

Analysis of Flowering Time Using a Massive Maize Mapping Panel

Edward S. Buckler^{1,2} and The Maize Diversity Project^{1,2,3,4,5,6,7}

¹ USDA-Agricultural Research Service;

² Cornell University, Ithaca, NY;

³ Cold Spring Harbor Laboratory, NY;

⁴ University of California-Irvine, CA;

⁵ North Carolina State University, Raleigh, NC;

⁶ University of Missouri, Columbia, MO;

⁷ University of Wisconsin, Madison, WI

The maize genome is a source of tremendous phenotypic and molecular diversity. Such abundant variation was first used by Native Americans to adapt maize to the tropics to the Andes to Canada. The long-term objective of our group is to understand how a complex trait like flowering time is controlled and evolved. To study complex traits, we have developed a design that can use both linkage and association approaches to provide high resolution and statistical power. The maize nested association mapping (NAM) panel is the product of crossing 26 highly diverse maize lines to B73, and then 5000 recombinant inbred lines were produced, phenotyped, and genotyped. This is the largest complex trait study of its kind, and it provides important insights into the nature of a genetic architecture for a species. We will discuss genetic architecture in terms the QTL distribution, effect size, sharing of QTL, correlations between traits, relationship to recombination, epistasis, interactions with the environment, and the QTL distribution relative to population structure.

We are currently testing the limits of linkage versus association mapping on this population. Through NAM, known QTL have been validated, but the full power of this system is being enabled with the ongoing sequencing of the parental lines by next generation sequencing technology and further high density genotyping. We will discuss the progress in identifying several other novel QTL down to the gene level. Large collaborative populations, association analysis, and genomic tools will likely revolutionize the study of complex traits.