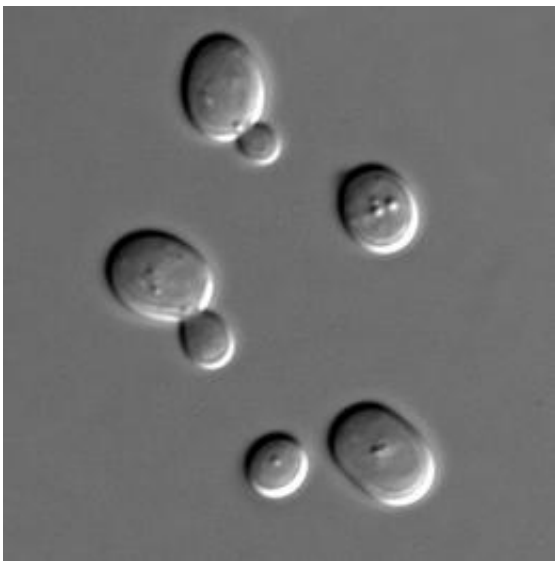


Researchers show how historical contingencies constrained evolution of a yeast regulatory network

July 9 2015, by Bob Yirka



Sacharomyces cerevisiae cells in DIC microscopy. Credit: Wikipedia.

A team of researchers with the University of California has found a way to show how historical contingencies constrained the evolution of a gene regulatory network. In their paper published in the journal *Nature*, the team describes how they conducted a genetic analysis of brewer's yeast in a way that allowed them to gain a new perspective on the regulatory network that led to the current genome of the group of fungi. Aaron New and Ben Lehner of Universitat Pompeu Fabra in Spain, offer a *News & Views* piece on the work done by the team in the same journal

issue.

In this research effort, the team looked at historical contingency—where a sequence of events led to a present state in a biological context. In ordinary life, historical contingencies occur all the time, looking over the life a person has lived, for example, would reveal many such instances, where decisions were made that led to a new state, and where another decision was eventually made based on what had occurred thus far, and on and on—mapping historical contingencies over time leads to what is known as a [regulatory network](#)—a depiction that illustrates the impact of all the contingencies that have occurred. In the biological sciences historical contingencies apply to evolutionary changes that occur over a certain period of time, and the regulatory network allows [researchers](#) to see which changes were contingent on which prior changes. Such work is challenging, which is why the researchers chose brewer's yeast to study—not only does it have a reasonably simple genome, as New and Lehner, point out, but there are also genetic engineering tools that have been developed for its study that can be adapted for use across more than one species.

Studying historical contingency in organisms works because of the way genetics works—as a trait evolves, the genome changes. Also, sometimes, changes that occur are lost due to changes in the environment, but the genome retains some of the DNA that came about due to the original change, and that too can be used in creating a regulatory network. In this new work, the researchers reconstructed the evolutionary path of two mating types in brewer's yeast, dubbed "a" and "α"—both cause genes to be switched on when exposed to pheromones. As part of their analysis they were able to show the evolutionary path that the types took as each was impacted by events, leading to contingencies and thus were able to construct a regularity network. They were also able to show, as New and Lehner, note that understanding the evolution of individual genes must involve the evolution of regulatory

networks.

More information: Intersecting transcription networks constrain gene regulatory evolution, *Nature* (2015) [DOI: 10.1038/nature14613](https://doi.org/10.1038/nature14613)

Abstract

Epistasis—the non-additive interactions between different genetic loci—constrains evolutionary pathways, blocking some and permitting others. For biological networks such as transcription circuits, the nature of these constraints and their consequences are largely unknown. Here we describe the evolutionary pathways of a transcription network that controls the response to mating pheromone in yeast. A component of this network, the transcription regulator Ste, has evolved two different modes of binding to a set of its target genes. In one group of species, Ste binds to specific DNA binding sites, while in another lineage it occupies DNA indirectly, relying on a second transcription regulator to recognize DNA. We show, through the construction of various possible evolutionary intermediates, that evolution of the direct mode of DNA binding was not directly accessible to the ancestor. Instead, it was contingent on a lineage-specific change to an overlapping transcription network with a different function, the specification of cell type. These results show that analysing and predicting the evolution of cis-regulatory regions requires an understanding of their positions in overlapping networks, as this placement constrains the available evolutionary pathways.

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