

New genetic tool helps researchers to analyze cells' most important functions

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Although it has been many years since the human genome was first mapped, there are still many genes whose function we do not understand. Researchers from the University of Gothenburg, Sweden, and the University of Toronto, Canada, have teamed up to produce and characterize a collection of nearly 800 strains of yeast cells that make it possible to study even the most complicated of genes.

One common way of studying the role of [genes](#) in cells is to remove a gene and investigate the effect of the loss. Genes are very similar in both [yeast](#) and people, which is one reason why the baker's and brewer's yeast [Saccharomyces cerevisiae](#) has become a firm favourite with geneticists – and in yeast it is easy to make this kind of genetic change.

However, this does not work for many genes as the loss causes the cells to die. These are known as essential genes and are therefore difficult to study. This is a major problem for researchers as essential genes are often involved in crucial life processes. These essential genes are also the most well-conserved over long evolutionary distances, like between humans and yeast.

Together with researchers from the University of Toronto, Anders Blomberg and Jonas Warringer from the University of Gothenburg's Department of Cell- and Molecular Biology have produced a collection of nearly 800 strains of [yeast cells](#) where the function of these essential genes can be studied. This new genetic tool is now being made available to other researchers.

"The trick is to use temperature-sensitive mutants for the genes you want to study," says professor Anders Blomberg. "These mutants have amino acid changes, which make the resultant protein sensitive to higher temperatures but able to function normally at normal temperatures. And at intermediary temperatures one can set the desired activity of the mutant protein."

The Gothenburg researchers have worked for many years on characterising the changes in yeast mutants that result from genetic changes or environmental factors automatically and on a large scale. They will continue to develop and characterize the new collection of yeast cells to facilitate the systematic analysis of the function of all essential genes.

Provided by University of Gothenburg

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