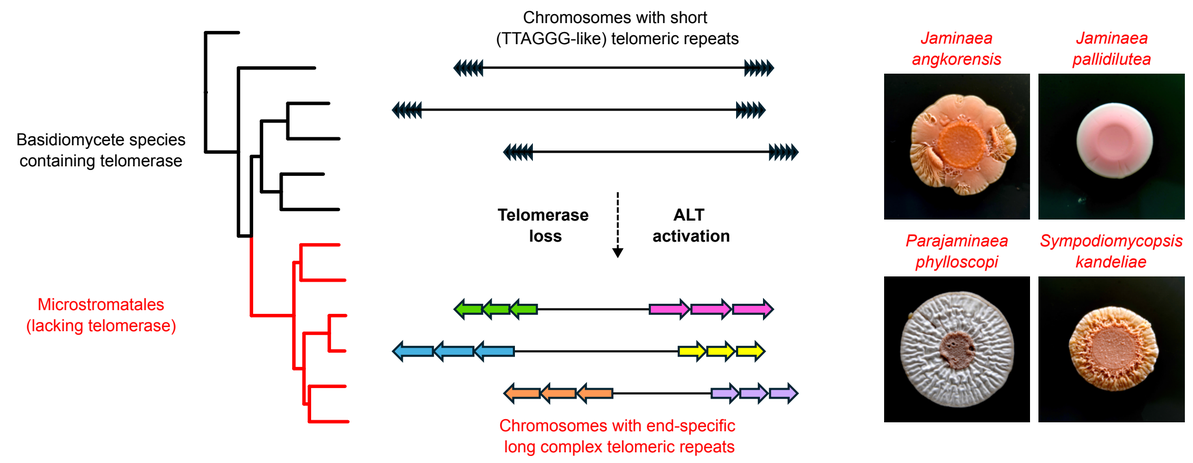
Noncanonical Chromosomal-End-Specific Telomeric Arrays in Naturally Telomerase-Negative Yeasts

A Bioinformatics Perspective

Abstract

In most eukaryotes, chromosomal DNA terminates with tandem repeats of a short G-rich motif, such as the canonical TTAGGG sequence. The arrays of telomeric repeats are maintained by telomerase or by alternative lengthening of telomeres (ALT). Here we report that nuclear chromosomes of several basidiomycetous yeasts classified into the order Microstromatales carry unusual telomeres. We demonstrate that instead of TTAGGG-like repeats these telomeres are composed of unique tandem arrays which are in most cases specific to a particular chromosomal end. In contrast to other basidiomycetes, the Microstromatales genomes lack orthologs coding for the telomerase catalytic subunit Est2 and a shelterin component Tpp1 indicating that noncanonical telomeric arrays are maintained by a telomerase-independent mechanism. We hypothesize that in a common ancestor of Microstromatales the loss of telomerase and Tpp1 was compensated by activation of an ALT mechanism, which promoted amplification of various motifs and formation of distinct telomeric arrays at most chromosomal ends.

Graphical abstract



Bioinformatics analyses

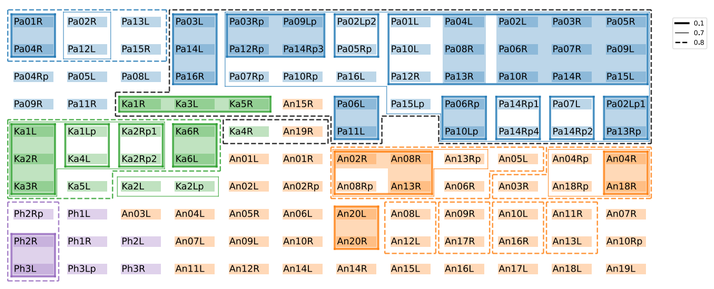


Figure 1. Single-linkage clustering of telomeric motifs using Jaccard containment measure on multi-sets of 7-mers (substrings of length 7). Although some motifs are identical or highly similar, there are many motif pairs with little similarity suggesting high turnover.

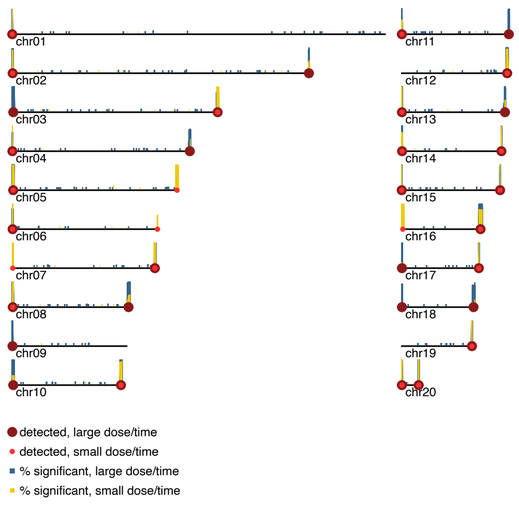


Figure 2. DNA was extracted from cells and treated with BAL-31 enzyme which digests chromosomal ends. Both treated and control DNA were sequenced on MinION sequencer. Depletion of 21-mers in the treated samples was tested by one-sided Fisher exact test with Bonferroni multiple testing correction. Windows of length 1kb more than 50% covered by significant 21-mers are highlighted. Each chromosomal end was significant in at least one experiment, confirming telomeric nature of identified repeats. This analysis inspired our subsequent work [Petescia et al. 2025].

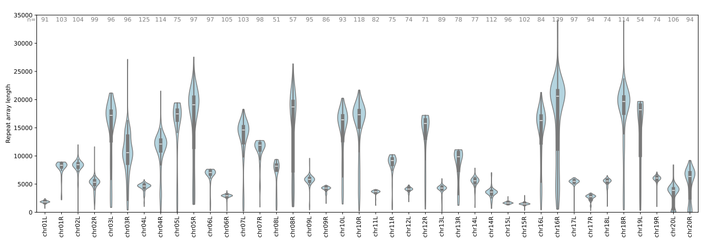
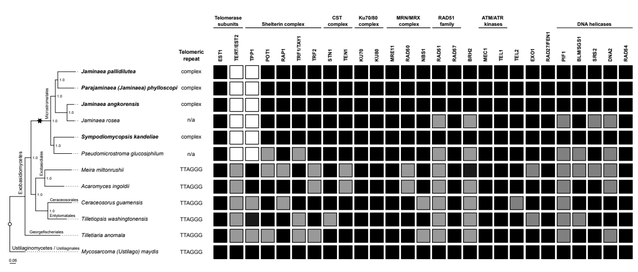


Figure 3. Length distribution of telomeric arrays. The lengths were estimated from nanopore reads by a custom profile hidden Markov model to capture the cyclical nature of the motifs as well as sequencing errors. The lengths of individual motif arrays differ more than 10-fold.

Phylogeny and gene loss



References

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- Petescia, A., Denti, L., Gafurov, A., Hodorová, V., Nosek, J., Brejová, B. and Vinař, T., 2025. Alignment-free Detection of Differences Between Sequencing Data Sets. iScience.

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