

# Genetic study suggests humans may be evolving in a way that prevents alcoholism

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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

A pair of researchers with the University of Pennsylvania has found evidence suggesting humans may be evolving in a way that will prevent alcoholism in the future. In their paper published in the journal *Nature Ecology & Evolution*, Kelsey Elizabeth Johnson and Benjamin Voight describe their study which involved analyzing data from the 1000 Genomes Project looking for emerging gene variants and what they found.

Humans are, of course, still evolving, which suggests studies looking into the ways we are evolving might be important. In this new effort, Johnson and Voight analyzed [genetic data](#) from the over 2,500 people whose DNA ended was used in the 1000 Genomes Project. More specifically, they looked for emerging variants in different population groups that might shed some light on the [evolutionary changes](#) that we are currently undergoing. They report that they were able to identify five genetic "hot spots"—resistance to malaria in African populations, an amino acid change in Europeans, two sections of DNA left over from interbreeding with Neanderthals, and finally, an ADH variant.

The ADH gene is responsible for inducing production of [alcohol dehydrogenase](#), an enzyme that breaks down alcohol into acetaldehyde, which is then converted to acetate by another process. The researchers note that the variants seem to protect against alcoholism, though how that might happen is still unclear. They theorize that it might break down alcohol faster, causing drinkers to feel sick almost right away—a side-effect that would almost certainly deter drinkers from further consumption. They further theorize that it is possible that over the past 1000 years or so, people, particularly those in their reproductive years, who drank a lot wound up killing themselves off before reproducing—a trend still in evidence today as young people who drink and drive frequently wind up dead before they have a chance to make babies.

The researchers report that there was an anomaly in the data,

however—ADH variants were not nearly as prevalent in European and American populations as they were in others. They suggest this might have been due to overlooking the markers in the data.

**More information:** Kelsey Elizabeth Johnson et al. Patterns of shared signatures of recent positive selection across human populations, *Nature Ecology & Evolution* (2018). [DOI: 10.1038/s41559-018-0478-6](https://doi.org/10.1038/s41559-018-0478-6)

## Abstract

Signatures of recent positive selection often overlap across human populations, but the question of how often these overlaps represent a single ancestral event remains unresolved. If a single selective event spread across many populations, the same sweeping haplotype should appear in each population and the selective pressure could be common across populations and environments. Identifying such shared selective events could identify genomic loci and human traits important in recent history across the globe. In addition, genomic annotations that recently became available could help attach these signatures to a potential gene and molecular phenotype selected across populations. Here, we present a catalogue of selective sweeps in humans, and identify those that overlap and share a sweeping haplotype. We connect these sweep overlaps with potential biological mechanisms at several loci, including potential new sites of adaptive introgression, the glycoporphin locus associated with malarial resistance and the alcohol dehydrogenase cluster associated with alcohol dependency.

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