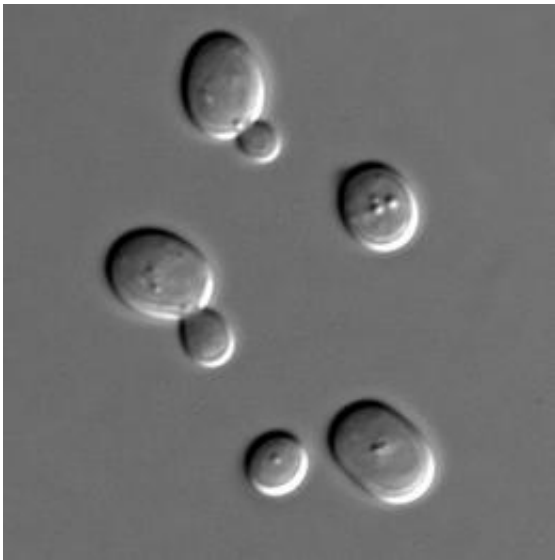


How yeast doubled its genome—by mating between species

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Sacharomyces cerevisiae cells in DIC microscopy. Credit: Wikipedia.

The common baker's yeast (*Saccharomyces cerevisiae*) is used to make bread, wine and beer, and is the laboratory workhorse for a substantial proportion of research into molecular and cell biology. It was also the first non-bacterial living thing to have its genome sequenced, back in 1996. However, when the sequence of that genome emerged it appeared that the scientists were seeing double - the organism seemed to have two very different versions of many of its genes. How could this have happened?

Researchers from the Centre for Genomic Regulation (CRG) Barcelona, Spain, writing in the Open Access journal *PLOS Biology* in a paper publishing 7th August, have now proposed a new theory to explain this phenomenon; the answer involves an ancient mating event between two distinct species, and may have implications for our own genomes.

Since the initial observation, scientists had assumed that about 100 million years ago the entire genome had somehow been duplicated, and that subsequently and although some genes had been lost, the yeast kept two copies of many genes and used them to acquire new functions that helped it to survive.

Such "whole genome duplications" are now known to be surprisingly widespread; for instance, we know that whole genome duplications were important in the early evolution of vertebrates (our own genomes bear the hallmarks of two separate ancient whole genome duplication events) and that it is a very common phenomenon in plants, especially cultivated ones such as wheat.

The CRG scientists Marina Marcet-Houben and Toni Gabaldón used advanced [computational methods](#) to study the origins of the whole genome duplication in yeast to gain a more thorough understanding of this phenomenon, which is thought to have played a key role the evolution and adaptation of the species. Unexpectedly, they show that the appearance of duplicated genes was not caused by a simple duplication of the whole genome but rather by a mating ("hybridization") event between two different species. Their proposal, which is at odds with the currently most widely accepted theory in the scientific community, provides new insight into this key process during genome evolution and the origins of species.

"When we first saw the results of our study, we thought there had been some kind of mistake," explained Toni Gabaldón, the lead investigator

of the study, head of the CRG Comparative Genomics Group and ICREA Research Professor. "Honestly, when the results are not what you expect and contradict what is established, the first thing you do is think that they were affected by some kind of problem. But once all the potential problems have been discarded, you begin to interpret the data objectively, without preconceived ideas, and to do real science. That's when we started to consider the different possible explanations and to work on a new idea,"

The work of Marcet-Houben and Gabaldón revealed that, for yeast, hybridization was indeed behind the duplication of some genes. The researchers analyzed genomic data with computational tool, based on cutting-edge computational methods, and designed by the Gabaldón group, to study the yeast family tree. This tool allowed the researchers to reconstruct gene duplications and to determine what happened in evolutionary time, making it a computational equivalent of carbon-14 dating for fossils. To their surprise, they found that the age of some duplicated genes seemed to be much greater than that predicted by the theory for the whole genome duplication event. Rather than supporting a genome duplication event at the time when yeast evolved to have twice the number of chromosomes, their data indicated that the duplicated genes had begun to diverge long before. This result suggested the possibility of hybridization between species. In this case, the [genes](#) that have been duplicated still differ from each other, so that their divergence preceded the duplication of the chromosome.

Gabaldón added, "It's one of those magical moments of research when, once you open your mind enough, you can surrender to the evidence in the data and discard what you had considered as a proven fact to adopt an entirely new paradigm, no matter how implausible it seems at first. Afterwards you reel in your new paradigm and see that it also explains other independent observations. Scientifically it has been a challenging and rewarding experience. "

The hybridization hypothesis has strong implications on how we interpret the origin and evolution of duplicated genomes. For instance, we no longer need to imagine that massive and rapid changes are necessary to generate new functions from duplicated genome regions, since hybridization combines the properties of the two parental lines from day one and opens the door to new ecological and evolutionary opportunities.

Being able to "look" at 100 million-year-old genomes will now allow us to deepen our knowledge about genomes as well as about the evolutionary mechanisms that lead to diversifying and acquiring new function. This challenging and innovative work will have major implications on how we interpret the functional and evolutionary consequences of genome duplication. It also highlights the importance of basic research for understanding genomes, evolution and diversity.

More information: Marcet-Houben M, Gabaldón T (2015) Beyond the Whole-Genome Duplication: Phylogenetic Evidence for an Ancient Interspecies Hybridization in the Baker's Yeast Lineage. *PLoS Biol* 13(8): e1002220. [DOI: 10.1371/journal.pbio.1002220](https://doi.org/10.1371/journal.pbio.1002220)

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