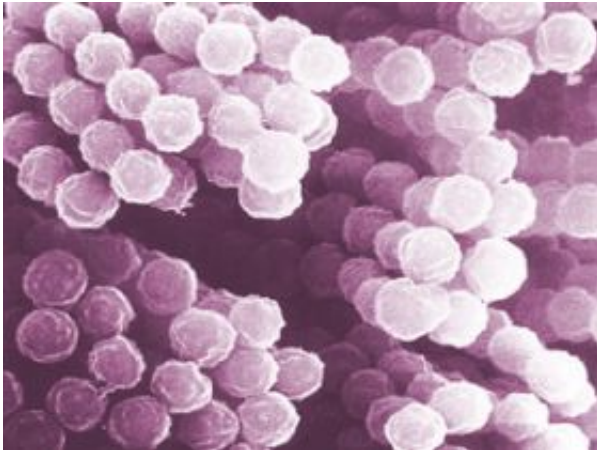


Team probes history of genes with new tool

September 11 2007



A scanning electron micrograph of one of the seventeen fungal species analyzed in the study. Image courtesy / Janice Carr, Centers for Disease Control and Prevention

The wheels of evolution turn on genetic innovation -- new genes with new functions appear, allowing organisms to grow and adapt in new ways. But deciphering the history of how and when various genes appeared, for any organism, has been a difficult and largely intractable task.

Now a team led by scientists at the Broad Institute of MIT and Harvard has broken new ground by developing a method, described in the September 6 advance online edition of *Nature*, that can reveal the ancestry of all genes across many different genomes. First applied to 17 species of fungi, the approach has unearthed some surprising clues about

why new genes pop up in the first place and the biological nips and tucks that bolster their survival.

"Having the ability to trace the history of genes on a genomic scale opens the doors to a vast array of interesting and largely unexplored scientific questions," said senior author Aviv Regev, an assistant professor of biology at MIT and a core member of the Broad Institute. Although the principles laid out in the study pertain to fungi, they could have relevance to a variety of other species as well.

It has been recognized for decades that new genes first arise as carbon copies of existing genes. It is thought that this replication allows one of the gene copies to persist normally, while giving the other the freedom to acquire novel biological functions. Though the importance of this so-called gene duplication process is well appreciated -- it is the grist for the mill of evolutionary change -- the actual mechanics have remained murky, in part because scientists have lacked the tools to study it systematically.

Driven by the recent explosion of whole genome sequence data, the authors of the new study were able to assemble a natural history of more than 100,000 genes belonging to a group of fungi known as the Ascomycota. From this, the researchers gained a detailed view of gene duplication across the genomes of 17 different species of fungi, including the laboratory model *Saccharomyces cerevisiae*, commonly known as baker's yeast.

The basis for the work comes from a new method termed "SYNERGY", which first author Ilan Wapinski and his coworkers developed to help them reconstruct the ancestry of each fungal gene. By tracing a gene's lineage through various species, the method helps determine in which species the gene first arose, and if -- and in what species -- it became duplicated or even lost altogether. SYNERGY draws its strength from

the use of multiple types of data, including the evolutionary or "phylogenetic" tree that depicts how species are related to each other, and the DNA sequences and relative positions of genes along the genome.

Perhaps most importantly, the method does not tackle the problem of gene origins in one fell swoop, as has typically been done, but rather breaks it into discrete, more manageable bits. Instead of treating all species at once, SYNERGY first focuses on a pair of the most recently evolved species -- those at the outer branches of the tree -- and works, two-by-two, toward the more ancestral species that comprise the roots.

From this analysis, Regev and her colleagues were able to identify a set of core principles that govern gene duplication in fungi. The findings begin to paint a picture of how new genes are groomed over hundreds of millions of years of evolution.

Source: MIT

Citation: Team probes history of genes with new tool (2007, September 11) retrieved 1 June 2023 from <https://phys.org/news/2007-09-team-probes-history-genes-tool.html>

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