

## 199. Genomics of Bioenergy Grass Architecture

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**Project Goals:** Understanding the genetics of plant architecture has taken on new importance with invigorated efforts to develop plant genotypes optimized for production of biomass for use in fuels or chemical feedstocks. We will increase knowledge of genetic determinants of components of plant architecture that are important to the ‘design’ of crop genotypes optimized for production of biomass from a range of environments, also characterizing allelic and haplotype variation in salient sorghum genes toward their deterministic utilization, and enabling new integrative queries of these and other results to accelerate discovery and utilization of genetic determinants in biomass crop improvement. This project fits closely with DOE missions of advancing energy security, scientific discovery, and environmental responsibility, and leverages and enhances the value of many existing resources.

**Abstract Text:** Variations in plant architecture are central to the yield potential of biomass crops under high-input conditions and are a key element of crop adaptation to marginal environments under which most cellulosic biomass production may occur. Optimal biomass productivity in temperate latitudes and/or under perennial production systems may require substantial changes to architecture of plants of tropical origin that have previously been adapted to annual cultivation. Sorghum is of intrinsic importance as one of the few crops suited to all proposed approaches for renewable fuel production, i.e. from starch, sugar, and/or cellulose; and as a model for functional genomics of bioenergy plants, in view of its C4 metabolism (unlike rice), its small genome (unlike many), and its low level of gene duplication resulting from ~70 million years of abstinence from genome-wide duplication (unlike switchgrass, Miscanthus, maize, sugarcane, and other grasses). Its remarkable diversity of morphologies make sorghum a particularly attractive model for dissecting the genetic basis of grass morphological diversity. Utilizing these advantages, we are employing forward genetics in three populations that broadly sample the eusorghum clade to obtain baseline QTL data for components of plant architecture and related traits, also assessing inter-relationships with one another and with perenniality; association genetics of positional and/or functional candidate genes to narrow the locations of QTLs, reveal haplotype diversity in trait-controlling regions, investigate roles in quantitative variation of major genes identified in other taxa, provide insight into the evolution and distribution of phenotypic variation in components of plant architecture and related traits useful toward numerous applications in sorghum genetics and breeding, and perhaps even identify functional variants in some instances; and facilitate integrative use of positional, diversity, and mutant information in discovery and utilization of genetic variation by using Gramene trait ontologies to ‘interleave’ (in silico) three well-characterized but to date isolated genetic resources. Collectively, these expected results will provide a foundation for deterministic improvement of sorghum itself, accelerate progress in dissecting the genetic control of plant architecture in the complex polyploid genomes of closely-related Saccharinae biofuel crops, and nurture new dimensions in plant functional genomics with novel integrative queries that may accelerate progress toward long-held goals and provide a powerful attraction to new investigators.

### Publications:

1. Wenqian Kong, Huizhe Jin, Changsoo Kim, Valorie H. Goff, Tae-Ho Lee and Andrew H. Paterson. 2014. Genetic analysis of vegetative branching in sorghum. *Theoretical and Applied Genetics* 127:2387-2403. DOI 10.1007/s00122-014-2384-x
2. Dong Zhang, Wenqian Kong, Jon Robertson, Valorie H. Goff, Ethan Epps, Alexandra Kerr, Gabriel Mills, Jay Cromwell, Yelena Lugin, Christine Phillips, Andrew H. Paterson 201#. *Comparative*

genetics of inflorescence and plant height components in divergent cereal lineages represented by sorghum (Panicoidae) and rice (Oryzoidae).

*This research was supported by the USDA National Institute of Food and Agriculture (NIFA), AFRI Competitive Grant no. 2012-67009-19718.*