OH 33 and 34 Mapping populations Manuscript

# What has been done already

## Abstract

The abstract is solid, general statement of manuscript objectives and then list how many QTL were found for each trait, and how many were novel.

## Introduction

Right now, the introduction for this paper is very similar to the one in my oil mapping manuscript. I start by talking about the importance of protein and oil as far as adding value to a soybean cultivar because of the main uses for soybean. Then I talk about the historical difficulty in improving oil, protein, and yield simultaneously due to the correlation structure among them and talk about some papers that explain how this is due to the competing metabolic pathways that influence each trait. Then I write about how there some limited success in the past with has been applying MAS to improve these traits, but that it is still difficult because there have been few stable QTL found which improve one or more of the traits without having a negative effect on the others. I talk about the large effect QTL on chromosomes 20 and 15 and focus on the findings of the studies which used the Danbaekkong as a high protein source, specifically that there is evidence that the alleles or genetic background donated by Danbaekkong can improve protein content without yield drag.

## Materials and methods

Basic description of the population development process including what parents were used for each population and what techniques were used to develop the population (SSD). Descriptions for how phenotype data were collected and how DNA was extracted for genotyping. What statistical methods and software were used to analyze the phenotype, and what software were used to make the linkage map and conduct QTL mapping along with the relevant thresholds that were used to declare QTL significance

## Results

A summary of the phenotype distributions including the range of phenotypes and their coefficients of variation for each population along with the correlations between the phenotypes for each population. Brant has already made a good summary table and a plot to show the distributions of the phenotypes with the parent values shown on the distributions. Next, some summary information about the linkage maps that were used for the QTL mapping including the number of markers and RILs used in each linkage map along with the average marker spacing on each map and how the marker spacing varies between LGs.

QTL mapping results are presented in the results section by listing how many QTL were found for each trait and on what chromosomes, the names of novel QTL are given here.

## Discussion

I have collected references for past manuscripts which have found QTL in the region of each non-novel QTL detected in this manuscript. Like in my oil manuscript, I compare the effect sizes and PVE of these past QTL with those found in the current manuscript.

# What needs to be done

## Introduction

Has there been an analysis done to see if the parents of this population had the Danbaekkong marker? Brant mentioned this was being verified.

## Materials and methods

* Verify locations and location names. The locations right now in the manuscript are Wooster, OH and Central Crops research Station in Clayton, NC. Want to double check that These are the appropriate names for the locations/research stations.
* Plot techniques: Plot length, seed rate, any other treatments that were done.
* More details about the population parent pedigrees would be good. I could make a diagram like I did for my oil manuscript for supplementary information or have the data ready in case the reviewers ask for it.
* More information about the population development if necessary. I was thinking including some quick details about over what years the population was developed by SSD and potentially in what locations the population development was done.

## Discussion

Brant mentioned that another collaborator was working on confirming if the parents used in this manuscript had the Danbaekkong alleles. In general, I think this is what I’ll need the most help with because I’m less familiar with the objectives as they relate to the presence/absence of these alleles, at the very least, I’d want to talk through this when we meet with everyone on zoom.

# Main points

* The abstract, introduction, results, and materials and methods sections are pretty solid right now, but I’ll keep adding to them as we go along.
* I have collected data (QTL location, effect size, R^2) from past manuscripts that have found QTL in similar locations to those found in this manuscript, where possible. I’m using this data to compare with our findings and to comment on the stability of the QTL found with our study and the implications on their effectiveness for MAS in the discussion section.
* There’s some details about plot techniques and experimental design that I don’t have right now, but I think would improve the materials and methods section.
* Brant mentioned we were checking for the presence/absence of the Danbaekkong in the parents, since I’m not as familiar with this objective of the manuscript I’d like to go over it with everyone during the meeting to make sure I’m on the same page
  + And then adjust the introduction and discussion sections accordingly to accommodate for the information.