

Genotemporality: The DNA Revolution and The Prehistory of Human Migration

A Review of David Reich, *Who We Are and How We Got Here: Ancient DNA and the New Science of the Human Past*.
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I am attracted to big books that promise a gold mine of research data. Several years ago I ran across a second-hand, mint-condition volume at extraordinarily reasonable cost: Luca Cavalli-Sforza's magnum opus, *The History and Geography of Human Genes* (1994), an enormous book: 9 ½ by 11 ¼ inches, 2 ½ inches thick, 1088 pages. It was rich in charts and statistics, with maps that traced out the spread of agriculture from its origins a few thousand years ago across whole continents. Cavalli-Sforza (1922-2018) spent the second half of the 20th century attempting to work out prehistoric human migrations from differences in the genes of today's human population, enriched "by bringing in as many relevant disciplines as possible, from historical demography to archaeology, paleoanthropology and linguistics, and perhaps ethnography, together with population and molecular genetics" (Cavalli-Sforza, 272). It was an ambitious and impressive goal—and ultimately beyond the capability of genetic science of the day; his work was done before the revolution in genetics that we might date from the complete sequencing of the human genome in 2001.

Though Cavalli-Sforza's work has been eclipsed by a tsunami of studies based on genetic sequencing, David Reich respectfully begins his book, *Who We Are and How We Got Here* (2018) honoring him: "This book is inspired by a visionary, Luca Cavalli-



**WHO WE ARE
AND HOW WE
GOT HERE**

**ANCIENT
DNA AND THE
NEW SCIENCE
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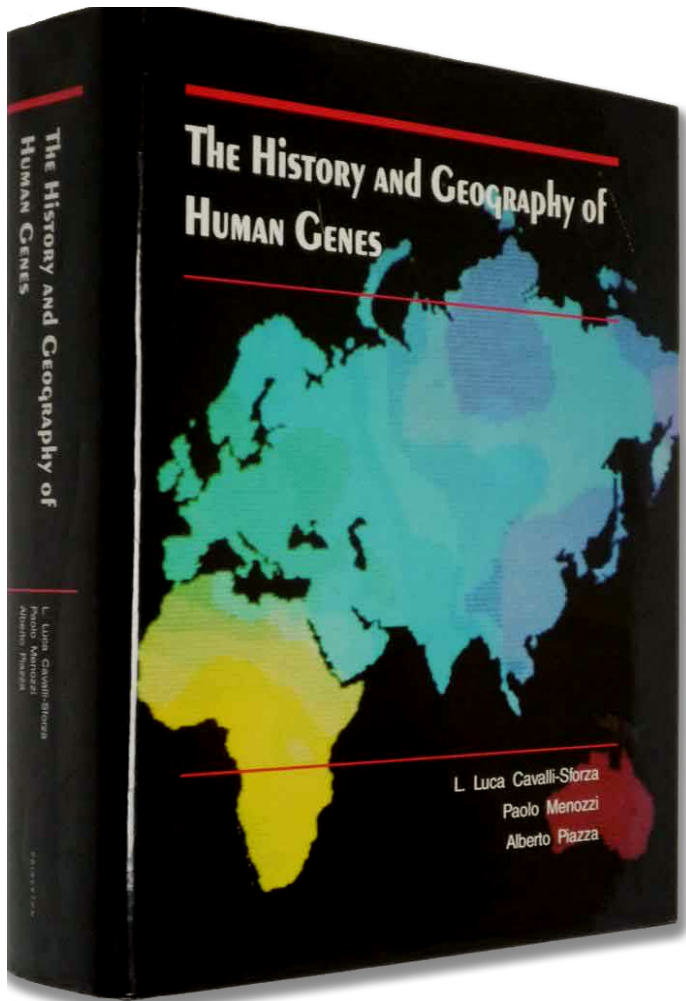
**DAVID
REICH**

"If you want to understand our origins over the course of the last 100,000 years, this book will be the best up-to-date account for you."

—JARED DIAMOND,

THE NEW YORK TIMES BOOK REVIEW

Sforza," noting that *The History and Geography of Human Genes* was the "high water mark" of his career. He was a pioneer in his early recognition of



David Reich began his 2018 book, *Who We Are and How We Got Here*, by honoring Luca Cavalli-Sforza, author of the 1994 book, *The History and Geography of Human Genes*.

“the full potential of genetics for revealing the human past, but his vision predated the technology need to fulfill it” (Reich, xi, xv). Reich, a professor of genetics at Harvard Medical School, now has a lab that is turning out genetic analyses at breakneck speed, with his major contribution being analysis of ancient DNA.

Prior to what Reich calls “the ancient DNA revolution,” the primary insight was the tracking of mitochondrial DNA in the female genome that suggested all humans had descended from a single female sometime around 160,000 years ago (Lewin

1987). The detective story of “Mitochondrial Eve” as she was dubbed was presented in Michael Brown’s *The Search for Eve* (1990), an unfortunate spillage of biblical imagery into serious science. Its twin was the tracking of Y chromosomes which were traced to an African male, “Adam” perhaps, who lived around 320,000 years ago. This huge variance in dates must have upset liberal interpreters of the biblical story who would like to have learned the primal couple lived together at a more scientifically respectable time. Reich’s updated contribution is the discovery that “the genome contains the stories of diverse ancestors—tens of thousands of independent genealogical lineages, not just the two whose stories can be traced with the Y chromosome and mitochondrial DNA” (Reich 10).

The most important benefit of DNA analysis is the ability to tease out dates for very ancient events that have left traces in the human genome. In some cases, the traces are found in separate, often distant, populations that show evidence of an earlier “ghost population” that can no longer be found and has most likely gone extinct, a kind of genetic triangulation where two vortices allow for locating the third. Developing a schedule for genetic changes that signal encounters between variant populations works toward a distinctive time scheme that we have termed *genotemporality* (Wood 2016), an evolutionary chronology based on DNA combinations, divergences, markers, and mutations. Genotemporality can be inferred from pieces of DNA that trace to mammalian, reptilian, amphibian, and marine ancestors (Shubin 2009), and even further back to genetic fragments incorporated into human cells from invertebrates and the earliest bacteria (Ryan 2009).

Reich’s approach is what he calls the “whole-genome perspective” (9-10); his territory is *Homo sapiens* with forays into hominid predecessors such as Neanderthals and Denisovans. Based on non-African DNA, modern humans appear to derive from a common ancestor between 60,000 and 50,000 years ago, a time during which a small population of migrants was leaving Africa along the southern coast of Arabia and

across South Asia according to emerging research on the so-called Southern Route (Armitage *et al.*, 2011). This route is confirmed by hominid remains from the East Africa to the United Arab Emirates, prehistoric floral and faunal resources on the prehistoric Arabian peninsula, undersea freshwater springs once above sea level on the South Arabian coast, and a sequence of genetic markers from Africa across South Asia.

Since the sequencing of the human genome, a revolution in DNA analysis has occurred. The reader should be forewarned: Reich is a clear and informative writer, but some of the analytical methods developed by geneticists are challenging, with masses of data that are growing exponentially. In colloquial idiom, we may have to replace “It’s not rocket science” with “It’s not genetic science.” At the level of the laboratory work, the power of sequencing is astonishing: in the period of 2006 from 2010 notes Reich, “the brute power of new machines” has “reduced the cost of sequencing by at least about ten thousandfold” (31). The results are equally astonishing. The most ancient DNA obtained comes from an individual found among a cluster of twenty-eight *Homo heidelbergensis* remains recovered from the Sima de los Huesos Caves in Spain. Dating to 400,000 years ago, these humans appear to be ancestors of Neanderthals following their split with modern human ancestors but before encounters that led to recombination of Neanderthal and modern human genes (Reich 71). Archaeological evidence from caves in Iraq, Croatia and France dating from 130,000 to 180,000 years ago indicate Neanderthal social and cultural sophistication (Reich 26-27); naturally, their genetic makeup was of great interest. The sequencing of DNA from Neanderthal bones from Croatia dating to 40,000 years ago led to the discovery that Neanderthals carried four to six percent of modern human DNA while modern humans contain two to three percent of Neanderthal ancestry—opening up fascinating questions of influences of each on the other.

The possibility of Neanderthal/*Homo sapiens* interaction was hinted at nearly forty years ago—

before genetic sequencing verified its occurrence—when Jean Auel mapped out her six-volume story of Earth’s Children®, beginning with *The Clan of the Cave Bear* (1980) in which Ayla, a *Homo sapiens* toddler, is found and reared by Neanderthals. The hint has become a reality in the new millennium. Analysis has revealed several prolonged contacts between *Homo sapiens* and Neanderthals; whenever they met, they mated. Precisely where these encounters occurred is conjecture, but the evidence suggests that the *Homo sapiens* population where the most influential encounter occurred is a “ghost population,” now long extinct, that cannot be definitively located other than deep in the Near East, possibly on or close to the Southern Coastal Route. This is one of several ghost population that recent DNA analysis has identified.

The most striking new Eurasian discovery is a hitherto unknown species of hominid from a finger bone and molar from Denisova Cave in Southern Russia. Gene sequencing of these miniscule finds (Krause *et al.* 2010) has revealed a whole new prehistoric hominid now known as Denisovans, cousins of Neanderthals, the two occupying overlapping territory in Central Asia. The Denisovan genes show interactions with Neanderthals in East Asia and ancestral connections with *Homo sapiens* in the isolated regions of New Guinea, Philippines, and Australia. Reich terms them “Australo-Denisovans”; the presence of Denisovan DNA in Island Southeast Asia and its absence in *Homo sapiens* elsewhere suggests mating encounters probably occurred beyond what was originally called “Wallace’s Line,” later “Huxley’s Line,” which separates Philippines, New Guinea, and Eastern Indonesia from the rest of Southeast Asia (Reich, 60-63).

Both Neanderthals and Denisovans occupied vast territories and were evidently descended from *Homo erectus* who found their way out of Africa twenty times earlier, 1.8 to 2.1 million years ago. The earliest finds of what Reich calls “Superarchaic humans,” now thought to descend from *Homo erectus*, were the 900,000 to one million-year old Java Man

(*Pithecanthropus*) remains found (1891-1892) in Indonesia; the 680-780,000 year-old Peking Man (*Sinanthropus*) skulls found (1923-1927) in China; the recent (2004) discoveries of one-meter tall inhabitants (“Hobbits”) of Flores in Indonesia of uncertain date but tentatively trace to *Homo erectus* ancestors in the region 700,000 to one million years ago; and the 1.8-million-year old skeletons uncovered (1991-2005) at Dmanisi in Georgia (Reich, 63-67). Remarkably, all of these *Homo erectus* descendants across Eurasia were displaced and eventually suffered extinction following the arrival of *Homo sapiens*. Whether these earlier humans were driven to extinction by the arrival of modern humans or were too few in numbers to survive is unknown. Possibly they lacked the innovative skills typical of the newly arrived *Homo sapiens*. We simply do not know. What we do know is that *Homo sapiens* were socially unified and they appear to have had superior technical and cognitive skills. Their numbers increased as they criss-crossed the Eurasian landmass; in fact, their movements were so complex that ancient DNA has barely cracked open the story of their migrations.

Maps of human movement out of Africa are overly simplified; they show radiating routes like spokes of a wheel across the planet—an image suggesting a branching tree that implies continuing divergence with no subsequent interaction between the branches. However, Reich points out that the metaphor of the tree is no longer effective for tracing population relationships which involve later encounters and genetic exchange between previously separate migrating groups (Reich, 77-78). These are revealed by analysis of ancient DNA. The power of genetic analysis acquired in the past few years has revealed a genotemporality relevant to several populations that have since vanished, one of which we have already mentioned. From northern Eurasia, DNA from Europeans and Native Americans reveals an ancestral population somewhere between, presumably in northern Russia or southern Siberia north of the Black and Caspian Seas. But this group which appears to have suffered extinction is another

“ghost population,” a second of several identified in the past decade.

Such ancestral sources of genetic encounters provide a challenge to long-standing metaphors. The branching tree is thus more aptly replaced with a complex web with multiple intersections. Digging for information about earlier populations from multiple analyses of present populations thus leads to surprising discoveries. We tend to think of dark skin, dark hair, and dark eyes as typical of Africa and the tropics of South Asia and blue eyes and blond hair as European. The blue-eye mutation has been dated to approximately 30,000 BP in the *Homo sapiens* population of prehistoric Europe. This led to an interesting combination of features: “western hunter-gatherers around eight thousand years ago had blue eyes but dark skin and dark eyes, a combination that is rare today” (Reich, 96). Thus the dark skin coloring of African migrants persisted in Europe for tens of thousands of years after departure from Africa.

Nearly twenty years ago, the distinctive markers of Native Americans were some of the earliest haplogroups identified and were thus designated A, B, C, and D. The migrations of people into the Beringian land bridge around 30,000 years ago and subsequent migration south into North America around 16,000 years ago followed the last glacial maximum. Here geological constriction simplified New World migration to a linear route in contrast with the interwoven maze of Eurasian migration. For half a century, this linear route was identified with a hypothetical “ice free corridor” from Alaska, through the Yukon and the Canadian province, Alberta, east of the Rockies into Montana. In the new millennium this route has fallen victim to precise genotemporal dating: dated remains of archaic migrants reveal they had reached North and South America centuries before an ice-free corridor was available. Meanwhile, a Western Coastal Route has come into prominence (Fahrenkamp-Uppenbrink, 2017). Genetic connections have been discovered down the Pacific coast of the Americas and these account for Native American

DNA similarities in the Southern United States and most of Central and South America. Some distinctive genetic differences mark a later migration into central and eastern Canada, perhaps following a much later opening of an ice-free terrain. Still later, as migrants moved along the Arctic Coast to Baffin Island and Greenland, they gave rise to Inuits and Eskimos. Unlike Eurasia where genetic analysis has identified ghost populations in certain areas that have suffered extinction, genetic evidence often supports continuity of a population in a region; as Reich puts it, “both the genetic and linguistic evidence support a scenario in which many of the present-day Native American populations are direct descendants of populations that plausibly lived in the same region shortly after the first peopling of the continent” (175).

Reich’s discussion of genetics in India appears in a chapter called “The Collision that Formed India”—an interesting analogy since the Indian subcontinent—a triangular adjunct to South Asia—was formed when a tectonic plate from the ancient supercontinent Pangea drove north from what is now Antarctic regions, initiating a collision with the Eurasian plate that began 50 million years ago and continues today. The result is a crushing and rippling of the Asia landmass that has raised the highest mountains in the world, the Himalayas, which are still buckling upward. Reich’s treatment of India’s populations focuses on the past 3,000 to 5,000 years, thus bypassing discussion of ancient southern-route migrants that entered India from the west sometime after 75,000 years ago, with some settling for the long term while others moved on to Southeast Asia.

Reich’s metaphorical “collision” applies to the much more recent incursion of Indo-European language speakers who migrated from the steppelands north of the Black and Caspian Seas through what are now Iran and Afghanistan, settling for several thousand years in the Indus River Valley, then moving on to northern India. This collision occurred when the indigenous Indian speakers of Dravidian languages were gradually pushed south where they now occupy

the lower third of the Indian triangle. This division of cultures was recognized more than two centuries ago when Sir William Jones identified Sanskrit cognates of European languages and proposed the Indo-European language family as common to Europe and India. What was recognized culturally in the eighteenth century can now be documented genetically. The arriving Indo-Europeans were of supreme cultural importance for the worldview they brought and developed in India, notably the two major religions, Hinduism and Buddhism, which eventually spread to Southeast Asia, and the epic literature that forms the foundation of today’s Indian culture: *The Mahabharata* and *The Ramayana*. They also brought a social caste system that marks a cultural divide between tribal people descendant from the ancient Dravidians and the higher status Brahmins and ruling elites.

Toward the end of *Who We Are and How We Got Here*, Reich tackles the issue of “rejoining Africa to the human story” (206-225). But this placement belies what we now know: that Africa is not the end of the story but the beginning—the original homeland of *Homo sapiens*. The “African Genesis” first unpacked by Robert Ardrey (1961) unfolded from 200,000 to 100,000 years ago, corresponding to the first half of *Homo sapiens*’ history. Reich’s interest, however, is on the much more recent period, particularly times when farming transformed the former forager-hunter populations of sub-Saharan Africa.

A limitation that affects genetic analysis makes African human ancestry particularly difficult to untangle. Africa’s tropical location leads to more rapid deterioration of genetic material. Thus the sequencing of ancient DNA from northern Eurasia is virtually impossible in Africa. For insight into the first hundred millennia of *Homo sapiens*’ history, one has to turn to paleoarchaeology, the human remains and tools of South African cave dwellers and the kinds of material-culture analysis of anthropologists such as Curtis Marean (2007) and Kyle Brown (2009). Consequently, Reich’s findings about human interaction and migration in Africa focuses on the past 10 to 15

thousand years. His contribution is in providing a foundation for human movement; as he notes, “It is in the area of shedding light on human migration—rather than in explaining human biology—that the genome revolution has already been a runaway success” (22). But innovative methodologies applied to recent DNA sometimes uncover situations of the more distant past. One such discovery is another ghost population in East Africa. Now extinct, this east coast population may be absent because of transitory presence during *Homo sapiens* migration from South Africa to the Horn of African and the Gate of Grief water crossing to southern Arabia.

In addition, as he points out in “The Genomics of Race and Identity,” genetic analysis provides a scientific tool for dismantling long standing prejudices about race. Theoretically this has been a theme on the agenda since the Emancipation Proclamation. Demythologizing race received a boost, as Reich points out, by Ashley Montague in *Man’s Most Dangerous Myth: The Fallacy of Race* (1942). Now, study of the human genome has removed all physical grounds for racial distinctions and provides a new foundation for racial equality and opportunity for everyone.

Making reference to Walter Libby’s development of Carbon 14 dating (Libby 1955), Reich refers to the genotemporality made possible by genetic analysis as the Second Revolution in Archaeology. Libby raised dating from the guesswork of Darwin, Lyell, and Kelvin to a scientifically grounded dating of biological remains. The innovations of the genetic revolution have added a relational dimension: “by sequencing the whole genomes from ancient people, it is now possible to understand in exquisite detail how everything is related. . . . There is every reason to expect an avalanche of major discoveries from ancient DNA over the coming years.”

Reich’s interest is on ancient DNA and specific clarifications that have come from sequencing it. Since the methodology is recent and samples of ancient DNA scarce, clarifications are discrete; most regions have not and cannot yet be accessed

by analyzing ancient DNA. The result is a series of illuminating discoveries with cursory connection. His book makes a useful companion for Alan Rutherford’s *Brief History of Everyone Who Ever Lived* (2017), previously reviewed in this journal (Wood 2018). It is worth noting again that *Who We Are and How We Got Here* is a densely-packed book; it pulls no punches in its explanations of the most advanced techniques of ancient DNA analysis. It has already spawned a 50-page Zip Read summary of its main ideas; as one reader writes, “All the info without all the time.” But plowing through Reich’s fuller treatment is advisable for anyone wishing to keep up with genetic analysis which is likely to become even more complex in the future.

The tradeoff for Reich’s richly dense explanations of methodology is a certain lack of continuity. Reich states his interest in migration and argues that migration is the theme most illuminated by his kind of analysis, but we should note that his separate clarifications do not yet cohere as a *sequential* narrative of the peopling of the Earth. This narrative will require connecting studies such as Reich’s and numerous others. The result should be a continuous narrative that begins in Africa and traces *Homo sapiens*’ migration to the most remote reaches of the planet.

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