

A gene divided reveals the details of natural selection

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In a molecular tour de force, researchers at the University of Wisconsin-Madison have provided an exquisitely detailed picture of natural selection as it occurs at the genetic level.

Writing today in the journal *Nature*, Howard Hughes Medical Institute investigator Sean B. Carroll and former UW-Madison graduate student Chris Todd Hittinger document how, over many generations, a single yeast gene divides in two and parses its responsibilities to be a more efficient denizen of its environment. The work illustrates, at the most basic level, the driving force of evolution.

"This is how new capabilities arise and new functions evolve," says Carroll, one of the world's leading evolutionary biologists. "This is what goes on in butterflies and elephants and humans. It is evolution in action."

The work is important because it provides the most fundamental view of how organisms change to better adapt to their environments. It documents the workings of natural selection, the critical idea first posited by Charles Darwin where organisms accumulate random variations, and changes that enhance survival are "selected" by being genetically transmitted to future generations.

The new study replayed a set of genetic changes that occurred in a yeast 100 million or so years ago when a critical gene was duplicated and then divided its nutrient processing responsibilities to better utilize the sugars

it depends on for food.

"One source of newness is gene duplication," says Carroll. "When you have two copies of a gene, useful mutations can arise that allow one or both genes to explore new functions while preserving the old function. This phenomenon is going on all the time in every living thing. Many of us are walking around with duplicate genes we're not aware of. They come and go."

In short, says Carroll, two genes can be better than one because redundancy promotes a division of labor. Genes may do more than one thing, and duplication adds a new genetic resource that can share the workload or add new functions. For example, in humans the ability to see color requires different molecular receptors to discriminate between red and green, but both arose from the same vision gene.

The difficulty, he says, in seeing the steps of evolution is that in nature genetic change typically occurs at a snail's pace, with very small increments of change among the chemical base pairs that make up genes accumulating over thousands to millions of years.

To measure such small change requires a model organism like simple brewer's yeast that produces a lot of offspring in a relatively short period of time. Yeast, Carroll argues, are perfect because their reproductive qualities enable study of genetic change at the deepest level and greatest resolution because researchers can produce and quickly count a large number of organisms. The same work in fruit flies, one of biology's most powerful models, would require "a football stadium full of flies" and years of additional work, Carroll explains.

"The process of becoming better occurs in very small steps. When compounded over time, these very small changes make one group of organisms successful and they out-compete others," according to Carroll.

The new study involved swapping out different regions of the yeast genome to assess their effects on the performance of the twin genes, as well as engineering in the gene from another species of yeast that had retained only a single copy.

"We retraced the steps of evolution," the Wisconsin biologist explains.

The work shows in great detail how the ancestral gene gained efficiency through duplication and division of labor.

"They became optimally connected in that job. They're working in cahoots, but together they are better at the job the ancestral gene held," Carroll says. "Natural selection has taken one gene with two functions and sculpted an assembly line with two specialized genes."

Source: University of Wisconsin-Madison

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