

Epigenetics may explain Neanderthals' extinction

Late last year, scientists unveiled the complete genome of a female Neanderthal whose 130,000-year-old toe bone had been found in a cave in Siberia. As it turned out, her sequence of some 3 billion DNA letters was not all that much different from mine or yours. The researchers identified only about 35,000 places in the genome where all modern humans differ from our ancient hominid cousins. And only 3,000 of those were changes that could impact how genes are turned on and off.

But if our DNA is so similar to Neanderthals, why were they so...different? They were brawnier than our ancestors, with short but muscular limbs, and big noses and eyebrows. They didn't carry certain genetic variants that put modern humans at risk of autoimmune disease and celiac disease. And although they lived alongside our ancestors as the latter migrated into Europe, for some reason the Neanderthals didn't survive.

Part of the answer undoubtedly lies in the way the Neanderthal genome actually worked — a complex process that depends not only on the underlying DNA code, but on the way genes get turned on and off. DNA molecules are constantly interacting with chemicals that control which genes can be activated. For example, a methyl group (one carbon and three hydrogen atoms) can latch on to the genome and help switch on or off the expression of nearby genes.

Read the full, original story: [From ancient genomes to ancient epigenomes](#)