

Getting to the Root of Enamel Evolution

Connecting genes to hominin teeth shows evidence of natural selection

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The skulls of a human, a gorilla and a macaque -- three of the species in which researchers looked at the genomics of enamel evolution. Photo Credit; Les Todd, Duke Photography

DURHAM, NC - Along with our big brains and upright posture, thick tooth enamel is one of the features that distinguishes our genus, *Homo*, from our primate relatives and

forebears. A new study, published May 5 in the *Journal of Human Evolution*, offers insight into how evolution shaped our teeth, one gene at a time.

By comparing the human genome with those of five other primate species, a team of geneticists and evolutionary anthropologists at Duke University has identified two segments of DNA where natural selection may have acted to give modern humans their thick enamel.

Teeth have been an invaluable resource for scientists who study evolution, the authors said.

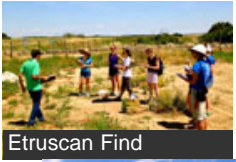
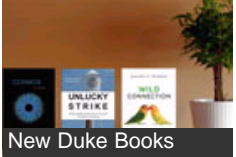
"The fossil record is always the most complete for teeth," said coauthor Christine Wall, associate research professor of evolutionary anthropology at Duke. "And enamel thickness has long been a key trait used to diagnose fossil hominins and reconstruct their diets and life histories."

Clear differences in enamel thickness among primates have been

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linked to diet. Of the six species included in this study, fruit- and leaf-loving gorillas and chimpanzees have the thinnest enamel; omnivorous orangutans, gibbons and rhesus macaques have an intermediate thickness; and humans possess the thickest enamel, well suited to crushing tough foods.

"Teeth also preserve their growth bands," Wall said, referring to the way enamel is deposited in layers, like concentric tree rings. "So in terms of understanding fossils, teeth can tell you how old a juvenile was when it died, or how long it takes for teeth to develop -- so you can compare between living and extinct species."

All of this makes tooth enamel one of the few traits that's both found in the fossil record and amenable to genomic analyses, Wall said.

The team set out to identify some of the genetic changes that contributed to humans acquiring thicker enamel. The work is part of a large-scale investigation of the links between genes, physical characteristics and diet during human evolution.

"We decided to look just at genes that have a known role in tooth development," said Greg Wray, professor of biology at Duke. The team chose four genes, each of which codes for a protein involved in tooth formation (enamelysin, amelogenin, ameloblastin and enamelin), making the genes good candidates for seeing evidence of positive selection, but not necessarily the only ones involved in tooth evolution, Wray said.

Publicly available data provided the sequences for the four genes across six species -- except in the case of the gorilla and orangutan, whose DNA the team isolated themselves.

The researchers then fed the sequences to a software program that pinpointed which base pairs had changed between the species, and where changes had accumulated at an accelerated rate. "That's when we know a gene is under positive selection," said first author Julie Horvath, director of the genomics and microbiology lab at the Nature Research Center in Raleigh, NC and research associate professor of biology at North Carolina Central University.

They used the concept of genetic drift to reach this conclusion. Drift is a phenomenon in which changes to the DNA sequence accumulate at



Teeth are common in the fossil record and full of information, making them an excellent candidate for combining fossil and genomic studies.

Photo credit: Les Todd, Duke Photography

an expected rate, Horvath said. When changes add up faster than expected, it suggests to scientists that the affected genes are under positive selection -- that they give organisms some kind of advantage.

Previous research had shown positive selection on one of the genes, called MMP20, also known as enamelysin. The present analysis confirmed that MMP20 shows the distinct signature of natural selection acting on tooth enamel thickness in humans. They also found another gene, called ENAM or enamelin, which is under positive selection.

Selection pressure did not affect ENAM and MMP20 in the protein-coding region, where even slight changes can dramatically alter or destroy a gene's functionality. Instead, ENAM and MMP20 showed positive selection changes in their regulatory regions, a sequence slightly upstream or downstream in the DNA that controls how a gene is transcribed.

"This study provides the important bridges between morphology, developmental processes, and their underlying genetic regulating mechanisms," said Timothy Bromage, professor of biomaterials and biomimetics at New York University, who was not involved with the study. "Already the results of the reported work are whittling away the many layers of regulation and evolution of enamel structure."

By connecting genes and fossils across species -- and in the future, across different age groups -- the team hopes to build a roadmap for untangling how the many pieces of natural selection are linked.

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