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COVID-19 risk from hybridization with Neanderthals: what does it mean?

We have known for a decade that, due to different hybridization events between species, modern humans carry in our genome a certain Neanderthal trace that approaches 2% on average, somewhat higher in East Asia, somewhat less in Europe and in Middle East, and around 0.3% in Africa. By the way, in my case it is 1.2%.

Determining what is the relationship of Neanderthal genomic regions with certain phenotypic traits is complicated, since there are usually different genes involved. In some cases, a more specific link can be established, such as the one in question: the crossing between modern humans and Neanderthals identified in the Neanderthal genome of Vindija (Croatia), 40,000 years old, left a trace in 6 genes on chromosome 3 that It is implicated with an increased risk of severe COVID-19, as seen from a study of 3,199 patients with this disease.

Not all humans today have this Neanderthal variant, but we do noticeably do so in 30% of the South Asian population. For example, at least 63% of the population in Bangladesh have a copy of this variant. Among East Asians it has only been seen in 4%, and among Europeans in 8%. Europeans who carry two copies of this variant have a 3 times greater risk of suffering from the disease, and 1.75 times those who have a copy, compared to those who do not carry it.

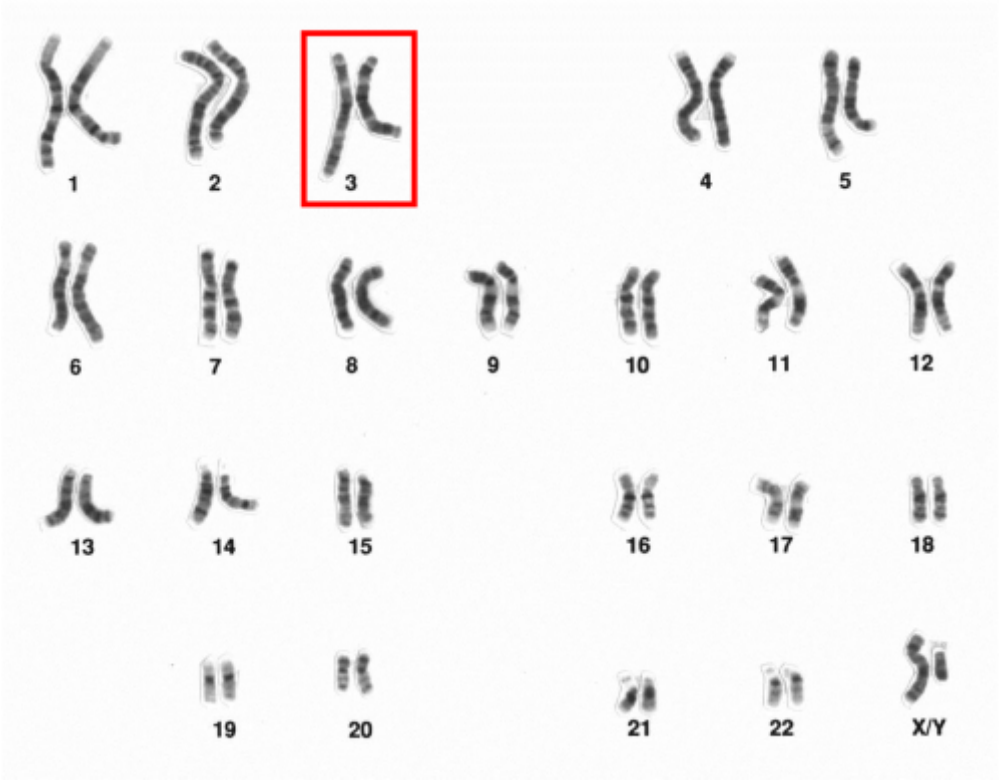
This is what the article says. Now, there are a number of considerations to keep in mind:

- This work by Hugo Zeberg and Svante Pääbo is still in the pre-publication phase and has not yet been peer reviewed.
- It is not the only risk associated with suffering from this disease in a serious way. In other words, these genetic regions are related to one of the risks of suffering from it, but there are others.
- The study does not imply that Neanderthals suffered from COVID-19, much less that this disease was a cause of its extinction, as I have read. The focus is to understand why COVID-19 is more dangerous for some people than for others, why that genetic expression may be a greater risk for certain humans.
- Would this partly explain why there is a high death rate among people of Bangladeshi descent in the UK, or a lower incidence of the disease in Africa? For now, hypotheses can only be considered pending new work.

- It should be remembered that possible relationships of the Neanderthal trace in our genome have been found with other problems: Down syndrome, schizophrenia, autism, type 2 diabetes, Crohn's disease, lupus, biliary cirrhosis, asthma, hay fever, allergies ... But also with improvements in our immune system, which equipped modern humans with new receptors that gave immunity against certain local diseases in their expansion through Eurasia, and also with capabilities to adapt quickly to colder environments.

Related article : *What's new with our Neanderthal DNA (https://wp.me/p4Bi9E-yc)* | *Nutcracker man*

Reference : *Zeberg, H. & Pääbo, S. (2020) (https://doi.org/10.1101/2020.07.03.186296) . The major genetic risk factor for severe COVID-19 is inherited from Neandertals (preprint)*



(https://nutcrakerman.files.wordpress.com/2020/07/human_male_karyotpe_high_resolution_-_chromosome_3.png)
Human male Karyotype after G-banding. Chromosome 3 highlighted. Credit: National Human Genome Research Institute

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