



Editorial

All sciences are based on evidence to support the theories and proposals they formulate.

In paleoanthropological research, especially when we talk about anthropological genetics, and specifically about ancient DNA (aDNA) research, one of the most important evidences are the fossil remains, since it is from them that the future of this field of research.

Going far back in time, Georges Cuvier would give way to proposals for mass extinctions based on his paleontological findings; of course, this would imply the questioning of creationism and the dominant religious thought of the time. Remnants that look like current creatures, but aren't, sloths that look like current ones, but aren't. It wouldn't take long to find someone who looked like us, but wasn't.

In 1924, the discovery of Raymond Dart would change many things. Other primate-like fossils had been found before; but none that had any particular human feature that we could recognize as similar to us as the foramen magnum at the base of the skull of the Taung child, which indicated bipedalism. From here and from many other later findings, a human phylogeny would be built which, in its beginnings, would be based mainly on morphoscopic and morphometric analyses; however, technological development allowed us to analyze and understand DNA and with it a world of hypotheses, answers and possibilities opened up. To be able to extract this material from very old samples.

One of the great challenges of doing research with ancient DNA is that over time and like soft tissue, it degrades. The older the remains are the more damaged we will find the DNA.

Before carrying out any analysis, understanding all the external factors that could affect the obtaining of the material was fundamental to guarantee that the information, in fact, was the desired remains. To do this, understanding the pattern of DNA damage helped to discern between modern DNA (contaminating, coming from the handling of materials, caused by the same research team at the time of excavating, for example, and obtaining and moving the remains) and the associated DNA (from agents inherent to the environment in which they are deposited, understood as the genetic information of bacteria, fungi, plants, animals that could be in contact with the remains, such as rodents and insects frequently) of the target or endogenous DNA, the genetic material of the remains in question. But what is this pattern of damage?

Among the characteristics it presents, it is known that a process called "cytokine deamination" occurs, where, by degradation, the cytokine loses the amino group becoming thymine, thus, when sequencing is obtained, we have an excess of T and we can realize this by the law of base complementarity. It also happens that the DNA obtained is not very long sequences, it is highly fragmented and the older it is, the smaller the lengths found tend to be, and finally: : the coverage in the analyzes is usually low, also 1X, 2X... very high results



are not usually obtained.

Once the damage pattern had been distinguished, it was necessary to learn which were the best areas of a skeleton to store endogenous DNA, that is, that of the individual or that of the remains. Currently, it is known that the best areas to take samples are: the petrous fragment of the temporal bone (in the skull) and the teeth, since, due to their multiple layers, the material inside is better encapsulated and preserved; however, this extraction technique required the loss of the selected fragment, since it is crushed in order to digest it and obtain DNA.

This particularity of the method perfected by Nadin Rohland and Michael Hofreiter in 2007 means that, in general, ancient DNA work is considered a destructive method, therefore, part of the protocols indicate that it is important to keep a record of the fragments that will be used, as a photographic record. Many recommend a 3D model to be able to replace the piece in the collections, as well as a detailed description so that other researchers have access to this information if required.

It is important to note that an important advance was made thanks to Essel *et al.* (2023) who managed to develop a non-destructive method for the samples, which consists of a series of incubations in sodium potassium buffer at temperatures of 21, 37, 60 and 90°C, finding favorable results for the investigations.

There is now a dilemma: once the data is generated, who owns it? The answer to this is complicated and still under debate. While a large part of the scientific community advocates free access to the data generated, many others prefer to keep them for themselves, and

since there are no regulations in this regard, each work team is free to do what it sees fit, especially because genetic data repositories also involve an effort to maintain and this may generate more doubts than answers: Who would guarantee the maintenance of these databases if they were public? Wouldn't we have to know for what purposes the genetic data are used if not for research, these questions are more about research ethics and cooperation between working groups.

Unfortunately, the global south has a technological backwardness that has prevented us from analyzing the samples held in different places, because yes, we have many individuals and samples, but analyzing them is still not very feasible due to the cost involved. This has also led to the creation of almost exclusive lines of research depending on who has access to the data and the capacity for analysis, however, there are efforts to develop these investigations, people interested in making it possible and that, as more information we have, more we understand the relationships between human groups both current and past, as well as we come to see the interconnection between species, since we humans are one more organism on this planet.

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