

Tuning Plant Development to Environments Boosts Yield

Flowering time in wheat is described as the appearance of the distinctive seed-bearing spikes. However, the wheat spike is formed before the crop begins its rapid increase in height during spring and early summer. This initial period of spike development is critical for capturing carbon resources during and after this phase and then maximizing grain number and ultimately yield. The timing and duration of the developmental phases are regulated by genetic variation controlling phenology. An IWYP Project “**A Genetic Diversity Toolkit to Maximize Harvest Index by Controlling the Duration of Developmental Phases**”, led by Simon Griffiths at the John Innes Centre, with other colleagues in the UK, Australia, Argentina, Spain and Mexico, aimed to develop a catalogue of known and new phenology QTL/alleles for use by breeding programs globally to maximize harvest index (HI) and grain yield in varieties for different environments.

What Solutions have been Identified?

- New evidence that breeders use some genes of major effects not previously well understood (e.g., a version of *Vrn-D3*, versions of *ELF-3*, and a QTL with effects on HI for which *TOE-1* is a candidate).
- New QTL characterized for their effect on HI and yield from wheat landraces in the AE Watkins collection.
- Beneficial alleles in germplasm such as HIBAP and Near Isogenic Lines (NILs) created in CIMMYT backgrounds. Higher grain numbers arise from enhancing floret survival, with the best combinations of phenology alleles.
- Improved understanding of how phenology genes/QTL interact, enabling better use in breeding.

What has been transferred to the wheat improvement pipelines?

- Building on the UK investment, new CIMMYT Nested Association Mapping (NAM) populations were created and made available to geneticists and breeders along with high density genotyping data.
- Molecular genetic markers now used routinely by CIMMYT to select new lines for international field trials.

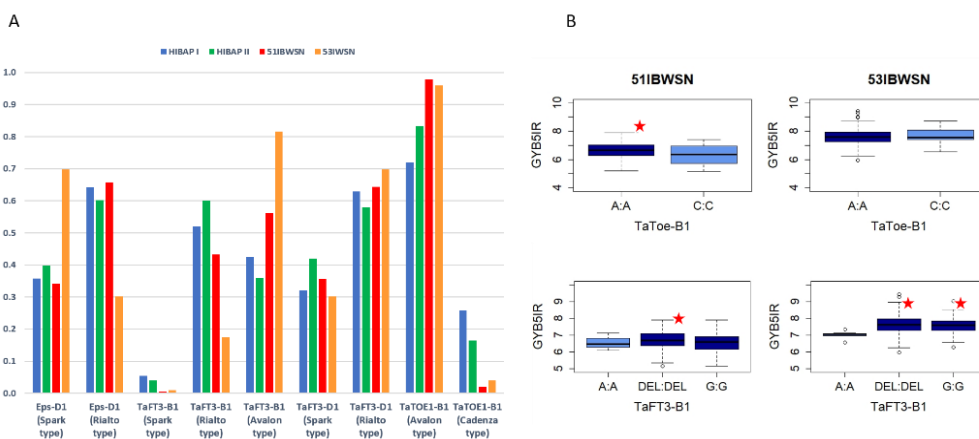
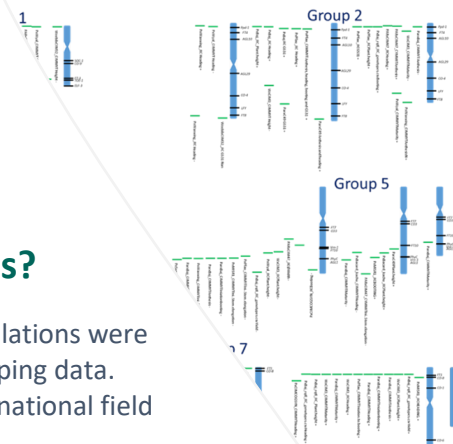


Figure 1. Effect of novel candidate genes, *TaTOE-B1* and *TaFT3-B1*, advantageous for stabilizing the expression of yield and HI. A) Frequency of alleles in High Biomass Association Mapping Panel I and II, 51st and 53rd International Bread Wheat Screening Nurseries (IBWSN). B) Boxplots using grain yield under irrigated conditions (GYB5IR) show the effect for alleles at both genes in 51IBWSN and 53IBWSN.