

Potential for Genetic Improvement of Wheat Quality Traits In Hard Spring Wheat

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Importance of Wheat Quality

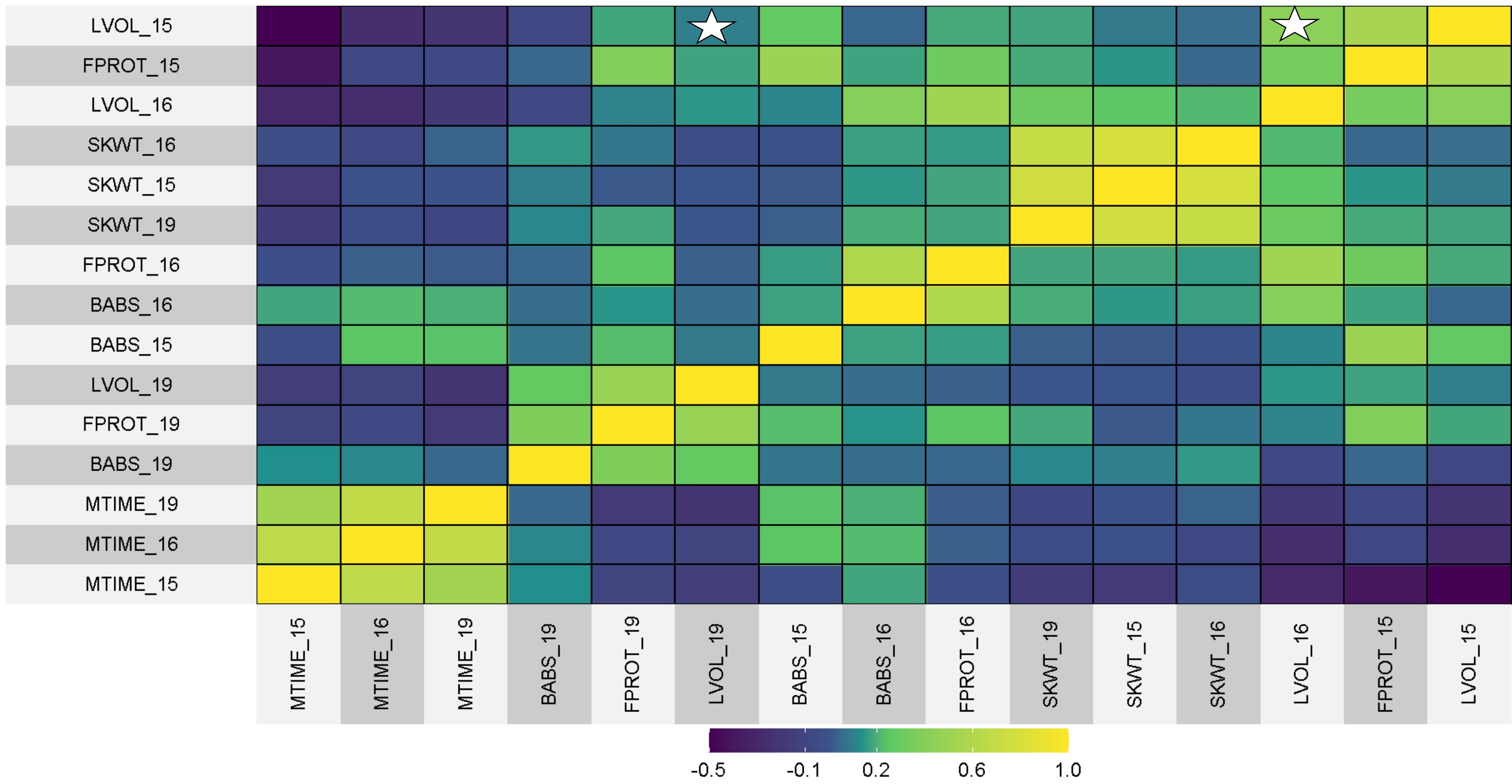
Spring wheat cultivars must have acceptable wheat quality traits to be marketable to millers and consumers. The hard wheat market class should have high protein content and protein strength along with good bread making qualities (2). The improvement of quality traits within wheat market classes can be slow due to costly phenotyping and limited to later generations in the breeding program. Development of molecular markers or statistical models that can differentiate between acceptable and unacceptable wheat quality will save time, money, and increase genetic gain of quality traits (3).

Background

A population of recombinant inbred lines was developed by crossing two hard wheat cultivars, Kelse and Scarlet. Kelse and Scarlet were selected for this study because they carry the same alleles for genes known to have a major impact on wheat quality. Both parents carry the same alleles at loci controlling High Molecular Weight Glutenin production on 1A,1B, and 1D. However there appeared to be segregation between the parents for loci controlling Low Molecular Weight Glutenins on 1B and 1D short. The goal of creating this population was to discover new genes impacting wheat quality that would otherwise be masked behind the outsized impact of segregation for High Molecular Weight Glutenin alleles. The population was advanced through single seed descent to the F6 generation at which time 180 recombinant inbred lines were genotyped with both genotyping by sequencing and the Illumina Infinium 90k Wheat Chip. A linkage map was created using 2,550 total markers. The population was grown over three years at Spillman Agronomy Farm in Pullman, Washington and phenotyped for sixteen quality traits at the Western Wheat Quality Laboratory. For this poster, only data for the five quality traits described below will be discussed (5).

Abbreviation	Trait	Description
BABS	Bakewater Absorption	Amount of water needed to add to dough for breadmaking
FPROT	Flour Protein	Percent Protein content of milled wheat flour
LVOL	Loaf Volume	Volume of a baked loaf of bread with a set weight of dough
MTIME	Mixing Time	Optimum mixing time for dough
SKWT	Single Kernel Weight	Average weight of a wheat kernel

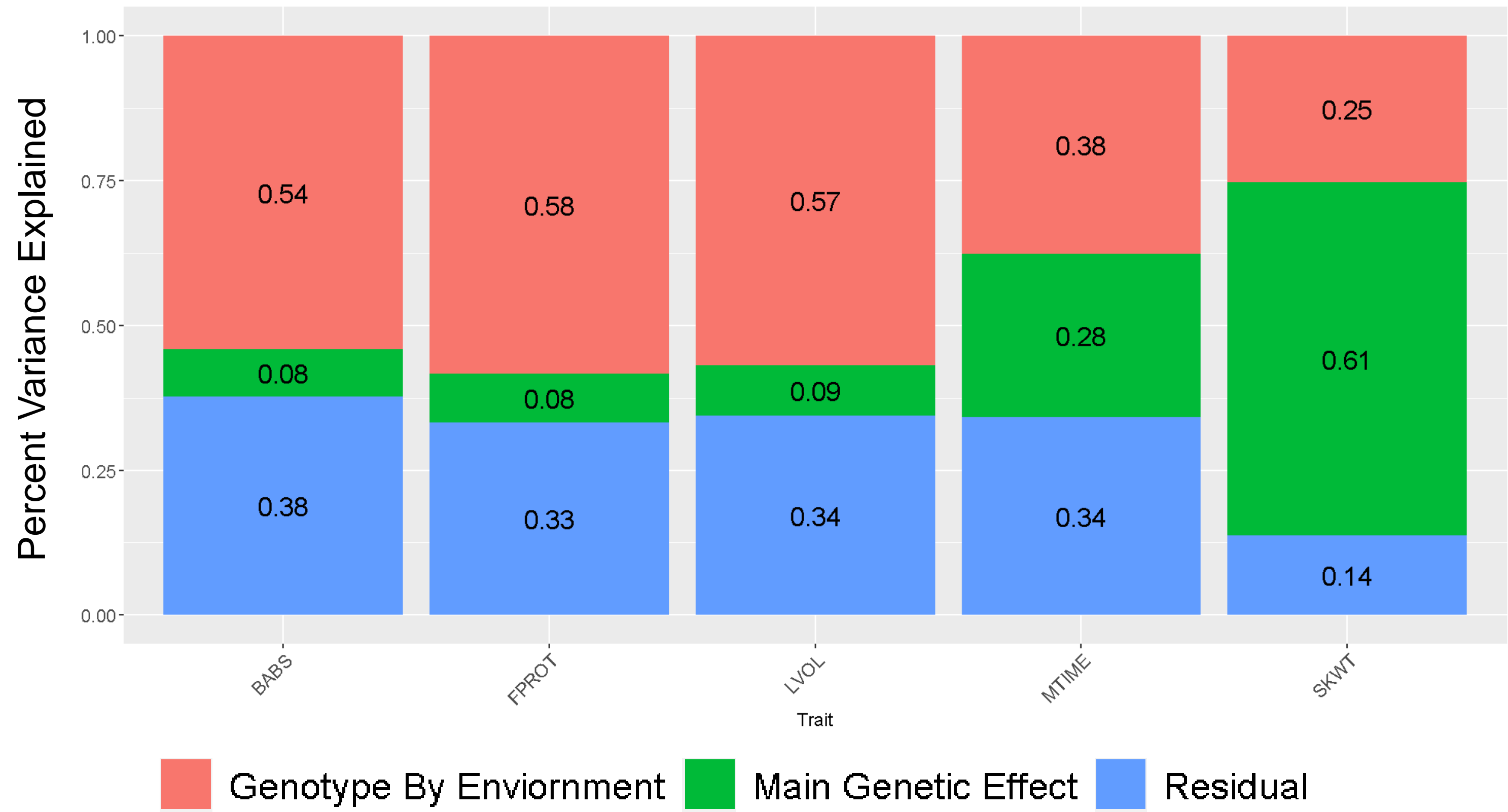
Correlation Between Traits By Year



The relationship between traits changes between growing seasons. For example, the LVOL data between 2015 and 2016 is highly correlated, while the 2019 LVOL data is weakly related to both 2015 and 2016 LVOL data. The white stars highlight these datapoints.

Variance Component Analysis

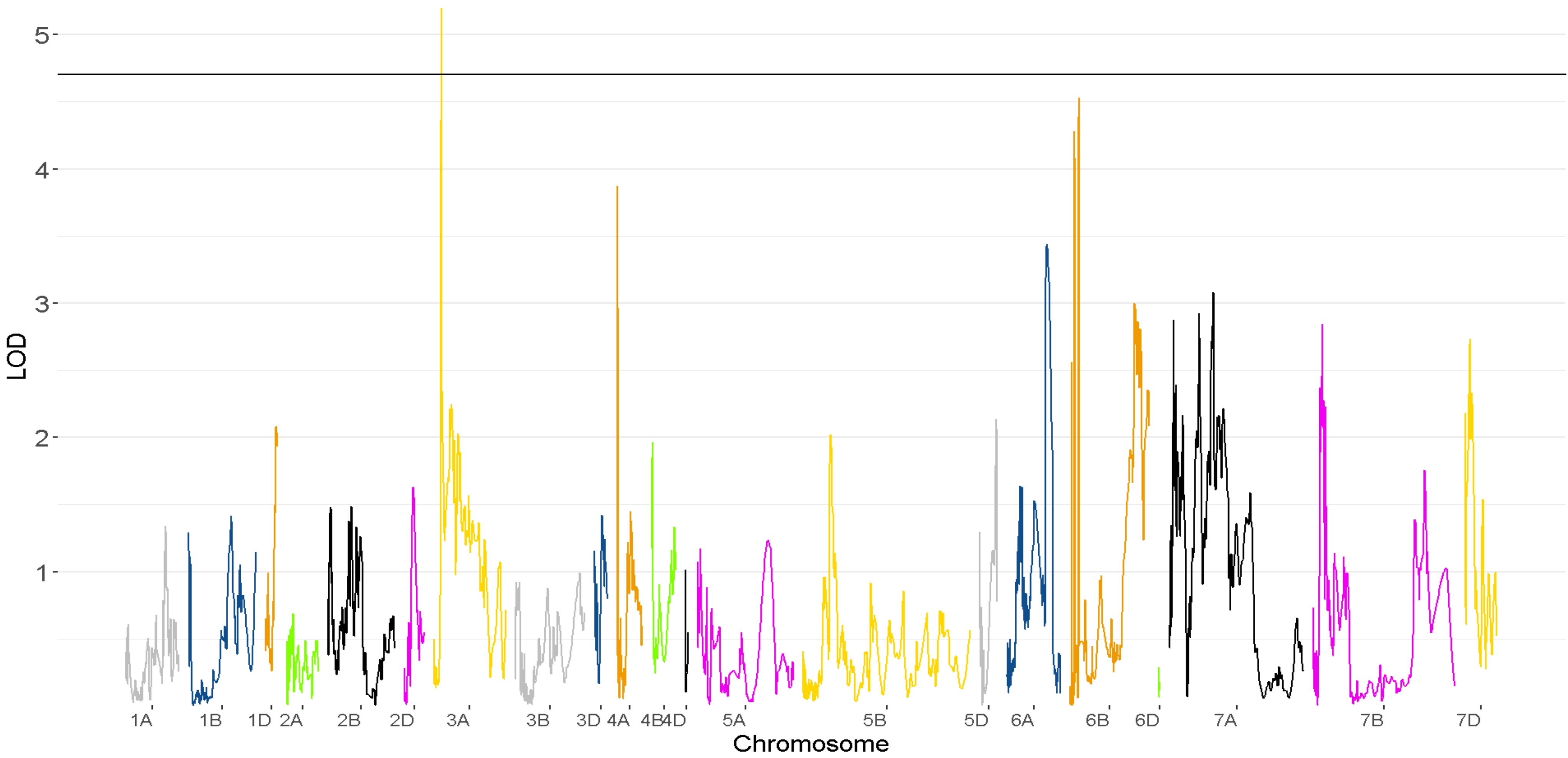
Estimation of variance components in the population was performed for the five studied wheat quality traits over the three growing seasons. A GBLUP model was created per trait to estimate the main additive genetic effect, growing season specific additive effects, and residual error using a realized relationship matrix within the population using BGGE(1). BABS, FPROT, and LVOL had greatest portion of variation explained by genotype by environment interactions while SKWT was mainly controlled by the main additive genetic effect.



QTL Mapping

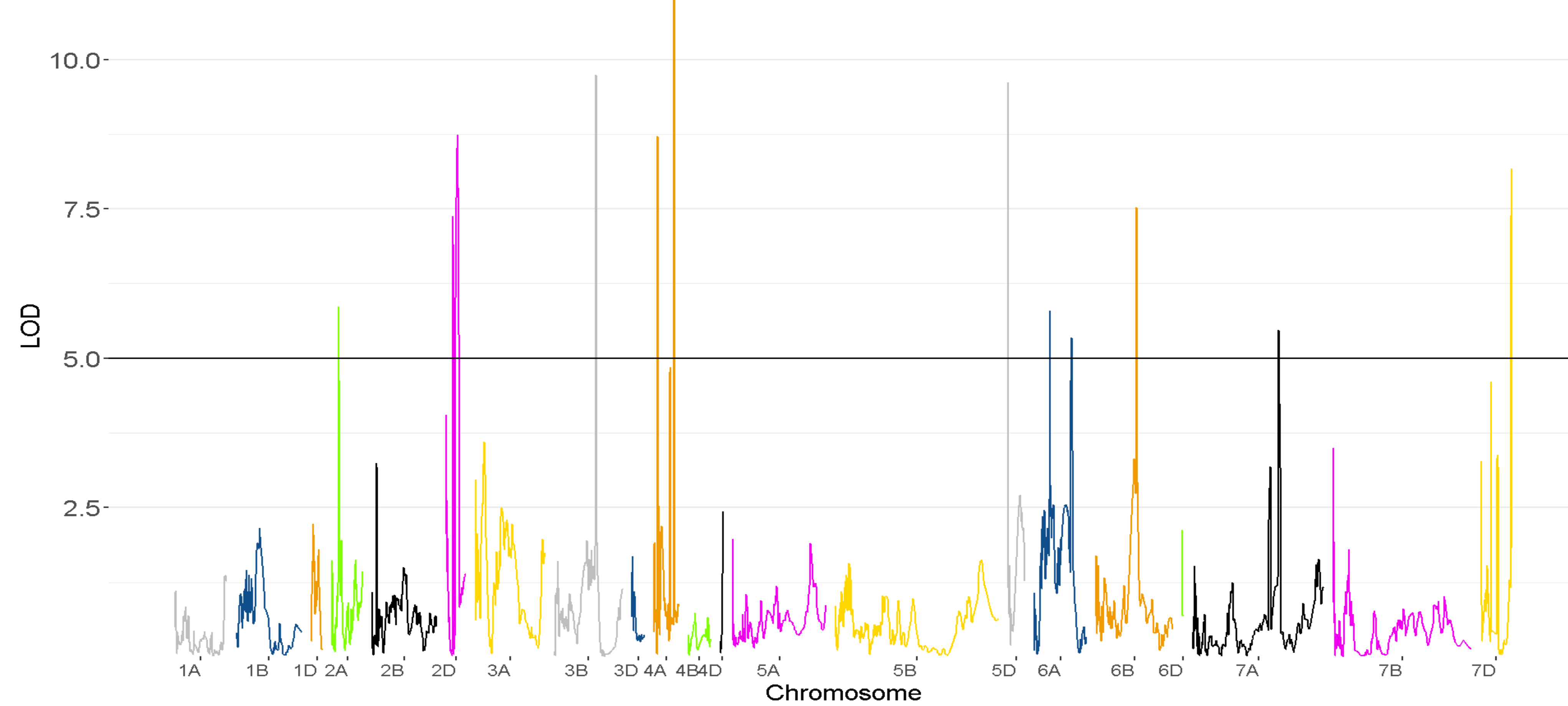
Due to large genotype by environment interactions, multi-environment QTL mapping was performed with QTL IciMapping software using the multi-environment additive effects model (4). 1,000 repetitions of permutation testing at Alpha .05 was performed to determine significance of results.

Loaf Volume (LVOL) Mapping Results



Loaf Volume analysis revealed a region on 3A short that explained 12% of the variation across all years. The Kelse allele for this locus had a positive effect on loaf volume in 2015 and 2016, while having a negative effect in 2019.

Single Kernel Weight (SKWT) Mapping Results



Kernel Weight analysis revealed several regions with additive effects consistent across all years, in some cases on the same chromosome. Both parents provided allelic variants that increased or decreased Kernel Weight. All markers above the LOD permutation test threshold explained 45% of the variation in the three years of data.

Conclusions

The amount of variation that could be explained by significant loci varied across the five studied traits. Mapping for BABS revealed two significant loci explaining 13% of the variation in total. FPROT only had one significant mapping result explaining 4% of the variation in the data. MTIME had eight significant results explaining 40% of the variation over the three years. One significant result for MTIME was found on 1B short and possibly colocalizes with a known gene controlling Low Molecular Weight Glutenins. Very little of the variation for FPROT, LVOL, and BABS could be explained through QTL analysis, suggesting that the traits are highly polygenic in populations fixed for High Molecular Weight Glutenin loci. Traits like SKWT or MTIME that had several significant results still had minor additive effects per significant locus. Multi-environment genetic analysis with QTL mapping or GBLUP was able to reflect the variation in phenotypic data across years, showing that both approaches can be used to improve hard wheat quality.

Sources

- (1)Granato, I., Cuevas, J., Luna-Vázquez, F., Crossa, J., Montesinos-López, O., Burgueño, J., & Fritsche-Neto, R. (2018). BGGE: A new package for genomic-enabled prediction incorporating genotype × environment interaction models. *G3 Genes/Genomes/Genetics*, 8(9), 3039–3047. <https://doi.org/10.1534/g3.118.200435>
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- (3)Kiszonas, A. M., & Morris, C. F. (2018). Wheat breeding for quality: A historical review. *Cereal Chemistry*, 95(1), 17–34. <https://doi.org/10.1094/cchem-05-17-0103-fi>
- (4)Li, S., Wang, J., & Zhang, L. (2015). Inclusive composite interval mapping of QTL by environment interactions in biparental populations. *PLOS ONE*, 10(7). <https://doi.org/10.1371/journal.pone.0132414>
- (5)*Wheat Analysis System – Description of Abbreviations*. Western Wheat Quality Laboratory . (n.d.). <https://wwql.wsu.edu/wheat-was/wheat-was-abbrev/>