A new method furthers understanding of evolutionary genetics

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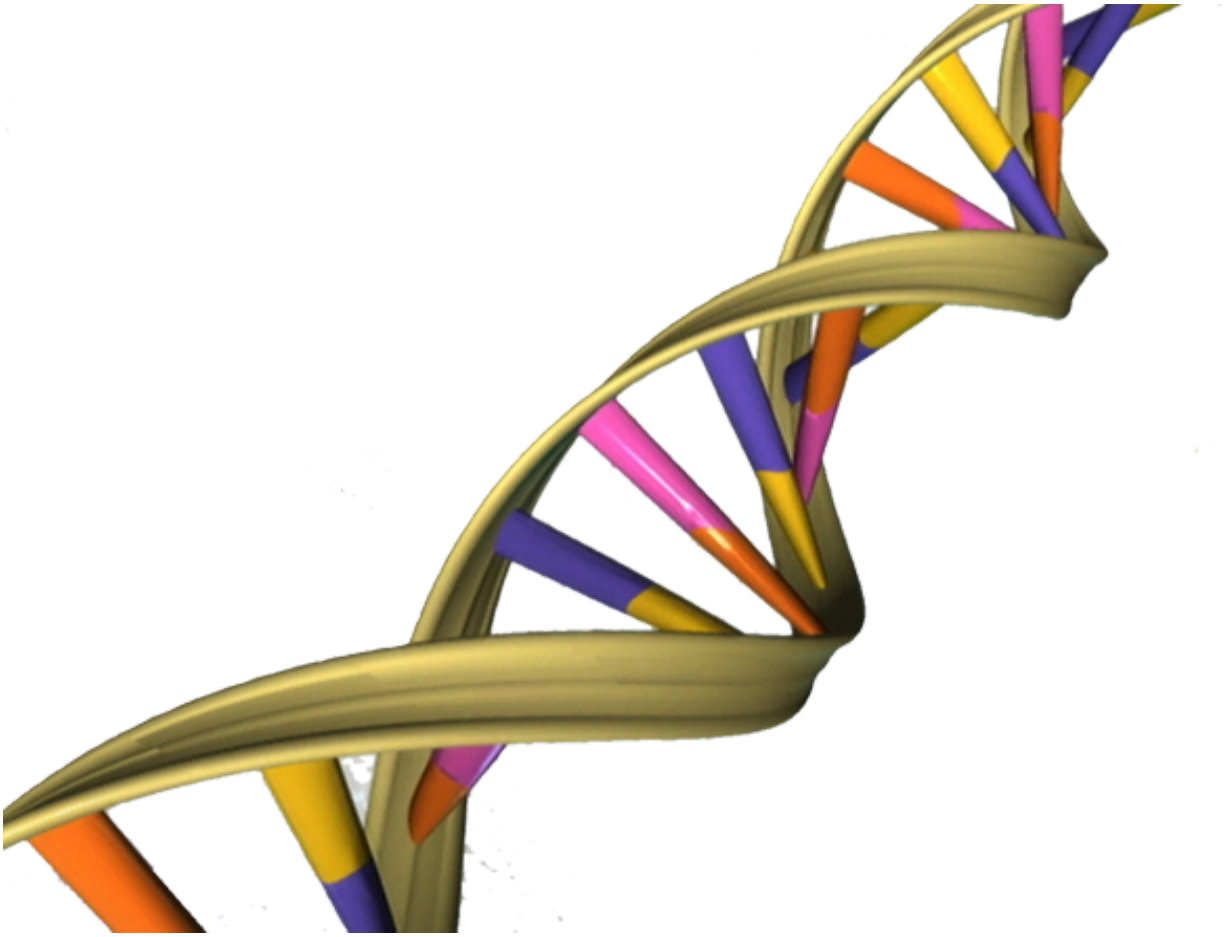

A depiction of the double helical structure of DNA. Its four coding units (A, T, C, G) are color-coded in pink, orange, purple and yellow. Credit: NHGRI

Since Darwin, evolutionary biologists have been fascinated by how different organisms are from one another. The ultimate goal is to understand how mutations in DNA, the genetic blueprint, shape the growth and behavior of animals, plants, and microbes around us. Standard research tools have been available for some time to study the genetics of closely related individuals—for example, the variation of lactose intolerance between humans. But understanding differences between long-separated species has remained a challenge. Publishing online in *Nature*, Buck Institute professor Rachel Brem and her colleagues have broken through this roadblock by focusing on distantly-related species of yeast, the single-celled organism used to make beer, wine and bread.

"Yeast is an easy system to work with and a good model for more complicated organisms," said Brem. "It was a great platform for us to develop a method for discovering what makes species unique."

The researchers first noted that some species of yeast were much better than others at deriving energy from galactose, a sugar found in plant materials. Brem and her collaborators then identified seven locations in the yeast DNA at which the species had distinct genetic information, at sites that regulated how galactose metabolism genes turned on and off as the cells grew. Ultimately, the researchers showed that these regulatory changes were the reason why yeast species used galactose differently.

"What our work shows is that research in genetics is no longer limited to surveys of close relatives," said Brem. "So we can start to understand how species of malaria parasites acquired different infectious behaviors over time, and develop new species-specific treatments. And we can figure out how short-and long-grained rice developed their respective shapes in the ancient past, and make new rice varieties. We are excited about future work far beyond yeast."

The work could have implications for research on aging, said Buck professor Gordon Lithgow. His lab studies tiny nematode worms in order to uncover genes and small molecules that prolong lifespan. As an example, Lithgow sites the *Caenorhabditis* family of nematodes which contains widely divergent species, some of which have significant differences in lifespan. "These animals have incredibly different genomes, even though they look identical under the microscope," he said. "Tools like this give us an opportunity to compare their DNA - what are the genes that account for their lifespan changes? It's the first step in understanding how we might exploit those differences in order to extend healthspan."

More information: Jeremy I. Roop et al. Polygenic evolution of a sugar specialization trade-off in yeast, *Nature* (2016). DOI: 10.1038/nature16938

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