

Quantitative Trait Loci for Leaf Carbon Isotopic Signature and Transpiration Efficiency in the C₄ grass *Setaria*

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Project Goals: The objectives of this project are to 1) identify the gene regulatory and metabolic networks important for adaptation to low water availability and high-density plantings and to gain a greater understanding of the physiology underlying these adaptations and 2) develop technologies to precisely control gene insertion and replacements events for large scale engineering of pathways in model and target feedstocks.

Abstract: Leaf carbon isotopic composition ($\delta^{13}\text{C}_{\text{leaf}}$) in C₄ plants is a proposed proxy for transpiration efficiency (TE) suitable for high throughput phenotyping. To test this, we studied the C₄ plants *S. viridis* (A10) and *S. italica* (B100) to determine the relationship between TE and $\delta^{13}\text{C}_{\text{leaf}}$. We found that $\delta^{13}\text{C}_{\text{leaf}}$ differentiated between well-watered and water-limited plants and correlated with plant- and leaf-level measures of TE (Ellsworth et al., in review). Following this experiment, we used a population of 217 recombinant inbred lines (RIL) derived from A-10 and B-100 to identify quantitative trait loci (QTL) relating to $\delta^{13}\text{C}_{\text{leaf}}$ and TE under both well-watered and water-limited conditions. The experiment was conducted in the Bellweather Phenotyping Facility at the Danforth Center where plant size and water use was measured daily. Leaf $\delta^{13}\text{C}$ was significantly more negative in the water-limited treatments ($P < 0.0001$). Additionally, TE and $\delta^{13}\text{C}_{\text{leaf}}$ had co-localized QTL on chromosome 7 and 9. Additionally, the additive effects associated with these QTL were in opposite directions corroborating the negative relationship between TE and $\delta^{13}\text{C}_{\text{leaf}}$ commonly reported in C₄ plants. Plant size and transpiration also had the same co-localized QTL as TE and $\delta^{13}\text{C}_{\text{leaf}}$. Two unique QTLs were found for TE that were not present for either plant size or transpiration on chromosome 5 and 9, suggesting these two QTLs are independent of either biomass production or transpiration. Having identified the same QTLs for $\delta^{13}\text{C}_{\text{leaf}}$ and TE, we are

moving closer to finding a genomic control of TE and to using marker-assisted approaches to select for TE in C₄ plant breeding programs.

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