ROM

Summer 2012 **$5.95** CAN

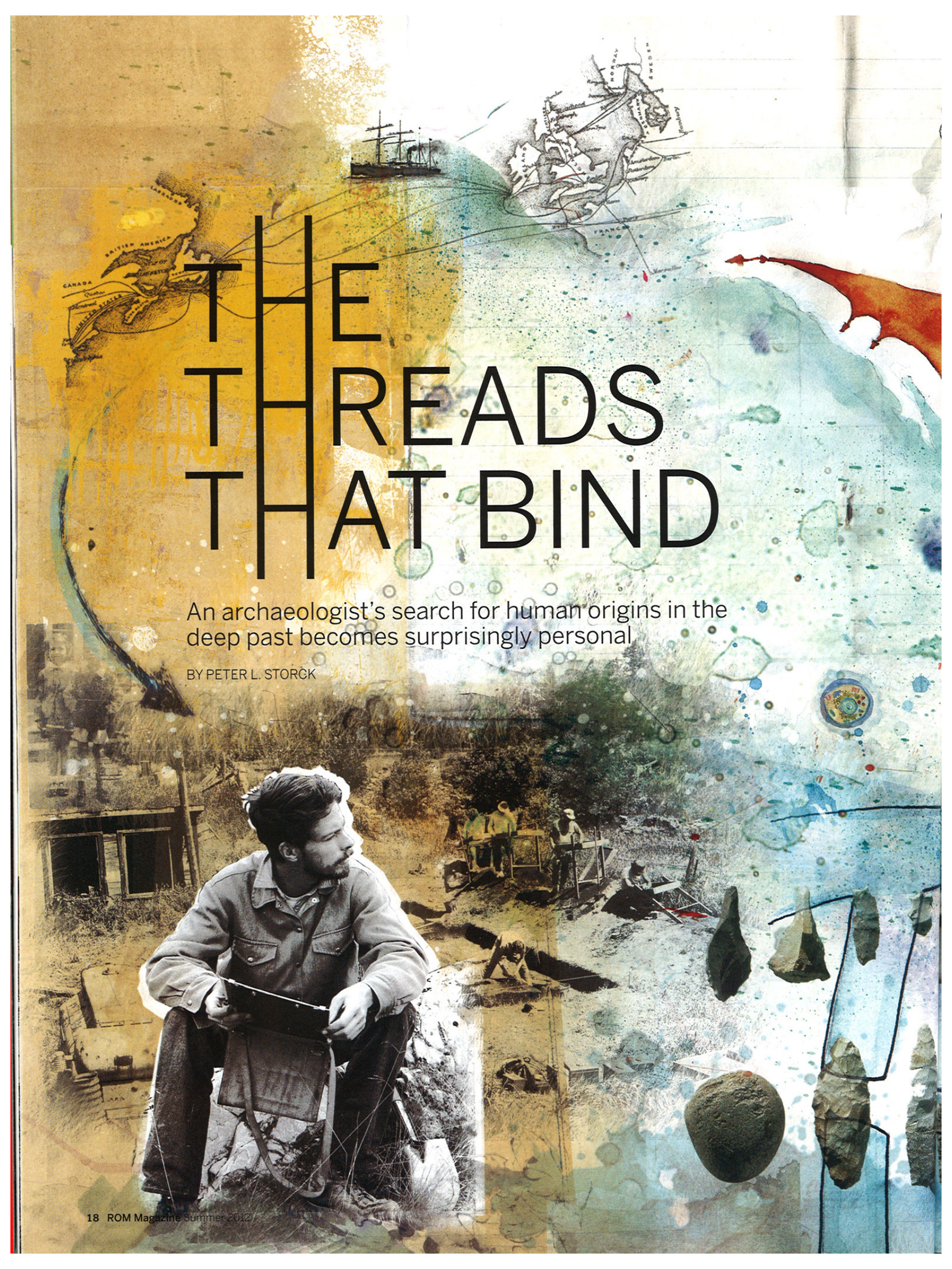
Magazine *of the* Royal Ontario Museum

DINO-EGG HUNTERS: Succeeding in the clutch / **FROM THE LOST WORLD:** A remote river in Guyana reveals a strange new kettle of fish / *Ancestry.DNA:* The surprising find of an archaeologist's search for ancestral roots / *Plus:* **JAMES CHATTO** on piscatorial platters and MARK KINGWELL on living forward

THE THREADS THAT BIND

An archaeologist's search for human origins in the deep past becomes surprisingly personal

BY PETER L. STORCK



Artist concept by Janice Kun

Top, left: With a childhood friend on the first day of kindergarten, 1945 or 1946.

Top, right: With a VW van purchased in 1964 for Master's thesis fieldwork.

Middle: Fieldwork at the Banting site, 1973.

Bottom: Geological testing at Banting, 2004. The site has since been destroyed by urban development.

For much of my life I've lived in the past. As a child, I began collecting fossils of ancient corals several hundred million years old from an abandoned rock quarry near my home. Years later, at university, I bonded firmly to the past when I took my first course in human evolution. And after I became a curator at the ROM, I buried myself in the past for nearly three decades, searching the beginning of the archaeological record for traces of the first people to occupy Ontario at the end of the Ice Age—hunter-gatherers, called Early Paleo-Indians, who lived some 11,000 years ago.

But lately, I've been paying much more attention to the more recent past, and other origins. My own. Something I had neglected for nearly a lifetime. I wondered about the influences that shaped me: the end of WWII during my childhood, the Korean War and the Cold War during my adolescence, and the Vietnam War during my student years at university. These decades have left me with emotional scars. During that period my family declined, nearly becoming extinct because of premature deaths from cancer, heart disease, tuberculosis—deaths that denied me ongoing connections in life. I've tried to compensate for those losses by creating a family history from a scattering of surviving documents, photographs, and memory fragments withered from neglect. Little survived, and there are no elders left who can answer questions about things I experienced as a child but did not—and still do not—understand and to explain events that occurred before I was born. Delving deeply into my own memories has often been uncomfortable, emotional. It has stimulated dreams in which I talk with my father and grandfather and other relatives who were lost to me, asking them about their lives, telling them about mine—and revealing how they have influenced, even in death, the way I have lived my own life.

During this period of looking inward, I also began searching for the origins of the four paternal lines that converged with my birth—the ancestries of my two grandfathers and two great-grandfathers. One of these ancestries is still a mystery. It may lead me to mid-18th century England, but the trail has gone cold. The other three led to western Europe between the 18th and the 16th centuries. But there the record stopped, at least so far as my patrilineal ancestry was concerned. And I had virtually no documentation of my maternal ancestry, the female lines that married into the male ancestries. Fortunately, maternal ancestry can be revealed through genetics. And, surprisingly, those genes can be traced back much further in time than the surnames of my male grandparents.

But lately, I've been paying much more attention to the more recent past, and other origins. My own.

Back to the Ice Age

The genes that tell us about our maternal ancestries are, in a strict sense, not even ours. They are found in the DNA of small bodies—called mitochondria—that occur in the cytoplasm (outside the nucleus) of each cell in our bodies. The mitochondria produce enzymes that allow our cells to use oxygen—giving them energy.

Mitochondrial DNA (mtDNA) is inherited only through the mother from eggs produced by the female germ/sex cells. The mitochondria in male sperm cells are lost during or after fertilization, leaving only the mother's mtDNA in the developing embryo's cells. This means that maternal ancestry (of males as well as females) can be traced back in time from child to mother to grandmother to great-grandmother, and so on, right back to the beginning of the chain, to a point in time when "signature" mutations (or changes) first appeared—marking the start of that female lineage.

I learned all this rather late in my search for the origins of my own family, from a book written for the general public, *The Seven Daughters of Eve*, by Bryan Sykes, a geneticist at the Institute for Molecular Medicine at Oxford University in Britain. From more than 10,000 samples of mtDNA obtained from people across Europe, Sykes and his colleagues identified seven major genetic lineages (and more recently an eighth).

For this analysis, geneticists use only part of the mtDNA—a very short segment called the "control region," which is only 1,000 chemical base pairs long compared with the 16,500-plus base pairs in the entire mtDNA chromosome (and 3,000 million base pairs in DNA from the nucleus of a cell). The specific sequence of base pairs at certain "marker" locations in the control region defines each of the major genetic lineages in Europe.

The approximate age of each lineage could then be calculated from the average number of mutations in each and the estimated rate of mutation—the larger the number of mutations, the older the lineage. Similarly, researchers determined that each lineage most likely originated in the geographic region where people of that lineage have the greatest genetic variation today.

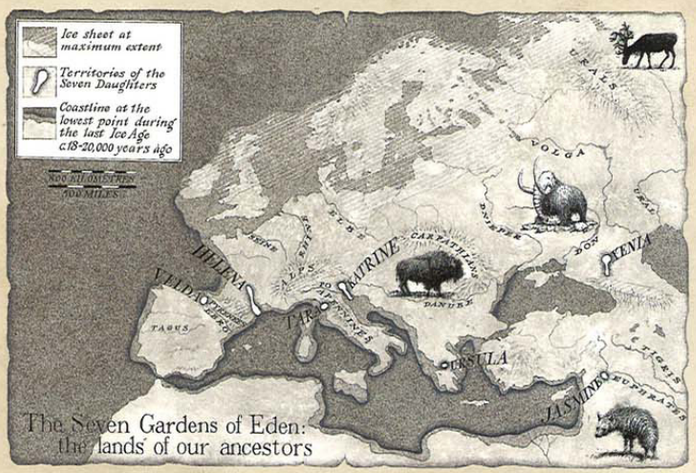
From this, Sykes and his colleagues constructed a diagram they thought revealed the population history of Europe from the time modern humans first arrived, perhaps 40,000 years ago (overlapping the Neanderthals), through to the appearance of agriculture 10,000 to 8,000 years ago.

I was intrigued by this and, on a whim, sent a swab of saliva containing my DNA to Oxford Ancestors Inc. and asked them to tell me which of the seven lineages I belong to. About three months later I got my answer. In the 400 base-pair sequences that were examined, mutations were found at four "marker" locations: 129, 223, 304, and 391. This pattern put me into a genetic lineage called X.

The letter X was the original laboratory designation of this lineage. Later in Sykes's research, when it appeared that mtDNA studies could reveal maternal ancestry and perhaps even the population history of Europe, the seven (now eight) lineages were given popular names derived from the geographic regions where they appear to have originated. Lineage X was given the name Xenia (from the Greek word for hospitable). It includes approximately seven percent of today's native-born Europeans. Significantly, the lineage is believed to have originated on the eastern edge of the Black Sea in the northern Caucasus and can be traced back in time to a female who lived approximately 25,000 years ago.

This Eve-like person, one of the seven daughters in the title of Bryan Sykes's book and matriarch of the Xenia clan, is not the only woman in lineage X who was alive at the time; however, she is the only one who left an unbroken line of female descendants. And male descendants, such as myself, who inherited their mtDNA from her.

Lineage X—Xenia's clan—has two other important characteristics. It can be subdivided into three branches, based on the distribution of people today who have inherited Xenia's mtDNA. Two branches spread to central Europe and as far west as France and Britain. The third branch, largely confined to Eastern Europe, must also have spread farther east. Much farther, since about one percent of Native Americans are also descendants of Xenia. I was stunned when I first read this. Because if true, it was strangely ironic.



Top: Two pathways of genetic ancestries to the New World: 25,000 years ago to present day.

Bottom: Origins of the genetic lineages described by Bryan Sykes in his book *The Seven Daughters of Eve*.

Top map: Claire Louise Milne. Bottom map: Hand Made Maps Ltd.

Artist's interpretation of Early Paleo-Indians caribou hunting in Ontario 11,000 years ago.

People of the Mammoth Steppe

As a curator, I focused my research on the lives of Early Paleo-Indians, one of the earliest colonizing peoples of the New World and the first people to occupy Ontario. There are many questions but the most fundamental concerns their origins. There is no doubt that the New World was colonized by peoples from Siberia, and northeast Asia generally, at the end of the last Ice Age. And while no Early Paleo-Indian sites have been found in northeast Asia (the culture apparently having developed in North America), Paleo-Indian stone tool technology has a Eurasian Upper Paleolithic look to it. It is this that identifies the ultimate Eurasian origins of the people who would evolve into North American Early Paleo-Indians roughly 12,000 years ago, if not slightly earlier.

Twenty-five thousand years ago, when the people of Lineage X lived in the Black Sea region, the Ukraine to the northwest was occupied by Upper Paleolithic hunter-gatherers famous for the large, domed winter houses they built of interlocked mandibles, tusks, and bones of woolly mammoth. The people of Lineage X were probably closely related to those in the Ukraine. Indeed, at the time, Upper Paleolithic peoples were widespread in Eurasia and occupied a vast steppe called the Mammoth Steppe, named after the largest mammal in that environment—the woolly mammoth. Other cold, steppe-adapted animals also lived there—woolly rhino, caribou, woolly horse, steppe bison, saiga antelope; and predators—lions, wolves, cheetahs, hyenas, bears. South of the continental ice sheet, the Mammoth Steppe extended from western Europe across Russia and Siberia (which was largely ice-free) to Alaska and the Yukon Territory (also largely ice-free). Most archaeologists believe that when Eurasian Upper Paleolithic peoples spread north and then east, colonizing recently de-glaciated lands during the final retreat of the ice sheets, some groups crossed a land bridge exposed by lower sea levels between Siberia and Alaska and then moved south into the central part of the North American continent. Some of those colonizing groups may have been the ancestors of Early Paleo-Indians and also descended from Lineage X, Xenia's clan. As I am. If so, over a nearly 30-year career I had been studying very distant relatives, people to whom I am related in a measurable way—despite the 460 or so generations that separate us, longer still if I calculate from the more distant origin of Lineage X.

Looking Again, at the Other Half

The results of my mtDNA analysis were so interesting that I asked the same genetics laboratory to do an analysis of the genes in my Y chromosome. This is the chromosome that determined my sex, inherited only through males.

The analysis of a short segment of the DNA in my Y chromosome at 15 marker locations produced a genetic signature that is useful in tracing ancestries over several tens of generations. More importantly (for my interest in determining origins), the signature can also be correlated with one of several genetic groupings, technically called haplogroups or clades, in another system of genetic classification that is useful in interpreting long-term evolutionary history. In this system, the genetic signature of my Y chromosome can be correlated with a high level of confidence with a clade given the letter designation "I" and the popular name Wotan, the name of the German god of battles. This name was chosen because it reflects roughly the geographic area where people with this genetic signature live today. The highest frequencies of this signature occur among people in western Eurasia: in Armenia and Georgia (40%), Germany (20%), northern Europe (the Scandinavian countries, 30 to 33%), as well as in eastern England (33%), Scotland (15%) and Wales (11%). The frequencies in the British Isles probably reflect Saxon, Danish, and Norse influences.

Interestingly, the number of mutations in the Wotan clade suggests that it originated roughly 25,000 years ago in the Ukraine. This is consistent with my mtDNA, inherited maternally, which is thought to have originated at about the same time and in the same general region. Thus, my ancestry on both the male and female sides is clearly from western Eurasia. The "German" identity, revealed by three of the four surnames of my grandparents, came much later, first appearing, so far as genealogical records are concerned, between the 16th and 19th centuries, before Germany became unified. My proto-German ancestors emigrated to the New World (and another branch to Fiji in the Pacific) in the mid 19th century.

Much earlier, at the end of the Ice Age, other peoples to whom I am related through my mtDNA moved eastwards from the Ukraine and the Caucasus toward the New World. Several hundred generations later their descendants camped for a brief period on an island in a glacial lake. There, ten thousand years later, in another geological epoch and roughly an hour's drive northwest of Toronto, I discovered archaeological debris on the farm of Edward Banting* from a former camp occupied by Early Paleo-Indians. Although I didn't realize it at the time, a circle had closed.

My ancestry is the sum of the histories of all of my genes, not just the narrow pathways revealed in my mtDNA or my Y chromosome. In its entirety, my DNA—those helical threads of sugar and phosphate molecules coiled around nucleic acids—contains other histories in the long trail of descent from my late Ice Age ancestors and, before them, various forms of humans, pre-humans, primates, mammals—and earlier still to the very origins of heredity, and life itself. The past is within us, curated like museum collections in our DNA and in our memories. In life, in family, these are the threads that bind.

* **Edward Banting** was a nephew of Sir Frederick Banting, one of the co-discoverers of insulin, and Edward's farm had been Frederick's boyhood home. More information on the archaeological site is found in Storck's book for the general public, *Journey to the Ice Age*, published by the University of British Columbia Press in association with the ROM. It is available in the ROM Museum Store, at bookstores, and online.

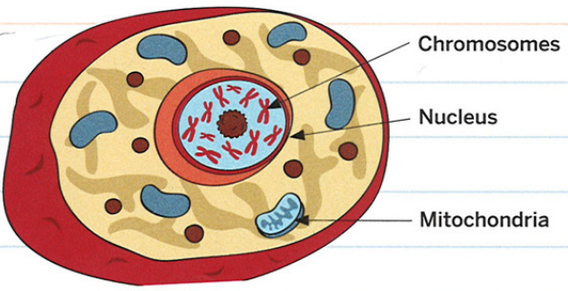
Illustration: Ivan Kocsis, ROM

DNA 101

DNA is a molecule found in every cell of every living organism (with the exception of some viruses). It stores the instructions for all aspects of an organism's development and functioning, coding for all traits: eye colour, height, number of fingers and toes, etc. The double helix structure of DNA is one of the most iconic images in biology, often seen in modern culture in everything from crime shows to ads for hair shampoo. DNA's two long intertwined strands are made up of subunits called nucleotides. Nucleotides themselves are composed of sugars, phosphate groups, and one of four kinds of bases—adenine, guanine, cytosine, and thymine. These bases play a crucial role: the bonds between bases of opposite strands hold the two strands together, and the order in which different bases occur along the molecule holds the genetic code.

There are 3 billion base pairs in the human genome, a blueprint carried in every cell in our bodies. If you took all the DNA molecules from a single one of your cells and put them end to end they would stretch to almost 2 metres in length. Lined up, all the DNA molecules from the estimated tens of trillions of cells in your body would be long enough to reach from the Earth to the sun and back again more than 100 times.

Except for identical twins, no two people in the world have exactly the same DNA sequence. This diversity is the result of mutation—the process whereby one base along the sequence either becomes switched for a different one or deleted, or a new one is inserted. Mutations can be the result of environmental factors, such as radiation or exposure to mutagenic chemicals, but most often they arise from errors introduced when DNA is replicated just before a cell divides—in other words, they are copying errors.



Mutations are not inherently bad. They are, after all, the raw material for evolution and without them we would not be here. They can be detrimental when their occurrence disrupts important genes. Hemophilia, the impairment of the body's ability to control blood clotting, for example, is one disease caused by a genetic mutation. But sometimes mutations confer benefits, such as the ability to digest lactose. This ability is lost by most mammals shortly after they are weaned. Several human populations have independently acquired mutations that allow them to use milk as a nutritious food source into adulthood. Such beneficial mutations have rapidly spread through pastoral societies.

Most mutations, however, seem to make no difference at all—either because redundancy in the genetic code minimizes their impact or because they occur in the large portion of our genome that doesn't appear to code for anything. These neutral mutations are the ones that scientists compare to trace human ancestry. **—O. H.**

How genetics is helping scientists reveal human history

The tools used to uncover the history of humans from our earliest origins to the rise and fall of ancient civilizations have traditionally been the trowel and shovel. In the last few decades a new tool has been added to this inventory: DNA sequencing.

To study human ancestry and migration, DNA researchers have initially focused on the Y chromosome and the mitochondrial genome because of the unique way these parts of the DNA are inherited. The mitochondrial genome (mtDNA) is inherited by sons and daughters exclusively from the mother while the Y chromosome passes down from father to son with no contribution from the mother. The remainder of the genome is more difficult to interpret because a process called recombination mixes together the sequences of both father and mother in a child's DNA.

Y chromosome and mtDNA sequences agree with the fossil evidence that points to Africa as the birthplace of our species and they reveal that most of the genetic diversity within our species is still found on that continent. The evidence also suggests that the rest of the world was colonized by just a small group of humans who left Africa between 70,000 and 125,000 years ago. As they spread throughout the world, different populations grew and diversified over the millennia, accumulating genetic mutations along the way.

Scientists can now compare the DNA sequences of people all over the world and, working backwards, reconstruct a family tree for the whole species. Back in 1981, a researcher by the name of S. Anderson was the first person to have his entire mitochondrial genome sequenced. Today, when we analyze an individual's mtDNA, this original sequence—referred to as the Anderson sequence or the Cambridge Reference Sequence (CRS)—is the one to which it is compared. "Mutations" are simply any base pair along the sequence that differs from the Anderson sequence.

Tracing our ancestry using the Y chromosome is more involved because compared with mtDNA there is less variation between individuals in this chromosome. The process is fundamentally similar, the difference being that the reference sequence is not from an actual individual but from a theoretical common male ancestor. Worldwide, there are now more than 30 recognized major mtDNA haplogroups, or lineages. At the moment, Europeans are the most extensively sampled population (the seven or eight haplogroups mentioned in "The Threads That Bind"), but an ever-increasing database of haplogroups and their geographic distribution is helping to untangle the history of the movements of peoples around the world.

Recent advances in genomic sequencing have gone beyond using just mtDNA and the Y chromosome, and have shown that the modern human gene pool contains DNA from other hominid species, such as Neanderthals and the yet-to-be-described hominid recently discovered in Denisova Cave in Russia. All this new evidence is revealing that our family tree is even more complicated than anyone ever imagined.

OLIVER HADDRATH is a technician and DNA expert in the Ornithology section of the ROM's Department of Natural History. Haddrath was one of the first to sequence a mitochondrial genome from an extinct bird species, the giant moa.

Illustration: Claire Louise Milne