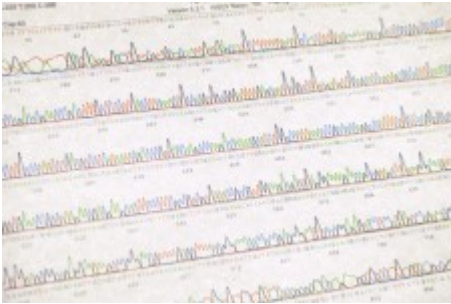


Yeast Can Do a Lot More Than Make Beer - They Can Tell Us Which of Our Genes Cause Disease



By Julianna LeMieux — April 7, 2016



The completion of the Human Genome Project in 2003 brought with it the hope of being able to see into the future, imagining answers to questions such as “Will I get cancer?” and “When will I die?” becoming part of routine medical care.

Because genome sequencing technology has evolved incredibly rapidly, a person can have their whole genome sequenced for \$999 by companies such as Veritas Genetics. That’s because sequencing a genome is easy. What is not easy is deciphering what the sequence data mean. It is a *much* more complicated process to figure out the underlying biology behind (1) what protein each gene makes; (2) how that protein functions normally; (3) how each alteration in the DNA (mutation) changes that particular protein, and (4) what diseases those changes might cause.

The difference between having a DNA sequence and predicting and treating diseases is the difference between being able to sing the alphabet song, as most 4-year-olds can, and being able not only to spell “querulous” but also to be able to say what it means (whiny). Although you cannot learn to read without knowing the alphabet, it is useless to know the alphabet without the ability to put those letters together into words.

A group from the Donnelly Centre for Cellular and Biomolecular Research at the University of Toronto and the Lunenfeld-Tanenbaum Research Institute has developed a new biological technique to uncover some of the information that is locked within the human DNA sequence. More specifically, [they have developed a method to identify whether a genetic mutation causes disease in humans](#). [1]

They do it using a powerful genetic tool that is also found in almost every kitchen -- baker’s yeast or, *Saccharomyces cerevisiae*. This may seem far-fetched, but, 31 percent of the genes found in this yeast are very similar to human genes and some of these similar genes happen to be the ones that cause human disease.

The way the researchers accomplish this begins by creating mutated strains of yeast that grow

slowly. For yeast, growing slowly is like having a “disease” because something in the cell is not functioning properly. Next, they insert a human gene into the slow growing yeast. If the human gene is normal (will not cause disease in a human) the yeast will be able to use that gene to grow normally. If the human gene causes disease, the yeast will still grow slowly.

In an effort to prove that this assay works well, the group tested 179 variants from 22 known disease causing genes and found that 82 percent of them did not help the yeast grow -- a higher success rate than current prediction models performed by computers.

This assay, of course, has limitations. Many human diseases, such as autism, are genetically complicated, resulting from complex gene interactions that we are just beginning to understand. However, this assay, coupled with other biological and computational methods, could play a role in harnessing the information that lies in our DNA sequences in order to diagnose and treat diseases more accurately and effectively.

[Genome Res. 2016 Mar 14.](#) ^[1] [Epub ahead of print] An extended set of yeast-based functional assays accurately identifies human disease mutations.

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[1] <http://www.ncbi.nlm.nih.gov/pubmed/26975778>