

Evolution of a natural gene network explored by Yale researchers

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Scientists have extensive knowledge of how mutations of single genes during evolution can have a fitness cost or benefit for the host organism. However, genes are often embedded into complex regulatory networks. The role of these gene networks in evolution is less well understood.

Yale researchers systematically assessed how the activity of a natural gene network evolved and came up with some surprising insights. Genes in networks are regulated by bits of genetic material called promoters. So the Yale team combinatorially swapped promoters of a sugar metabolism network between two species of yeast and then methodically analyzed the effects on the [yeast cells](#).

They found that swapping the promoter GAL80, which mediates a [negative feedback loop](#), substantially altered network activity and the fitness profiles of yeast cells.

"We have little empirical evidence about how evolution occurs at the gene network level," says Murat Acar, professor of molecular, cellular and developmental biology, and of physics, a researcher in the Systems Biology Institute at West Campus, and senior author of the study.

"Elucidating the role played by negative-feedback regulation on cross-species network activity differences adds to our understanding."

The work also offers an example of how quantitative systems biology approaches can help reveal key principles of gene network evolution, which will be essential for our fight against such pressing public health problems as antibiotic resistance, Acar said.

The findings are reported Feb. 11 in the journal *Nature Communications*.

Provided by Yale University

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