

Draft genome of the wheat A-genome progenitor *Triticum urartu*

Bread wheat is one of the most important food crops worldwide, and provides about 20% of the calories consumed by humans. To accelerate wheat improvement, a substantial amount of research has been conducted on the genome. Prof. Wang Jun with his team published their research findings in an article “draft genome of the wheat A-genome progenitor *Triticum urartu*” in *Nature* (2013, 496(7443): 87–90).

They sequenced *T. urartu*, which is the progenitor species of the A-genome of the diploid wild einkorn wheat. The genome of the annotation of the assembly was performed. Under a gene prediction research, they predicted 34,879 protein-coding gene models in total. In the miRNA research, they found the gene (TRIUR3_06170) of miRNA MIR5050 responded to cold treatment, which provides a new resource for investigating the regulation of cold adaptation through miRNA. Given that NB-ARC domain proteins function mainly in disease resistance, they analyzed the genes encoding R proteins in the *T. urartu* genome and identified 593 such genes. These analyses indicate that there was a specific expansion of R genes in the *T. urartu* genome.

The gene families of *T. urartu* were compared with those of rice, maize, sorghum and *B. distachyon* using OrthoMCL (Figure A). In the *T. urartu* assembly, a total of 8715 scaffolds, harbouring 14578 genes were mapped to 45 chromosomal regions of the wheat A genome. They showed the utility of the *T. urartu* draft genome sequence for finding agronomically important genes through identifying the *T. urartu* homologue of OsGASR7, a gibberellin-regulated gene that controls grain length in rice. They found two haplotypes (H1 and H2) for TuGASR7 in 92 diverse *T. urartu* accessions collected from different regions. H1 was significantly associated with greater values of grain length and grain weight (Figure B). They also verified that the *T. urartu* assembly also served as a rich resource for the development of genetic markers for molecular breeding through genomic selection.

Their *T. urartu* draft genome sequence provides new insights into the A genome that is shared by many polyploid wheat species. The large set of gene models and abundant genetic markers anchored in sequence scaffolds, together with the emerging genomic resources from bread wheat, promise to accelerate deeper and more systematic genomic and breeding studies of bread wheat that are required to meet the future challenges of food security and sustainable agriculture.

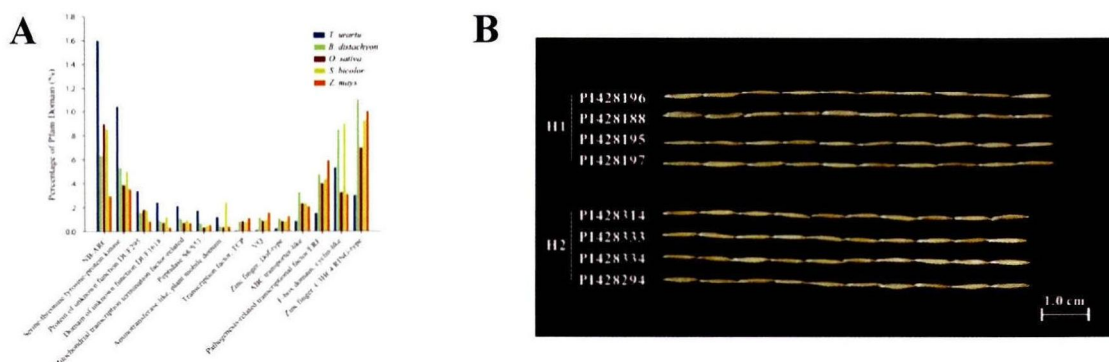


Figure **A** Comparison of protein families with different Pfam domains among the five species. Fourteen Pfam domains with significant differences ($P < 0.001$, Fisher’s exact test) in their percentages between *T. urartu* and the other four grass species are shown. **B** Typical grain lengths for the two detected TuGASR7 haplotypes, H1 (top panel) and H2 (bottom panel). For each haplotype, the seeds from four representative *T. urartu* accessions were photographed.