

## Epigenetics can help humans understand our ancient past

Some types of epigenetic modifications are directly influenced by environmental factors. Thus, characterizing and understanding the “epigenome” can help us understand the ways in which factors like diet and other life experiences affect our physical bodies. This research is still very new but we are already finding out, for example, that nutrition, stress, and social rank can have significant phenotypic effects, and that these effects can even be passed on from parent to offspring across several generations.

What if we could study the epigenome in ancient human populations? We could potentially stand to learn a great deal about past societies and individual lives in the past, in ways that we can't get at by studying archaeology or genetics alone. My labmate Rick Smith has just published a new study showing that methylation can be measured in ancient human populations. Using this approach, it may be possible to learn about how past environments affected human health.

The very early research in paleo-epigenetics has been mainly proof-of-concept. Because methylated cytosines degrade differently than un-methylated cytosines after death, DNA damage patterns have been used to infer methylation in the ancient genomes of a [43,000 year old mammoth](#) (Briggs et al. 2010), a [38,000 year old Neandertal](#) (Gokhman et al. 2014), and the [ancient Saqqaq individual](#) from Greenland (Pendersen et al. 2014). But damage-based approaches are somewhat crude, and can only provide general estimates of methylation. The most precise method—an approach known as bisulfite sequencing, which captures all (undamaged) methylated cytosines—had only been successfully used once on a [26,000 year old bison](#) (Llamas et al. 2012).

**The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis. Read full, original post: [The Promise of Paleo-Epigenetics](#)**