THE INTEGRATION OF HIGH-THROUGHPUT PHENOTYPING AND GENOTYPING-BY-SEQUENCING TO GENETICALLY DISSECT THE PHYSIOLOGICAL RESPONSES OF COTTON TO A HOT, ARID ENVIRONMENT

Michael Gore
USDA-ARS, U.S. Arid-Land Agricultural Research Center
Maricopa, AZ
Pedro Andrade-Sanchez
University of Arizona, Maricopa Agricultural Center
Maricopa, AZ
David D. Fang
USDA-ARS, Southern Regional Research Center
New Orleans, LA
Andy French
Doug Hunsaker
USDA-ARS, U.S. Arid-Land Agricultural Research Center
Maricopa, AZ
Jesse Poland
USDA-ARS, Kansas State University
Manhattan, KS
Jeff White
USDA-ARS, U.S. Arid-Land Agricultural Research Center
Maricopa, AZ
Arizona Phenomics Consortium
USDA-ARS, University of Arizona
Maricopa, AZ

Abstract

In the past century, cotton has been adapted to the low desert, irrigated production areas of central Arizona. Despite progress, it will be perhaps a greater challenge to further increase the yield and quality of cotton in this period of global climate change and diminishing fresh water supplies. Genetic improvement of cotton via modern plant breeding is the most sustainable and economical approach to address these eminent problems. However, the development of superior heat tolerant and water-use efficient cotton cultivars has been slowed by the polygenic inheritance and relatively lower heritability of economical traits in stress environments. Moreover, there is limited knowledge of the key genes that underpin physiological and biochemical traits that relate to improved productivity under high temperatures and water deficit.

To that end, we developed and evaluated genotyping-by-sequencing (GBS) and field-based high-throughput phenotyping (HTP) tools for dissecting the genetic architecture of complex traits that are potentially important for higher cotton yield in the southwestern United States.

With a cotton recombinant inbred line (RIL) population (TM-1xNM24016) cultivated under well-watered and water deficit treatments, we demonstrated that simultaneous proximal remote sensing of canopy spectral reflectance and canopy temperature could be achieved over the growing season with a high-clearance tractor carrying replicated sets of sensors. We found both canopy temperature and normalized difference vegetation index (NDVI) to have a statistically significant time-by-treatment interaction and moderate to high heritability under both well-watered and water-deficit conditions. As a complement to field-based HTP, we conducted GBS on an Illumina HiSeq platform to score nearly 400 single nucleotide polymorphisms (SNPs) across the TM-1xNM24016 population of ~100 RILs. This simultaneous SNP discovery and genotyping was performed without a reference genome sequence or custom designed genotyping assays. We will next integrate these HTP and GBS data to conduct time-related QTL analysis. This research illustrates how powerful modern plant breeding tools can be leveraged in the genetic improvement of cotton.