

Trait components of whole plant water use efficiency are defined by unique, environmentally responsive genetic signatures in the model C₄ grass *Setaria*

Ivan Baxter^{1,3*} (ivan.baxter@ars.usda.gov), Max Feldman¹, Asaph B. Cousins², Patrick Z. Ellsworth² and **Tom Brutnell**¹

¹Donald Danforth Plant Science Center, St. Louis, MO 63132, ²Washington State University, Pullman, WA 99163, ³USDA-ARS, Plant Genetics Research Unit, St. Louis, Missouri, USA`

url: <http://foxmillet.org>

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: Plant growth and water use are interrelated processes influenced by the genetic control of both plant morphological and biochemical characteristics. Improving plant water use efficiency (WUE) to sustain growth in different environments is an important breeding objective that can improve crop yields and enhance agricultural sustainability. However, genetic improvements of WUE using traditional methods have proven difficult due to low throughput and environmental heterogeneity encountered in field settings. To overcome these limitations the study presented here utilizes a high-throughput phenotyping platform to quantify plant size and water use of an interspecific *Setaria italica* x *Setaria viridis* recombinant inbred line population at daily intervals in both well-watered and water-limited conditions. Our findings indicate that measurements of plant size and water use in this system are strongly correlated; therefore, a linear modeling approach was used to partition this relationship into predicted values of plant size given water use and deviations from this relationship at the genotype level. The resulting traits describing plant size, water use and WUE were all heritable and responsive to soil water availability, allowing for a genetic dissection of the components of plant WUE under different watering treatments. Linkage mapping identified major loci underlying two different pleiotropic components of WUE. This study indicates that alleles controlling WUE derived from both wild and domesticated accessions of the model C₄ species *Setaria* can be utilized to predictably modulate trait values given a specified precipitation regime.

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