Genome Wide Association Study of Multiple High-Throughput Phenotyping Experiments to Identify Genetic Loci Controlling Water Use Efficiency in C4 Grass Setaria

Collin Luebbert[1], Greg Ziegler[1], Charles Pignon[1], Allen Hubbard[1], Louis Connelly[1], Jennifer Barrett[1], Hui Jiang[1], Max Feldman[1], Todd Mockler[1], Andrew Leakey[2], Darshi Bannan[2], Rachel Paul[2], Patrick Ellsworth[3], and Ivan Baxter[1]

[1]Donald Danforth Plant Science Center
[2]University of Illinois
[3]Washington State University

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Abstract

Irrigation of crops accounts for a significant portion of fresh water consumption. In order to utilize this resource more efficiently, it is necessary to engineer crops that can more efficiently use water. Water use efficiency, defined as the ratio of plant growth to water used, is a complex property of plants affected by many different factors. Despite this complexity, genetic variability has been able to be identified in a number of different crops. The C4 model species Setaria viridis remains under-studied in this regard and consequently we sought to identify promising genetic loci contributing to variation in water use efficiency. In order to accomplish this goal we leveraged the high-throughput phenotyping platform at the Donald Danforth Plant Science center to grow S. viridis in well-watered and water-limited conditions. This automated system enables strict control of watering regimes as well as measures of plant traits extracted from photographs using computer vision. Combining these two sets of data allows for direct measurement of whole-plant water-use efficiency on a daily basis which was used as a response variable in a genome wide association study. Significant associations were found for water-use efficiency and related traits. These loci were then prioritized further by pooling information across each day of an experiment and across multiple experiments to zero in on the most likely locations of genes responsible for driving water-use efficiency in S. viridis.

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[1]Donald Danforth Plant Science Center, St. Louis, MO, USA
[2]University of Illinois, Urbana, IL, USA
[3]Washington State University, Pullman, WA, USA

ORCiD: 0000-0002-8665-5950

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