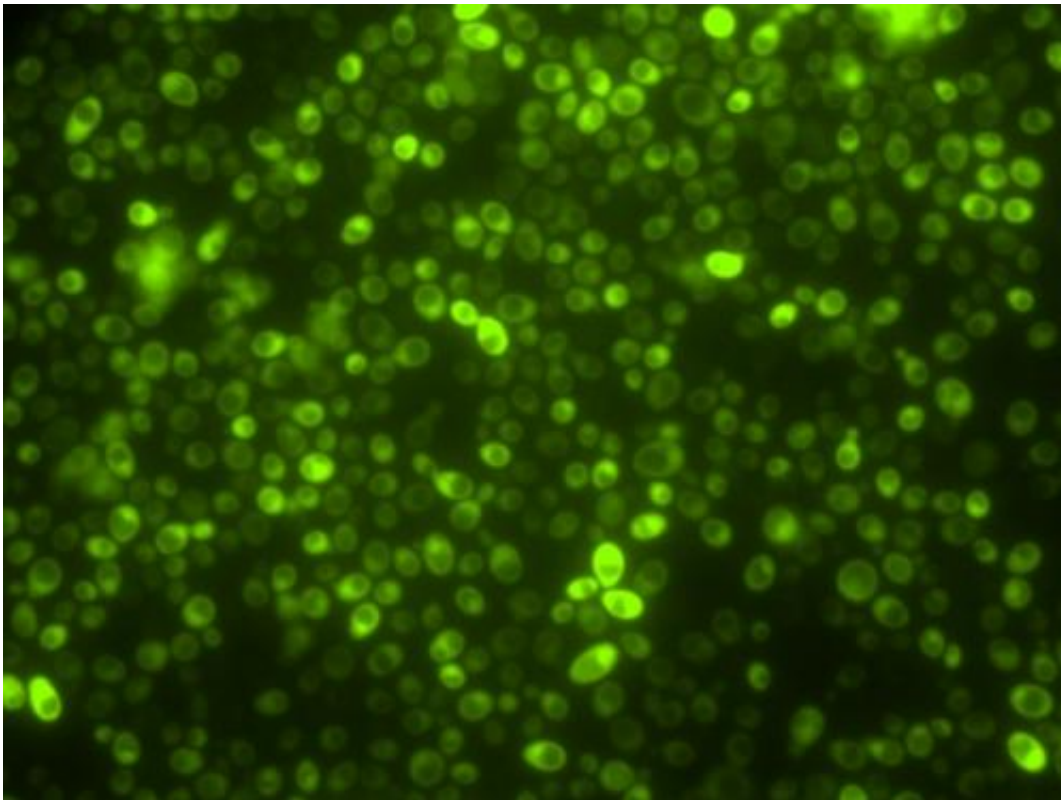


Scientists develop new approach to study how genetic variants affect gene expression

January 10 2014, by Kim Irwin



Yeast cells expressing proteins.

(Medical Xpress)—Each individual carries a unique version of the human genome. Genetic differences can influence traits such as height, weight and vulnerability to disease, but precisely what these genetic variants are and how they exercise their impact is mostly unknown. UCLA researchers have now developed a novel approach to study the

ways in which these individual differences affect how strongly certain genes are "expressed"—that is, how they are translated into the proteins that do the actual work in cells.

Using different strains of a yeast called *Saccharomyces cerevisiae*, a single-celled fungus, they studied hundreds of thousands of genetically different yeast cells—orders of magnitude more than previously examined—making their approach statistically powerful and significantly more revealing about how [genetic differences](#) influence [gene expression](#).

They also directly studied [protein levels](#), an approach that differed from earlier work, which focused on levels of messenger RNA (mRNA), the intermediate molecules that cells use to read genes and translate them into proteins. While mRNAs are easier to measure than proteins, their levels don't always correspond to protein levels.

The two-and-a-half-year study found that the [protein expression](#) of a typical gene is influenced by many more genetic variants than previously thought and that the effects of genetic differences on mRNA levels corresponded much more closely to the effects on protein expression than seen earlier. Additionally, there is a complex web of variants that affects a large fraction of the proteins in cells.

The work could shed light on the study of disease risk in humans, as genetic variants that influence disease often act by affecting the expression of genes. Clinical applications may eventually flow from a better understanding of the process of genetic variants and protein expression.

The research appears in the Jan. 8 early online edition of the journal *Nature*.

More information: "Genetics of single-cell protein abundance variation in large yeast populations." Frank W. Albert, Sebastian Treusch, Arthur H. Shockley, Joshua S. Bloom, Leonid Kruglyak. *Nature* (2014) [DOI: 10.1038/nature12904](https://doi.org/10.1038/nature12904)

Provided by University of California, Los Angeles

Citation: Scientists develop new approach to study how genetic variants affect gene expression (2014, January 10) retrieved 9 April 2024 from <https://medicalxpress.com/news/2014-01-scientists-approach-genetic-variants-affect.html>

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