

Transposable elements dynamics in the face of hybridization: insights from the wild yeast *Saccharomyces paradoxus*

Mathieu Hénault*, Souhir Marsit, Guillaume Charron and Christian R. Landry

Département de Biochimie, Microbiologie et Bio-informatique, Département de Biologie, Institut de Biologie Intégrative et des Systèmes, PROTEO, CRDM, Université Laval, Canada * [@mathieu_henault](https://twitter.com/mathieu_henault)

Background

Transposable elements (TEs) are mobile genetic elements that can profoundly impact the evolution of genomes and species. A long-standing hypothesis states that TEs could be reactivated in hybrids¹. This could fuel hybrid evolution with a higher mutation supply, but also cause reproductive isolation between species if high TE loads render hybrids inviable or sterile. We test this hypothesis using the undomesticated yeast *Saccharomyces paradoxus*². Using population genomic data³, we show that no Ty LTR-retrotransposons reactivation occurred in the natural hybrid lineages. We performed mutation accumulation (MA) experiments on artificial hybrid lineages⁴ and show that evolution of Ty copy number highly depends on the individual hybrid genotypes and is not predicted by the genetic divergence or Ty abundance of the parents. **a.** Hypothesis of TE reactivation in hybrids **b.** Phylogeny of North American *S. paradoxus* **c.** Hybridization history among *S. paradoxus* NA lineages

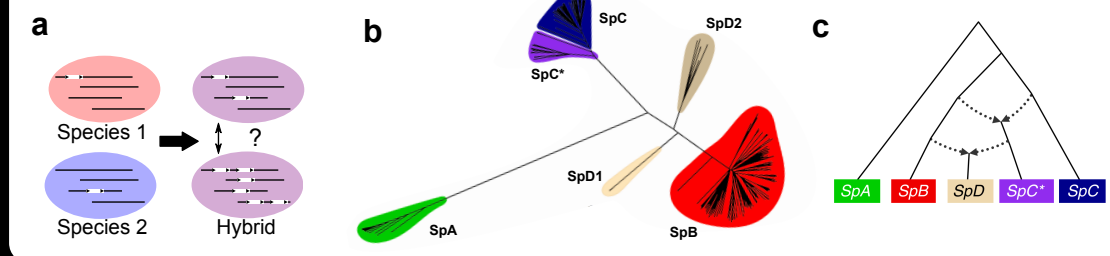


Figure 1

Ty copy numbers (CNs) in natural lineages. **a.** CNs of full-length elements (top) and solo LTRs (bottom) in six whole-genome assemblies based on long reads. **b.** CN variation in active Ty families measured as log2 normalized read depth (NRD) over Ty consensus sequences for 208 wild strains.

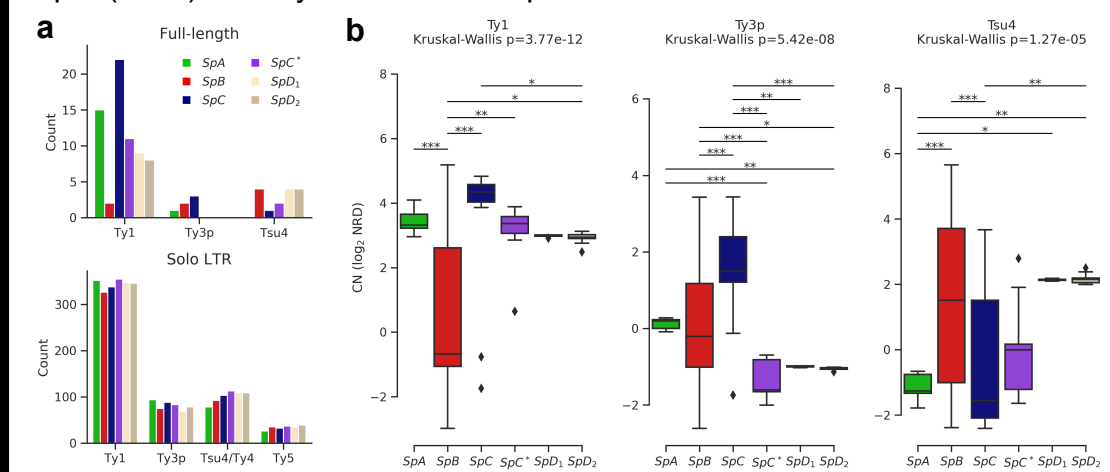


Figure 2

Evolutionary dynamics of Ty families in natural lineages. **a.** Distributions of minimum nucleotide divergence between LTR sequences. Numbers: counts of LTR sequences. Heatmaps: FDR-corrected p-values for pairwise Kolmogorov-Smirnov tests (red dots: $p < 0.05$). **b.** LTR divergence and conservation. Horizontal positions: Ty orthogroups clustered from conserved (left) to private (right). Color map: minimum nucleotide divergence. Red dots: LTRs that belong to full-length elements.

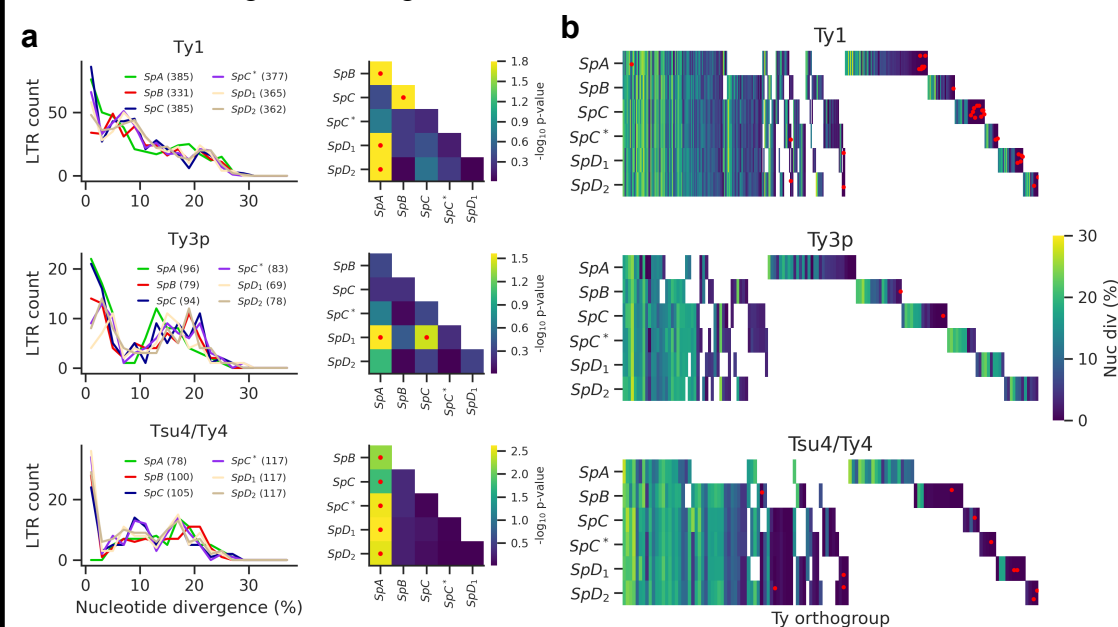


Figure 3

Design of the MA experiment on artificial hybrids. **a.** Artificial hybrids generated to initiate MA experiments span various levels of divergence. **b.** Single-cell bottlenecks on yeast populations allow mutations to accumulate with minimal selective constraints.

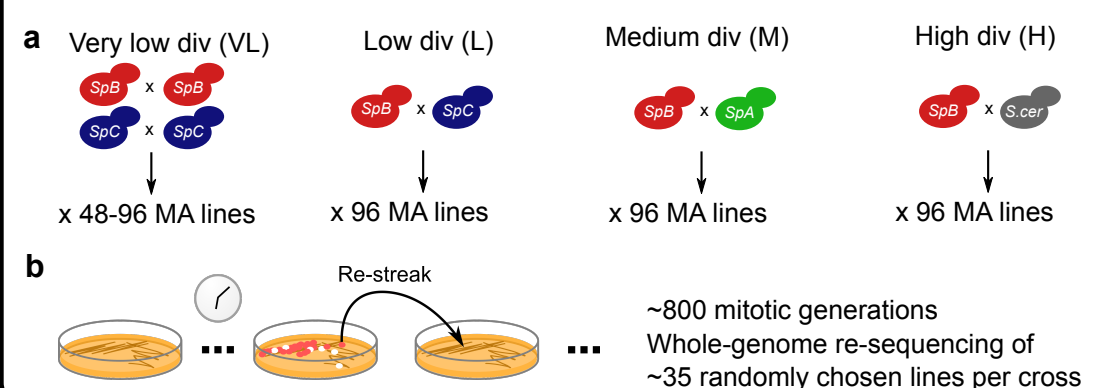
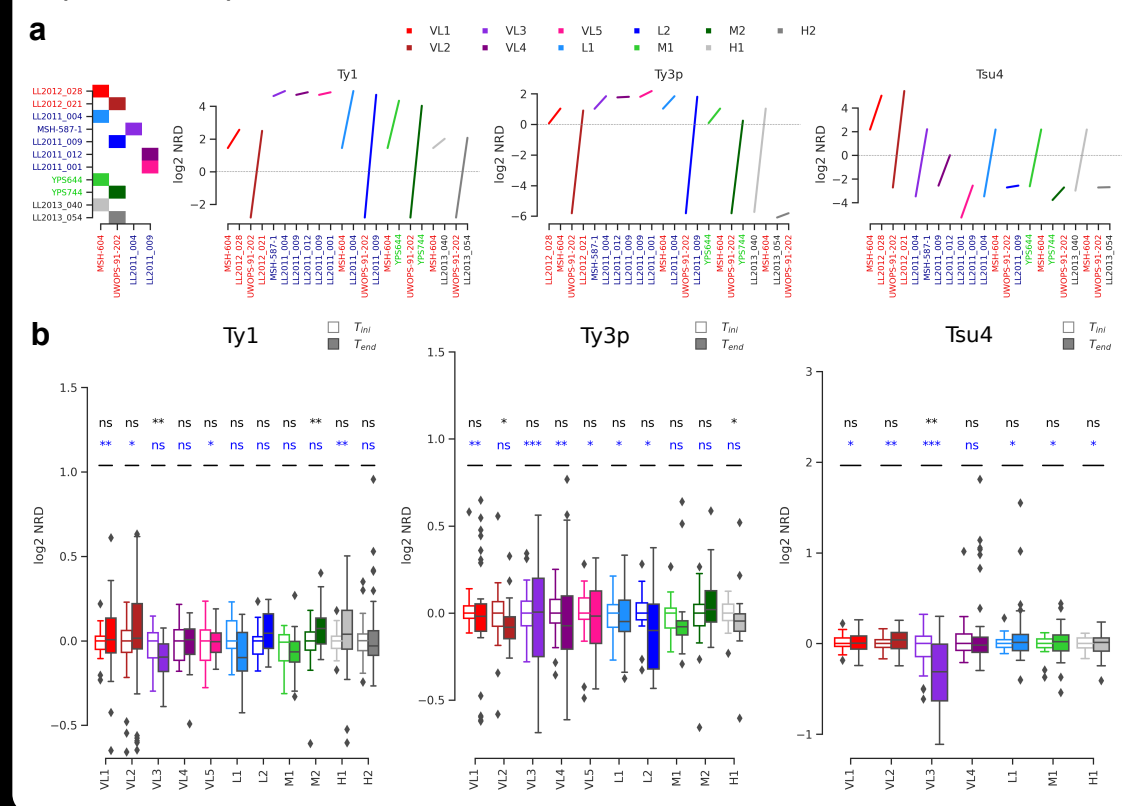


Figure 4

Ty CN variation in the MA hybrids. **a.** Design of the MA hybrid crosses and CNs in the haploid strains used. **b.** CN variation between the onset (T_{ini}) and the end (T_{end}) of the MA experiment. Black: FDR-corrected Wilcoxon p-values. Blue: FDR-corrected Brown–Forsythe p-values. ns: $p \geq 0.05$, *: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$.



Conclusions

- Natural hybrid lineages show no reactivation of Ty elements
- Natural pure lineages show extensive variation in Ty CNs and evolutionary dynamics
- MA on artificial hybrids reveal no systematic effect of hybridization, with CN variation poorly predicted by parental genetic divergence or Ty CNs

References

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