

**“Who We Are And How We Got Here: Ancient DNA and the New Science of the Human Past”, by David Reich, Oxford University Press, 2018. (South Asia Edition) Rs. 495/-**

**Outlook, 24 October 2018. “Leap into out branches”.**

In 2010, a team of paleo geneticists at the Max Planck Institute for Evolutionary Anthropology, led by the Swedish biologist Svante Pääbo published an astonishing result- they had managed to sequence the entire Neanderthal genome and found that there had been interbreeding between the Neanderthals and the West Eurasian humans. In a sense, the field of paleo genetics had finally come of age. Paleo genetics or the science of using genetics to study ancient humans and other populations relied heavily on the enormous advances in the technology to extract and sequence genomes since the Human Genome project. David Reich, a member of this team went on to establish his own laboratory at Harvard. Reich’s new book is a popular exposition of the revolutionary potential of paleo genetics to understand humanity’s origins and “histories”.

The workhorse of paleo genetics is the DNA molecule. The DNA molecule is a helix shaped molecule which is the blueprint for life. It consists of arrangements of 4 bases denoted by the letters, A, T, G and C whose ordering determines the coding of amino acids and hence the production of different proteins in a cell. During replication, sometimes there is an error in the copying of the bases and a wrong base is added to the new DNA strand. These errors or mutations are what form the basis on which natural selection operates. Interestingly, the rate at which mutations accumulate in a genome is constant over generations which allow us to determine how long back two segments shared a common ancestor. What we have is a kind of biological stopwatch.

The DNA in a cell is actually of two kinds- the nuclear DNA or nDNA which is what we usually refer to as our genetic code and a second type of DNA found only in structures known as mitochondria which are outside the cell nucleus. The mitochondrial DNA or mDNA is much smaller than the nuclear DNA and therefore much simpler to sequence. More importantly, mDNA is only passed down from the mother and hence reflects a purely matrilineal heritage.

With the coming of advanced gene sequencing machines, sequencing DNA from living populations can now be done rapidly and in a relatively straightforward manner. Doing the same from samples of ancient populations is on the other hand, extremely challenging. The DNA in ancient remains degrades with time, the sample gets contaminated by microbes and fungi and finally there is a chance of contamination from human handling. Nevertheless,

with the pioneering efforts of Pääbo and others to overcome these challenges, there are now several laboratories, including that of David Reich which are carrying out this work.

The book under review offers an overview of how the study of ancient DNA has radically transformed our view of prehistory. Sometime around 2 million years ago, an archaic species of humans emerged in Africa which was not just the ancestor of us Homo sapiens, but also of at least two other archaic populations: Neanderthals and Denisovans. Around 700,000 years ago, the Neanderthals and modern humans separated while the Denisovans separated from the Neanderthals at a later date. The Denisovans primarily inhabited the eastern part of the Eurasian continental mass while the Neanderthals were concentrated in Western Eurasia. Modern humans migrated out of Africa around 50,000 years ago.

Reich traces the origins of modern humans including the peoples of modern Europe, the Indian sub-continent, East Asia as well as Native Americans. The determination of the lineages of these major population groups reads like a detective story where scientists follow clues from anthropology, archaeology and even linguistics to finally establish our origins with genetic evidence. Though the book is written in an easy to follow style and the technical aspects are explained lucidly, the various case studies can be a bit confusing. The terms for various populations and their chronologies are easy to mix up for the lay reader.

There are several take-home messages from the various case studies in the book. Firstly, there are no “pure” populations anywhere. All of us today share our ancestry with other populations. The multitude of interconnected populations has contributed to each of our genomes. This however does not mean that the repeated admixtures of populations over time have made population differences meaningless. In fact, populations are different; both in the average and in their variation. Thus, scientific analysis does show real genetic differences on the average between members of different groups. To not accept this is to deny scientific facts. On the other hand, accepting it does not mean that one needs to accept racism or sexism. As the author says, we already accept much larger differences that exist among individuals within a population and aspire to treat them with equal respect. The differences across populations are on an average much smaller and so there is no reason to treat them differently.

In less than a decade, genetics has already revolutionised the study of our past. The future will undoubtedly throw up many more surprises. This book is essential reading for anyone who wants to understand how we know what we know about our ancestors. And, as the subtitle suggests, in doing this, it sheds some light on Who we are. In these days of increasing identity politics, it serves as a reminder of our shared heritage at the most fundamental level.

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