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Noncanonical chromosomal-end-specific telomeric arrays in naturally telomerase-negative yeasts

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In most eukaryotes, chromosomal DNA terminates with tandem repeats of a short G-rich motif, such as the canonical TTAGGG sequence. 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. In this poster, we will show various bioinformatics analyses applied to explore sequencing data from these species.

Pracovisko fakulty (katedra)/ Department of Faculty

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Tlač postru/ Print poster

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