Understanding Natural Variation and Selection for Nitrogen Use Efficiency in Maize using Population Genetics

Nirwan Tandukar (ntanduk@ncsu.edu)[1], Fausto Rodríguez Zapata[2], Jung-Ying Tzeng[3], James Holland[4], Rubén R Álvarez[1,2]
[1]Department of Genetics and Genomics, North Carolina State University, NC
[2]Department of Molecular and Structural Biochemistry, North Carolina State University, NC
[3]Department of Statistics, North Carolina State University, NC
[4]USDA-ARS and Department of Crop and Soil Sciences, North Carolina State University, NC

Nitrogen Use Efficiency (NUE) is an important factor in crop productivity, determining how effectively plants utilize nitrogen (N) fertilizers. NUE is commonly defined as the grain yield per unit of nitrogen supplied. Enhancing NUE is essential for sustainable agriculture, as it reduces dependency on N fertilizers and minimizes environmental impacts. Aspartate is a key metabolite in N metabolism, acting as a precursor for the biosynthesis of essential amino acids such as lysine, threonine, and methionine. It plays a crucial role in N assimilation. Modifications in aspartate metabolism could directly influence NUE by improving N remobilization efficiency under low-N conditions. Natural genetic variability among crop populations offers opportunities for improving N metabolism and NUE. Natural allelic diversity in genes related to N uptake and assimilation has been shown to enhance NUE in various species. In sorghum, genetic variation in NUE-related traits has been documented, with certain alleles conferring superior N uptake and metabolic efficiency. In this study, we utilized Genome-Wide Association Studies (GWAS) and Fst analysis to identify key genetic loci associated with NUE in maize. Our results highlighted the aspartate metabolism pathway as a critical component in N assimilation and redistribution. Through GWAS, we pinpointed a candidate gene significantly associated with N-related phenotypes, suggesting its potential role in regulating nitrogen metabolism. Additionally, Fst analysis of Indian Chief and Jarvis maize populations, which have undergone long-term selection (14 rounds) for yield that is also selected for N accumulation in seeds, revealed independent selection signals at different steps in the aspartate pathway. These findings indicate that modifications in aspartate metabolism may contribute to improved NUE under selective pressure. Future work will focus on functional validation of these candidate genes or whole pathways through CRISPR-based gene knockouts and overexpression studies. Several other metabolic pathways were also found to be under selection, though they are not discussed in detail here. These pathways may work in conjunction for roles in N uptake, transport, assimilation, and remobilization. When developing new high-NUE maize varieties, it is essential to take these additional pathways into account.