

Discovering genes that control wheat spike development

Inflorescence (spike) architecture is a major component of yield determination in wheat, as the number and arrangement of spikelets and florets control the maximum number of potential grains. Despite spikelet and floret fertility being key yield-related traits, very little is known about the genes that control inflorescence development. An IWYP Aligned Project “**Investigating the potential for allelic variation of key inflorescence development genes to increase yield potential in wheat**”, led by Scott Boden at the University of Adelaide (formerly John Innes Centre), is identifying genes that regulate the number and arrangement of spikelets on a wheat inflorescence, which will then be combined with analysis of phenology to propose strategies for improving grain production and quality.

What Solutions have been Identified?

- Genetic analysis has identified an HD-ZIP III transcription factor that regulates vascular development of wheat, and boosts spikelet number when gene expression is higher due to mutation of a conserved microRNA complementary site (**Figure 1**). This trait is associated with a ~25% increase in grain protein content (GPC), meaning simultaneous improvements in both grain yield and quality (**Figure 2**) could be possible. These alleles are named *Diss-D1* and *Diss-A1* (Diss = Dominant Inheritance of Secondary Spikelets).
- Allelic variation for *TEOSINTE BRANCHED1* significantly influences inflorescence architecture in European and Australian breeding lines, with novel variants identified on the B (*TB-B1b*, mapped to chromosome 4B) and D (*TB-D1b*, mapped on chromosome 4D) genomes. Lines tetrasomic for chromosome 4D also showed additional paired spikelets (**Figure 3**). The researchers have also shown that *TB1* suppresses tillering¹ and stem elongation² and are investigating the potential to modify tillering and height using these new alleles of *TB-B1* and *TB-D1*.
- Additional genetic variation was found for a locus on chromosome 2D that also modifies inflorescence architecture and is associated with improved floret fertility.
- Mutants with modified inflorescence architecture can produce grain with significantly more protein, providing additional novel variation for improvement of grain quality traits (**Figure 2**).

What has been transferred to the wheat improvement pipelines?

- NILs containing novel variant alleles for the genes that alter inflorescence architecture and grain quality to be introgressed into adapted germplasm, both in CIMMYT and Australia.
- Gene-specific KASP molecular genetic markers for *TB-B1* alleles.

Figure 2. Having identified that *Diss-A1* and *Diss-D1* mutants (blue dashed lines) produce grain with more protein the research team found that multiple paired spikelet-producing mutants with either fertile (blue) or infertile (green) secondary spikelets produce grain with more protein than wild-type (cv. Cadenza, red dashed line) suggesting a genetic link between spikelet architecture and grain quality.

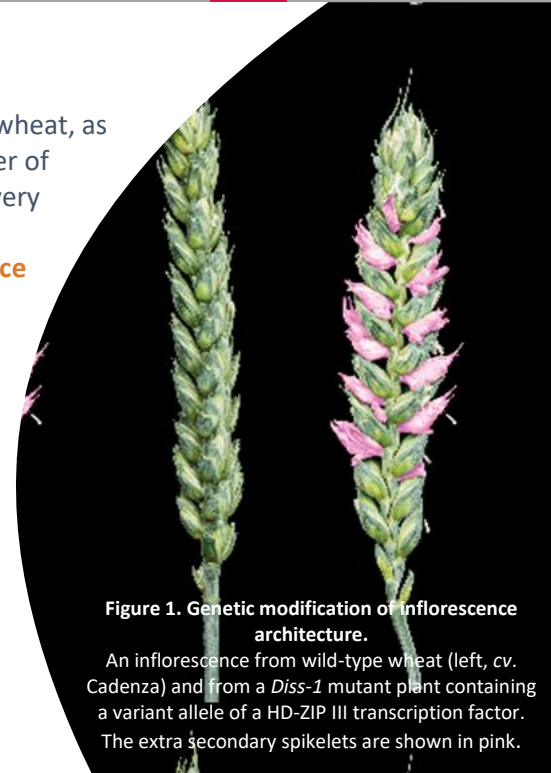


Figure 1. Genetic modification of inflorescence architecture.

An inflorescence from wild-type wheat (left, cv. Cadenza) and from a *Diss-1* mutant plant containing a variant allele of a HD-ZIP III transcription factor. The extra secondary spikelets are shown in pink.

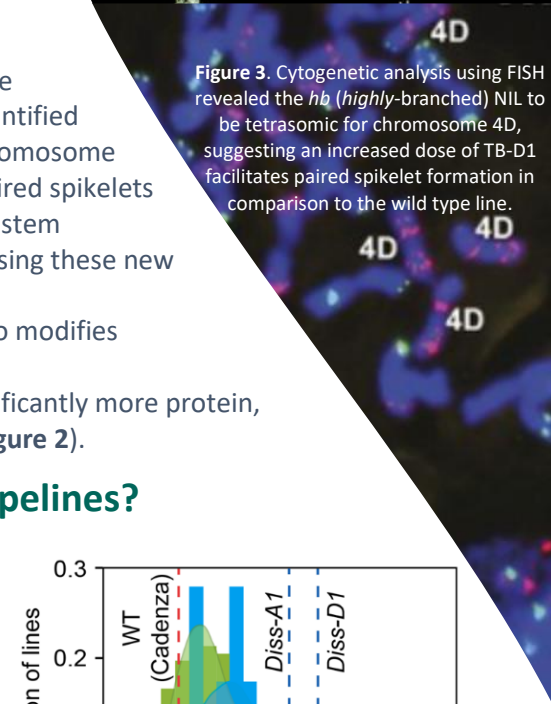


Figure 3. Cytogenetic analysis using FISH revealed the *hb* (highly-branched) NIL to be tetrasomic for chromosome 4D, suggesting an increased dose of *TB-D1* facilitates paired spikelet formation in comparison to the wild type line.

