

Family trees for yeast cells

May 13 2013

Researchers at the Institute for Systems Biology in Seattle and the Luxembourg Centre for Systems Biomedicine (LCSB) at the University of Luxembourg have jointly developed a revolutionary method to analyse the genomes of yeast families. The team of Dr. Aimée Dudley from the ISB and Dr. Patrick May from LCSB published their paper in the renowned scientific journal *Nature Methods* on May 12th. It describes a new method called BEST: Barcode Enabled Sequencing of Tetrads.

Baker's yeast is one of the most powerful and widely used organisms in genetic research because of the ability to perform a technique called tetrad analysis. Matings between two yeast "parents" produce four yeast "children" or spores that stick together as "tetrads". To genetically analyse these progeny, one needs to physically separate ("dissect") the four spores of each tetrad. The current method for doing this is extremely labour-intensive and has remained essentially unchanged for 75 years. A number of methods have tried to circumvent this manual process, but until now, none has been able to capture a crucial piece of information, the tetrad relationships between the spores.

The research team designed a new method that is several hundred times faster and is based on the following principles: First, two [DNA sequences](#) are added to the cells: A short sequence, called a barcode, that labels spores that come from the same tetrad and additionally a GFP ([Green Fluorescent Protein](#)) reporter gene. This fluorescent reporter allows the separation of tetrads away from other types of [yeast cells](#) by FACS sorting. Then, the four spores of the tetrad are disrupted using a

specific [enzymatic reaction](#) and allowed to grow up as individuals. Ultimately, the barcode and the same 2-3% of each individual's genome are sequenced allowing the spore strain to be placed in the correct position of the family tree for further genetic analysis.

"Identifying the genes that underlie complex traits requires extremely large numbers of progeny and high volumes of DNA sequencing," says Patrick May. "BEST combines the power of a gold standard genetic technique with ultra-high-throughput genome sequencing in a way that will enable the study of problems that were previously not possible."

More information: Ludlow, C. et al. (2013) High-throughput Tetrad Analysis. *Nature Methods*, 2013. www.nature.com/nmeth/journal/v...full/nmeth.2479.html

Provided by University of Luxembourg

Citation: Family trees for yeast cells (2013, May 13) retrieved 26 April 2024 from <https://phys.org/news/2013-05-family-trees-yeast-cells.html>

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