GENETIC FINGERPRINTS

Imagine a genetic recipe as 46 very long pieces of string, each piece of string representing the DNA molecule that makes up one of the 46 chromosomes. A restriction enzyme works like a pair of molecular scissors. Wherever it recognizes a specific sequence of DNA letters, it cuts the string. Because different people have different DNA sequences, the places where the strings are cut are different for each individual. So after the strings have been chopped up, each person has their own unique combination of string fragments, which vary in size and number.

everyone has a unique fingerprint

DNA FINGERPRINTING

*** Genes are a part of what defines our identity. Their visible signatures, in the form of fingerprints or blood types, have long been used to identify individuals in criminal investigations and paternity disputes. But in addition to these traditional methods of fingerprinting and blood typing, DNA technology has provided some powerful new tools for sniffing out suspects. DNA fingerprinting has made it much more difficult for criminals to, literally, get away with murder.**

THE ONE AND ONLY

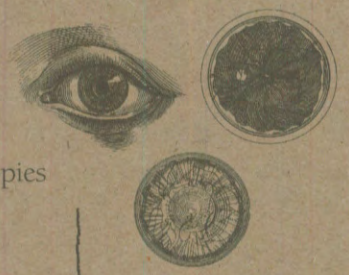
* Fingerprints have been used for identification purposes since the early 1800s. ***Everyone has his own unique set of fingerprints***. Even identical twins, who share an identical set of genes, display slight differences in the fine pattern of skin ridges that make up their fingerprints. So differences in fingerprint patterns are due not only to genes, but to environmental factors during fetal development.

* Fingerprints are an accurate way of matching a suspect to the scene of a crime. Unfortunately, criminals are only too aware of this, so they wear gloves to conceal their tell-tale marks of identity. But short of turning up in a plastic bubble, they cannot avoid leaving behind fragments of skin, hair, and other bodily tissues—all of which contain copies of their unique genetic recipe.

only a plastic bubble would not leave any trace

* DNA FINGERPRINTING was first developed in the 1980s by **Alec Jeffries** at the University of Leicester, in England. What makes the technique so powerful is its sensitivity. A tiny speck of tissue provides sufficient copies of a genetic recipe to obtain a genetic fingerprint. This is why the technique has been so widely adopted by forensic scientists.

* After the genetic recipe has been extracted from a tissue sample, restriction enzymes are used to cut it up into smaller fragments which can be separated from one another by gel electrophoresis.



retinal scans can also be used as identity checks

Eye-dentity

Scientists recently discovered that each of us has a unique pattern of blood vessels on the retinas of our eyes. ***Retinal scans*** *are therefore now being used by the security conscious as additional proof of an individual's identity.*

Technology

Although the technology underlying genetic fingerprinting is state-of-the-art, the principle behind its use differs little from traditional fingerprinting. A DNA fingerprint is a mark of a person's identity—but one based on their unique DNA sequence, rather than the unique pattern of ridges on their fingertips.

get the DNA onto paper

KEY WORDS

GENOME: all the DNA in the genetic recipe of an organism

SOUTHERN BLOTTING: a method of transferring DNA fragments from a gel onto a piece of nylon paper, and then visualizing the fragments through **hybridization** with a DNA probe. The technique's name has nothing to do with compass bearings—it was named after its inventor, **Ed Southern**.

AUTORADIOGRAPH: an image of the distribution of radioactive particles produced on a radiation-sensitive film

PICKING OUT THE PRINT

* Even after the DNA fragments have been separated on a gel, they will still be invisible. The DNA can be stained with ethidium bromide, but there won't be enough of it to show up under ultraviolet light. So another method, known as "Southern blotting," is needed to visualize the chopped-up DNA fragments.

SOUTHERN BLOTTING

* First, the DNA fragments have to be transferred from the gel onto a piece of nylon paper. This is laid on the top of the gel and, under pressure, the DNA fragments are forced through the gel onto the paper, where they stick fast to the long polymeric molecules of the nylon. Moving the DNA from gel to paper doesn't change the relative positions of the fragments to one another.

UNZIPPING

* The next stage is to incubate the paper at a high temperature. This unzips each of the double-stranded DNA fragments into their two complementary strands. Again, the locations of the different sized fragments on the paper remains unchanged.

PROBING

* Then comes a really nifty bit of molecular trickery. A solution containing a DNA PROBE is added to the paper. The probe is a bit of artificially made single-stranded DNA sequence, usually about a few hundred DNA letters long, that has been tagged with a radioactive isotope.

finding the DNA sequence is as easy as ABC

* In DNA fingerprinting, the DNA probe has the same sequence as one of the junk DNA sequences found in multiple copies in all human genetic recipes. When the single-stranded DNA probe is added to the nylon paper, it will bind to any DNA fragments that contain a complementary sequence. Since the junk DNA sequence is ubiquitous throughout the human genome, the probe will bind to a large number of fragments.
* Finally, the locations of the DNA fragments that bound to the radioactive probe are revealed by overlaying the nylon paper with a piece of radiation-sensitive film. When the film is developed then, at last, we have a visual picture of the DNA fragments.

hybrids are interbred

Hybridization

In biology, hybridization has two meanings. It can refer to interbreeding between two different species or varieties, or it can mean complementary base pairing between two DNA strands from different sources (i.e. a DNA probe and a DNA fragment).

your DNA gave it away

chance plays a part in DNA fingerprinting

THE NECESSITY OF CHANCE

* Once a DNA fingerprint has been obtained, the next job is to find a suspect whose own DNA fingerprint matches the one found at the scene of the crime. Because the chance of two different people sharing the same DNA fingerprint is extremely low, a profile match can be presented as fairly damning evidence in court.

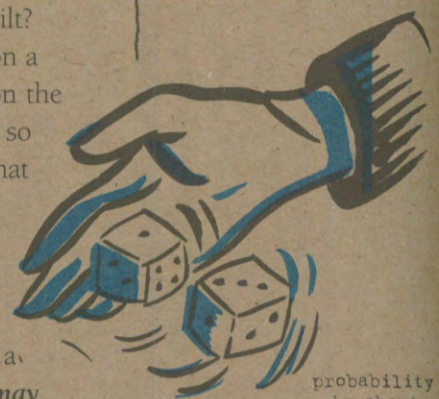
REASONABLE DOUBT

* If the DNA fingerprint of a suspect does not match the one obtained from the tissue samples found at the scene of a crime, then the two DNA samples must have come from two different people, so the suspect is exonerated. But what happens if the DNA fingerprints do match up? Is this conclusive proof of guilt?

* Securing a conviction based on a matching DNA fingerprint rests on the assumption that fingerprints vary so much between different people that the chance of two people sharing the same fingerprint is low. But although everyone has their own unique genetic recipe, DNA fingerprinting only samples a proportion of that recipe. ***There may be a chance, however slim, that two people do in fact share the same DNA fingerprint as revealed by genetic testing.***

SUSPECT DNA

DNA data banks have been established in the U.S. and Britain. Screening the catalog of fingerprints is the first step in tracking down possible suspects.



probability is about measuring the likelihood of events

guilty! (or innocent?)

* So scientists have to work out the probability of a chance match. Despite the fact that the DNA fingerprint from the scene of the crime matches that of the suspect, the scientist has to work out what the chances are that it came from someone else.

PROBABILITY

* The estimate of PROBABILITY has to be based on a sample population of which the suspect is a member. This is important, because ***two people from the same ethnic group are more likely to share genes, and therefore DNA fingerprints, than two people drawn at random from the population as a whole***. However, working out the probability of chance matching is never an exact science, and lawyers can exploit this element of doubt in court. In Britain some people have been convicted on DNA evidence alone—but without additional incriminating evidence, this is still quite rare.

Incompetence

There are more prosaic reasons why DNA evidence may not stand up in court. Any suspicion of incompetence in the way tissue samples were collected from the crime scene, or during the laboratory testing itself, can lead to allegations that the samples were contaminated by DNA from other sources.

do I have to repeat myself?

REPEAT AFTER ME...

* Other forensic DNA technologies have emerged since the introduction of DNA fingerprinting. PCR techniques have been incorporated into the forensic scientist's tool box, to uncover the repetitive DNA sequences that are scattered throughout our genetic recipes.

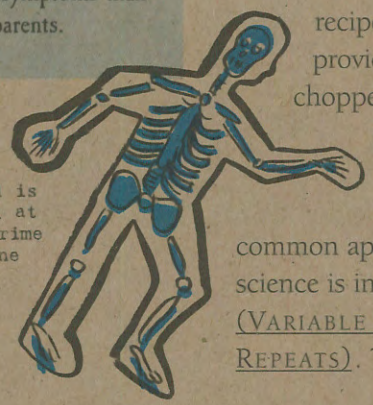
FRAGILE-X SYNDROME

Fragile-X syndrome is a relatively common congenital mental disorder in humans caused by a tri-nucleotide repeat sequence stuck in the middle of a gene on the X chromosome. How the sequence got there is a mystery, though it may have been part of a jumping gene. The repeat sequence completely disrupts the gene's function. With each generation the number of repeats increases—with the result that children always have worse symptoms than their parents.

TANDEM REPEATS

* One of the problems for forensic scientists is that unless the tissue samples they collect from crime scenes are relatively fresh, the genetic recipe within the cells of the tissue will have become degraded. In other words, microbes will have begun chopping it up. For obvious reasons, this can make conventional DNA fingerprinting impossible.

* But ***PCR has the advantage that it only requires a small section of intact DNA***, rather than the genetic recipe in its entirety. It will work provided the DNA has not been chopped slap-bang in the middle of the sequence you want to amplify.



speed is vital at the crime scene

* One of the most common applications of PCR in forensic science is in the study of VNTRs (Variable Number of Tandem Repeats). These are noncoding

could we identify a criminal from a genetic profile?

sequences, found throughout the genome, made up of endless "tandem repeats"—for example, ATATATATATATAT. The number of repeats varies enormously between individuals. When these regions are amplified by PCR, different people produce tandem repeats of different lengths, which can be separated by size using gel electrophoresis. And because PCR produces so many copies of the amplified sequence, there is no need to fool around with the long-winded complexities of Southern blotting. The DNA can be visualized by staining it with ethidium bromide and viewing it under ultraviolet light. ***By looking at many of these individual tandem repeat sequences, scientists can produce a DNA profile that is similar to a DNA fingerprint.***

TWOS, THREES, FOURS...

Repetitive sequences don't just come in repeats of twos. Threes, fours, and much larger repeat units are well known. All these repetitive sequences have much higher mutation rates than coding genes, and changes involve the addition or deletion of one or more of the repeated units.

If the Face Fits...

When trying to solve a crime, police forces often publish an artist's impression or a computer-originated composite picture of a suspect, based on the recollections of eyewitnesses. In the future, a genetic recipe may be all that is required to build a picture of a criminal. Scientists in the UK are currently constructing a database containing the genetic recipes of a group of volunteers plus detailed 3-D images of their faces, in order to see how well DNA can predict facial features.

sitting on the tree of descent

CLUES TO THE PAST

★ Evolutionary change ultimately comes about through the steady accumulation of new mutations in DNA. By comparing the DNA sequences of different species, it's possible to trace their evolutionary history. DNA sequencing has even offered insights into our own biological past.

ONLY CONNECT

Taxonomy is the study of the classification of living things. Gone are the days when taxonomists spent endless lonely hours measuring the lengths of bones. Nowadays, they spend equally endless lonely hours sequencing genes from different species to work out how they are related to one another.

excuse me, could you tell me the way to my evolutionary history

SPLENDID ISOLATION

★ Imagine the following hypothetical evolutionary scenario. A population of aardvarks is happily minding its own business when a splinter group suddenly decides to head off for greener pastures. Each individual in the splinter group will take with it the aardvark genetic recipe. But as the years pass, genetic changes will begin to accumulate in the two isolated populations. The extent of this divergence will be correlated with the length of time they have lived apart.

★ The aardvarks illustrate the general principle that ***the longer the interval since two populations or species shared a common ancestor, the greater is the difference between their DNA sequences***. So, by reversing the logic, we can use the DNA sequence differences between species to work out the evolutionary relationships between them.

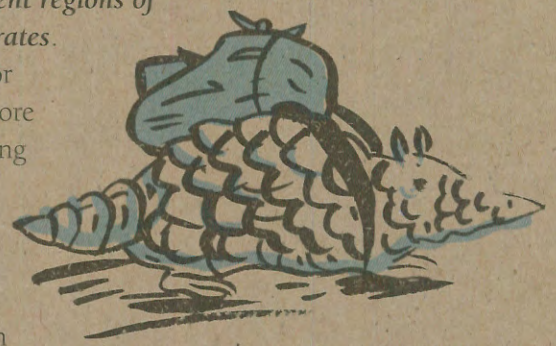
VARIABLE RATES

★ The choice of which genes to look at is an important one. ***Different regions of DNA evolve at different rates***. Noncoding sequences, for example, evolve much more rapidly than protein-coding genes, because mutations can steadily accumulate in the genetic garbage without any detrimental effects on the organism.

★ Slowly evolving genes are not very informative for investigating the evolutionary relationships of closely related species, because they will have accumulated few, if any, differences. In general, fast-evolving genes are used to distinguish closely related species; and slowly evolving genes are used for distantly related species.

Close relatives

DNA sequencing has shown that chimpanzees are our closest living evolutionary relatives. DNA sequences of humans and chimps differ by only 2.5%. Given that the genetic recipes of humans differ from one another by an average of about 1%, this means that our own genetic recipes differ from those of chimps by about 20 DNA letters in every thousand.



aardvark heading off to form a new group

Africa may be the cradle of human history

DETECTING DIFFERENCES

DNA differences between human populations are slight. Mitochondrial DNA is often used to distinguish human populations, because it has some noncoding genes that evolve at a very high rate, making differences relatively easy to detect.

the genetic history of African peoples has been studied

GEOGRAPHICAL GENES

✱ Tracing the ancestry of families, populations, and nations is a popular pastime among historians and archaeologists. Cultural artifacts and other human remains contain clues to our past, and their geographical distribution has illuminated patterns of human ancestry and migration. But genes contain much more reliable clues, and DNA technology is adding an extra dimension to studies of human history.

OUT OF AFRICA

✱ Before DNA technology, the only way of investigating early human origins was through their fossil remains. Because these are difficult to date accurately, there has always been ample scope for speculation and conflict over when and where humans first originated. One theory suggests that *Homo sapiens* evolved simultaneously in Africa, Europe, and Asia. An alternative "out of Africa" theory postulates that humans had an exclusively African origin and subsequently spread to other parts of the world. Geneticists go for the latter theory.

✱ A number of recent genetic studies have found that DNA differences between modern African populations are much greater than those between populations

African populations may be the oldest in the world

from other parts of the world. That more DNA differences have accumulated within African populations implies that ***African populations are older than other human populations.***

MAKING A DATE

✱ DNA data provides support for the "out of Africa" hypothesis. But geneticists have been able to go further with this information and actually put an estimate on the time when humans first evolved. This calculation rests on the assumption that mutations accumulate in the DNA at a steady rate, like a ticking clock. By counting the number of accumulated differences and knowing the rate at which mutations occur, you can extrapolate backward to pinpoint a date of origin. Using this technique, it has been estimated that ***humans originated about 100,000 years ago***.

Genetic baggage

When some human populations decided to pack their bags and leave Africa, they didn't just take their suitcases, language, and culture; they took copies of their genes as well. Like languages and cultures, the present day distribution of genes records patterns of human migration. The geographical patterns of genes in modern humans suggest that Europeans wandered into Europe via the Middle East about 45,000 years ago. Native American people seem to derive from two separate migrations, both from Asia, around 10,000 and 30,000 years ago.

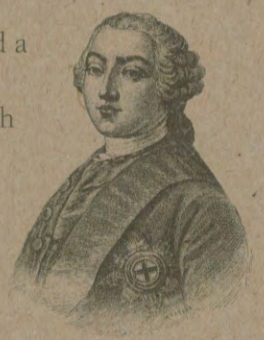
the werewolf condition may be a genetic disorder

MIGRATION AND MADNESS

* The history and movement of populations leaves its mark on the present day distribution of genes. The global distribution of the dominant genetic disease porphyria variegata provides one of the most striking examples of this phenomenon.

HEADING SOUTH

* In most parts of the world, porphyria variegata is very rare. But among the Afrikaans-speaking people of South Africa, it is much more common. Today, about one out of every 300 Afrikaners has the disease. Afrikaners are descendants of a Dutch couple who married and founded a settlement in South Africa in the late 17th century. Although porphyria is rare in Holland, by chance either one or both of the couple must have had the porphyria gene in their genetic recipes.



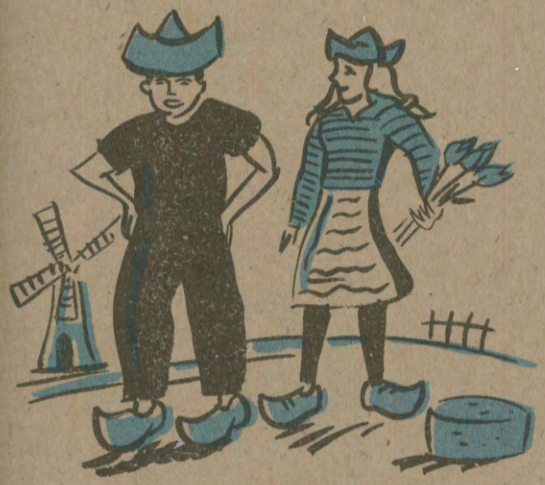
King George III may have suffered from porphyria

Werewolves and Kings

The legend of the werewolf may have originated with the disease porphyria variegata. The effects of the disease are very variable, but in extreme cases sufferers can experience such diverse symptoms as extreme sensitivity to light, excessive hair growth on exposed skin, blood-red urine, and bouts of madness. It has been suggested that the disease was responsible for the "madness" of the English King, George III.

INBRED DISEASES

* The Dutch couple produced a large family, so the gene would have been passed on to some of their children and grandchildren, and so on. Although the settlement grew rapidly, language and religious barriers meant that the population was effectively cut off from the outside world and was therefore exposed to the dangers of INBREEDING.



porphyria was brought to South Africa by the first Dutch settlers

* The genetic risks of inbreeding provide a good biological reason why incest has become a cultural taboo in most human societies. Close relatives share more genes in common with one another, including the genes which cause disease—so if you marry a close relative and have children, there is a much greater chance that you will produce a child with two copies of a disease-causing gene.

REMOTE RISKS

Wherever communities remain small and are isolated by religious, cultural, or geographical barriers, there is a much greater risk of a genetic defect spreading in a population through inbreeding. For example, a recessive genetic disease called **BIDS syndrome**, which causes extremely brittle hair and intellectual impairment, is relatively common in the religiously isolated Amish community of North America, but unknown elsewhere.