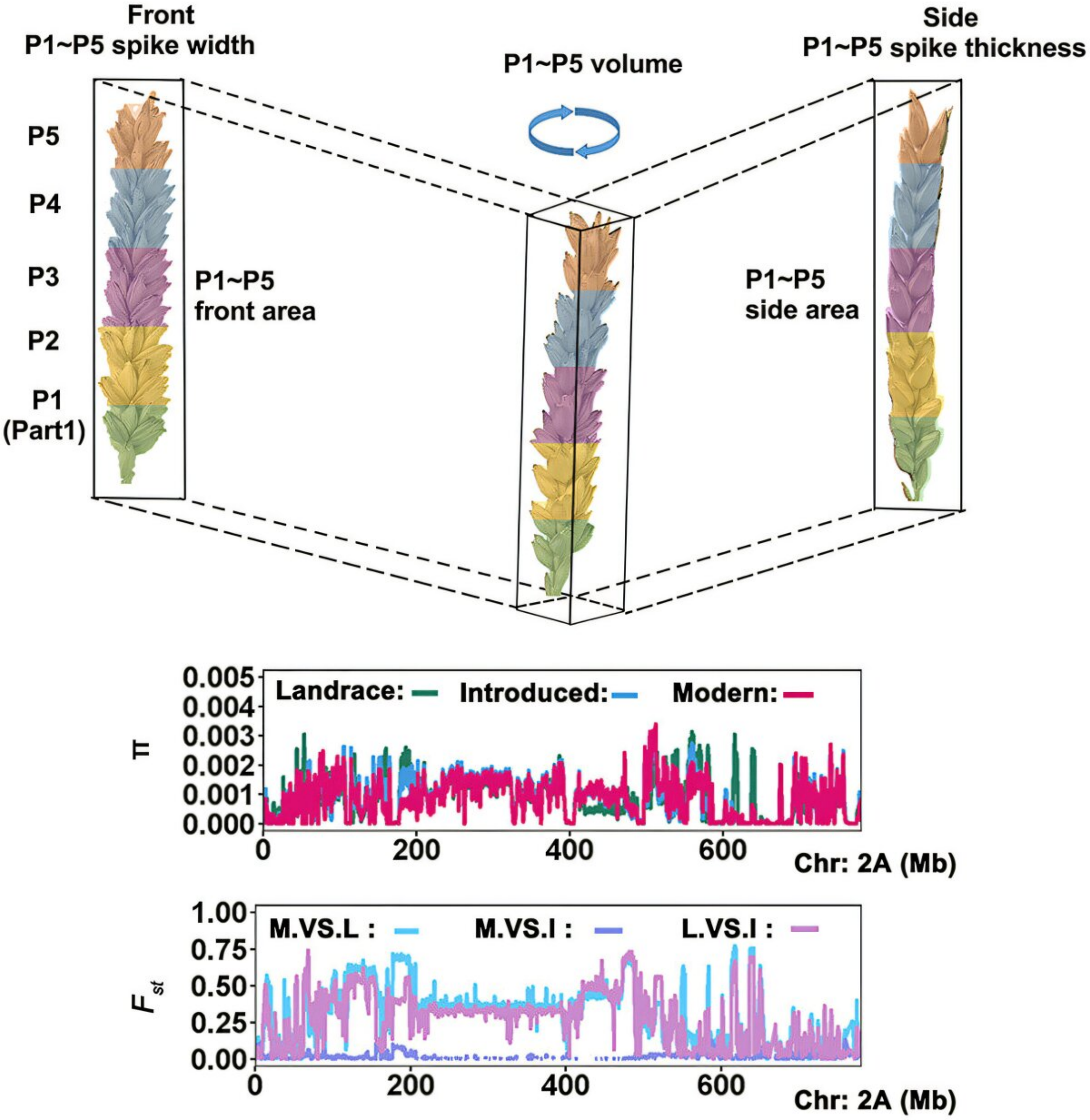
High-throughput phenotyping platform uncovers genetic basis of wheat spike morphology evolution

September 3 2025



Credit: *Cell Reports* (2025). DOI: 10.1016/j.celrep.2025.116120

A collaborative research team led by Lu Fei from the Institute of Genetics and Developmental Biology (IGDB) of the Chinese Academy of Sciences (CAS) and Guo Zifeng from the Institute of Botany of CAS, together with their colleagues, has pinpointed key genetic factors shaping wheat spike morphology—a critical trait for yield—using a high-throughput phenotyping platform.

Their findings, published in *Cell Reports*, offer molecular targets to boost wheat yields via precision breeding.

Wheat spike morphology directly influences grain number per spike and grain weight, two major components of yield. However, traditional manual measurements have been unable to capture detailed variations across different spike regions, limiting efforts to uncover the underlying genetic mechanisms.

To address this, the research team developed an image-based high-throughput phenotyping platform, employing 3D segmentation technology to accurately measure spike parameters such as length, width, thickness, area, and volume. For the first time, they systematically quantified 54 spike morphological traits, laying a crucial data foundation for in-depth genetic analysis of spike architecture.

Using genome-wide association studies (GWAS), the researchers identified 288 significantly associated genomic regions in a global panel of 306 wheat accessions and pinpointed 303 key regions in 1,053 Chinese-bred cultivars. They revealed that geographical differentiation and breeding selection trends in spike morphology (e.g., intercontinental differences in spike volume) are primarily regulated by haplotype combinations.

Notably, different haplotypes in the 2D chromosomal region (containing TaDA1 and Rht8 genes) significantly modulate spike length and width. The negative correlation between spike length and width/thickness, commonly observed in global landraces, was overcome through modern breeding by selecting synergistic haplotypes (e.g., C-trait3-2D.1, C-trait9-1A.4, and C-trait15-5B.2).

An analysis of China's century-long breeding history showed that although spike length remained stable, continuous increases in spike width and thickness led to a significant boost in spike volume.

Of particular interest, haplotypes controlling spike volume in different spatial partitions (P1–P5) exhibited directional enrichment during modern breeding. For instance, the frequency of the advantageous haplotype C-trait51-5B.2 surged from 12.6% to 61.14%. Molecular validation demonstrated that the favorable haplotype of TraesCS1D02G068300 could increase spike volume by 53.23%.

This critical finding not only confirms that haplotype stacking is an effective strategy for yield enhancement, but also provides key theoretical foundations and valuable genetic resources for molecular design of high-yield wheat varieties.

More information: Kuocheng Shen et al, Dissection of genomic drivers of spike morphology changes in wheat by high-throughput phenotyping, *Cell Reports* (2025). DOI: 10.1016/j.celrep.2025.116120

Provided by Chinese Academy of Sciences

Citation: High-throughput phenotyping platform uncovers genetic basis of wheat spike morphology evolution (2025, September 3) retrieved 4 October 2025 from https://phys.org/news/2025-09-high-throughput-phenotyping-platform-uncovers.html