

Complete telomere-to-telomere assemblies of two sorghum genomes to guide biological discovery

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Chuanzheng Wei, Lei Gao, Ruixue Xiao, Yanbo Wang, Bingru Chen, Wenhui Zou, Jihong Li, Emma Mace, David Jordan, Yongfu Tao. 2024. Complete telomere-to-telomere assemblies of two sorghum genomes to guide biological discovery. *iMeta* 3: e193. <https://doi.org/10.1002/imt2.193>



Background



- Sorghum is the fifth cereal most produced in the world after wheat, rice, maize, and barley.
- Sorghum has outstanding tolerance and adaptability to abiotic stresses, including drought, salt, and alkaline, and heavy metal.
- Sorghum can accumulate biomass quickly and efficiently, showing great potential in the field of bioenergy.



Background

	<i>Sorghum bicolor</i> reference genome statistics	
	Version 1	Version 3
Number of pseudomolecules	10	10
Number of contigs	6929	2688
Scaffold sequence (Mbp)	659.2	683.6
Contig sequence (Mbp)	625.6	655.2
Scaffold N50 (Mbp)	64.3	68.7
Contig N50 (Mbp)	0.2045	1.5
Scaffold L50	5	5
Contig L50	838	71
Unmapped sequence (Mbp)	71.9	20.2
Estimated error rate	<1 per 10 kbp	<1 per 100 kbp

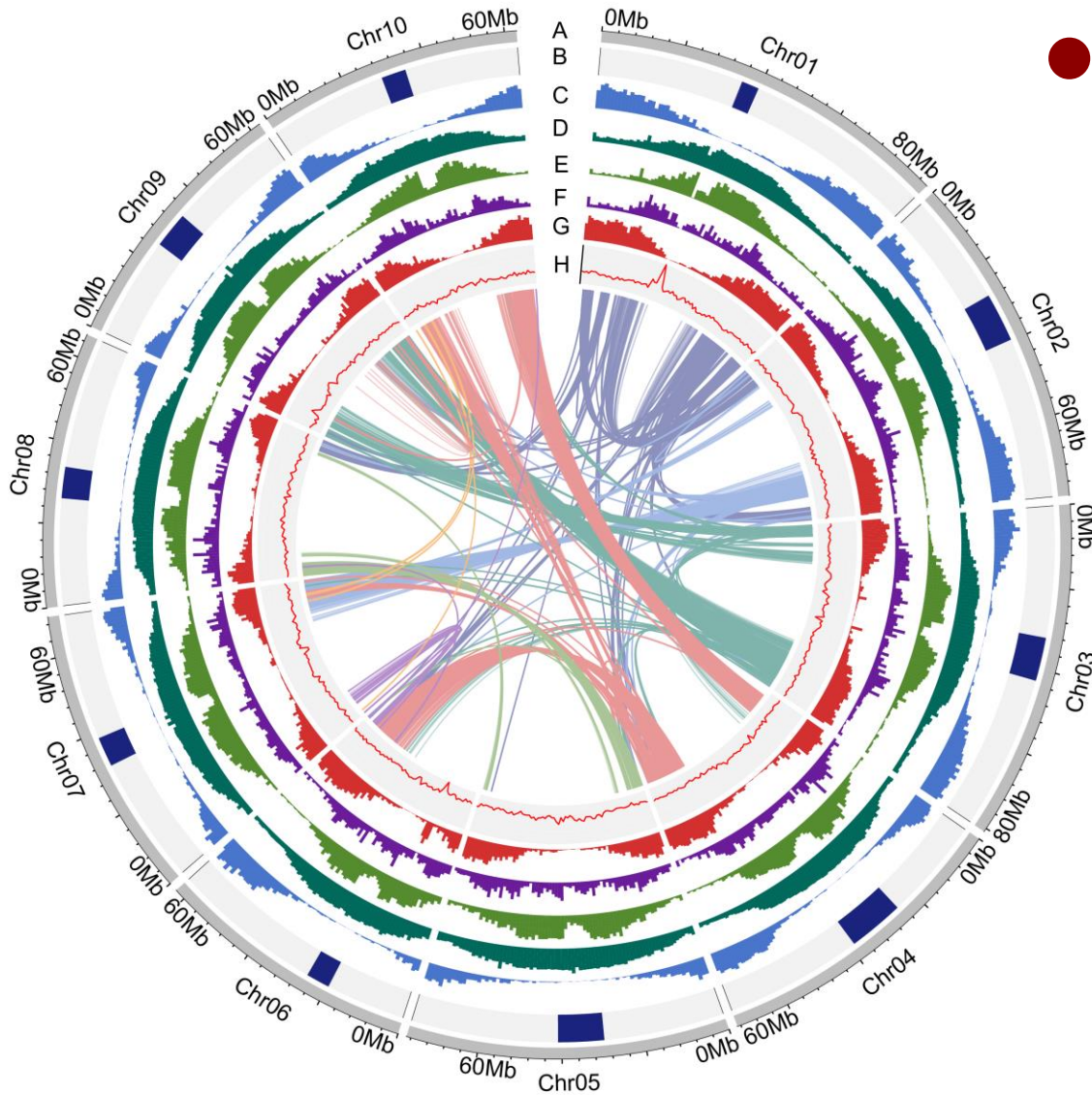
The previous reference genome of sorghum is the BTx623-v3 published in 2017;

Previously, several genome regions have not been accurately assembled, including 2,678 gaps and 18 incomplete splicing of telomeres.



Results

● Assembly of two T2T sorghum genomes

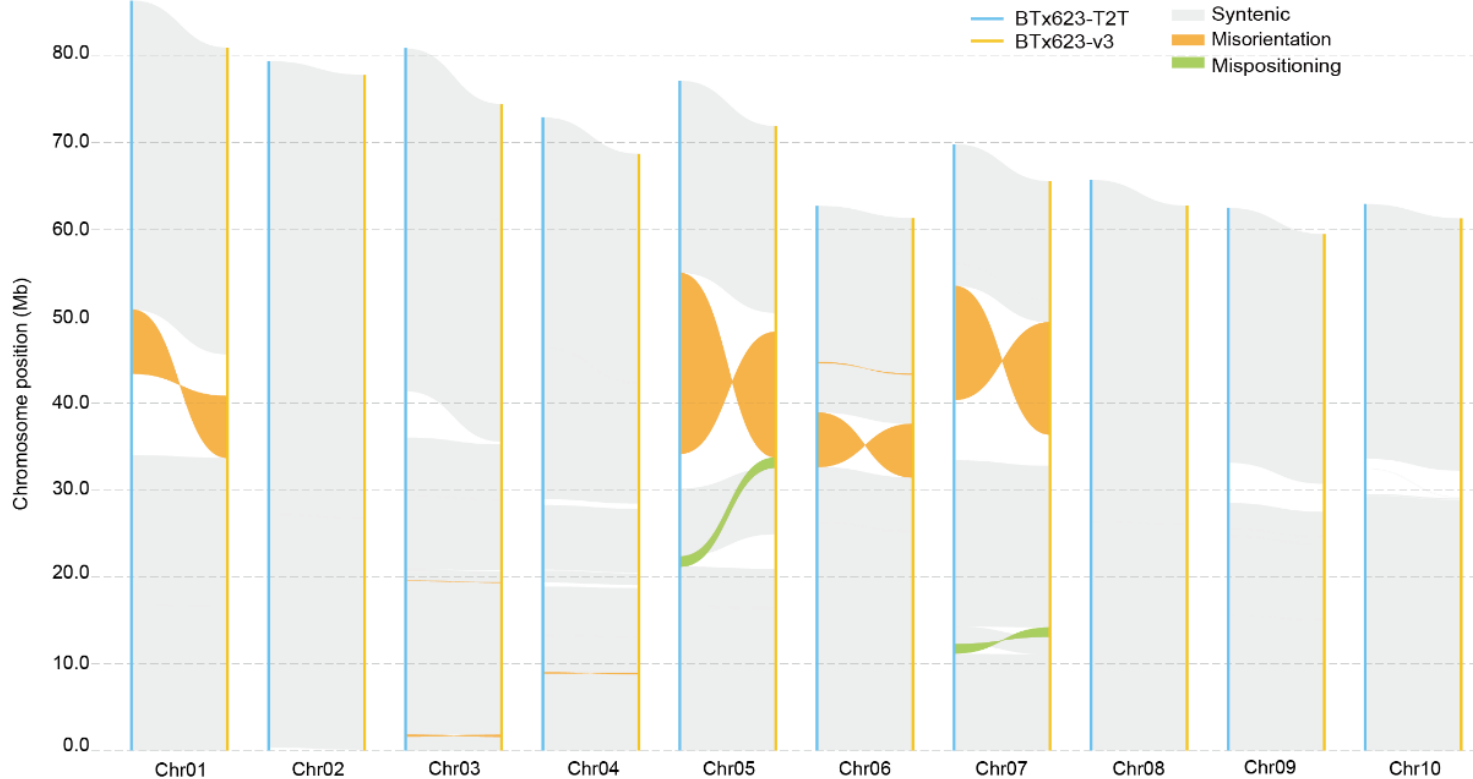
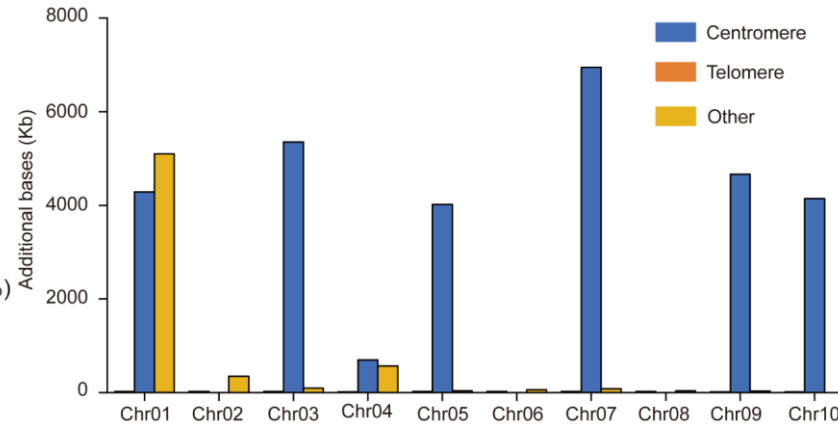
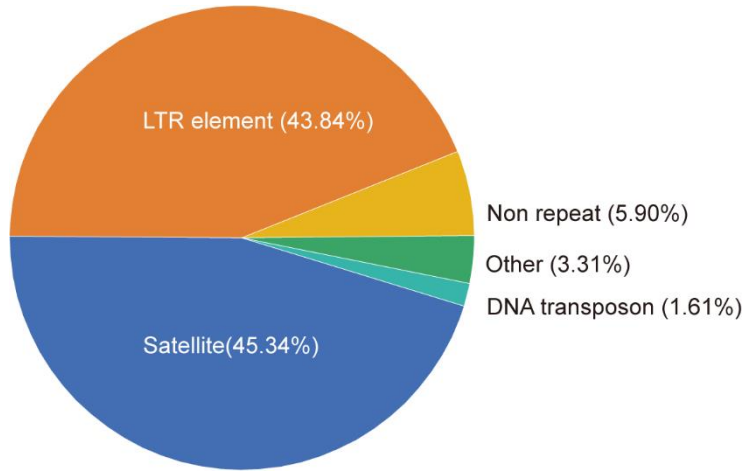


Summary of genome assembly

Parameters	BTx623-T2T	Ji2055-T2T
Chromosomal genome size (bp)	719899664	722964161
Contig N50 (bp)	72850042	73908011
L50	5	5
LTR Assembly Index	25.17	24.07
HiFi mapping rate	100%	100%
ONT mapping rate	99.99%	99.85%
BUSCO	98.5%	98.6%
Genome quality value score(QV)	70.93	71.98
Base error rate	3.87×10^{-7}	3.99×10^{-7}



Results



- T2T genome identified assembly errors in previous genome

- All gap areas are filled.

- 36.25 Mb of newly assembled sequence and 133 novel genes

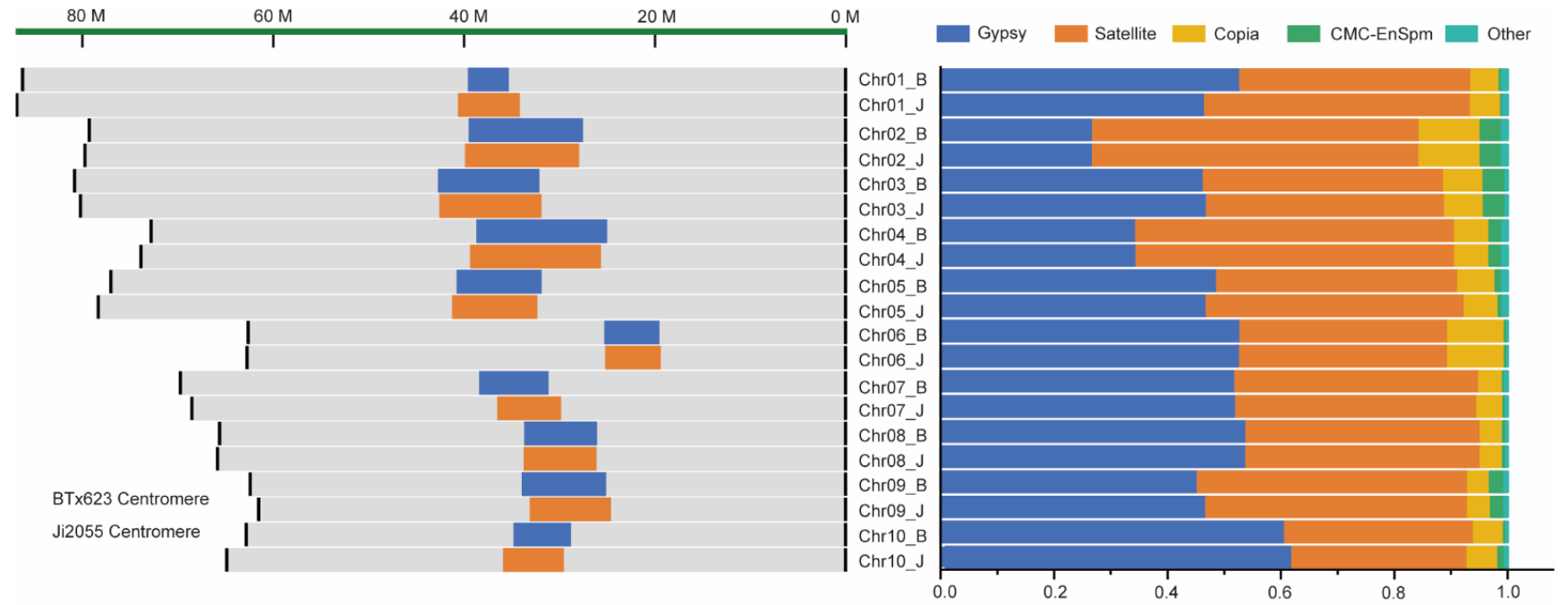
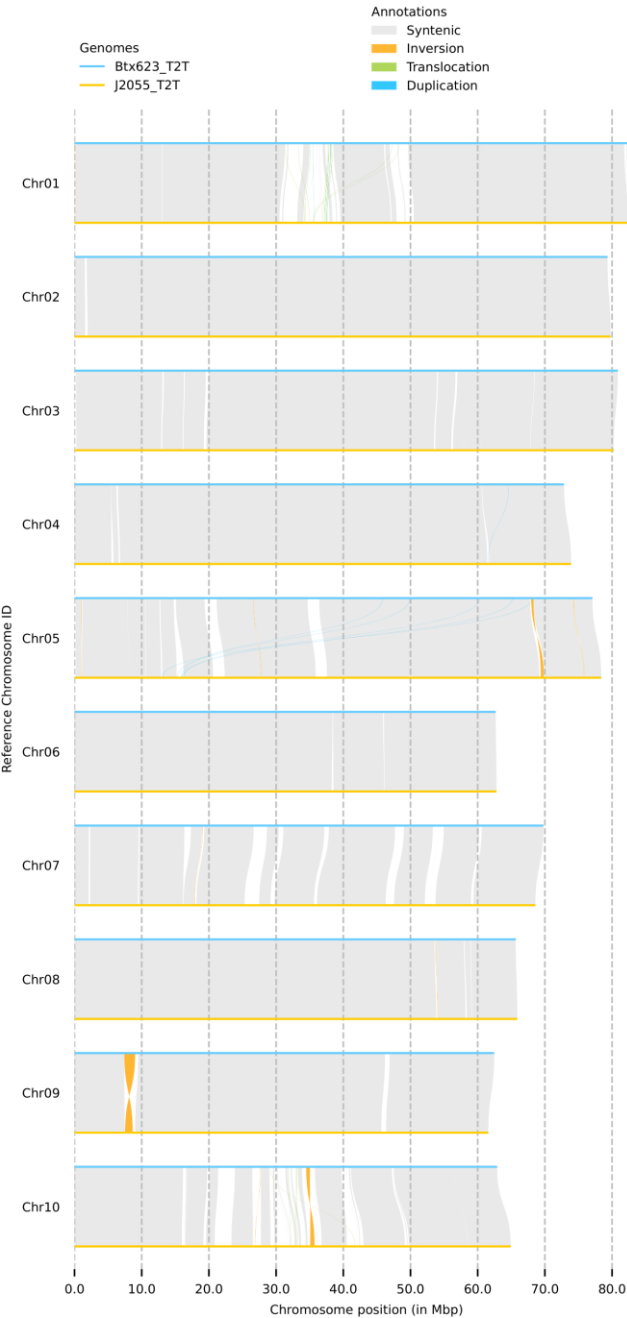
- the misorientation of four genomic regions and the mispositioning of two over 1 Mb sequence segments

Results



● Sequence variation between two T2T genomes

- There are obvious variations in the staining of the centromeric regions of chromosomes 1 and 10 between T2T genomes.
- Six inversions larger than 50Kb were found in non-centromeric regions.





Summary

- Complete telomere-to-telomere assemblies of BTx623 and Ji2055 sorghum genomes.
- The assembly of two sorghum T2T genomes corrected the genome errors in current reference.
- Sequence variation were discovered in the sorghum reference genome, BTx623 and a popular Chinese inbred line, Ji2055.

Wei, Lei Gao, Ruixue Xiao, Yanbo Wang, Bingru Chen, Wenhui Zou, Jihong Li, Emma Mace, David Jordan, Yongfu Tao. 2024. Complete telomere-to-telomere assemblies of two sorghum genomes to guide biological discovery.

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