

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

The other yeast genome

ArticleInfo		
ArticleID	:	4407
ArticleDOI	:	10.1186/gb-spotlight-20020221-01
ArticleCitationID	:	spotlight-20020221-01
ArticleSequenceNumber	:	73
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	3
ArticleHistory	:	RegistrationDate : 2002-2-21 OnlineDate : 2002-2-21
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

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In the February 21 *Nature*, an international consortium of laboratories, led by the British Nobel laureate Paul Nurse, reports the complete sequence of the fission yeast *Schizosaccharomyces pombe* (*Nature* 2002 **415**:871-880). The depth of sequence coverage was about eight-fold. The three chromosomes make up a 13.8 Mb genome, which is similar in size to that of the budding yeast *S. cerevisiae*, but considerably smaller than the other sequenced eukaryotic genomes (fruitfly, nematode worm, human and *Arabidopsis*). The authors predict a maximum of 4,940 protein coding genes, which is about six hundred less than *S. cerevisiae* and considerably less than the largest prokaryote genomes, emphasising that the differences between prokaryotic and eukaryotic functions does not reside simply in the total number of genes. The *S. pombe* genome is also less compact than that of *S. cerevisiae*, with one gene every 2.5 kb and longer intergenic regions. The *S. pombe* centromeres are 300-1000 times larger than those of its yeast cousin. There are also many more introns (4,730 in 43% of genes) than in *S. cerevisiae* (5% of genes); this suggests greater opportunity for alternative splicing and protein variants with different regulatory roles. The authors have carried out extensive comparison with other sequenced genomes. The *S. pombe* proteome has homologs in common with both *S. cerevisiae* and *C. elegans* (67%), with *S. cerevisiae* alone (16%), with *C. elegans* alone (3%), as well as apparently unique proteins (14%). They found around fifty *S. pombe* proteins that resemble human proteins implicated in disease; these include several cancer-related proteins linked to DNA damage repair, the cell cycle and genome stability. Comparison with prokaryote genomes indicates the minimal sets of proteins that are specifically important for eukaryotic cell organization and functions. These include those involved in chromatin organisation, nuclear transport, the cytoskeleton and protein stability or modification. Comparison of all the eukaryote and prokaryote genomes available allowed the authors to speculate that "the evolutionary transition from unicellular prokaryotic to unicellular eukaryotic life may have been more complex than the transition to multicellular life."

Editor's note

Readers interested in the comparative genomics and evolutionary history of *Schizosaccharomyces pombe* might like to read the following articles previously published in *Genome Biology*:

Minireview: Where does fission yeast sit on the tree of life? **Matthias Sipiczki.** *Genome Biology* 2000, **1(2)**:reviews1011.1-1011.4<http://genomebiology.com/2000/1/2/reviews/1011>

Minireview: Membrane traffic between genomes **John Armstrong.** *Genome Biology* 2000, **1(1)**:reviews104.1-104.4<http://genomebiology.com/2000/1/1/reviews/104>

References

1. *Nature*, [<http://www.nature.com>]
2. The yeast genome directory.
3. *Schizosaccharomyces pombe* GeneMaps, [<ftp://ftp.sanger.ac.uk/pub/yeast/pombe/GeneMaps>]
4. Proteome database registration, [<http://proteome.com/databases>]
5. Minireview: Where does fission yeast sit on the tree of life? Matthias Sipiczki. *Genome Biology* 2000, 1(2):reviews1011.1-1011.4, [<http://genomebiology.com/2000/1/2/reviews/1011>]
6. Minireview: Membrane traffic between genomes John Armstrong. *Genome Biology* 2000, 1(1):reviews104.1-104.4, [<http://genomebiology.com/2000/1/1/reviews/104>]