

Advancing plant telomere-to-telomere genome research with PlanT2T

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Telomere-to-telomere (T2T) genome assemblies provide previously unsequenced regions such as telomeres, centromeres, and repetitive sequences. This advancement marks a significant milestone in plant genomics research. However, four years after the release of the first plant T2T genome, their adoption remains limited. We identify several contributing factors:

1 **Insufficient Functional Annotation:** T2T genomes often lack comprehensive functional annotations compared to traditional genomes, hindering their utility for researchers.

2 **Limited Accessibility:** Approximately 29.12% of T2T genomes are not readily accessible post-publication, and about 65.93% available in public databases (e.g., GWH, Figshare, Zenodo, GitHub) lack real-time query and interactive features.

3 **Absence of a Centralized Research Community and Specialized Tools:** There's a notable lack of a centralized, active plant T2T genome research community to drive studies forward, coupled with a scarcity of tools specifically designed for T2T genome analysis.

To address these challenges, we have developed PlanT2T (<https://bis.zju.edu.cn/plant2t/>), an integrated platform offering:

1 **Enhanced Structural and Functional Annotations:** Each T2T genome is thoroughly annotated, including predictions of telomere and centromere positions, gap analysis, BUSCO and GC-content assessments, transcription factor and regulator predictions, protein function insights (GO, KEGG), structural domain identifications, physicochemical property analyses, structural predictions, and OrgDB construction.

2 **Interactive Genome Pages:** PlanT2T features over 180 interactive genome pages enriched with extensive omics data, allowing users to upload, analyze, browse, access, and share genomic information seamlessly.

3 **A Suite of Analytical Tools:** The platform includes more than ten online analysis tools, ranging from conventional utilities like BLAST, JBrowse, GO, and KEGG enrichment analyses, to proprietary algorithms for telomere and centromere identification. By providing an easy-to-use, comprehensive platform, PlanT2T overcomes the barriers to the widespread adoption of T2T genomes in plant research, making it a valuable resource for the plant genomics community.