Yeast cells optimize their genomes in response to the environment

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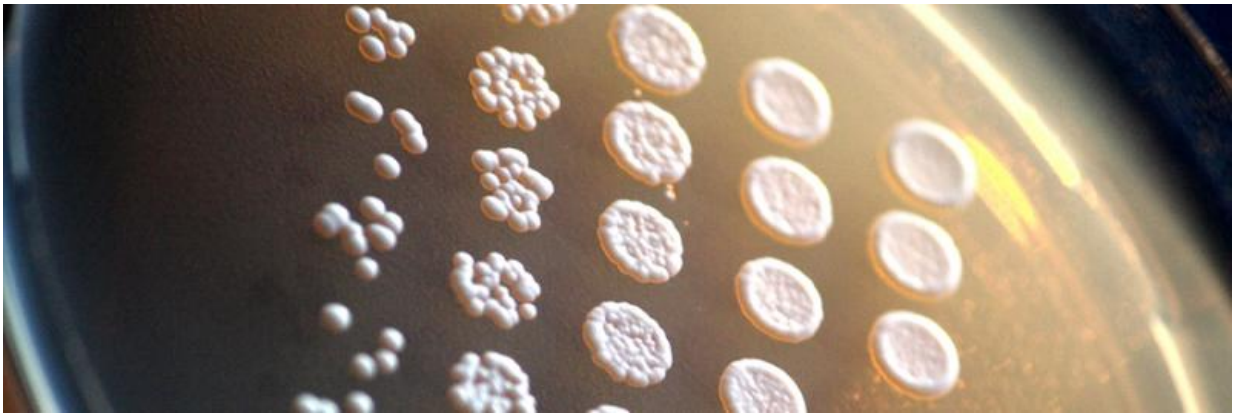

Yeast colonies on an agar plate. Image: Rainis Venta [CC BY-SA 3.0 via Wikimedia Commons]

Researchers at the Babraham Institute and Cambridge Systems Biology Centre, University of Cambridge have shown that yeast can modify their genomes to take advantage of an excess of calories in the environment and attain optimal growth.

The ability to sense environmental nutrient availability and act accordingly is a critical process for all organisms. Changing behaviour in response to nutrients can occur at many levels: the activity of proteins can be varied or new genes can be activated to produce a different set of proteins. Research published in the latest issue of *PNAS* reveals that

yeast go one step further and actually modify their genomes to act optimally in the current environment.

We think of the information in our genome as stable, only changing occasionally through random mutation. However, a handful of genes in organisms from yeast to mammals are known to change rapidly at specific times and in specific cell types. A good example of this is the system which creates immune diversity in vertebrates. How these systems are controlled is a major question as mechanisms that cause genome change can be very dangerous if mis-directed. This is especially true for single-celled organisms like yeast, for which a genome change affects not just an individual but is passed down to all its descendants.

This research looked at the genes encoding ribosomes - the factories that produce proteins in cells. To create an entire new cell requires the synthesis of a huge amount of proteins by the ribosomes, and a vast proportion of cellular resources are used in producing enough ribosomes to allow cells to divide at the maximum possible speed. TOR is a signalling pathway that coordinates growth rate in response to nutrient availability and controls the rate of ribosome synthesis. TOR signalling is conserved from yeast to mammals and controls numerous processes, one notable example being the response to caloric restriction which slows growth and can extend lifespan.

In the paper published in *PNAS*, the researchers show that TOR also responds to caloric excess, instigating a pathway that increases the number of ribosomal DNA genes in the genome. Yeast engineered to carry a sub-optimal complement of ribosomal DNA genes are known to undergo gene amplification to correct this deficit, but it was not known why. The researchers found that these cells perceive the normal environment as containing an excess of calories because they struggle to produce enough ribosomes to maintain normal levels of protein synthesis . TOR signalling responds to this caloric excess and initiates ribosomal

DNA gene amplification. Amplification of the ribosomal DNA genes provides a long term, heritable increase in ribosome synthesis capacity to enable optimum reproduction rate and make best use of available nutrients. It will be fascinating to now ask whether TOR can also drive genome changes in higher organisms in response to an excess of calories, and what effects this might have on health and lifespan.

More information: *PNAS Early Edition*
www.pnas.org/cgi/doi/10.1073/pnas.1505015112
www.pnas.org/content/early/201 … /1505015112.full.pdf

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