

*A bit of saliva can tell
the story of an entire people.*

*Since scientists learned
to identify the human genome
letter for letter, they can sometimes*

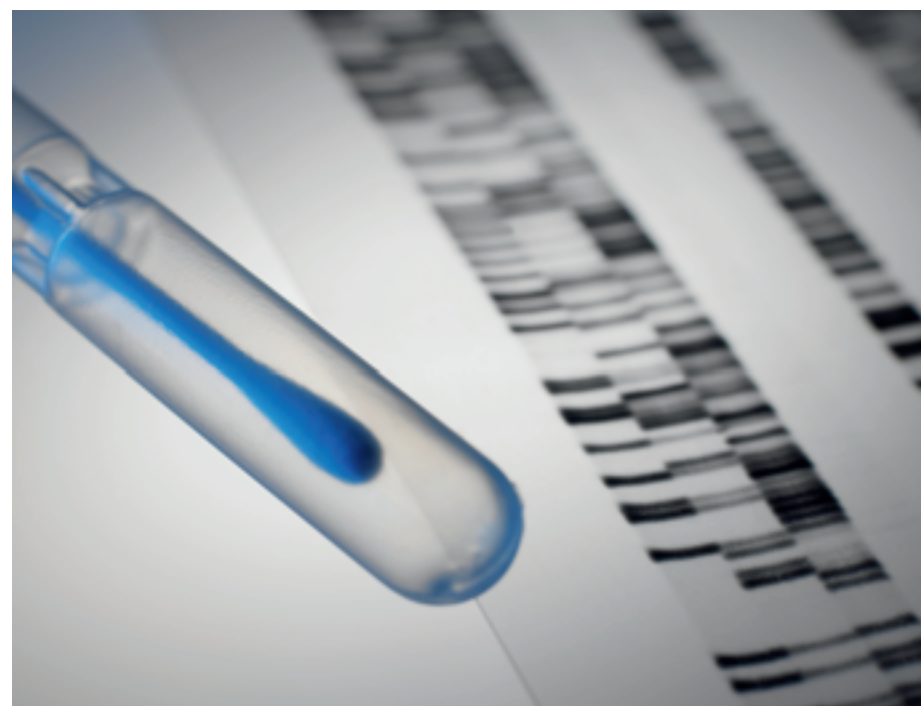
gain more information from it than they can from potsherds or yellowed papers. Thus,

MARK STONEKING and his colleagues at the **MAX PLANCK INSTITUTE FOR EVOLUTIONARY ANTHROPOLOGY** use it to investigate, for example, how various peoples gradually dispersed.

Genes Take to the Road

This here is the extracted, highly purified DNA from the cells in saliva. Each tube contains the sample from one individual," says Sean Myles. He reaches over to place it in the styrofoam container with the others, then puts the collection back in the freezer. It's just a few drops of clear, frozen liquid at the bottom of a tapered, transparent plastic tube, but they reveal secrets about entire cultures, about the conquest of new territories and migrations to the remotest corners of the Earth. They tell of liaisons or rape, cultural exchange or centuries of isolation. And the contents of these drops provide clues about the development of mankind.

Sean Myles is a doctoral student in Mark Stoneking's Molecular Anthropology research group at the Max Planck Institute for Evolutionary Anthropology in Leipzig. The team specializes in, among other things, examining the consequences of migration on planet Earth. Where did the ancestors of a region's inhabitants originate? To what extent did immigrants intermix with natives? Or did they completely displace them? Peoples that migrate leave tracks behind them. Not only in language and culture, but also in the genes of those they encounter. It is precisely these genetic tracks that Mark Stoneking and his staff are looking for.



The genome harbors history: Using saliva samples – here a Q-tip in a sample tube –researchers decode how population groups migrated.

Human genes are actually very poorly suited for determining the origins of a population group, as they get hopelessly stirred up in every new generation: not only are paternal and maternal genes distributed to offspring completely at random – which is why everyone has an individual gene makeup – but the associated chromosomes also exchange entire genetic segments. With every generation, this recombination makes it difficult to decipher population history.

Luckily for the molecular geneticists, however, there is one thing

that escapes recombination: the DNA in certain cell organelles, the mitochondria. This DNA is not affected by the gene exchange of the DNA in the cell nucleus, since mitochondria multiply (like bacteria) through simple division. Thus, these tiny powerplants in our cells are all descendants of the mitochondria from the plasma of the maternal ovum. This means it is possible to trace the origin of the matrilineal line of a human population group using the mitochondrial DNA, or mtDNA for short. On one hand, this



Human trails: The red arrows mark the migration of modern man, probably starting from East Africa; violet shows Neanderthal territory.

is good, but on the other hand, it isn't, as it means that we only ever learn half the story.

The molecular geneticists get the other half of the story from the Y-chromosome, the second genetic island of tranquility: the Y-chromosome in the cell nucleus is what makes a person a man. Because it has no matching partner with which to exchange genes on the maternal side, its gene sequences remain largely intact and can be used to trace back the paternal line.

But the genetic researchers don't want too much tranquility in the gene sequence, either. If nothing changes at all, then there will also be no differences in genetic patterns between population groups. A source of variety is needed. And it exists: mutations. The random but rare exchange of individual letters in the base sequence is the sole cause of changes in the mtDNA and the DNA of the Y-chromosome. It happens seldom enough that not too much is changed, and yet frequently enough to give the researchers the key tool they need to determine the ancestry and origins of human populations.

When these mutations are passed on from one generation to the next, they become genetic markers for a population group. The researchers categorize multiple sequences and their typical mutations into hap-

logroups. These can differ greatly in frequency between populations, and are named after letters of the alphabet. The haplogroup L, for example, with its sub-groups L1, L2 and L3, occurs only in Africa. M and N originated in East Africa, but they also exist in Eurasia and America. Haplogroups A to D are found in the New World, just as in Asia, and G, Y and Z are found primarily in Siberia.

SALIVA SAMPLES FOR SCIENCE

The typical mutations in the DNA of a population group tell Mark Stoneking where they mingled with the resident population on their way from one region to the next. "Cell material from the saliva or mucous membranes of 20 to 50 non-related persons in a group is sufficient," says the scientist.

The genetic markers allow the researchers to trace migration waves throughout human history, from the first major journey out of Africa some 100,000 to 50,000 years ago, to the first colonization of the New World probably around 12,000 to 13,000 years ago, to the conquest of the Pacific island paradise of Polynesia about 5,000 years ago. Even migrations that took place just a few hundred years ago can still be studied with these genetic methods. This is because extensive sexual contact

between the men and women of two peoples quickly has an impact that Stoneking and his colleagues can detect as a genetic contribution in the genomes of these population groups.

Because widespread sexual contact leaves such clear evidence behind, genetic analysis is a good tool for clarifying questions that, to date, anthropologists, ethnologists, linguists and archaeologists have been able to answer only fragmentarily. For instance, regarding the spread of agriculture. Scientists consider the transition from nomadic hunters and gatherers to settled farmers around 10,000 years ago to be the greatest cultural revolution in the history of man. "But it is still unclear today how agriculture and animal husbandry spread across the world," says Stoneking.

Theoretically, there are two possibilities: either people take the idea with them to new regions when they travel, or the idea goes traveling through people's minds, with residents of other regions picking it up while its inventors remain in their original location. Mark Stoneking tested these hypotheses in a region that experienced precisely this change in relatively recent history: India.

"There, we have aboriginal groups that still live as hunters and gatherers, others that have long practiced



Yearning for new horizons: The beginning of a journey from the island Kitawa in Melanesia. Researchers are still puzzling over how the Pacific Ocean was colonized.

PHOTO: AGENTUR FOCUS – GEORGE STEINMETZ / MPI FOR EVOLUTIONARY ANTHROPOLOGY

“However, the evidence in the genetic pattern of the Y-chromosome also indicates that men and women dispersed differently,” explains Sean Myles. In the case of New Guinea, for example, it appears that the conquerors had no chance against the home advantage. They landed on the island’s coast – and clearly lost their women to the native men. “A glorious conquest it apparently wasn’t, at least in New Guinea,” says Myles.

LANGUAGE MIX IN THE MELTING POT

However accurate the genetic analyses of the molecular anthropologists might be, to rely on the gene sequences alone would be foolhardy. “We must constantly take a step back and look at the bigger picture,” says Stoneking, who has been trying to unite the two camps involved – the natural and social sciences – for years. Genetics can help unveil se-

crets that other fields such as linguistics and archaeology can’t decipher. But geneticists, too, must sometimes rely on the aid of their colleagues. “We can’t do without the knowledge of the other disciplines. We need them, for example, to formulate our hypotheses,” says Stoneking.

As in the case of the Kalmyks, a tribe of currently about 150,000 people living north of the Caspian Sea along the Lower Volga in a region that belongs to Russia. The Kalmyks live right next door to a true melting pot: the Caucasian region between the Black and Caspian Seas, where there are more than 50 different ethnic groups and where, on an approximately 700-kilometer-wide strip of land, languages of four different language families are spoken on both sides of the Caucasus Mountains.

Ivan Nasidze, a member of Stoneking’s team, took on this region. And there is a very simple explanation as

to why – apart from the fact that it is a very exciting region for a population geneticist: “I was born there,” says the Caucasian in a deep voice and with a satisfied grin beaming from below his mustache.

Historical sources tell us that the Kalmyks originally came from Mongolia. Around 300 years ago, their ancestors emigrated from a region more than 4,000 kilometers away. Their Mongolian parentage is still apparent today, and can be heard, as well, as they still speak Mongolian. But 10 to 12 generations are a long time, and one would expect that the immigrants would have since mingled with their Russian neighbors. “After all, this also occurred in a comparable timeframe in North America with Europeans and Afro-Americans,” says Ivan Nasidze.

But Nasidze’s genetic analyses show that the Kalmyks did not warm up

agriculture, and groups that have just changed their way of life to agriculture and animal husbandry in the past 3,000 years,” explains the native Californian who has been conducting his research in Leipzig for seven years now. Such an investigation would not be possible in Europe – and not just because there are no longer any hunters and gatherers: “We also don’t know the genetic pattern of the people who lived in Europe before farming spread here.” There are, however, such aborigines still living in southern India.

Comparing the genetic patterns of both the maternal mtDNA and the male Y-chromosome yield the same result: the new farmers of southern India are more closely related to India’s inveterate farmers than to the aboriginal hunters and gatherers. Thus, over the course of millennia, farmers carried their ideas with them when they penetrated into new regions and mingled with the local population.

This finding, which Stoneking, in collaboration with Indian colleagues, published in the journal *SCIENCE* in 2004, shows that agriculture and animal husbandry spread because farmers spread their technology through migration. “However,” says Mark Stoneking, “it also shows that cultural processes have the power to change human genetic variation.” Or, to put it another way: great achievements make people extremely sexy.

RIDING THE WAVES FROM ISLAND TO ISLAND

Genetic analyses have also shed light on a question that scientists have been debating for two centuries – even if the genes can’t fully clarify the issue: the settlement of the island world of the Pacific Ocean, from Hawaii in the north, the Indonesian islands in the west, New Zealand in the south and the Easter Islands far in the east. Although there are numerous archaeological remains that help explain the history, and linguistic

analyses show what influences helped shape the languages of the inhabitants of Melanesia, Micronesia and Polynesia, it remains unclear even today how man conquered the last unpopulated islands.

Archaeological finds prove that humans lived in New Guinea for the first time as many as 30,000 years ago. The second big wave probably followed 5,000 to 6,000 years ago – the Austronesian migration, which was also the last great human migration wave. With boats, dogs and pigs, the migrants rode the waves of the Pacific from island to island.

One of the main hypotheses states that the migrants started out from Taiwan, passing the Indonesian islands fairly quickly, then moving past New Guinea and out into the world of the Pacific islands. The proponents of this “Express Train” theory had, to date, seen no evidence of any intense interaction with, for example, the native inhabitants of New Guinea. The fact that the inhabitants of this enor-

mous island kingdom all speak closely related Austronesian languages supports the theory of fast dispersal.

However, only part of the genetic data suggests this. An analysis of the mtDNA underscores the Express Train model. “We find Asian mtDNA patterns in 95 to 100 percent of the people, and the variation is very similar, too,” says Mark Stoneking. But the Y-chromosome, so the male line, tells a slightly different story: the Y-chromosomes also exhibit contributions from the original inhabitants from the first immigration wave. And what does this mean specifically? To begin with, that there was, indeed, pretty extensive contact between the old and the new settlers. The trek eastward continually experienced delays.



DNA sample collection: Sean Myles collects cheek swab samples from the inhabitants of the Solomon Islands in Melanesia.

