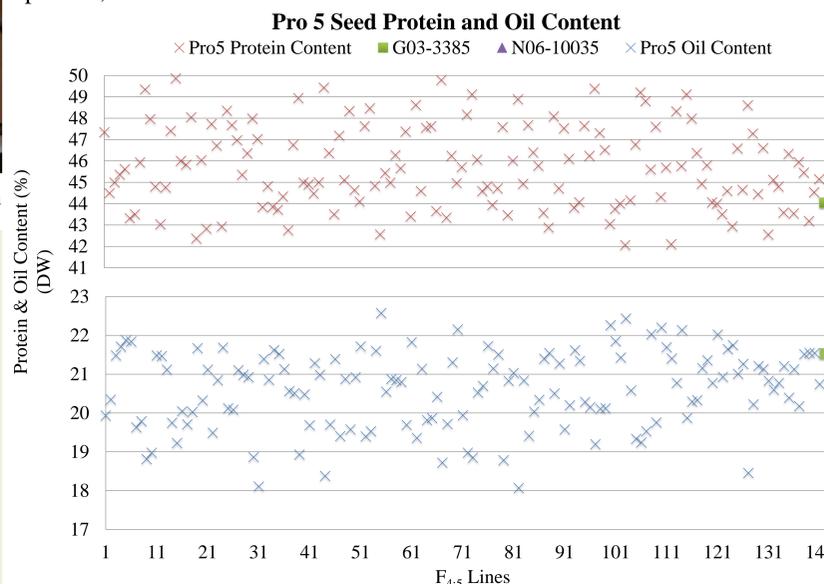
* Indicates the highest value in each category

^ Indicates the lowest value in each category



Parents N06-10035 and G03-3385 with a sample of their F_{4.6} progeny.

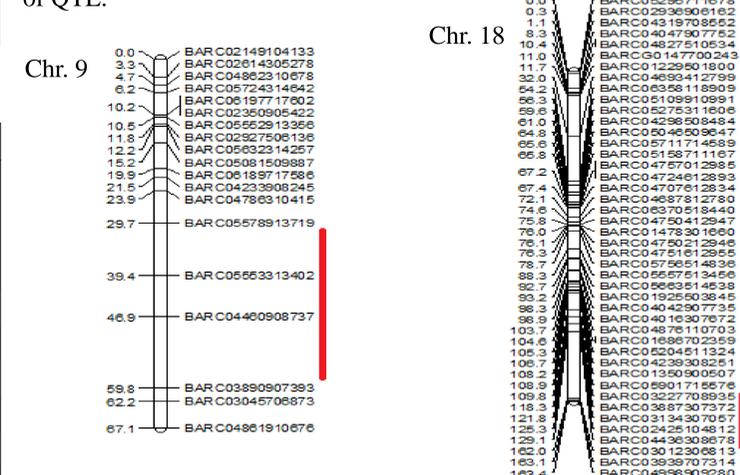
Figure 1. Percent protein and oil content of the Pro 5 population, including parents, in 2012.



Molecular Marker Analysis

- Confirmed Chr. 20 high protein allele from 'Danbaekong'.
- Putative high protein QTL detected on Chr. 1, 9, 18, and 20 using 2012 protein data with R²: 2.97%, 0.04%, 4.50%, and 50.01%, respectively.
- Positive alleles for increased protein content from N06-10035: Chr. 9 and 18 (Figure 2).

Figure 2. Positive alleles for increased protein content from N06-10035 detected on chromosomes 9 and 18. Red line indicates approximate position of QTL.



Conclusions

- Preliminary phenotypic and molecular analysis indicate that N06-10035 and N06-10011 carry high protein QTL that are different from the QTL in the Korean PI 'Danbaekong' and these QTL have smaller effects.
- Germplasm lines with high protein content and acceptable oil levels could be developed from these populations.

Future Work

- SSR markers are being added to the genotypic data.
- Protein content of samples from the 2013 field season are being determined / analyzed, and these data will be added to the QTL analysis.

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