

Leaf carbon isotope composition in *Setaria*: genetic contribution and potential for high throughput screening for water use efficiency in C₄ plants

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Project Goals: 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 understand 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: Increasing whole plant water use efficiency (yield per transpiration; WUE_{plant}) through plant breeding can benefit the sustainability of agriculture and improve yield under drought. To select for WUE_{plant} a high throughput method of phenotyping must be developed, and the genetic architecture of traits such as transpiration efficiency (TE_i ; rate of CO₂ assimilation relative to stomatal conductance) must be better understood. Leaf carbon stable isotope composition ($\delta^{13}\text{C}_{\text{leaf}}$) has been proposed as a high throughput proxy for TE_i , and there is a negative correlation between $\delta^{13}\text{C}_{\text{leaf}}$ and both WUE_{plant} and TE_i in the C₄ model grass species *Setaria*. Therefore, a water limitation experiment was conducted where transpiration, biomass, WUE_{plant} , and $\delta^{13}\text{C}_{\text{leaf}}$ were measured on a recombinant inbred line (RIL) population of *Setaria viridis* and *S. italica* to better define the genomic control of WUE_{plant} and TE_i . Three quantitative trait loci (QTL) for $\delta^{13}\text{C}_{\text{leaf}}$ were co-localized with transpiration and biomass, but not with WUE_{plant} . However, $\delta^{13}\text{C}_{\text{leaf}}$ was negatively correlated with WUE_{plant} when WUE_{plant} was calculated for allele classes based on the allele combinations of the three QTL for $\delta^{13}\text{C}_{\text{leaf}}$. This negative relationship suggests that variation in WUE_{plant} across these allele classes is in part due to differences in TE_i . In this C₄ grass population, multiple traits can influence WUE_{plant} ; however, the analysis of $\delta^{13}\text{C}_{\text{leaf}}$ provides insights into how TE_i contributes to WUE_{plant} . The data presented here suggests that $\delta^{13}\text{C}_{\text{leaf}}$ can be used in marker-assisted breeding to select for TE_i and to better understand the genetic architecture of TE_i and WUE_{plant} in C₄ species.

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