I. MSMC project title

MSMC 16-386: Identification and Evaluation of Domesticated Soybean Lines Derived from Wild Soybean Crosses with Increased Levels of Protein and Value-Added Amino Acids

II. Time period covered

April 1st, 2016 – March 31st, 2018

III. Project leaders and co-primary investigators

PI: Andrew Scaboo, University of Missouri
Co-PI: Pengyin Chen, University of Missouri
Co-PI: Ed Large, University of Missouri

IV. Layman's summary

During the past two years, we have evaluated a core collection of *Glycine soja* plant accessions from the USDA germplasm collection via a genome wide association study, three *Glycine max* x *Glycine soja* hybrid populations via nested association mapping, and two *Glycine max* x *Glycine soja* hybrid populations via bulk segregate analysis.

Thus far, we have grown all of these populations in replicated multi-location field experiments for the last two years. The field experiments have been largely successful over the last two growing seasons, although we discuss only 2016 results in this report. We will complete the entire analysis, including 2017 data, during the spring of 2018. We have found experimental lines that have the potential to be good parents for improving the protein and amino acid content in elite soybean varieties, and we have also identified several genomic regions, or quantitative trait loci (QTL), that are associated with seed protein and amino acid content.

Although we are currently unable to identify specific genes controlling these traits, we can use this information to develop new plant material and experiments to eventually understand the genetic architecture of these traits.

V. State your objectives in question form and discuss how your results answer these objectives

The objectives of this project were to answer two questions:

- Can we develop soybean germplasm, with *Glycine soja* (wild soybean) in the pedigree, with higher protein and essential amino acids?
- Can we identify genomic regions (QTL) and genes that are associated with improved seed protein and amino acid composition?

Can we develop soybean germplasm, with Glycine soja (wild soybean) in the pedigree, with higher protein and essential amino acids?
We have developed hundreds of experimental lines, with *Glycine soja* (wild soybean) in the pedigree, with improved protein and amino acid content. Yet there are only a handful of lines with seed yield potential acceptable for advancing for use in breeding when developing high-yielding soybean varieties with improved seed composition.

Can we identify genomic regions (QTL) and genes that are associated with improved seed protein and amino acid composition?
We found three QTL (chromosome 20, 15, and 14) associated with seed protein content using nested association mapping with three unique *Glycine max* x *Glycine soja* hybrid populations across 4 locations in MO during 2016 (Figure 1), and we found one QTL (chromosome 13) associated with both seed aspartic acid and glutamine content using genome wide association mapping of a core collection of *Glycine soja* (Figures 2 and 3).

Figure 1. Manhattan plot identifying QTL associated with total protein content using nested association mapping with three *Glycine ma*x x *Glycine soja* populations.

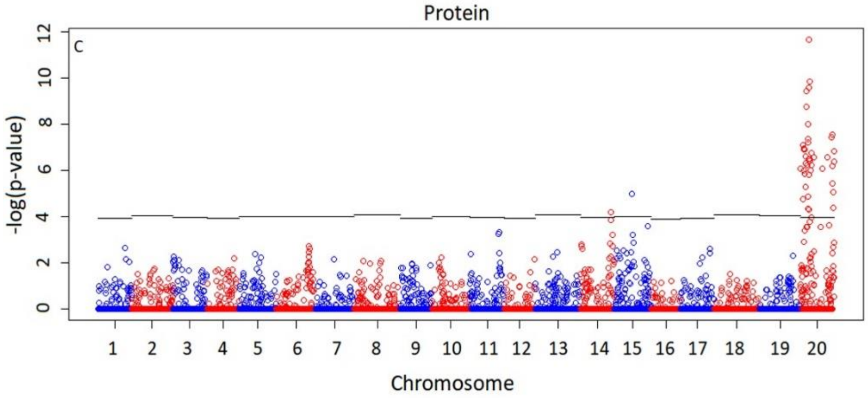


Figure 2. Manhattan plot identifying QTL associated with seed aspartic acid content in a *Glycine soja* core collection.

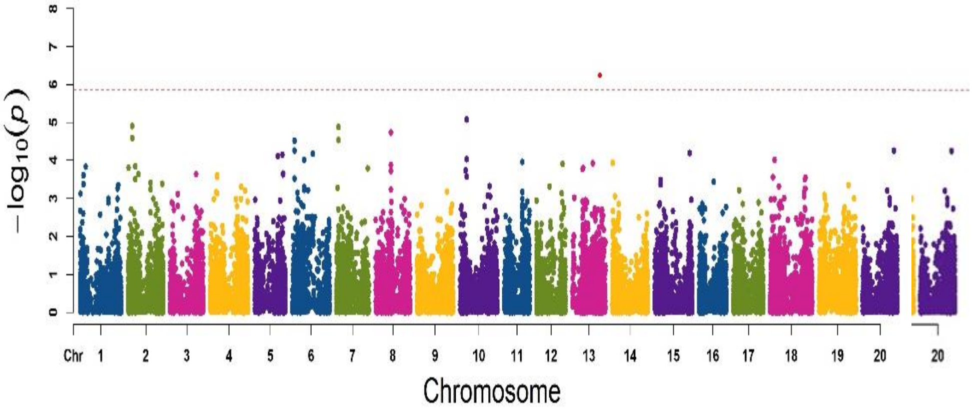
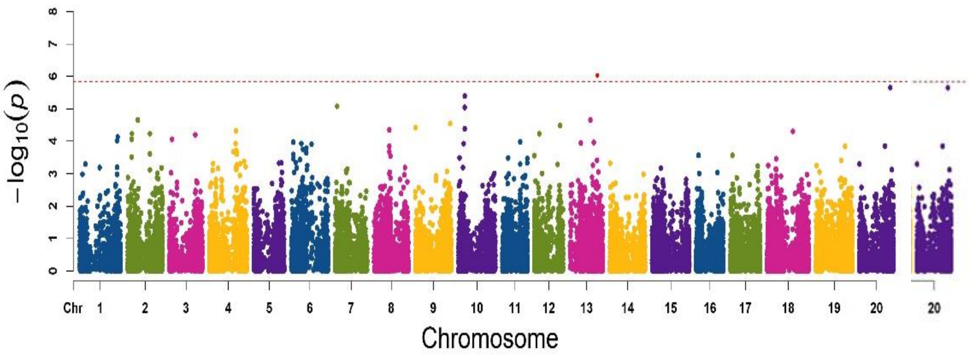


Figure 3. Manhattan plot identifying QTL associated with seed glutamine content in a *Glycine soja* core collection.



VI. Please answer the following:

A. How do your results benefit Missouri soybeans growers?

We found QTL's with positive allelic variation and effect in *Glycine soja* and expect to leverage this information to improve the protein and amino acid composition of the cultivated soybean. In addition, the utilization of wild soybean in breeding programs will help to improve the poor genetic diversity of soybean cultivars in North American, and prevent future yield limitations due to lack of genetic diversity.

B. Estimate financial return for the average Missouri soybean producer.

The financial return for Missouri farmers from this project will be in the long-term increases in profitability and productivity due to improved soybean genetic potential.

C. Do your results benefit the environment?

Our results do not directly benefit the environment.

D. What products or processes can be commercialized from this research?

Two main avenues can commercialize soybean germplasm and varieties: a) licensing to private companies for sale as varieties and b) licensing to private companies for use in their respective breeding programs.

1. List disclosure(s) of inventions or plant varieties submitted to the MU Tech Transfer Office

None at present

2. Identify potential disclosure(s) of inventions or plant varieties.

Soybean germplasm from this project has the potential to be developed as disclosed inventions in the future

E. How would you commercialize these products or processes?

Two main avenues can commercialize soybean germplasm and varieties: a) licensing to private companies for sale as varieties and b) licensing to private companies for use in their respective breeding programs.

F. If no specific products or processes were produced, how do you plan to make your results available to producers or industry?

The results of our research will be released in the form of peer-reviewed publications, as well as communicated in the form of presentations at scientific and farming related conferences.

G. Is additional time or research required before your results can be used by producers and industry?

Yes, some of our 2017 analyses are still in process, and will be fully completed with the funds already utilized. Moreover, we plan to continue this research with a new proposal that expands the research on seed protein and amino acid composition.

VII. List publications by type (popular press, thesis, journals, other) written or planned.

La et al., Characterization of a USDA core collection of wild soybean (*Glycine soja* Siebold & Zucc.) accessions for seed composition and agronomic traits. 2018. Crop Science (accepted with revisions December 2017)

VIII. List cost of original project and actual expenditures. *The U.S. Department of Agriculture requires that we ask for budget information, including the number of hours spent on the project, the number of dollars remaining on*

***account, as well as a breakdown of expenses. You are required to provide this information in your report.* Please also include names and titles/positions of those whose time has been charged to this project.**

As of April 10th, 2018 the account balance is $1,686.00. $33,146.08 has been spent on salary and wages, $10,597.74 has been spent on fringe benefits, and $15,188.15 has been spent on operating expenses. The encumbered dollar amount is $3,962.03.

IX. List equipment purchased with MSMC funds, identifying inventory, and serial number.

None