

## Revealing an Important Gene for Yield in Wheat

The production of wheat grain is highly influenced by spike architecture. Overall, grain yields are influenced by three components: spikes per unit land area, grains per spike and grain weight. Two sub-components, the number of spikelets per spike and the number of grains per spikelet, are responsible for the final number of grains per spike. Therefore, a better understanding of the genetic control of spikelet development would aid in identifying new approaches to increase grain number without decreasing grain weight. A project led by Liuling Yan at Oklahoma State University and part of the recently completed Coordinated Agricultural Project (CAP) “**Validation, Characterization and Deployment of QTL for Grain Yield Components in Wheat**” (see IWYP Science Brief No. 32, October 2022), used QTL mapping and map-based cloning approaches to identify the genetic control of spikelet nodes per spike (SNS). They identified a gene in this project that functions not only to increase grain number but also enhances spike number thereby increasing grain yields in wheat. The recent results were published in *Science* (<https://bit.ly/3khAyZH>). Further, a scientific educational video was recently developed describing the *TaCol-B5* story (<https://bit.ly/3wbcCtA>).

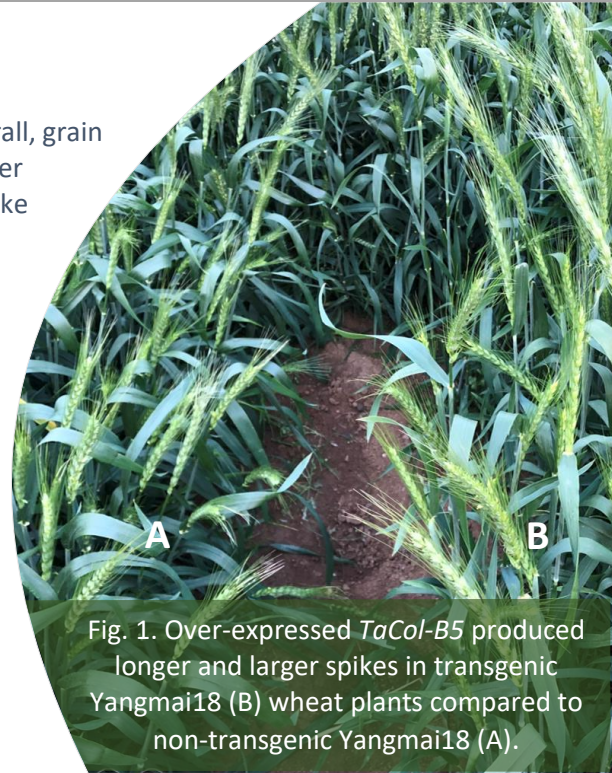


Fig. 1. Over-expressed *TaCol-B5* produced longer and larger spikes in transgenic Yangmai18 (B) wheat plants compared to non-transgenic Yangmai18 (A).

## What Solutions have been Identified?

- Identification of a major QTL for SNS, *Qsns.osu-7B*, mapped to the long arm of chromosome 7B. This QTL accounted for over 40% of the total variation found.
- The gene responsible for this QTL was cloned and when constitutively overexpressed in transgenic wheat it increased both SNS and spike numbers (Figure 1) leading to an increase of field based-grain yield by approximately 12%.
- The cloned gene, *TaCol-B5*, encodes a CONSTANS-like protein orthologous to COL5 in other plant species which has been shown to have a role in promoting cell proliferation and differentiation. The Ser<sup>269</sup>/Gly<sup>269</sup> substitution in *TaCol-B5* for the higher yield and *Tacol-B5* for the lower yield resulted in differential protein phosphorylation by *TaK4* (Figure 2).
- The favorable allele of this gene is present in wild Emmer wheat ecotype Zavitan but in very low frequency (~2%) in a global collection of modern wheat varieties (Figure 3).

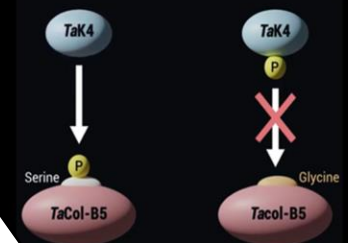


Fig. 2. Differential phosphorylation of *TaCOL-B5* by *TaK4*.

## What has been Transferred to the Wheat Improvement Pipelines

- *TaCol-B5* was found to be present in winter wheat cultivars ‘Billings’ and OK1059018. Several breeding lines/populations are being converted with these donors.
- The CIMMYT parental line carrying the favorable allele of this gene used in the initial genetic mapping study is now being used at the IWYP Hub at CIMMYT to test the overall effect of *TaCol-B5* on yield in diverse genetic backgrounds and different environments.



Figure 3. Percent frequency of *TaCol-B5* in a survey of >1600 global wheat accessions.