High Fidelity Detection of QTL for Biomass Production from Rapid Imaging of a C4 Grass Crop in the Field

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Project Goals: The development of next generation bioenergy feedstocks that meet the demands of an emerging bioenergy economy requires exponentially accelerated crop improvement relative to the gains of conventional plant breeding. Recent advances in sequencing technologies have improved evaluation of genetic variance within germplasm collections. However, applying this genomic knowledge to detect genotype-to-phenotype associations is limited by our current ability to phenotype large mapping populations cheaply and quickly, especially for complex traits such as biomass. This necessitates the development and testing of diverse technologies that can assess plant physiology and growth in non-destructive and high-throughput ways. This study tested the use of hemispherical photography as a means to detect QTL for biomass production and demonstrates the fidelity and potential of rapid imaging as a high-throughput phenotyping technique for quantitative genetics studies on field grown bioenergy feedstocks.

Current rates of crop improvement are inadequate to meet demands for high productivity agriculture that is ecologically sustainable and resilient to global environmental change. High-throughput, non-destructive methods for assessing plant growth and function are a widely anticipated solution to the "phenotyping bottleneck" that currently limits discovery of genotype-to-phenotype relationships for crop breeding and biotechnology. However, proof of concept is needed to demonstrate that a high-throughput phenotyping technique can be applied to field trials of grass crops to detect the genetic architecture of a productivity trait as effectively as destructive harvest techniques. This study demonstrates the fidelity of hemispherical photography as a method to detect quantitative trait loci (QTL) for above-ground biomass production that co-localize with results from destructive harvests in a recombinant inbred population derived from a *Setaria italica* x *Setaria viridis* cross. Plant area index (PAI) was estimated from hemispherical photographs acquired in 8 person-hours. Total above-ground, vegetative, leaf, stem, and panicle masses were estimated by a destructive harvest and weighing protocol requiring 150 person-hours. Five clusters of QTL for biomass traits were identified. All clusters included QTL for PAI and leaf mass. Fewer clusters included QTL for vegetative mass (4 QTL), total above-ground mass (3 QTL) and stem mass (2 QTL). There was not overlap between QTL clusters for PAI and those detected for traits associated with bushiness and partitioning to seeds. This demonstrates the potential for a non-destructive, high-throughput phenotyping technique that is cheap and scalable to replace destructive and slow harvest methods for discovery of genotype-to-phenotype relationships for grass crop biomass production.