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How yeasts evolve

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The publication in [Nature](#) this week of four yeast genomic sequences seems to have confirmed the controversial idea, introduced in 1997, that whole genome duplication occurred in *Saccharomyces cerevisiae* (*Nature* 2004, **430**:35-44).

The very high-coverage sequences - with virtually no gaps - of four species of yeast reveal evidence of tandem gene duplication, segmental duplication (coduplication of tens to hundreds of genes), and whole genome duplication, said study coauthor Giles Fischer, who worked with Bernard Dujon and others at the Centre Nationale de la Recherche Scientifique in France. "One of the major forces that has driven evolution is gene duplication followed by gene loss," Fischer said, "but we did not find only one single mechanism of gene duplication, we found three."

"During the last 2 or 3 years, about 10 novel yeast sequences have been completed, and now the comparison of these sequences has brought one conclusion which is very clear," said André Goffeau, a professor at the Institut des Sciences Vie, Université Catholique de Louvain, Belgium, who wrote an accompanying News and Views article. The [proposal](#) of whole genome duplication in *S. cerevisiae* - first put forward by [Ken Wolfe](#), professor at the department of Genetics, Trinity College Dublin - "is now fully proven without doubt," Goffeau told us.

"Dujon was one of the people who was most opposed to this hypothesis," Wolfe, who was not involved in the study, told us. He said that in 2000, the French group did limited sequencing of 13 species of yeasts and drew the conclusion that there was no evidence to support the genome duplication idea. "It wasn't even draft sequencing, it was 0.2-fold coverage," said Wolfe. "They've completely turned around and changed their minds now - very gratifying for me."

"I think that all the mechanisms that we see in this group of species are probably conserved all over the kingdom of life," Fischer said, noting that yeast species are more different from each other than man is from marine invertebrates, fish, birds, and mammals.

The four yeast genome sequences published were from *Candida glabrata*, a human pathogen; *Kluyveromyces lactis*, commonly used in genetics studies; *Debaryomyces hansenii*, a salt-tolerant yeast; and *Yarrowia lipolytica*, a methane-using yeast. "The molecular divergence as measured by the percentage of identity between homologous proteins is very high between these yeasts," Fischer said.

"One can see that the finer details of the evolutionary trajectories at the genomic level can be quite different even within a single phylum," said Anthony Poole, from the Department of Molecular Biology and Functional Genomics at Stockholm University. "We tend to be biased by what we see, and if we look at a fish and a human we tend to think they're fairly different looking species, whereas yeasts all look to the same to us. It's why far more detailed studies have to be carried out."

Poole, who was not involved in the study, said that previous analyses using smaller data sets had led to more and more generalizations. "When you have a comparative data set like this, there's all sorts of interesting questions that will come out of it."

References

1. *Nature*, [<http://www.nature.com/>]
2. Molecular evidence for an ancient duplication of the entire yeast genome
3. Ken Wolfe, [http://www.tcd.ie/Genetics/staff/Ken_Wolfe.html]