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EXPLORING THE ORIGINS OF MANKIND THROUGH THE EVIDENCE OF DNA

(AN ANTHROPOLOGICAL VIEW)

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Somewhere in the grasslands of sub-Saharan Africa between 140,000 and 170,000 years ago, a woman walked the savannah with a small group of other Paleolithic hunter-gatherers. She belonged to the genus *Homo sapiens sapiens*, an anatomically modern human being, and she likely had dark-pigmented skin. We know nothing else about her except one important fact: she gave her mitochondrial DNA to a large progeny of her descendants, and through them, became the mother, in an unbroken, umbilical female line, of all members of the human race living today all over the world. Scientists have dubbed her "Mitochondrial Eve," and while she was not the only woman living at that time, her lineage and DNA imprint is the one that has survived, and today there are eighteen major subgroups of her descendants living around the globe. At the time a group of scientists at Berkeley announced Eve's discovery in 1987, the study captured the public's imagination. *Newsweek* ran an issue with the headline, "The Search for Adam and Eve," and featured a nude African couple sitting under a tree with a snake.

Undoubtedly this Eve had a partner who was the father of all of mankind, but scientists have determined through the genetic study of the Y-chromosome that the common male-line ancestor of humanity lived much more recently – just 60,000 years ago and also in Africa – and he is separated from us today by about 2,000 generations. They have dubbed him "Y-Chromosomal Adam," and their estimate of when he lived is based in part on the worldwide diversity and distribution of Y-chromosomes and a calculation of their mutation rates. This estimate also has something to do with human sexual behavior over

thousands of years and a condition known as "variance in reproductive success." Over time, more women have the opportunity to reproduce than men. A single man may share his Y-chromosome with the offspring of many women, while other men never have the opportunity to reproduce. Hence there is more diversity worldwide among the DNA we inherit from our mothers than we do from our fathers, and that female or mitochondrial DNA extends further back in time.

What implication does the discovery of this genetic Adam and Eve have for us today? Why should we care about ancestry and genetics, and what does it all mean in terms of our own identity? Here at the beginning of the twenty-first century, we are in the midst of a revolution in our understanding of the origins of humankind and how our species came to populate the Earth. The mapping of the human genome and the application of the study of DNA to the field of anthropology has allowed scientists to begin to unlock the mystery of ancient human development and migration in a way that the fossil record alone has been unable to do. All of us carry within our genetic make-up clues about our deep ancestry. By collecting DNA samples from thousands of distinct population groups around the globe, geneticists have begun to find answers to questions that have eluded anthropologists for decades. The conclusions they have reached, just in the last few years, have had profound implications for our understanding of what makes us human, what constitutes race, and how all of us the world over share a much more recent genetic connection than what scientists only a generation ago had supposed.

The key to unlocking these long-held secrets lies in the study of Y-chromosomal and mitochondrial DNA. As we reproduce, we pass down to our children our DNA through our genes, half coming from the father and half from the mother. Each human genome or

total DNA sequence contains about 30,000 genes, and these are reshuffled during replication, a process known formally as "recombination." Two types of DNA do not get reshuffled, however. We all know than when a father contributes a Y-chromosome, together with an X, a fertilized egg will become male. This Y chromosome is passed down from father to son over many generations, and while mutations can and do occur, they generally do so infrequently, providing scientists with an almost perfect mechanism for studying male-line genetic lineages far back in time.

Mitochondrial DNA is located outside the cell nucleus where the genome is found, an area of the cell known as the mitochondrion, which is part of the cytoplasm or main body of the cell. Like the Y chromosome, it does not get reshuffled with each generation, but instead is passed down by a mother to her children, though only her daughters will pass it down further to their children. Thus, mitochondrial DNA offers us a glimpse into our deep maternal ancestry, an inheritance passed from mother to daughter over thousands of years back to Mitochondrial Eve.

The mutations that occur in these two types of DNA are known as single nucleotide polymorphisms, known also as SNPs or "Snips," and they are important to understanding how the extended human family tree was formed. When a mutation occurs on the Y-chromosome or in the mitochondrion, it gets passed down to the descendants of that person. Thus, when a sample of Y- or mitochondrial DNA is analyzed, the results allow geneticists to sort that donor into a descendant group, known as a haplogroup, based on a line of heredity or set of genetic markers known as a haplotype. The challenge for scientists comes in trying to determine the mutation rates of these markers and using them to calculate timelines of divergence within population groups.

SNPs are of two basic types. Some are classified as Unique Event Polymorphisms – mutations that occur so seldom that they happened only once in human history. They are considered ancestral and define large groups of people around the globe. Other SNPs are classified as "derived" and are considered to be of much more recent origin. Both kinds of SNPs or markers are designated by letters and numbers, and some examples you will see on your map and your philogenetic tree. By studying the geographical proximity of haplogroups around the globe, anthropologists have gained insight into larger patterns of human migration and settlement. In effect, we now have a record of our remote ancestors' movements, stretching back thousands of years, in a way that had eluded earlier generations of scientists looking only at bones and artifacts.

Leading the drive to collect this genetic evidence is the Genographic Project, a five-year $40 million research effort funded in part by the National Geographic Society and IBM. To date it has gathered samples from as many as 100,000 indigenous groups with particular attention paid to small, isolated populations that have not mixed extensively with others. According to its spokesman, Spencer Wells, the project is strictly scientific, non-governmental, and non-profit. In Wells' own words, it "seeks to enable indigenous communities with information about their origins" in a way that is non-threatening, and it seeks to empower global communities, through knowledge, rather than exploit them. All participants are voluntary, and the data collected are not used for medical research.

The most startling and significant conclusion of the project thus far is that all of humanity shares a relatively recent common ancestry in Africa and that all genetic lines in all known population groups can be conclusively traced there. Prior to this discovery, anthropologists were divided into two groups: those who supported the so-called "multi-

regional hypothesis" for the origin of humans versus those who supported the "recent single origin theory," the view embraced and now largely proven by the Genographic Project.

The multi-regionalists, whose views held sway a generation ago and were best articulated by the late Carleton Coon, held that modern man developed simultaneously out of an earlier species on several continents during the Pleistocene Era. Coon had concluded that the racial characteristics separating humans were deep-seated in our past and that there were long-standing divisions that separated the races. This view has since been discredited. Modern-day multi-regionalists accept the theory of a recent migration from Africa, but they contend that as *Homo sapiens* moved into Europe and Asia, they encountered and interbred with other species of humans, including *Homo erectus*, the immediate forebear of modern humans in Africa, and *Homo neanderthalensis* or Neanderthal man, who lived in Europe from between 250,000 to as recently as 30,000 years ago and who differed from us genetically by only half a percentage point.

The debate is particularly focused at the moment on the Neanderthals, with scientists such as Milford Wolpoff of the University of Michigan and Bruce Lahn of the University of Chicago leading a theory in support of cross-breeding and arguing that all of us are descended from Neanderthals. Lahn has suggested that a version of the Microcephalin gene, a determinant of brain size, contains a haplotype that may have been passed by such cross-species contacts. Multi-regionalists also contend that there are similarities between sapiens and erectus skulls in different parts of the world, especially Asia, a term known as "regional continuity," and that in addition to cross-breeding, genetic drift occurred, with the genes of modern humans ultimately replacing those of more primitive

species over time. The complete sequencing of a Neanderthal genome by a German university later this year may shed more light on the question.

Most anthropologists now support the recent single origin theory, however. Evidence from the Genographic Project appears to show that modern humans evolved entirely and exclusively in Africa and then migrated out of that continent between 70,000 and 50,000 years ago. These migrations were probably encouraged by changes in climate, widespread drought in Africa, and decreasing food choices there. Once they reached Asia and later Europe, they replaced, rather than interbred with, other human species.

The widespread consensus that all roads of our deep ancestral past lead to Africa is supported not only by fossils, but by DNA, for Africa today remains the most genetically diversified continent on Earth, with strains of Y- and mitochondrial DNA found nowhere else. Among Y-DNA lineages, Africa is home to Haplogroup A, the oldest and deepest lineage in the Y chromosomal tree and found throughout Ethiopia, the Sudan, and among the San Bushmen of South Africa. Most geneticists believe that this haplogroup arose 60,000 years ago, before the great migrations out of Africa began. Haplogroup B, another very old lineage, is found throughout central and eastern Africa and is common among Pygmies. Members of A and B groups speak versions of click languages, which some anthropologists argue is a remnant of the oldest form of spoken language, perhaps spoken by all of our ancestors before their migration. Haplogroup E, associated with the Bantu tribe, is the most common African haplotype and is found especially in Cameroon, Nigeria, in southwest Africa, and among descendants of African slaves. These deep and ancient haplogroups are evidence against grouping the dark-pigmented peoples of Africa into a single race, and Wells has pointed out that there are great differences in body type,

facial characteristics, and even skin tones among these groups. Y-chromosomal Adam, our earliest common male-line ancestor, may have closely resembled a modern San Bushman, both in lifestyle and appearance.

If we look outside of Africa for the earliest evidence of modern humans, it may seem surprising that the second oldest fossilized specimen has been found in central Australia and is 40,000 years old. The discovery of the skeleton of Mungo Man in the 1970s puzzled scientists, at least initially, for there was no ready explanation for how he got to a continent far from Africa isolated by water. Additional testing has shown that his form of mitochondrial DNA has no modern match. Most scientists believe that part of this mystery involves the distribution of water and the ancient coastline of southern Asia. Sixty thousand years ago, much of Earth's water remained frozen in glaciers in the northern hemisphere. Before these glaciers melted, the coastline of Asia looked vastly different than it does today. Groups of hunter-gathers left Africa and followed the coastline around the Arabian Peninsula and India to reach what is now Sumatra and Java, all while still walking on dry land. They then crossed a short span of water at the Torres Strait to reach Australia about 50,000 years ago. Proving this hypothesis has challenged archaeologists, since most of the evidence for this migration is now under water. Genographic Project scientists believe that the modern Aboriginies descend from this ancient migration. Some evidence of their Haplogroup C with a SNP known as M130 has also been found in India, which appears to confirm this migration.

After this early move to Australia, a second one occurred from Africa into the Levant of southwestern Asia about 45,000 years ago. This population group first carried a Y-DNA SNP known as M89, a marker not found in Africa or Australia but is prevalent

throughout the northern hemisphere. According to Spencer Wells, this migration occurred after a great leap forward in human brain function, a time when language was becoming more complex and humans had begun to create very primitive artistic images. It may have coincided, as well, with a changing African climate, for there is evidence of widespread drought and the fact that the Sahara Desert expanded and retreated during different millennia – retreating so much at one point to encourage outward migration, but then expanding and locking descendants of M89 in Asia. Men with this marker had descendants with a new mutation, a marker known as M9, who lived about 40,000 years ago on the plains of Iran and south central Asia. They hunted game in the Asian steppes, and over the next thousands of years, their descendants moved eastward, cutting a dramatic path across the Asian continent. When they encountered the great mountain ranges of central Asia, they split into two groups. One group moved north of the Hindu Kush, while another, about 30,000 years ago, went south into what is now Pakistan and the Indian subcontinent. Both groups left a distinct genetic trail that can still be traced.

About 35,000 years ago those who went north of the Hindu Kush into central Asia had a new mutation or marker, known as M45. Descendants having both the M9 and M45 markers expanded northward, perhaps as far north as Siberia, where they followed huge herds of game and hunted woolly mammoths, a complex and highly developed skill. Some scientists suggest that it was precisely this skill that allowed them to survive in the harsh, cold climate of northern Asia, providing survival and problem-solving abilities that were passed down to their descendants. We will return to this group in a moment.

The other group of M9 descendants, who lacked the M45 marker, went south of the Hindu Kush about 30,000 years ago and entered the Indian sub-continent, where they

continued to expand eastward. Some of their descendants had a new SNP on their Y-chromosome, M175, and this group continued to press north and east along the Tien Shan mountain range. Eventually they made their way into what is now China, a land that had been inhabited by *Homo erectus* for about a million years. Some anthropologists believe there was some overlap between the two species and that interbreeding occurred, but others say the evidence thus far gathered shows a single genetic line directly back to Africa with no other markers present.

Ancient China was settled by groups of humans coming from both the north and the south. These northern waves of migrants were offshoots of the central Asian clan in southern Siberia, M45, while others with the M175 marker arrived from the south via India. As they moved inland and reached Mongolia, the two groups mixed together. Even so, evidence of these two distinct strands of Y-DNA can still be found in China today, as well as on the Korean peninsula. About 10,000 years ago, the population in this region began to expand significantly. A descendant of M175 began to feature a new SNP, M122, at a time when farming was first discovered in this region. Descendants of M122 developed a millet-based agriculture in what is now Shaanxi province, and then spread this knowledge along the Yangtze River into central China. About 5,000 years ago, their descendants began raising rice, and today, people with this M122 marker are still strongly associated with a culture and diet based on rice, and they are found throughout Southeast Asia, in Japan, and even in Tahiti.

Let us return to the Russian steppes and the clan with marker M45, the hunters of woolly mammoths. About 30,000 years ago, a descendant group of this clan with a new Y-DNA marker, M173, branched off of this Siberian group. They continued to hunt the

plentiful game in the Steppes through a broad stretch of grasslands and moved westward, eventually reaching Europe. Today, this marker, M173, is found in high frequency across Europe and among people of European descent. These early *Home sapiens* were known as Cro-Magnon, and they were responsible for creating the dramatic cave paintings of animals at Chauvet in France and at the Fumane cave near Verona, Italy. With complex brains and highly-developed language skills, they probably replaced, rather than interbred with, the Neanderthals who had lived in Europe for 200,000 years. The remarkable fact – a surprise for genetic anthropologists – is that this M173 clan came all the way from central Russia to populate the European continent when the Middle Eastern clan with marker M89, lived in much closer proximity along the Mediterranean. Yet M89 is not widespread in Europe, while M173 is. In fact, in the British Isles and Spain, which were settled heavily by Celtic peoples, it makes up 90 percent of the population.

Cro-Magnon people were hunter-gatherers, as were the Neanderthals, but they brought with them better tools and more efficient hunting skills, perhaps due to a more complex social network that had been honed and developed for thousands of years in central Asia. Cro-Magnons had longer life spans than Neanderthals, often surviving into their 50s, and some scientists surmise that older tribal members passed down important survival skills to younger members and were able to assist with childcare, giving them an important advantage over Neanderthals.

If Middle Easterners did not contribute significantly to the Y-DNA of Europeans, they did give Europe an important gift that allowed M173 to expand its population when it came close to dying out, and that gift was agriculture. We have already shown that agriculture appeared in China about 7,000 years ago, but it began even earlier in the

Middle East. Scientists have differing theories about where precisely it first originated. The excavations of archaeologist Kathleen Kenyon in the 1950s prove that it was practiced on the eastern slope of the mountains of Judah near the Biblical city of Jericho as early as 10,000 years ago. It also began about the same time in the Tigris and Euphrates valleys of ancient Iraq and soon spread to the Nile valley of Egypt and the Indus valley in India. In each of these regions a sudden transition occurred from hunting and gathering to a cereal-based agriculture of grasses that were the forebears of modern wheat and barley. A number of factors may have influenced this transition, including a changing climate at the end of the last ice age that brought long, dry summers and short wet winters, a climate that favored the growth of grains and grasses.

The discovery of agriculture marked the beginning of the Neolithic Era in human development. By creating their own food supplies instead of relying solely on foraging and hunting for sustenance, humans began taking more control of their lives, building communities and living in higher densities than they did as hunter-gatherers. With more food available, families grew larger, and more children began to reach adulthood. Agriculture also allowed humans to choose where they wanted to live so long as the land was productive for farming. And as they began to live in communities, their societies became more complex, ultimately leading to writing, commerce, and laws. It was a great leap forward that gave those with the knowledge of farming a considerable advantage over those without it. The downside, of course, was that as humans lived in higher concentrations, they became subject to new diseases and were sometimes decimated by epidemics. Social structures also became more complex, with more stratification than in hunter-gatherer societies.

A great deal of study in the last several decades has centered on the question of precisely how agriculture was introduced to Europe. Before advanced genetic studies, many scholars had theorized that the knowledge of agricultural practices followed specific gene pools. They assumed that this knowledge followed a Middle Eastern invasion of people familiar with these practices. As we have seen, however, the Y-DNA marker associated with early agriculture, M89, is not widespread in Europe, while the same is also true of mitochondrial lineages, 80 percent of which are also Cro-Magnon in origin. Evidence shows that where the Middle Eastern marker does exist, it is found in strongest concentrations in southern Europe, especially along the Mediterranean Sea, perhaps because the climate there was closer to that of the Middle East. From there, agricultural practices gradually spread inland into northern Europe probably through cross-cultural contacts, but not through the spread of genes. A new genetic marker, M172, began to appear in southeastern Europe about 10,000 years ago and is found heavily in Greece and the Balkans region. Since it is also found in the Middle East, it was also likely associated with farming practices.

Once farming did take hold in Europe, it had just as profound of an influence there as it did in the Middle East and China. Its introduction came at a critical time at the end of the last ice age, when Europe's total population had declined from 30,000 to just 15,000 people. Agriculture allowed the population to rebound significantly in size, and it also explains why Europeans today are not as genetically diversified as many other indigenous populations. The number of inhabitants underwent a severe bottle-neck before agricultural allowed it to rebound.

Another way for scientists to study world populations is through linguistics. Wells and other scientists associated with the Genographic Project have wondered whether genetic studies could either support or refute theories about the origin of languages in Europe and central Asia. The so-called Indo-European Language Theory was first advanced in 1786 when a British judge in India, who was a scholar of Sanskrit, noticed certain similarities in forms of grammar and roots of verbs that are also found in Greek and Latin. He theorized that all three languages must have sprung from a common source. More recent scientists have pondered whether the spread of this ancient form of Indo-European was also associated with the spread of agriculture. There are various theories about who spoke this ancient language, and many linguists focus on the Kurgans, an ancient warrior and horse-riding culture who lived on the Eurasian steppes ranging from the Ukraine to Mongolia to Afghanistan. They appear to have spoken a language called "proto-indo-European" or PIE, and spread it to these areas, perhaps 6,000 years ago. A Y-DNA marker known as M17 appears to have arisen between 10,000 and 15,000 years ago in southern Russia and today is found in high frequency from as far west as the Czech Republic to south central Asia, yet it is not found in high concentrations in the Middle East. Anthropologist Colin Renfrew is among a group who has suggested that M17 may be a Kurgan marker, spread through Eastern Europe and Asia by these ancient warriors. This theory remains unproved, and other scholars have proposed alternative theories. Studies linking genetics with linguistics are underway within other population groups and are likely to influence the course of future research in both disciplines.

Let us return again to our ancient clan group M45, the Mammoth hunters who lived on the steppes of Russia some 30,000 years ago. We have shown how one of its major sub-

clans with marker M173 branched off and went west into Europe, becoming the ancestors of many of us here today. About 20,000 years ago, a second sub-clan of M45, distinguished by a new Y-DNA marker known as M242, moved north-eastward into the frozen tundra of northern Siberia and adapted to the very harsh environment of what is now Kamchatka. There they developed tools that were distinct from those being made elsewhere in Asia, including weapon-points known as microliths, which were leaf-shaped and symmetrical.

About 15,000 years ago, a group of descendants from M242 with a mutation known as M3, crossed the land bridge at the Bering Straits and entered North America in at least two and possibly several waves of migration. Some may have taken a coastal route into what is now Washington State, while others may have followed a more inland route along an ice-free corridor at the eastern edge of the Rocky Mountains. Once established in North America, descendants with this mutation moved rapidly across the continent and settled deep into South America within a thousand years. Today this marker, M3, is found in 90 percent of the Native American populations. Like their ancestors in Asia, they crafted microlith stone arrow points and were adept at hunting musk ox, mammoths, bison, and reindeer.

Anthropologists continue to debate how many distinct waves of migration came to the Americas from Asia. Some believe that as many as five migrations contributed to the gene pool of American Indians in North and South America, with those in the north being more genetically diversified than those in the south. Some scholars believe that ancient Japanese and even Australian Aborigines may have made it all the way to the new world and left a genetic imprint here. Some linguists contend that the more than 600 different

languages spoken by various tribes are too diverse to have come from a single source. Others disagree and argue that a base language, known as Amerind, serves as the basis from which most other language groups descend, the others being Eskimo-Alut and Na-Dene, both of which are spoken in northern and western parts of Canada, and in the case of Na-Dene, also by the Navajo in the southwestern United States. Speakers of Na-Dene often have another Y-DNA marker, M130, which has also been identified in parts of China and Tibet. Significantly, this marker has also been found among many Pacific islanders.

With most of the world's populations now genetically mapped, scientists are still seeking samples from additional isolated indigenous groups to find traces of more ancient migrations. In many ways, the project is racing against the clock. We live in a twenty-first century world of unprecedented mobility. Tribes of indigenous peoples that once populated remote parts of Asia, Africa, and South America have moved in greater numbers to large cities in search of work, abandoning their traditional lifestyles. There they often intermarry with other groups. The genetic markers remain, but the original contexts in which they existed are increasingly becoming lost, rendering them of less value to anthropologists.

A variety of other issues are also raised by the study of genetics and anthropology. While the Genographic Project has noble scientific goals that seek to empower indigenous groups around the world with knowledge, its critics have expressed concern about genetic privacy and the possibility of unintended exploitation. Some groups face oppression and discrimination on the basis of their ethnicity and do not want their past

exposed through genetic testing. The recent genocide in Darfur, the Congo, and in Bosnia is evidence that deep-seated ethnic hatreds still exist in many parts of the world.

Some ethicists are concerned about the prospects of medical exploitation of DNA samples given for anthropological study. While originally intended only for the study of Y- or mitochondrial DNA, there are fears that other medical testing could be performed, leading to discoveries and patents for medicines that some see as exploitation of the donors. Yet others recognize the importance of studying genetic variation among population groups precisely because of the insight it offers in understanding the origin of certain diseases. Some ethicists have expressed concern about the possible creation of immortal cell lines kept alive in laboratories long after their donors are dead, which again could be used for scientific purposes against the original intent of donors.

There are other ethical roadblocks. Sometimes the evidence revealed in genetic testing conflicts with deeply-held religious beliefs, especially among the Australian Aborigines and some Native American groups who are unwilling to accept scientific conclusions that conflict with long-held cultural traditions. These fears may hinder the Genographic Project's effort to obtain more samples that will further illuminate our genetic story.

Even with these concerns, the project has been heralded as a major success, and there are many positive issues raised by the study of our ancient genetic patterns. The first and perhaps most important issue is the knowledge that we, as human beings, are all much more closely interconnected to one another than we once believed we were, even a generation ago. We all share a common Y-chromosomal father who lived 60,000 years ago and a most recent common ancestor who lived only 3,000 to 5,000 years ago, making us a globally interconnected family. This fact has profound implications on what

constitutes race and how we perceive one another. Skin color, hair type, and facial features are not the deep dividing points that Carleton Coon had asserted in the 1960s. Instead, they developed relatively recently in the human timeline. Indeed, most scientists prefer to use the term "distinctive populations" to describe people instead of "race," which is a culturally-loaded word with overtones of negative stereotyping. Two thousand generations ago, all of our ancestors had dark skin and were living in Africa. In a world where there is still so much hatred over religious, ethnic, racial, and cultural differences, the study of our common genetic heritage forces us to see the absurdity of these hatreds and take a broader view of our shared humanity.

The second consideration is that there is still much to value and celebrate in what we can still discern about our cultural and genetic heritage. It goes without saying that no culture should seek to either stamp out or subsume another in an effort to achieve cultural assimilation, even if its motives are altruistic. The Genographic Project stands in support of preserving remnants of indigenous peoples and isolated cultures around the world, and its scientists also support efforts to preserve associated languages and traditions before they are lost. The study of genetics, they contend, underscores the preservation of ethnic heritage around the world.

Third, the nature of this project is such that we can all participate, if we so choose. For about two hundred dollars, any of us can go online to the Genographic Project or to other firms such as Family Tree DNA and have ourselves tested. Men and women can have their mitochondrial DNA analyzed to determine which of the eighteen descendant groups of Eve we belong. For example, my mitochondrial DNA is Haplogroup H, the most common one in Western Europe to which 40 percent of Europeans belong. Men can also

test their Y-chromosome and learn about their deep male-line lineage. Women will need to recruit their fathers, brothers, or male cousins for such a test. My Y-chromosome has the Cro-Magnon mutation known as M173. Within this very large group, I belong to Haplogroup R, a very common one in Western Europe. The results are often more meaningful if done in the context of a larger surname study, when men of the same last name participate together and compare their data. My Beatty family has had such a project going since 2002 with 15p0 participants, and while many of us don't know exactly how we relate, we know that many of us share a close Y chromosomal match with a distinctive haplotype. Within Haplogroup R, we belong to R1b, a major subgroup found especially in the British Isles and Spain. We can narrow it even further and by looking at all of our SNPs, we can say that we are R1b1b2a2*, which puts us into a very narrow subgroup, but shows exactly how we fit into the larger genetic tree and what other surnames are close to ours. Each of you can do the same and see where you fit into this tree. DNA has revolutionized the study of genealogy and is being used more frequently to solve difficult research problems that written records, alone, cannot address.

Fourth, this genetic study challenges all of us the world over to be more accepting of people of mixed backgrounds, a mixing that will almost certainly accelerate as more populations settle in large urban areas and have children. This is not in itself a bad thing, but as I said, it makes the task of finding the original context of certain genes increasingly difficult for scientists. People who would never have met one another a hundred years ago are now producing descendants. Wells holds up the example of golfer Tiger Woods, who is a mixture of African, Southeast Asian, and European ancestry, and claims that he is the face of the future in many parts of the West.

The next frontier in genetic testing will likely expand from the limited study of Y- and mitochondrial DNA to the sequencing of entire genomes in search of particular genes and their global distribution. Already an international consortium has formed to sequence more than 1,000 complete genomes from various regional populations in search of more clues to our evolutionary past. With that sequencing, more ethical questions will likely be raised, but more knowledge will also be gained.

I return to the question I posed at the beginning of this lecture: what does it all mean for us, both collectively and individually? It seems clear that the on-going study of DNA in anthropology has begun to transform the way we see ourselves as humans. But it also produces this paradox: As more people become aware of their ancient genetic heritage, biology is both increasingly and at the same time decreasingly becoming a determinant of our identity. Cultural and historical distinctions, though sometimes blurred by genetic studies, still remain more important. Those who watched Henry Louis Gates's acclaimed PBS series on African American ancestry know that the genetic ties of blacks and whites in the United States are closely interwoven, and many blacks, who are culturally African-American, have Y-DNA haplotypes that are European. Conversely, some men who are culturally white are discovering that they have Indian, Asian, or even African haplotypes. For example, Thomas Jefferson's Y-DNA haplotype, K-2, was African, even though his immediate ancestors were English.

So, is DNA research abolishing our differences or allowing us a better way to embrace them? Or, conversely, is it doing just the opposite, creating more distinctions and barriers than previously existed? Many pundits are already weighing in on this question and the ways in which we should define ourselves by our genetic heritage.

Should we, as the writer Jon Entine suggests, move past the kumbaya phase of genetic study that celebrates our togetherness and concentrate instead on our differences? Doing so, he argues, allows us to use DNA as "an atlas and time machine that can transport us to Biblical times and beyond, awakening us to shared roots of civilization and the promise of designer therapies to target disease." He adds: "The only way to understand how similar humans are is to learn how we differ."

Steve Olsen, author of *Mapping Human History: Discovering the Past through Our Genes,* stresses the importance of not using our genetics in negative ways to influence how we perceive one another. He writes: "Our preferences, character, and abilities are not determined by the biological history of our ancestors. They depend on our individual attributes, experiences, and choices… [In the future] when we look at another person, we won't think Asian, black, or white. We'll just think: person." Both predictions, if realized, represent a certain irony, for while many philosophers have stressed the need to look past biology in our understanding of one another, it has taken the study of our ancient genetics to drive home a message of acceptance that we, as fellow human beings, should have embraced all along.

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