

# Wild about the evolution of domesticated yeast

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(PhysOrg.com) -- It lives all around us and is probably one of the earliest domesticated organisms. Humans have been using it for tens of thousands of years. There is evidence that the Ancient Egyptians used it for baking and brewing and today yeast is regarded by geneticists, because of its genetic similarities to humans and the powerful tools available, as the 'model' model organism.

Domesticated yeast has been at the forefront of every major breakthrough in genomics. But has our long association with yeast made it too domesticated? Does the highly selected yeast we now produce for laboratory experiments in any way influence the outcome of scientific research?

After five years searching for the answer a team of scientists, led by Ed Louis at The University of Nottingham and Richard Durbin a principal investigator at The Sanger Institute, believe that even after centuries of domestication, the yeast we tamed for science, brewing and baking is actually much the same as its closest relatives still living in the wild.

Ed Louis, a professor of genome dynamics at the Institute of Genetics at The University of Nottingham, said: "We didn't know much about the evolution of yeast and how much influence we had over the centuries by highly selecting for brewing, baking and laboratory experiments. We have established that yeast is, for example, more like cats than dogs in terms of their domestication. Like cats, and their relatives the lion and tiger, yeast is much more closely related than we thought and still looks

and behaves in much the same way as its wild cousins. Therefore it remains to this day one of the best models even for evolutionary studies.”

Until now little has been known about the evolutionary processes taking place within populations and different strains of domesticated yeast. Scientists examined the genome sequencing of over 70 different strains of yeast. These are strains of *Saccharomyces cerevisiae* (*S. cerevisiae*) commonly used in the production of laboratory research, baking, wine making and the production of sake. They were compared with its closest relative, *Saccharomyces paradoxus* (*S. paradoxus*) isolates, found mainly on oak tree bark.

Their research, which has just been published in *Nature*, has established the level of variation between different populations and species of yeast. There is as much genetic variation between yeast strains as there is between humans. As a result of this research geneticists have been able to develop the model data set necessary for building tools for projects such as comparing thousands of human genomes. Yeast is a good model for studying cancer and ageing as well as diseases associated with specific cellular defects — such as diabetes and Alzheimer's.

Dr Richard Durbin said: "We have been able to use the amazing power of modern DNA sequencing to obtain an unprecedented picture of the way the genes in this organism vary, and how it evolved. The tools we developed to study yeast are now being applied to the human genome, to help identify genetic variants that are involved in disease."

Provided by University of Nottingham

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