



The classic model organism *Schizosaccharomyces pombe* and other fission yeasts have a distinct evolutionary history from that of budding yeasts, but little is known about the details of fission yeast evolution. An extensive comparison of the genomes and transcriptomes of the four known fission yeasts now changes this situation. It provides an intriguing picture of conserved and divergent features of gene structure and regulation in fission yeasts, and gives an insight into metabolic evolution.

Rhind *et al.* sequenced and assembled the genomes of *Schizosaccharomyces octosporus*, *Schizosaccharomyces cryophilus* and *Schizosaccharomyces japonicus* and compared them with the *S. pombe* genome. They found a high level of amino acid divergence in *Schizosaccharomyces* spp.; for example, 1:1 orthologues between *S. pombe* and *S. japonicus* have an average of only 55% amino acid identity. From the level of divergence, the authors estimate that fission yeast

arose ~250 million years ago. Given this divergence at the amino acid level, the gene content and structure is surprisingly conserved: 4,218 of the ~5,000 coding genes have a single orthologue in each species. So, there might be unusually fast sequence evolution in fission yeast, or they might have an unusually slow rate of change in gene content.

Repeat-element distribution and regulation is strikingly different among the fission yeasts. For example, the most ancient of these yeasts, *S. japonicus*, has many more transposon families than the others — *S. octosporus* has no transposons. Furthermore, unlike the other fission yeasts, *S. japonicus* centromeres lack symmetrical arrays of repeats, which is likely to be due to the high level of transposition. The disappearance of transposons in the younger species correlates with the appearance of Cbp1 proteins, which are known to silence transposons in *S. pombe*. The authors suggest that the suppression of transposition might have led to

degeneration of transposons and evolution of symmetric centromeric repeats. Interestingly, they also found that small interfering RNAs map to transposons in *S. japonicus*, whereas they are known to be involved in silencing centromeric repeats (but not transposons) in *S. pombe*.

Rhind *et al.* also compared the transcriptomes of the fission yeasts and found that global patterns of coding-gene expression are largely conserved under different conditions, such as growth or stress. Intriguingly, in all four species, antisense transcription seems to regulate meiotic genes, but possibly by a different mechanism from that of antisense regulation in the budding yeast *Saccharomyces cerevisiae*.

Finally, although both fission and budding yeasts use aerobic alcohol fermentation, this study shows how this capability evolved independently in these lineages. The authors also provide insights into why fission yeasts depend on glucose rather than ethanol as a primary carbon source. This illustrates how the availability of the fission yeast genomes can improve our understanding, not only of these species but also of fundamental processes, including modes of genome regulation and microbial metabolism.

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ORIGINAL RESEARCH PAPER Rhind, N. *et al.* Comparative functional genomics of the fission yeasts. *Science* 21 Apr 2011 (doi:10.1126/science.1203357)

FURTHER READING Dujon, B. Yeast evolutionary genomics. *Nature Rev. Genet.* **11**, 512–524 (2010)