Population Structure and Association Mapping in the Historical University of Minnesota Corn Germplasm

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From the 1920’s through the 1980’s, the University of Minnesota Corn Breeding program developed and released hundreds of inbred lines, including A619, A632, and A654. Many of these inbreds, referred to as the “A” lines, were developed from Minnesota 13, a very erstwhile open pollinated variety grown widely across the upper Midwest. A shift in the corn breeding industry from relying heavily on publicly derived inbreds to a greater reliance on proprietary germplasm has left the University of Minnesota corn seed storage facility more of a seed morgue than a seed bank. This historical germplasm may serve as a reservoir of variation for kernel composition, disease resistant or agronomic traits. Furthermore, new allele mining techniques provide an opportunity to survey this germplasm as its allelic potential remains unknown.

The objectives of my research are to: 1) characterize the population structure and linkage disequilibrium of the historical Minnesota germplasm and identify groups of lines unique to the MN germplasm; and 2) map quantitative trait loci (QTL) for kernel composition, disease resistance and other agronomic traits.

In this study, we will be using 143 A inbred lines and 141 inbreds lines developed by public and private breeding programs. The inbreds developed in private programs have expired Plant Variety Protection certificates and represent a germplasm resource that is becoming available for the research community (Mikel and Dudley, 2006). The lines were genotyped using Illumina’s Maize SNP50 Beadchip, providing more than 56,000 SNP markers. Linkage disequilibrium and population structure within this mapping population will be characterized, seeking to identify germplasm groups that are unique to the MN germplasm. Comparisons of LD decay will also be made between the A lines and the whole population and among subpopulations.

The historical Minnesota corn germplasm represents a potential source of major QTL for secondary traits such as kernel composition and disease resistance that has gone underutilized; therefore we are employing genomewide association mapping which is a technique developed to map QTL utilizing a broad population or group of individuals. Association mapping allows for the survey of a greater diversity of individuals at a higher resolution compared to the traditional bi-parental methods (Yan et al., 2011). Northern Corn Leaf Blight (NCLB), a foliar disease caused by Setosphaeria turcica, has been shown to reduce yield in most corn growing regions of the world. Major genes for race specific resistance have been identified but have proven to be unstable in different environments; therefore the identification quantitative resistance loci may provide a more stable source of resistance (Welz and Geiger, 2000). Additionally, numerous QTL for kernel composition have been identified in bi-parental mapping populations; however
most of these studies were conducted in a single genetic background, the Illinois High Oil
ergmplasm, and little is known about the architecture of this trait in other genetic backgrounds
(Wassom et al., 2008).

The characterization of LD and population structure in this project will lead to
information on the germplasm organization of early maturing corn inbreds. Identification of
ergmplasm uniquely represented among the historical Minnesota inbreds will allow further
studies on useful genes that might be present in such germplasm. Identification of major QTL for
kernel composition, disease resistance, and agronomic traits will provide targets for breeding that
are present in adapted germplasm.

References

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