QTLs Affecting Sweet Corn Carbohydrate Content and Eating Quality in *sugary1*

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Introduction

There are three main endosperm genotypes for commercial sweet corn varieties: sugary (*su1*), sugary enhancer (*su1se1*), and supersweet (*sh2*). The "sugary enhancer" genotype is a double mutant *su1/su1, se1/se1* and has been one of the most widely grown in fresh market production. Sugary enhancer quality has been attributed to an excellent texture, good flavor, elevated sweetness, and a thin pericarp. However, inconsistencies in sugar and starch accumulation indicate other loci contribute to sugary enhancer quality.

Objective

Identify quantitative trait loci (QTLs) of modifier loci of sugary enhancer quality in a *su1* background in sweet corn (*Zea mays*), using F_5 recombinant inbred lines (RILs) derived by single seed descent (SSD).

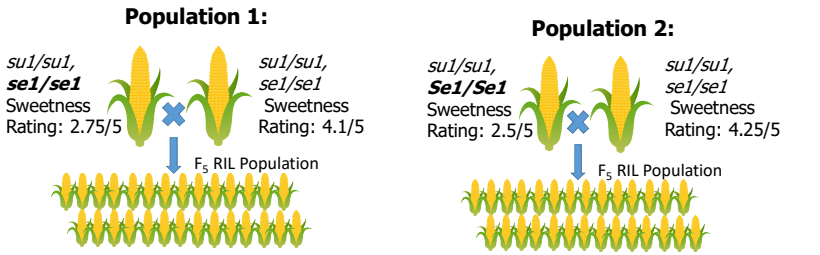
Methods

Field Analysis: Two RIL populations were derived from biparental crosses of sister lines of divergent sweetness, one heterozygous for *se1* and one homozygous. Once at F_5, families were self pollinated and harvested at eating stage and maturity. Finished inbreds were grown in an augmented RCBD with check genotypes to account for blocking and environmental effects at one location in Madison, WI in summer 2016 and two locations in summer 2017.

Phenotypic Analysis: Two ears were harvested at 21 DAP (fresh), kernel subsamples were frozen with liquid nitrogen, bulked, lyophilized, and ground. Two ears were harvested at 45 DAP (mature), dried at 32°C for eight days, kernel subsamples were bulked and ground. Total carbohydrate content was measured, including total polysaccharides, starch, phytoglycogen, sucrose, fructose, glucose, and total sugar. Closed sets of carbohydrate content for fresh and dry harvest dates were created using a NIRS FOSS DS2500 Feed Analyzer and were validated with a 10% random subsample using wet lab enzymatic assays.

Genotypic Analysis: DNA was collected from V2 stage leaves. Genotyping by sequencing (GBS) was conducted and a linkage map of 20,000 single nucleotide polymorphism (SNP) markers was created using TASSEL v5 and aligned to B73 RefGen_V3.

Statistical Analysis: Linkage map analysis was conducted using the R package R/QTL. Composite interval mapping (CIM) was used to create permutations at a 5% significance threshold and LOD scores were used estimate QTL positions.



Results

Figure 1: Distribution of Carbohydrate Components

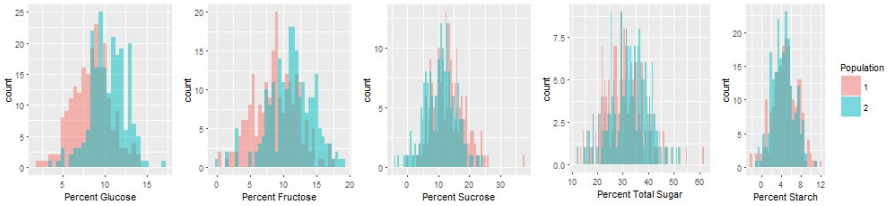


Figure 1: The distribution of ~~the~~ fresh harvest predicted values for glucose, fructose, sucrose, sugar, and starch.

Figure 2: Manhattan Plots of Selected Trait Data

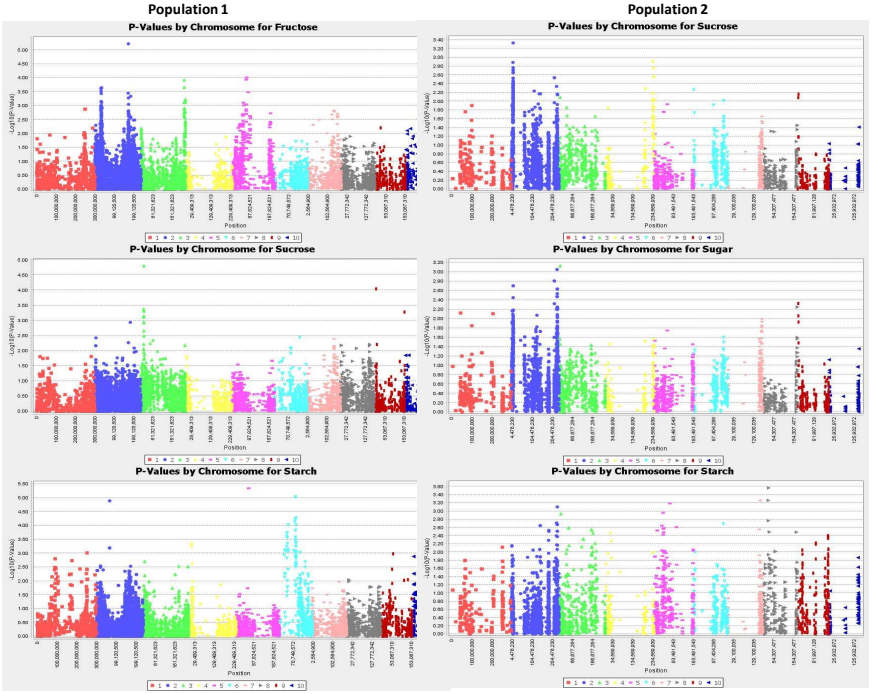


Figure 2: P-values from GLM analysis of fresh harvest trait analysis from populations 1 (15,427 sites) and 2 (4,916 sites). No significant markers were found for glucose and total sugar in population 1 and for glucose and fructose in population 2. Significance thresholds are not shown.

Figure 3:Prediction Models for Carbohydrate Components

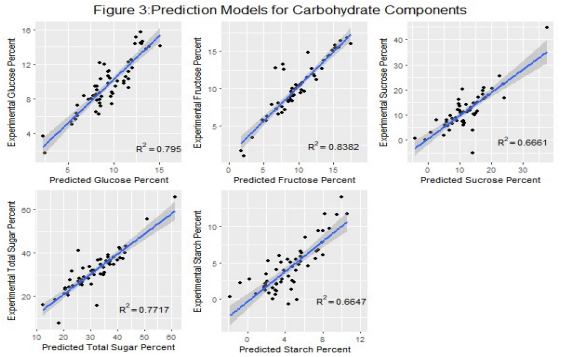


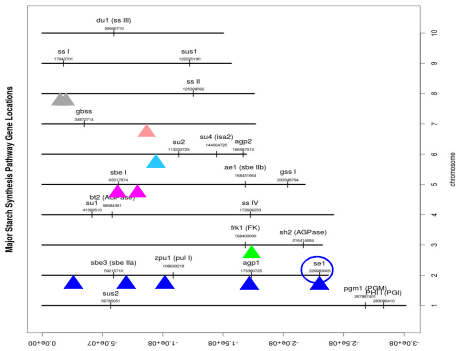
Figure 3: Prediction models for fresh harvest carbohydrate traits. Phytoglycogen and dry harvest traits were not included due to insufficient prediction power.

Discussion

Fresh harvest carbohydrate traits are quantitatively inherited with normal distributions. In Population 1, 4 QTL for starch and 1 QTL for fructose, sucrose, and glucose each were found. In Population 2, 4 QTL for starch and 1 QTL for sucrose and sugar each were found. The marker for *se1* on the end of chromosome 2 is significant in both populations and has a larger allelic effect in population 2 as was expected.

The marker depression on chromosome 4 is likely the large non-segregating *su1* linkage block.

The prediction models show carbohydrate traits can be estimated by NIR for more high throughput phenotyping. Our ultimate goal is to fine map genes that significantly affect *se1/su1* carbohydrate content and use marker based selection to improve sweet corn eating quality.



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