

**Nefeti Mheni**

## **Association Analysis and Genome-wide Selection for Early Maturity in Wheat**

### **Abstract**

Crop phenology is an important component of wheat adaptation to climate change. A few major genes and QTLs, along with minor genes have been reported to control variation for flowering and maturity in wheat. This study aimed to 1) identify QTLs for heading date (HD) 2) evaluate the accuracy and relative efficiency of genomic selection (GS) versus phenotypic selection for HD 3) assess the stability of alleles and genomic selection models for HD in spring and winter wheat. We used a soft winter wheat (SWW) panel phenotyped for HD in North America, and a hard spring wheat (HSW) panel phenotyped in the United States and Arusha Tanzania. The panels were genotyped with SNP markers. The analysis of genotype by environmental interaction produced two clusters of environments for each population with one cluster consisting of environments that produced a large range of HD and the other a narrow range. In both winter and spring wheat we detected seven very significant ( $p < 0.0005$ ) QTLs associated with HD. Within each population the QTL effects were consistent between clusters of environments. Very few QTLs were found to be common between the two populations, and the few that were in common had minor effects in either population. The accuracy and relative efficiency of GS was higher in the HSW population than the SWW population. We have identified nine genotypes that flower earlier than the existing commercial Tanzanian wheat varieties. The selected genotypes will be used as a resource in our breeding program for creating early flowering wheat varieties adapted to the Tanzanian environment.