

CROP GENOMICS

Optimise wheat A-genome

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Credit: Hong-qinq Ling, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences

The wild einkorn wheat *Triticum urartu* (Tu) is the A-genome progenitor of tetraploid (AABB) and hexaploid (AABBDD) wheat. A draft genome of Tu was published in 2013, but a better reference sequence is urgently needed by scientists and breeders. Hong-Qing Ling, from the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, and colleagues have now completed a high-quality Tu genome using multiple methods.

Assisted by technologies like BAC-by-BAC sequencing, PacBio sequencing, linked-read sequencing and optical mapping, the researchers assembled a high-quality genome of Tu with contig and scaffold lengths significantly increased. The genome includes 41,507 predicted protein-coding genes. Repetitive elements cover 81% of the whole sequence, with bursts of retrotransposons that repeatedly expanded the genome.

In comparison with other grass genomes, Tu-specific or wheat specifically amplified gene families were found to associate with stress response or vernalization. Large-scale retrotransposon-mediated structural rearrangements occurred during A-genome evolution, as revealed by comparing the A genomes among Tu, tetraploid and hexaploid wheat. An evolutionary model of the Tu chromosomes was proposed based on co-linearity analyses.

Resequencing of the transcriptomes clustered 147 Tu accessions into three groups, with differences in altitudes of origin and resistance to powdery mildew pathogen. The optimised wheat A genome represents valuable resource for agricultural genetic research and breeding in wheat and related cereal crops.

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