

## Researchers present new approach to identify key regulatory factors in wheat spike development

February 19 2024, by Zhang Nannan



Systematic identification of key regulatory factors for wheat spike development using multi-omics data. Credit: IGDB



Wheat, a globally important food crop, derives its yield from factors such as number of spikes per unit area, thousand-grain weight and grain yield per spike. Spike shape directly affects spikelet number, grain yield, and overall wheat productivity. Uncovering the key regulators of wheat spike development and investigating their molecular mechanisms holds great promise for precision breeding and molecular improvement of spike morphology.

In a <u>study</u> published in *Molecular Plant*, researchers led by Xiao Jun from the Institute of Genetics and Developmental Biology (IGDB) of the Chinese Academy of Sciences (CAS) presented an innovative approach. By integrating multidimensional omics, <u>population genetics</u>, and gene function analysis, the researchers outlined a systematic and efficient strategy to identify key regulatory factors in <u>wheat</u> spike development.

Through comprehensive sequencing of wheat spike transcriptomes, chromatin accessibility, and <u>histone modifications</u> at key developmental stages, they delineated the dynamic transcriptional and epigenetic landscape of wheat spike maturation, culminating in the construction of a transcriptional regulatory network (TRN).

By merging multidimensional omics with population genetics, the researchers pinpointed 227 putative regulatory factors influencing spike development, 42 of which have already been implicated in spike formation in wheat or rice.

Phenotypic screening of 61 novel genes using the KN9204 mutant library revealed 36 mutations, including TaMYC2-A1, TaMYB30-A1, and TaWRKY37-A1, altering flowering time or spike morphology. The functional characterization of TaMYB30-A1 underscored the efficacy of the TRN in deciphering gene functionality and its practical utility in wheat breeding initiatives.



Wheat Spike Multi-C	Omics Database (W	SMOD)	Home	Genes	WGCNA	TRN	Epigonomic Status	GWAS	Mutants	ID Conversion	Monuol
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1	The transcription regulatory networks play a crucial role in controlling oumerous biological processes in plants. In this study, we have produced a comprehensive multi-onics integrative network may during whest spike development. This may incorporate various data types, including gene expression, chromatin accessibility, multiple histone modifications, SNP information, and GWAS signals. We have constructed a co-expression network during whest spike development using RMA-seq data seligit stages. By information, and GWAS signals. We have constructed a co-expression network built a core transcription regulatory network that may drive various meristomatic cell identities to transition and form the spike architecture. These multi- omics data sources provide essential information for gene function analysis and deepen our understanding of genetic regulation in wheat spike development.										
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The wheat spike development multi-omics database (WSMOD). Credit: IGDB

At the same time, a comprehensive multi-omics database for wheat spike development, known as WSMOD, was launched. This platform provides researchers with convenient "all-in-one" access to various services, including gene information retrieval, co-expression analysis, TRN prediction, epigenetic map plotting, and mutant library search functions.

In summary, this study elucidates the dynamic transformations that occur during wheat spike development, which are shaped by both <u>gene</u> <u>transcription</u> and epigenetic regulation. It integrates multidimensional data including transcriptomics, epigenomics, and population genetics to unravel these processes. The construction of a wheat spike developmentspecific TRN represents a systematic, efficient, and accurate strategy for identifying key regulatory factors.



**More information:** Xuelei Lin et al, Systemic identification of wheat spike development regulators by integrated multi-omics, transcriptional network, GWAS and genetic analyses, *Molecular Plant* (2024). DOI: 10.1016/j.molp.2024.01.010

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