

COVID-19 AND... NEANDERTHALS

One haplotype of the locus mapping at chromosome 3: (chr3:45,859,651-45,909,024 hg19) represents a genetic risk factor for COVID-19 infection. Zeberg and Pääbo, in their paper in [Nature](#), pinpoint that this variant haplotype is one of the many genomic segments introgressed into Eurasians from Neanderthals. Indeed, the variant is absent in Africa. The frequency in Eurasia varies substantially, according to a supposed positive or negative selection. A positive selection occurred, very likely, in Bangladesh (protection from other infections?), where it is present, at least in heterozygosity, in about 63% of the population. The impact of the variant is better appreciated in UK where, in similar environmental conditions, individuals of Bangladeshi origin have about two times higher risk to die from COVID-19 than the general population.