29A

Early Interbreeding between Ancestors of Humans, Neandertals, and Denisovans within Africa

Gundula Povysil, Sepp Hochreiter

Institute of Bioinformatics, Johannes Kepler University, Linz, Austria

Since the release of high-coverage whole genome sequences of a Neandertal and a Denisovan, the interbreeding of ancestors of humans and other hominins outside of Africa has been intensively studied. In contrast to that, their interbreeding within Africa still lacks proper attention although hominins lived longer side by side within than outside of Africa and therefore had plentiful opportunities for admixture.

We investigate the genetic relationships of humans, Neandertals, and Denisovans by identifying very short DNA segments that these hominins share identical by descent (IBD). By focusing on rare variants, our method HapFABIA reliably identifies very short IBD segments that reveal events from a very distant past because shorter segments are presumably older than longer ones. Using the 1000 Genomes Phase 3 whole genome sequencing data, we extracted two types of very old IBD segments that are shared with Neandertals/Denisovans: (1) longer segments primarily found in Asians and Europeans that indicate introgression events outside of Africa; (2) shorter segments mainly shared by Africans that indicate interbreeding of ancestors of humans and other ancient hominins within Africa. These segments are not restricted to a single population of African descent, but are common in all African populations of the 1000 Genomes Project.

Our findings can help to shed light on selection processes that were initiated by interbreeding between hominin groups at different points in time. Furthermore, our results suggest that interbreeding with other hominins was a common feature of human evolution starting already long before ancestors of modern humans left Africa.