

New Genetic Markers for Stem and Spike Partitioning Traits to Enhance Harvest Index and Increase Grain Yield

There is strong evidence that during grain filling wheat yield (grain weight per spike and spikes per unit area) is sink limited because carbon accumulation is limited by the total storage capacity of the grains. Therefore, improving grain number per unit area is an important target in the genetic improvement of Harvest Index (HI) and yield potential. In a NIFA-IWYP Project “**Advancing Harvest Index In Wheat Through Genomic Enabled Physiological Breeding**”, led by Md Ali Babar at the University of Florida with other colleagues in the USA, UK and Mexico, wheat lines with optimized transfer of captured carbon to grains have been used to discover new genetic variation for carbon partitioning traits such as spike partitioning index (SPI), fruiting efficiency (FE), grains per unit of spike biomass at anthesis, number of fertile florets per spikelet and improved spike morphology. The teams have developed genetic markers associated with these traits to aid trait-based breeding. Increased HI in wheat from the current average could increase grain yields by up to 25%.

What Solutions have been Identified?

- Traits that differentiate useful and non-useful increases in biomass and optimize partitioning of useful biomass to increase HI, grain yield (GY) and grain number (GN).
- Evidence that SPI and FE are key traits for increasing HI.
- Data that show that the length of stem internodes 2 and 3 compete most with the developing spike for assimilates (SPI) so reducing these internodes would enhance HI and GN.
- Reduced glume, awn, and rachis partitioning and increased partitioning of lemma and palea further increase FE and grain number.
- Spike *Zeatin* (Cytokinin) and *Zeatin riboside* at GS45 (mid-boot) increases GN, FE, and HI.
- 61 KASP molecular genetic markers linked to target partitioning traits that influence grain yield from GWAS studies on a panel of 232 US facultative wheat lines and a panel of 150 lines in the CIMMYT High Biomass Association Panel (HiBAP).

What has been transferred to the wheat improvement pipelines?

- 18 validated KASP molecular genetic markers with significant allelic effects (5.6%-20.4%) for partitioning traits and which positively impact grain yield.
- Knowledge of which alleles for different partitioning traits should be combined to enhance HI and yield.
- US facultative wheat lines with the positive alleles for the various grain traits recommended (see below).

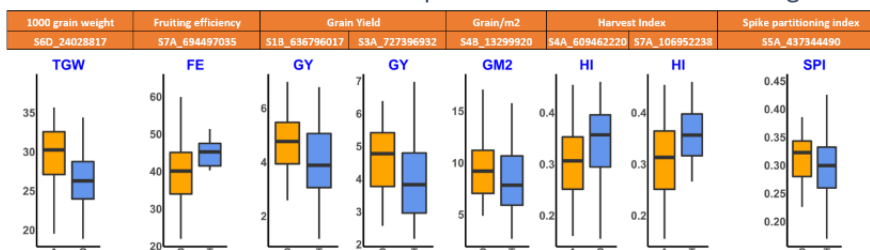


Figure 1. Examples of allelic variation at defined loci linked to targeted partitioning traits found in US facultative wheat lines