

Got Milk? Exploring the Evolutionary Connection between Milk Drinking, Lactose Digestion, and Sunlight

Milk, as the popular slogan goes, does a body good. It contains essential nutrients including fat, protein, sugar, as well as calcium, other minerals, and vitamin D needed for bones. Most people in the world lose the ability to digest lactose, the main sugar in milk, shortly after weaning. For these people, drinking fresh milk can lead to unpleasant bloating, flatulence, and cramps. However, about one-third of people in the world—mostly those whose ancestors originate in Europe, the Middle East, Africa, and southern Asia—continue to produce the enzyme lactase, which is responsible for lactose digestion, throughout adulthood. This trait is called lactase persistence, and recent genetic evidence has shown that it evolved independently in different parts of the world over the last 10,000 years as a result of strong natural selection.

Why lactase persistence has evolved under such strong natural selection remains something of a mystery. The most widely cited explanation is that in the absence of dietary sources for vitamin D and with insufficient sunlight to make vitamin D in the skin, early northern European farmers were at risk of bone disease. Milk is an excellent source of calcium and an adequate source of vitamin D. So, as this “calcium assimilation hypothesis” proposes, having the ability to drink fresh milk into adulthood could have led to a major survival advantage.

In a new article in *Molecular Biology and Evolution* journal, Sverrisdóttir et al. (2014) looked for the mutation that causes lactase persistence in Europeans (referred to as $-13,910^*T$) in the bones of early farmers from sunny Spain. They didn't find it! They then used computer simulations to estimate how much natural selection would be needed to push the frequency of $-13,910^*T$ up to what is seen in Iberia today (about one-third have the mutation). To their surprise, the answer was “a lot!”

What does this tell us about the calcium assimilation hypothesis? Well in Iberia, there is plenty enough sunlight

to produce vitamin D in the skin, so calcium deficiency shouldn't have been a problem for those early farmers. As Sverrisdóttir et al. (2014) reason, if selection was a necessary drive up for lactase persistence frequency in people for whom calcium deficiency was not an issue, then the calcium assimilation hypothesis could not be the main explanation for the observed frequencies of lactase persistence in the Iberian Peninsula today, and so not the only explanation for the evolution of lactase persistence in Europe. They conclude that other evolutionary selective pressures must have been at work to explain the presence of this trait in modern Europeans.

“Using ancient DNA and computer simulations, we show that strong natural selection has acted on lactase persistence in Iberia over the last 7,000 years. Sunlight in Iberia is sufficient to allow the synthesis of vitamin D in the skin for most of the year. It is therefore unlikely that the risk of calcium deficiency was the main driver for the evolution of lactase persistence (the calcium assimilation hypothesis) in this region. Additional evolutionary forces need to be identified to explain this example of strong natural selection in the genome of Europeans.”

Reference

Sverrisdóttir OO, Timpson A, Toombs J, Lecoeur C, Froguel P, Carretero JM, Arsuaga Ferreras JL, Götherström A, Thomas MG. 2014. Direct estimates of natural selection in Iberia indicate calcium absorption was not the only driver of lactase persistence in Europe. *Mol Biol Evol.* 31(4):975–983.

Joseph Caspermeyer^{*,1}

¹MBE Press Office

***Corresponding author:** E-mail: MBEpress@gmail.com.

doi:10.1093/molbev/msu052

Advance Access publication February 10, 2014

New Sequencing Tools Give a Close Look at Yeast Evolution

The baker's yeast *Saccharomyces cerevisiae* has been associated with human activities for thousands of years, being the primary biological agent in baking, brewing, winemaking, and other fermentation processes. It is also one of the most important model organisms in molecular biology and genetic research. For a long time, the history and evolution of this important yeast has been a complete mystery, but recent

advances in genome sequencing technologies allow it to be studied in greater detail.

Using next-generation sequencing, the authors Bergström et al. (2014) provide a detailed characterization of the genetic variation present within the baker's yeast species. They sequenced the genomes of 42 strains of *S. cerevisiae* and its closest relative *S. paradoxus*, which is an entirely wild species