



Two near-complete assemblies reveal R-subgenome structural and centromeric divergence associated with reproductive isolation in hexaploid triticales

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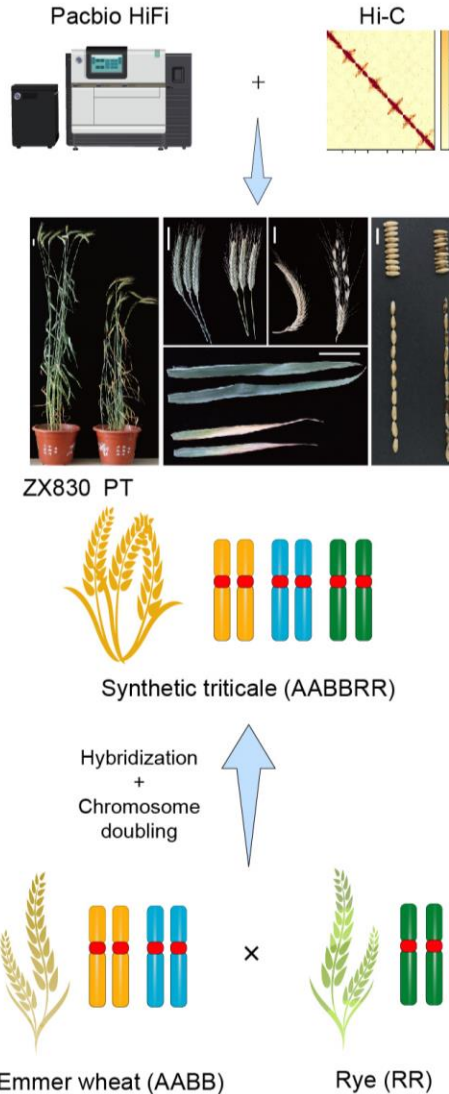


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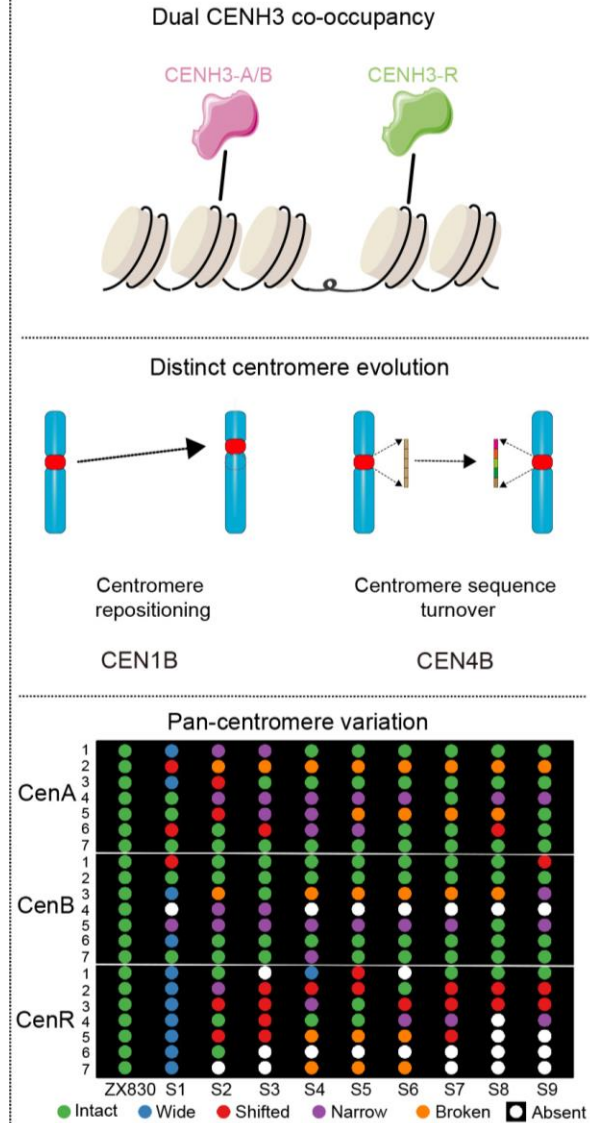


Introduction

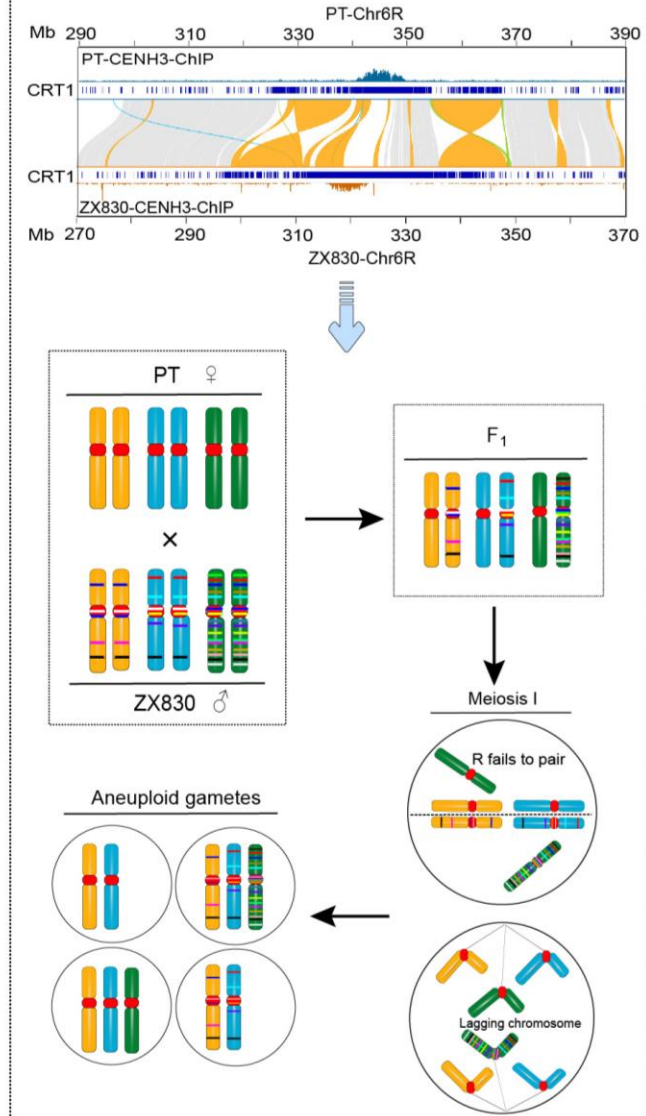
Near-complete genome assemblies



Post-polyploid evolution of centromeres



R-subgenome divergence associated with meiotic defects





Highlights

- Generated two near-complete genome assemblies of genetically divergent hexaploid triticales lines (ZX830 and PT).
- Development of subgenome-specific antibodies revealing dual loading of wheat and rye CENH3 at all functional centromeres in triticales.
- R-subgenome centromeres undergo size convergence, repeat turnover, and locus repositioning during post-polyploid evolution.
- Identified the R subgenome as the primary source of structural and centromeric divergence in hexaploid triticales.
- Centromeric divergence is associated with meiotic defects and reproductive isolation.

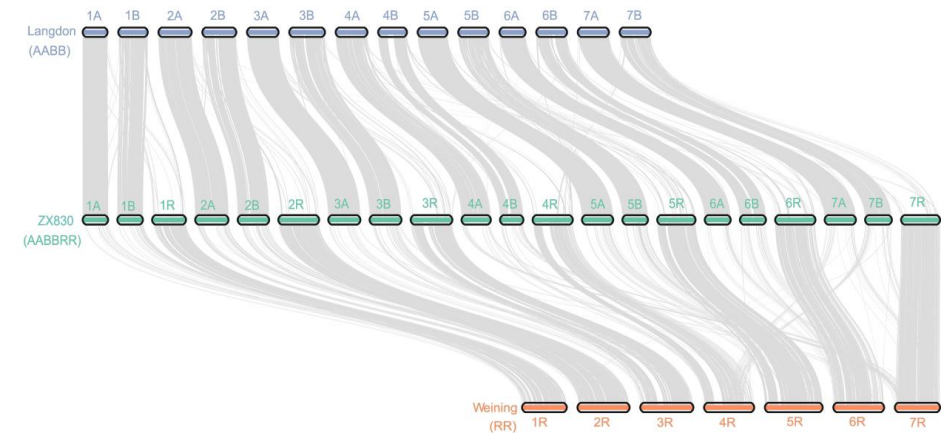
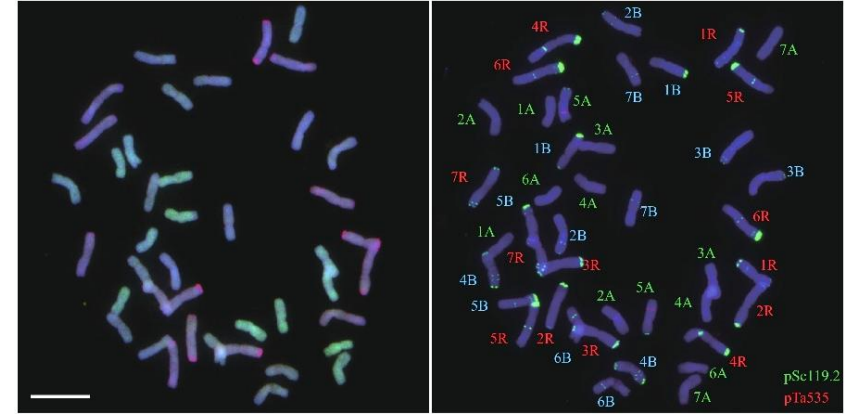
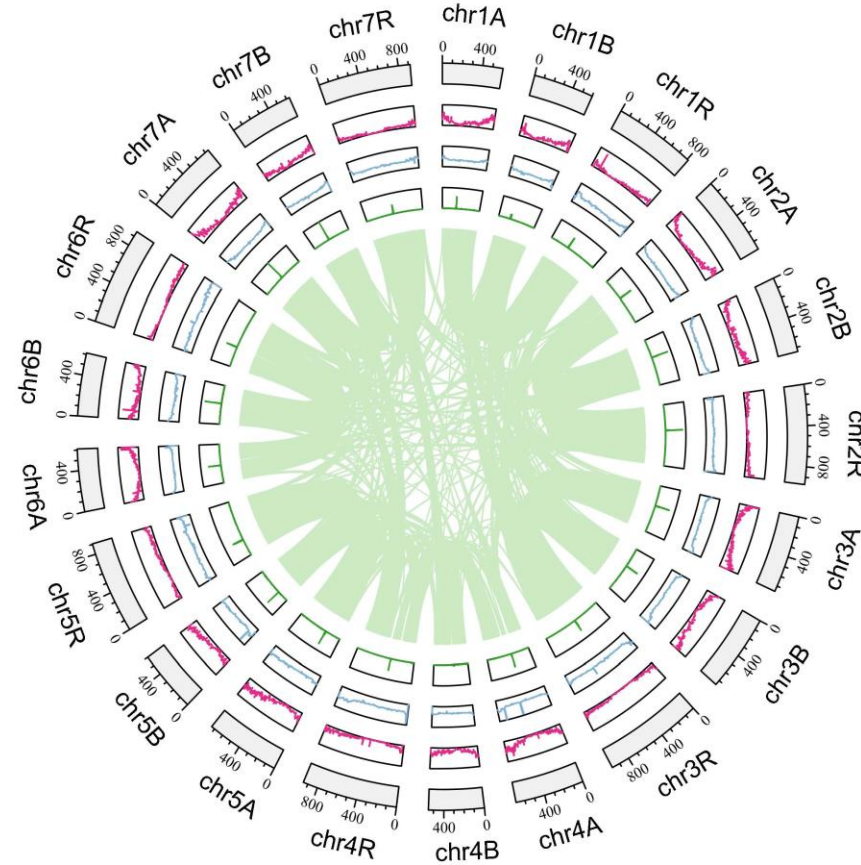


Near-complete assembly of hexaploid triticales ZX830

(A)



(B)

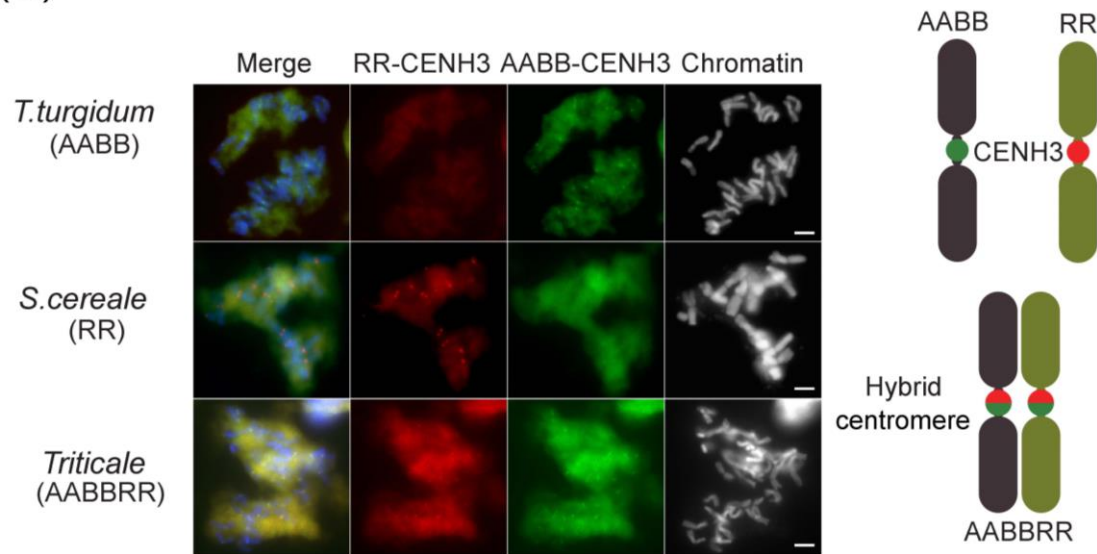


- We first generated a near-complete chromosome-scale assembly for the hexaploid triticales cultivar ZX830, spanning 15.9 Gb with a scaffold N50 of 755.7 Mb.

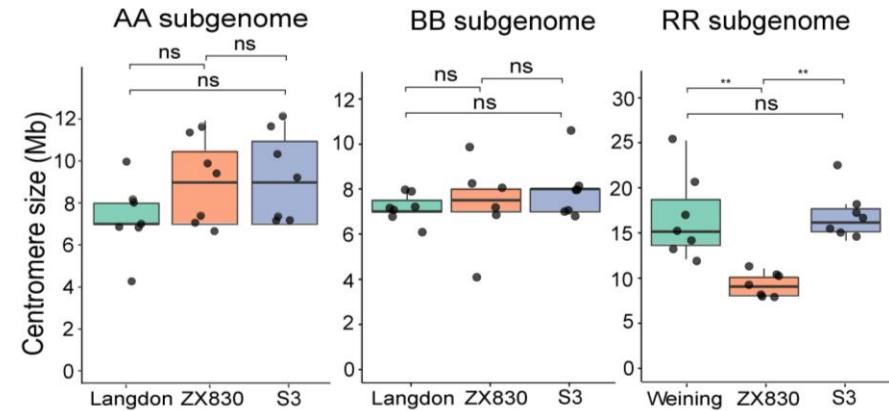


Centromere evolution and post-polyploid remodeling

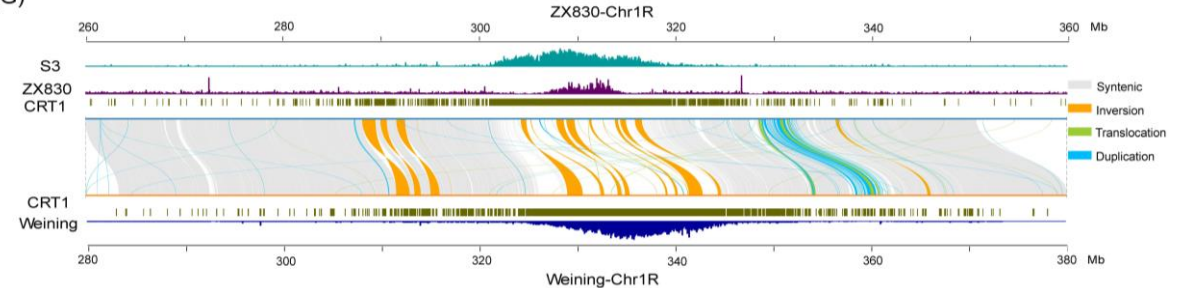
(C)



(F)

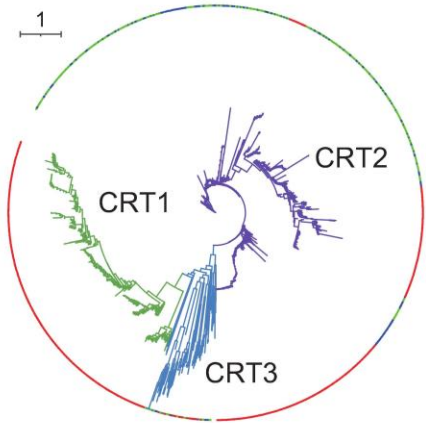


(G)

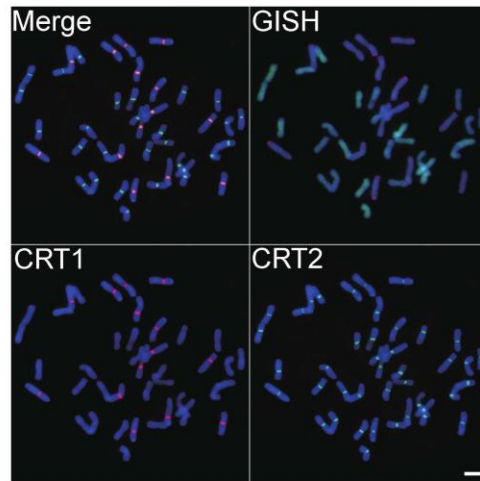


- Functional centromeres in hexaploid triticale are defined by dual loading of wheat and rye CENH3 on evolutionarily divergent sequences.
- Post-polyploid evolution drives extensive centromere remodeling, including size convergence, repeat turnover, and locus repositioning.

(D)

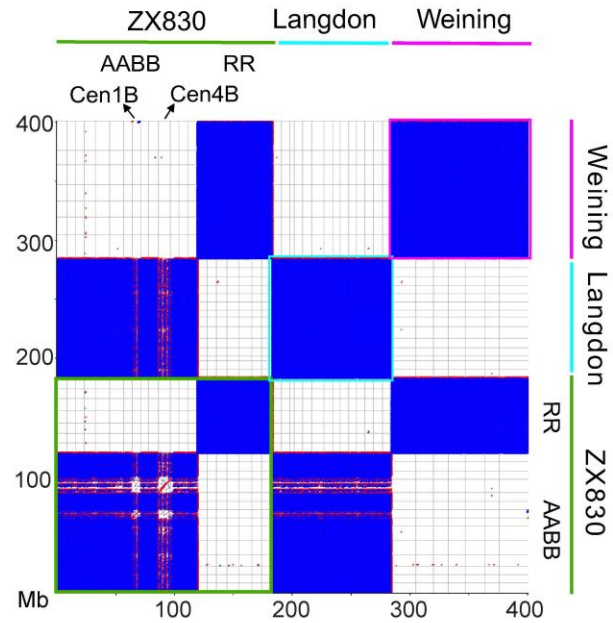


(E)

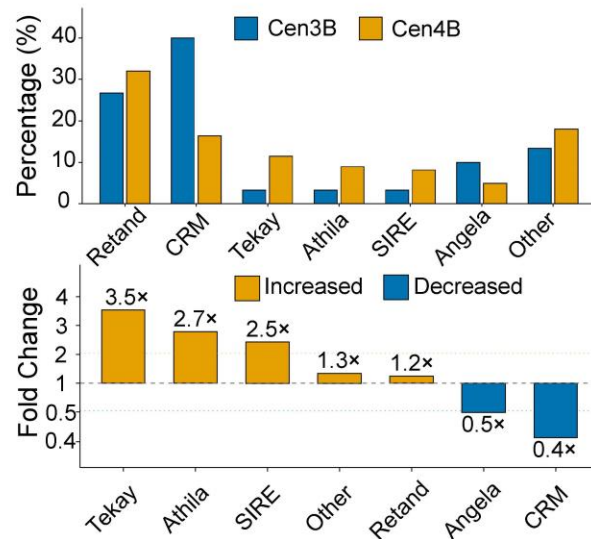


Distinct centromere evolutionary trajectories

(H)

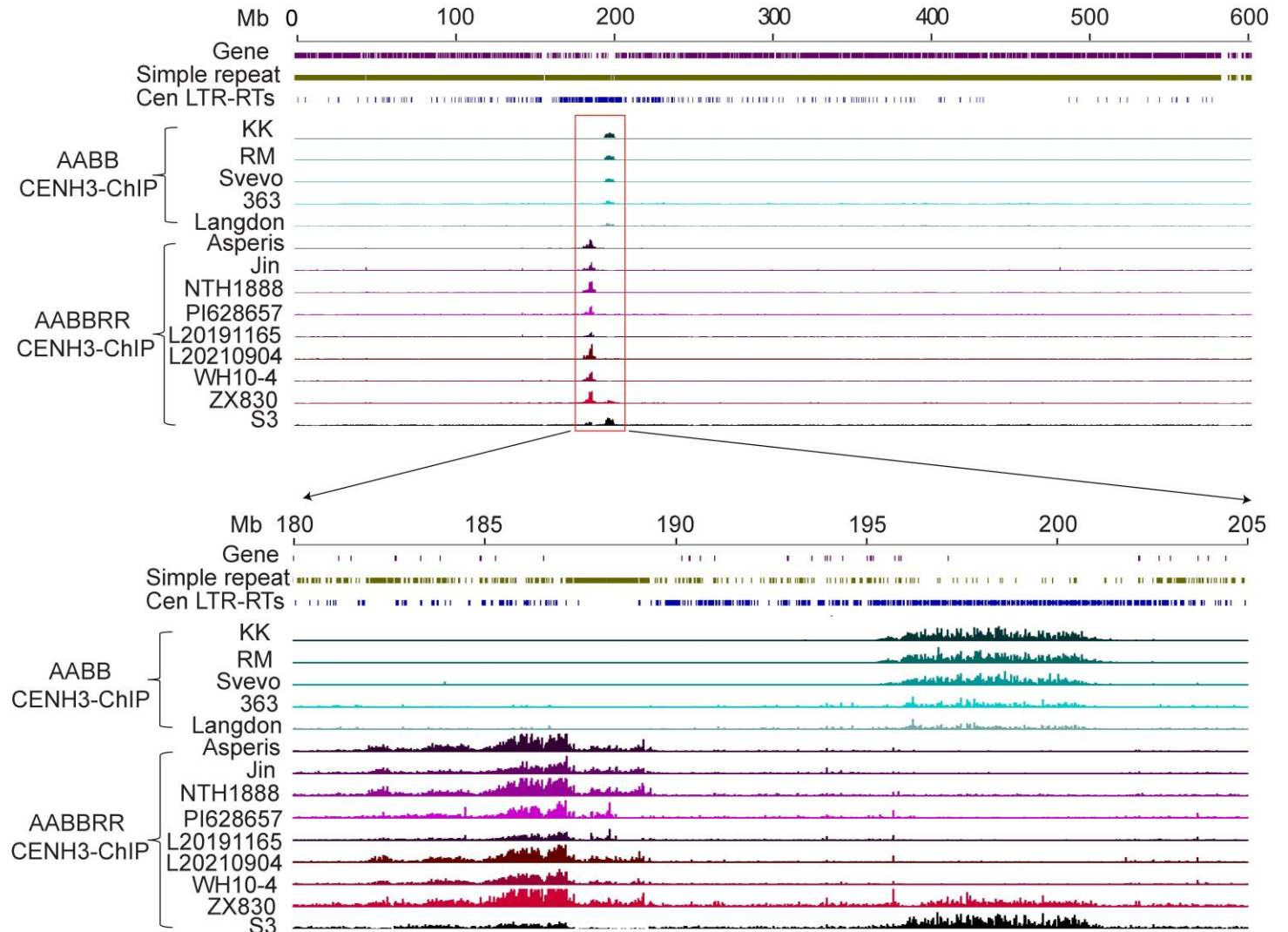


(I)



(J)

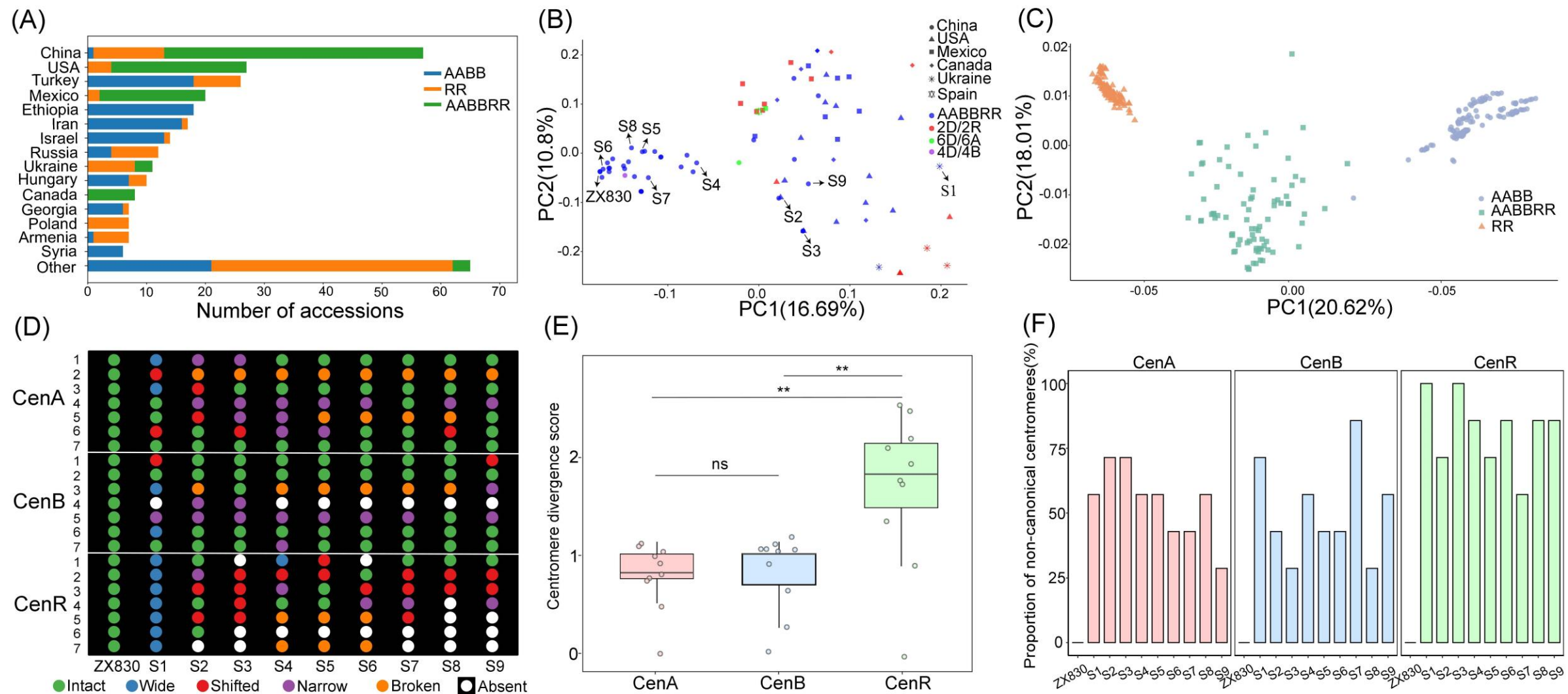
CENH3 ChIP-seq at CEN1B reveal centromere repositioning



- Distinct evolutionary trajectories reveal remarkable plasticity of centromere identity.



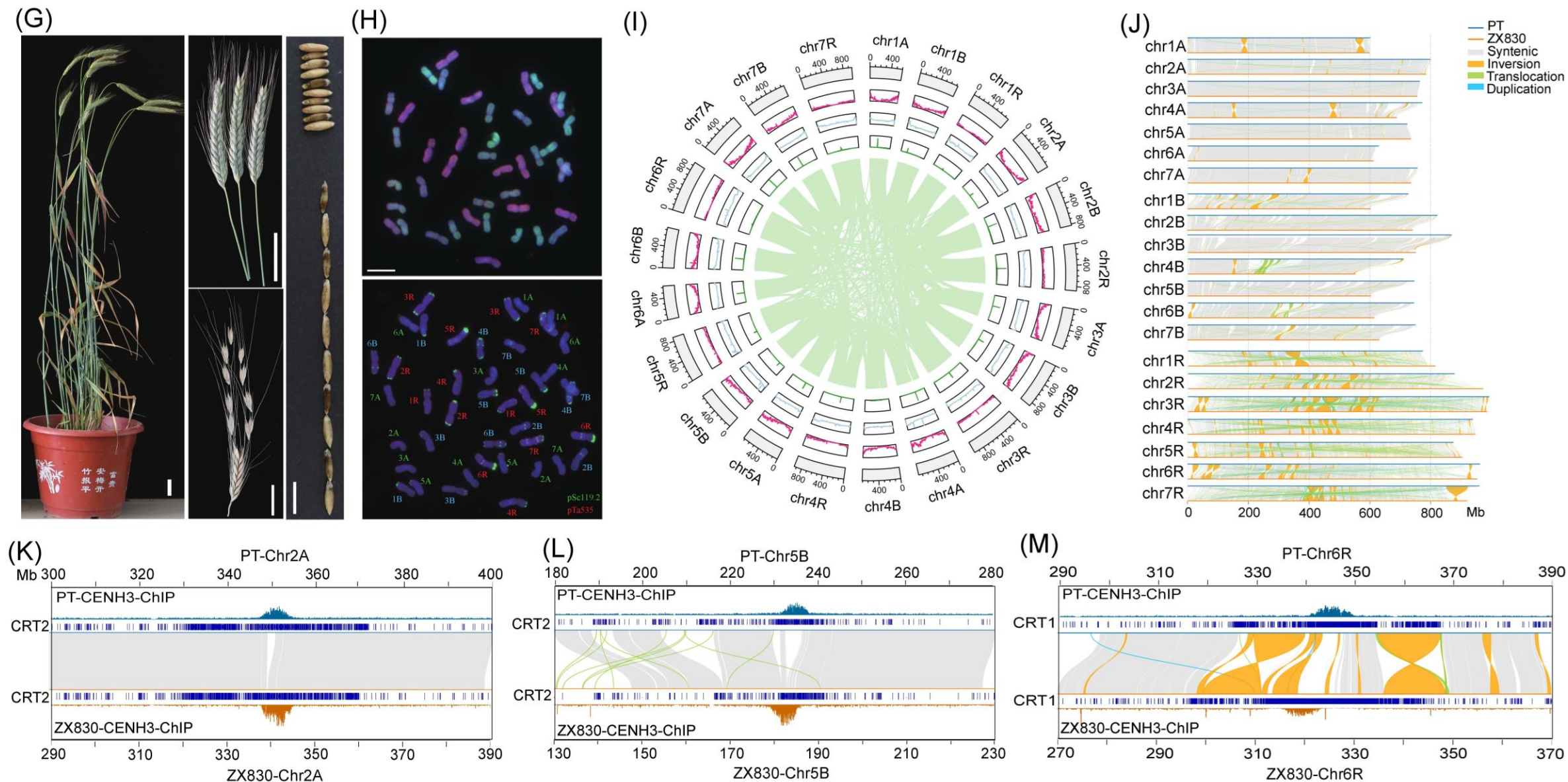
Population structure and pan-centromere variation



- Population-wide pan-centromere analyses reveal that the R subgenome is the principal axis of population divergence and centromeric diversification in hexaploid triticale.



R-subgenome structural and centromeric divergence

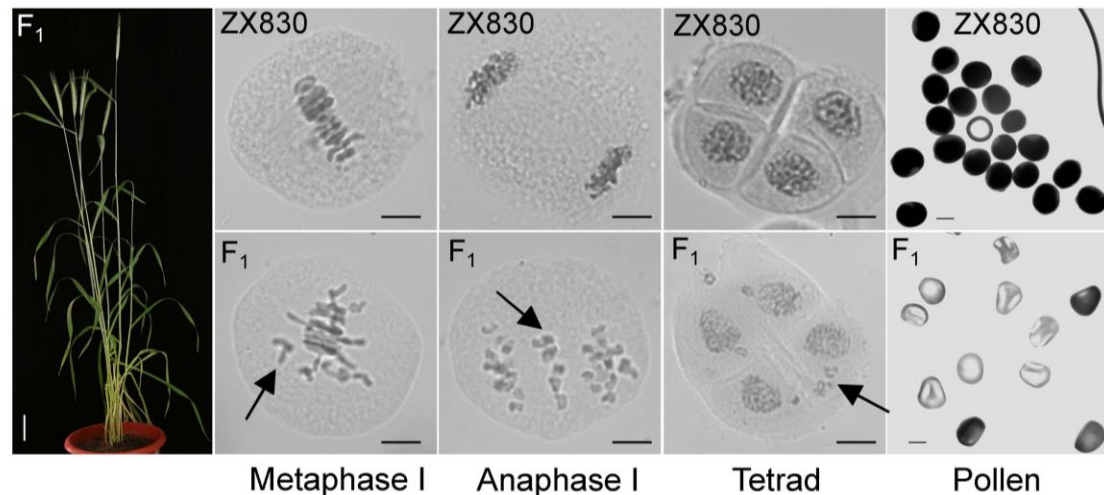


- PT exhibited the strongest structural and centromeric divergence relative to ZX830, particularly in the R subgenome.

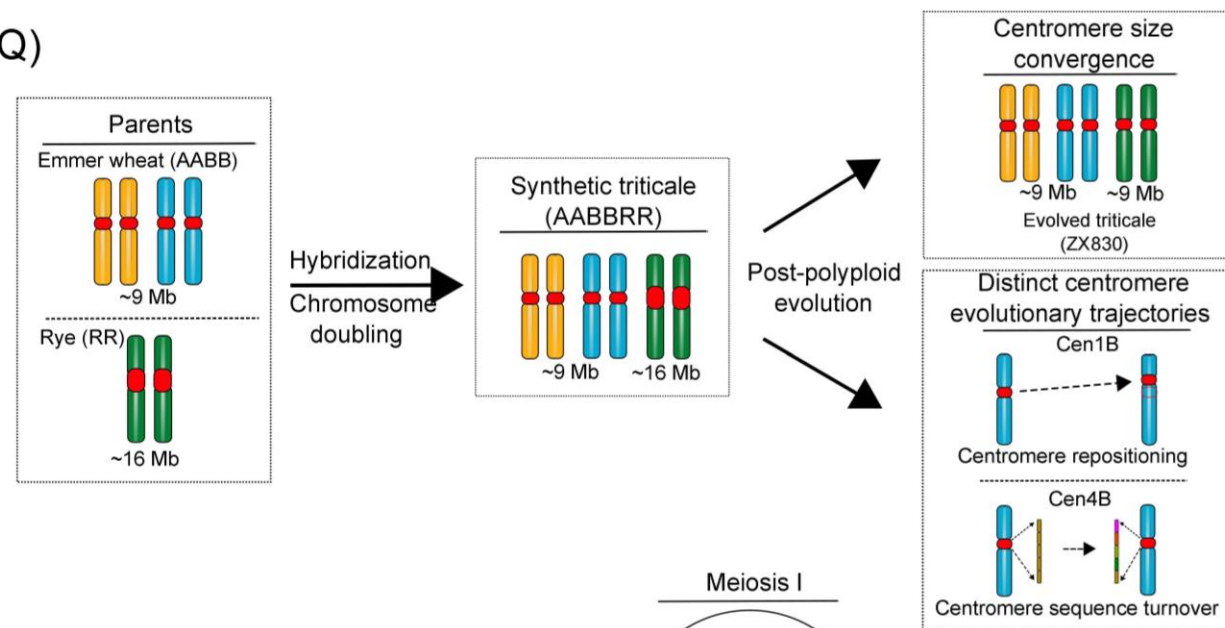


Meiotic defects and sterility in divergent triticales hybrids

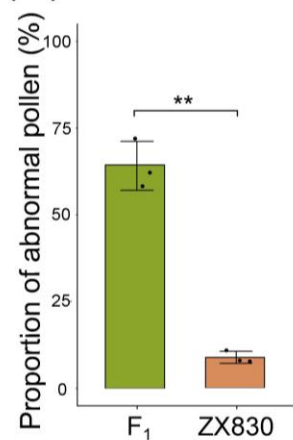
(N)



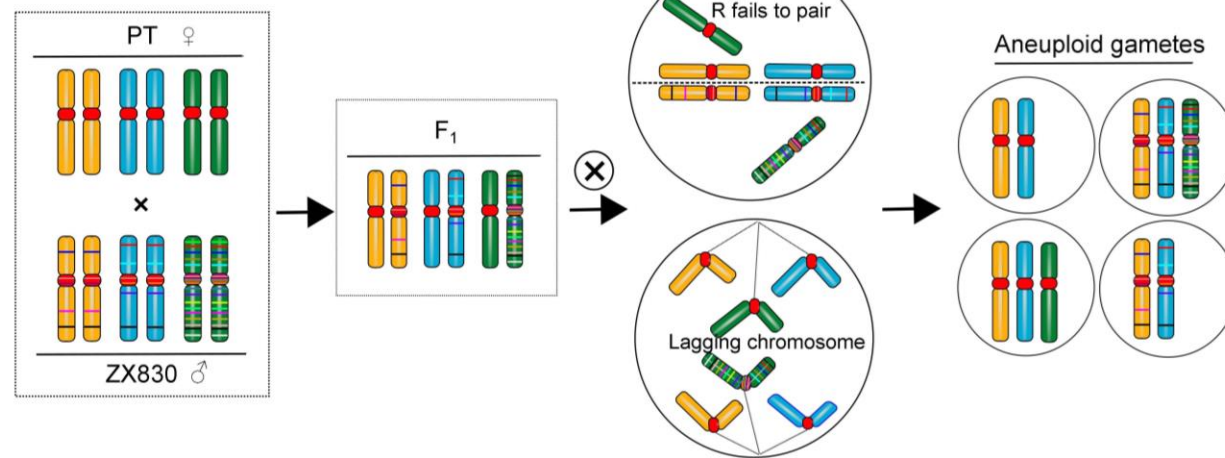
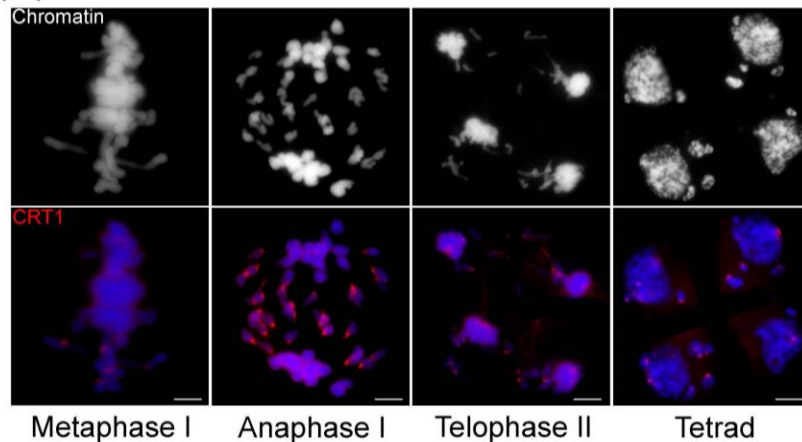
(Q)



(O)



(P)



R-subgenome divergence → chromosome mis-segregation → reproductive isolation



Summary

- ❑ This study generated two near-complete triticales genomes and the first pan-centromere landscape, providing a valuable resource for studying centromere evolution in allopolyploids.
- ❑ Functional centromeres are defined by dual loading of wheat and rye CENH3 on divergent sequences, demonstrating that centromere function relies on epigenetic compatibility.
- ❑ Post-polyploid evolution drives extensive centromere remodeling, especially in the R subgenome, which is associated with meiotic defects and reproductive isolation, establishing a genomic barrier during polyploid diversification.

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