Breeding For Healthier Wheat: Investigating the Genetic Basis of Grain Quality

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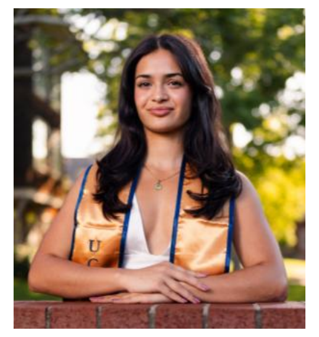


Introduction

- Approximately 75% of all US grain products are produced using wheat flour. (USDA, ERS)
- Wheat based products made with white flour can spike blood sugar quickly, which can increase risk for diabetes and obesity over time. (Li et al., 2022)

Glycemic Index Chart

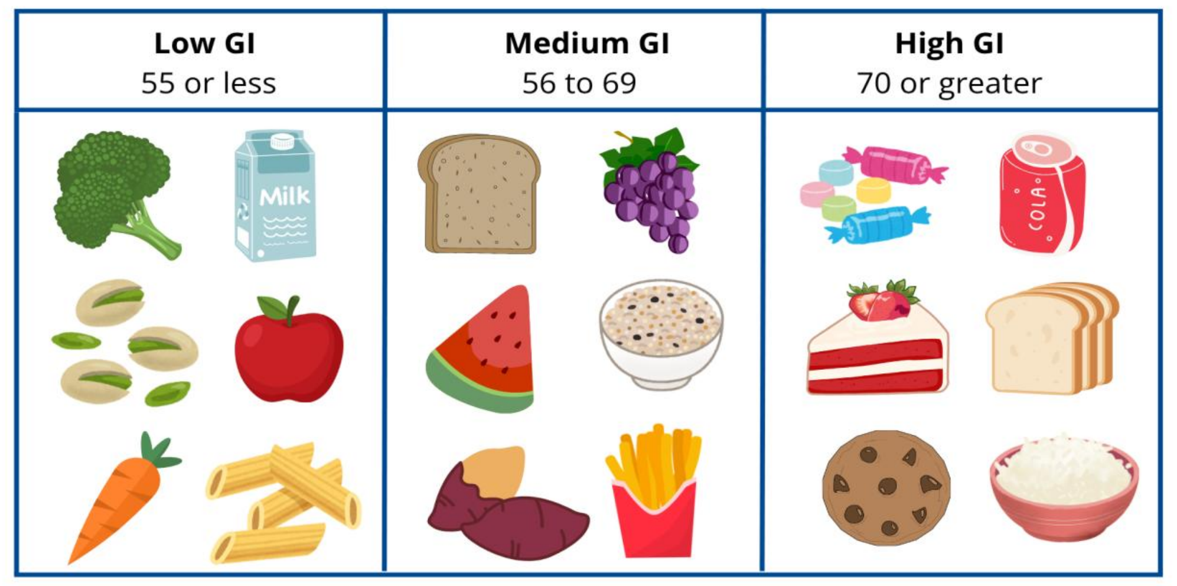


Figure 1. The glycemic index measures carbohydrate containing foods on a scale of 0 to 100 based upon how quickly they can increase blood sugar levels. Created using Canva.com.

- Currently, only about 20% of wheat grown in North Carolina goes to the milling and baking market.

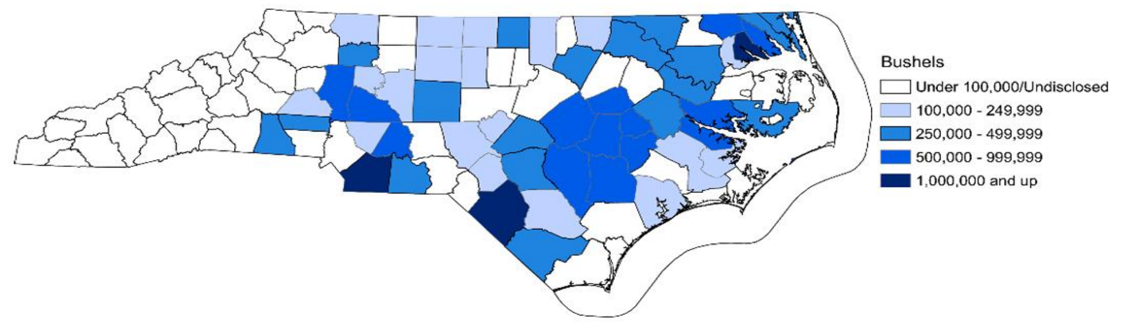


Figure 2. Winter wheat production (bushels/acre) by county in North Carolina in the year 2023. Adapted from USDA NASS.

Whole Wheat Flour vs. White Flour

- Whole wheat flour is rich in fiber, protein, vitamins, minerals, antioxidants, and phytochemicals and has a nutty taste.
- Most of the nutrients present in whole wheat are removed when it is refined to make white all-purpose flour.
- Refined white flour has an improved texture, better baking functionality, and a longer shelf life than whole wheat flour.

Bran

The bran is composed mainly insoluble dietary fiber, mainly cellulose and hemicellulose. It is also high in protein and micronutrients like phosphorus and potassium.

Endosperm

The endosperm is composed mainly of a carbohydrate called starch. Wheat starch can be broken down into two forms: amylose (unbranched) and amylopectin (branched).

Germ

The germ is the seed embryo and eventually develops into a young wheat plant. It is made up of protein, vitamins, and lipids (oils).

Figure 3. Cross section of a wheat kernel. Image Credit: Shailesh Acharya.

Objectives

1. Identify significant SNP-trait associations and quantitative trait loci (QTL) underlying twelve key grain quality traits.

2. Introgress traits from low-glycemic and low-gluten wheat varieties into North Carolina germplasm.

Genotyping-By-Sequencing (GBS) and Bioinformatics Pipeline

- This project utilized a collection of modern wheat lines from collaborative nurseries representing germplasm from the Southeastern United States.
- The DNA of each line is extracted and undergoes GBS which uses restriction enzymes to cut fragments of the DNA before sequencing.
- After sequencing, the GBS reads are aligned to the reference genome and single nucleotide polymorphisms (SNPs) are identified.

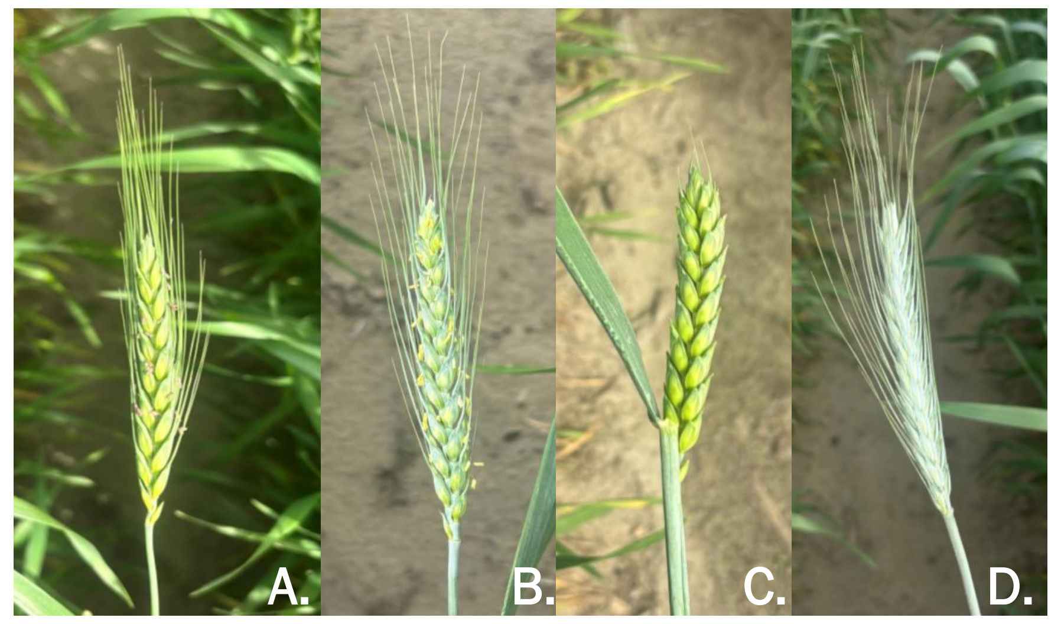


Figure 5. Heads of wheat in various stages of development from the NCSU yield trials.

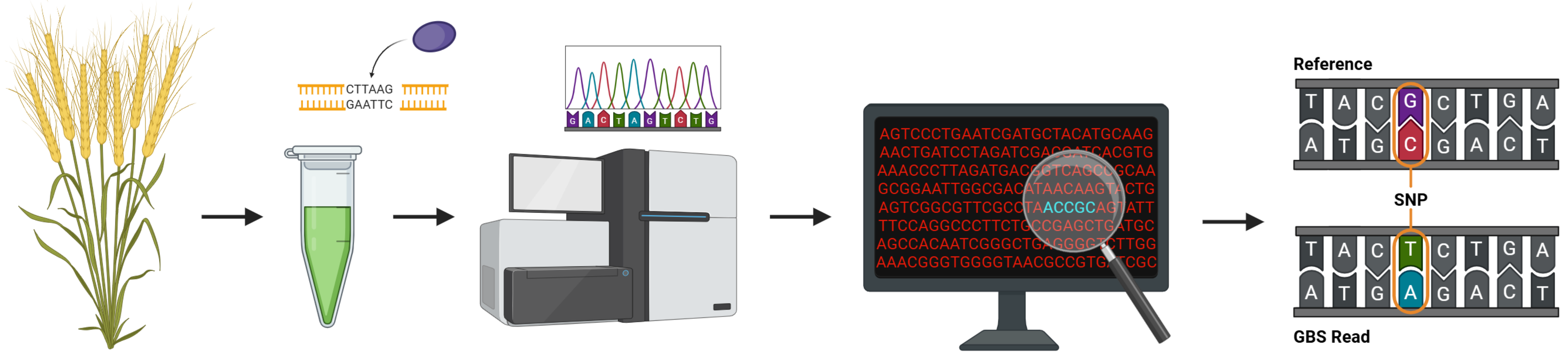


Figure 6. The GBS and Bioinformatics pipeline. Created using BioRender.com.

Results

- **52 significant SNP-trait associations were identified for eleven of the twelve grain quality traits, including key indicators for flour quality and gluten strength.**

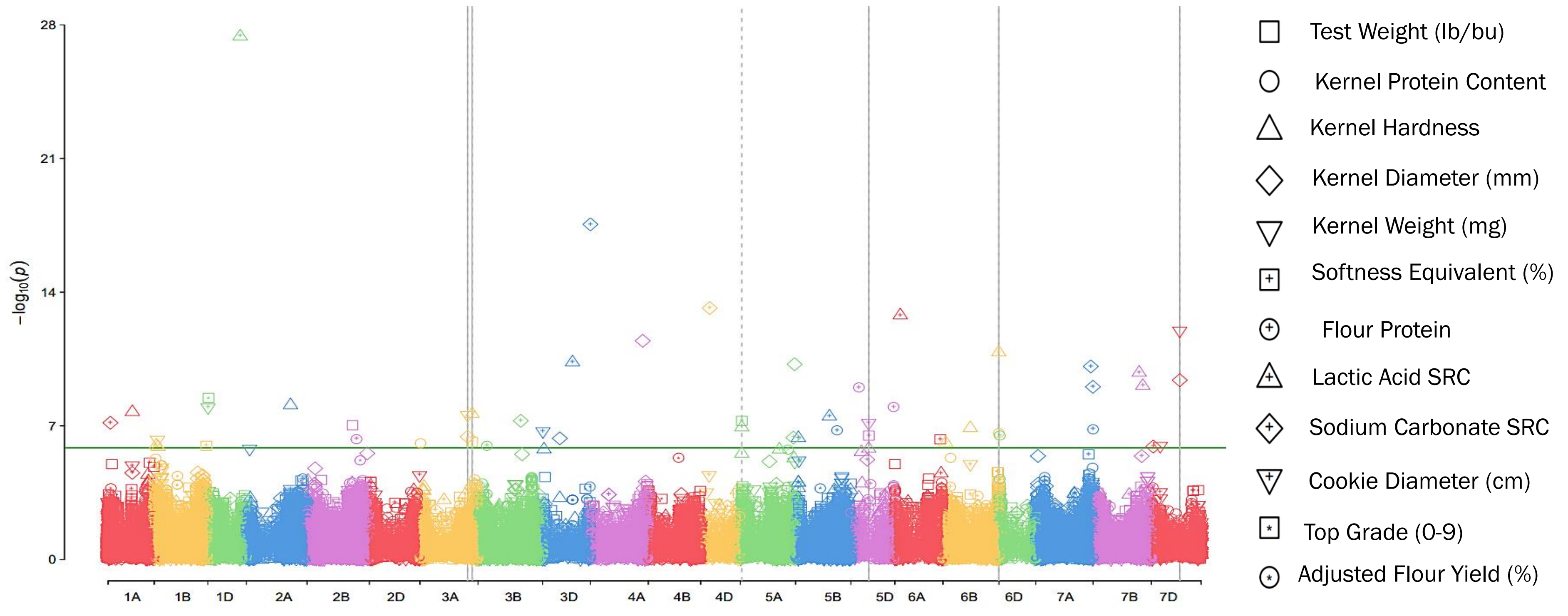
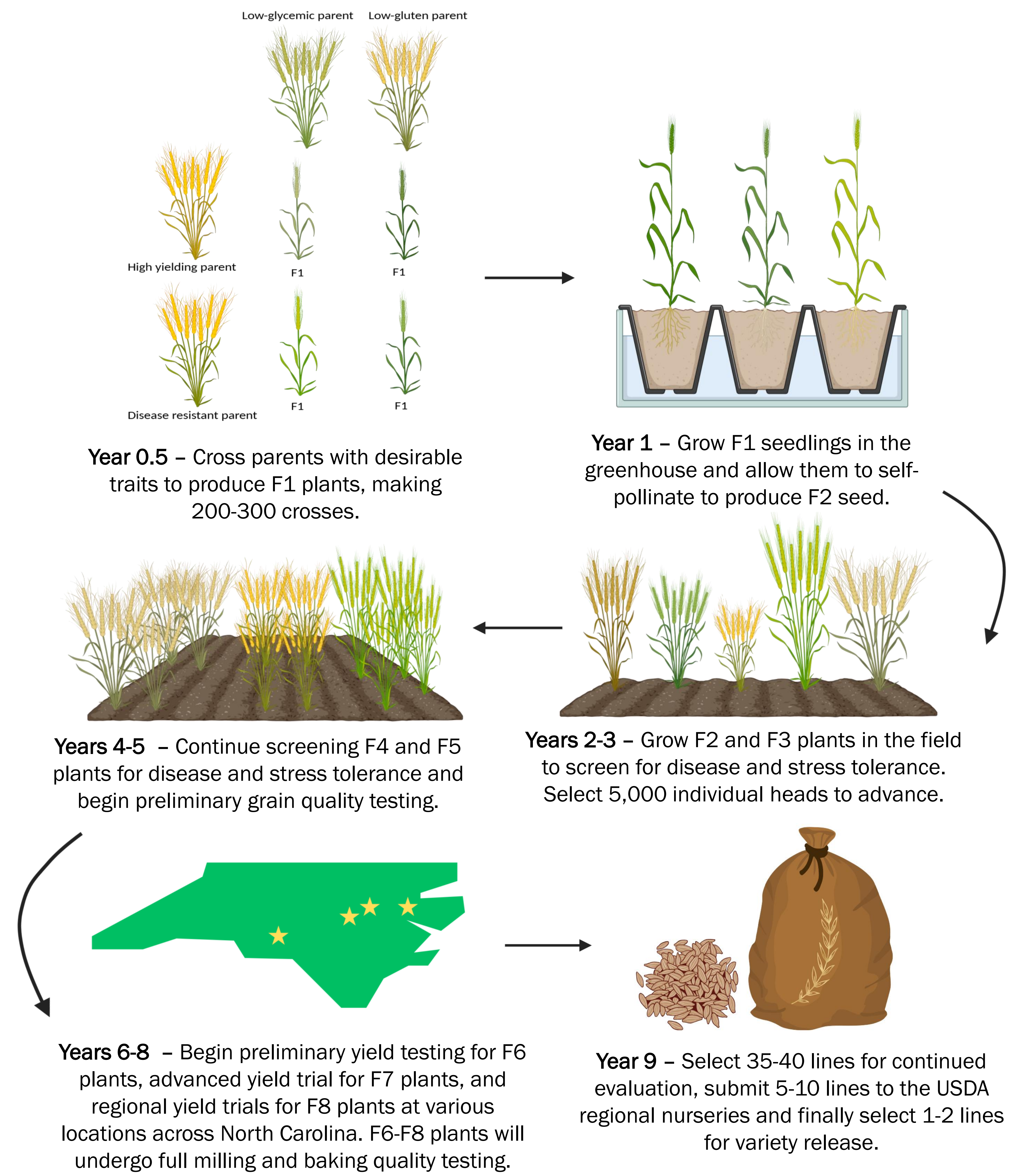


Figure 7. Manhattan plot identifying significant SNP-trait associations for the 12 grain quality traits. The dashed line indicates that two traits share a significant SNP in common. The solid line indicates that more than two traits share a significant SNP in common.

Grain Quality Crossing Block and Breeding Pipeline



Year 0.5 – Cross parents with desirable traits to produce F1 plants, making 200-300 crosses.

Year 1 – Grow F1 seedlings in the greenhouse and allow them to self-pollinate to produce F2 seed.

Years 2-3 – Grow F2 and F3 plants in the field to screen for disease and stress tolerance. Select 5,000 individual heads to advance.

Years 4-5 – Continue screening F4 and F5 plants for disease and stress tolerance and begin preliminary grain quality testing.

Years 6-8 – Begin preliminary yield testing for F6 plants, advanced yield trial for F7 plants, and regional yield trials for F8 plants at various locations across North Carolina. F6-F8 plants will undergo full milling and baking quality testing.

Year 9 – Select 35-40 lines for continued evaluation, submit 5-10 lines to the USDA regional nurseries and finally select 1-2 lines for variety release.

Conclusion

- The identified SNP–trait associations will be used to support selection decisions in the grain quality crossing block, as well as future work in genomic selection and prediction models.

References and Funding

USDA Agricultural Research Service
SunGrains
U.S. Wheat & Barley Scab Initiative