

Fingerprinting DNA from a single hair

A Florida court convicted a man last month on two counts of first-degree murder and necrophilia. Ten days earlier, a U.S. military court had sentenced a serviceman in Korea to 45 years for rape and attempted murder. In both trials, a technique called DNA fingerprinting — used to compare the defendants' genetic makeup with DNA contained in semen found on the victims' bodies — was pivotal in bringing about the guilty verdicts.

By identifying individuals as definitively as do regular fingerprints, DNA fingerprinting promises to revolutionize the analysis of semen, blood, hair and other samples left by criminals. Until recently, however, the forensic use of DNA fingerprinting had been somewhat limited because the method requires micrograms of DNA — that means several hairs, or blood and semen spots in amounts larger than what is often found at a crime scene. Now two research teams, taking different approaches, have developed DNA analyses that can be performed on nanograms of DNA, an amount typically found in a single strand of hair. This is an important benchmark because hair is commonly found at crime scenes.

One technique, devised by scientists at Cetus Corp. in Emeryville, Calif., and at the University of California at Berkeley, can even analyze very old, degraded samples of DNA. This not only enlarges the spectrum of criminal cases in which DNA typing is useful, but also opens the door for some interesting genetic studies in paleontology and archaeology. One Cetus researcher, for example, recently used the technique to examine the genetic sequence of DNA preserved in the muscle of a 40,000-year-old mammoth.

DNA fingerprinting was developed three years ago by geneticist Alec Jeffreys at the University of Leicester in England (SN: 12/21&28/85, p.390). Jeffreys observed that a number of DNA segments contain particular sequences of bases, the DNA building blocks, and these sequences are repeated many times. Most important, he noted that the number of repeat sequences in each of these regions — and hence each region's length — varies from one person to the next.

Jeffreys devised a technique that first cuts DNA into fragments. These are arranged according to length by electrophoresis, and then the ones that contain repeat sequences are tagged with radioactive probes, which allow these fragments to be visualized. The resulting pattern, which resembles a supermarket bar code, is a DNA fingerprint. With this method, the chances of two unrelated people having the same DNA fingerprint are, on average, 1 in 30 billion.

But in spite of its unusually high discriminating power, this approach has

some drawbacks for forensic work: It requires relatively fresh samples and relatively large amounts of DNA. Addressing the second problem, Jeffreys and researchers at Cellmark Diagnostics — the company that licenses the DNA fingerprinting patent — recently announced a modified, more sensitive technique. Instead of using the original repeat-sequence probes, which are relatively short molecules, the researchers made new "locus-specific" probes out of selected DNA fingerprint fragments. These larger probes are able to carry more radioactivity, enabling researchers to detect DNA at levels as low as 20 nanograms. This allowed the group to use the technique on a single hair root, according to Cellmark's David Green in Germantown, Md.

Scientists at Cetus have devised an even more sensitive technique and have used it to type samples containing less than 1 nanogram of DNA. In fact, they can work with as little as a single DNA molecule. Their method relies on a molecular copying process called polymerase chain reaction (PCR) gene amplification, which has been steadily changing the face of molecular biology since it was developed at Cetus three years ago. While traditional methods of copying genes or the proteins for which they code typically take weeks, PCR amplification can produce millions of copies in less than a day.

In the April 7 NATURE, Cetus' Russell Higuchi and Henry A. Erlich, along with Cecilia H. von Beroldingen and George F. Sensabaugh at the University of California at Berkeley, report that they have applied the PCR method to forensic samples of DNA. From both fresh and shed hairs, the researchers succeeded in making enough copies of one small DNA region, a portion of a gene, to perform three kinds of typing on it. By looking at differences in the length and/or base sequence of that gene, they could classify individuals into 21 different types. Unlike the Cellmark method, which requires long, intact DNA chains, the Cetus technique can copy and type DNA that has been degraded by long exposure to light or enzymes. The researchers typed several-month-old fallen hairs in which they had been unable to detect any DNA with conventional chemical means, and the group is currently working with police on DNA samples that are several years old.

Shed hairs typically contain less than 10 nanograms of DNA, and being able to type them is particularly important "because they're the most common hairs found in forensics," Higuchi says.

For both techniques at this stage, the cost of greater sensitivity is lower precision in distinguishing one person from another. Green estimates that with a test made of four of the new locus-specific

probes, the chances of two people having the same pattern would be 1 in a million, on average. (Sometimes the odds are much better: In the Korea case, the serviceman's pattern was so unusual that the statistics were 1 in 4.5 trillion.) The Cetus technique now is far less discriminating. But von Beroldingen expects that by looking at several different genes, her group will achieve comparable values within the next few years.

Because DNA typing can go much farther in zeroing in on a particular individual — as opposed to blood typing and other traditional forensic methods, which can at best simply narrow the field of suspects — both Britain's Home Office and the U.S. Federal Bureau of Investigation (FBI) have been closely following DNA fingerprinting. The FBI is evaluating a number of approaches, including the recent developments, and according to a spokesman, the bureau hopes to incorporate some form of DNA typing into its investigations by early fall.

While DNA fingerprinting figures prominently in a growing number of trials, it still may take some time before U.S. courts embrace DNA evidence as enthusiastically as do investigators and scientists. Right now DNA fingerprinting is being introduced into the courts on a case-by-case and state-by-state basis, says Cellmark's George Herrin Jr.

"It's a new technology, so no one, except the scientists, is really quite sure how to deal with it," he says. "It's thrown the legal system for a loop because it is much more powerful than any ID technique they've had other than normal fingerprints." — S. Weisburd

Farthest galaxy is cosmic question

Galaxies are the basic constituents of the universe. When and how they formed are fundamental questions for any theory of cosmology. Astronomers keep looking for ever-more-distant galaxies, because the farther away they are, the earlier the epoch at which we see them. Simon Lilly, a British astronomer working at the University of Hawaii at Manoa, has found a galaxy with a redshift of 3.4, which would put it four-fifths of the way back to the beginning of the universe.

This object, catalogued as 0902+34, is the most distant object now known for which there is good evidence that it is a galaxy. Some astronomers at the University of Arizona recently found infrared objects that seem to have redshifts greater than 6 (SN: 1/23/88, p.52) but have not been able to prove they are galaxies. Redshift, a displacement of the object's emissions toward the red end of the spectrum, is proportionate to the speed at which the object is receding from the observer. Distance can be calcu-

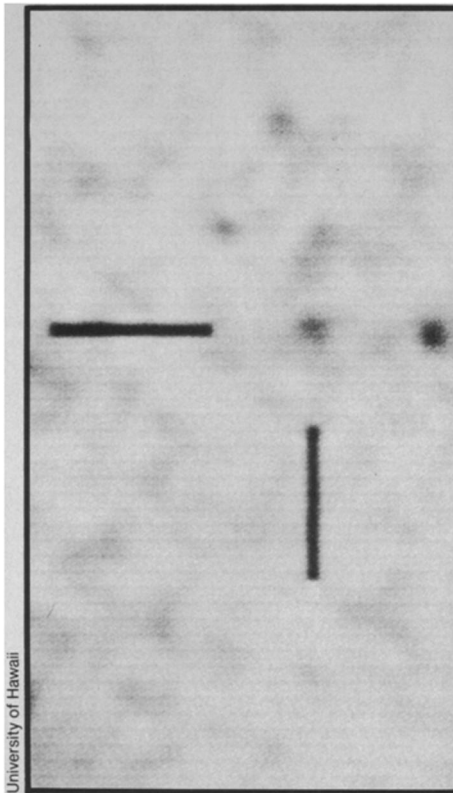
lated from the speed, but the computation uses the Hubble constant, which is so difficult to determine that astronomers cannot agree on its value. The value taken by Lilly makes the universe 15 billion years old, and on this basis 0902+34 is 12 billion light-years away. Other values of the Hubble constant yield ages for the universe between 10 billion and 20 billion years. Adopting any of them would change the distance to 0902+34 proportionately.

By whatever distance estimate, 0902+34 is far enough back in time to make trouble for a class of currently high-interest cosmological theories, the cold dark-matter theories, says Len Cowie, assistant director of the Institute for Astronomy at the University of Hawaii. Astronomers have a number of reasons for believing that a large amount of unseen, undetected matter pervades the universe. In most models this dark matter is composed of subatomic particles, neutrinos or maybe something more exotic. These models are divided into two classes according to whether the dark matter is hot or cold. The cold dark-matter theories appear to be the most popular at the moment, but the discovery of 0902+34 could make trouble for them, since they do not allow for galaxies as well formed as this one existing at such an early epoch.

Speaking from Mauna Kea, where he was observing, Lilly told SCIENCE NEWS that the discovery arose as part of a project to survey certain radio sources to see whether optical counterparts could be found for them. Since 1986 he has been concentrating on the dozen most promising ones chosen from his original sample. Object 0902+34 is the only one of the dozen or so that looks like a galaxy. A report will appear in *ASTROPHYSICAL JOURNAL*.

Although radio sources like 0902+34 are usually associated with very luminous galaxies, none appeared for this one when it was first studied in 1982. In his work on the object, Lilly used two telescopes, both on Mauna Kea, and a variety of recently developed, very sensitive recording equipment. In 1985, using the United Kingdom Infrared Telescope, Lilly detected a faint infrared source at the position of the radio source. Then, with the Canada-France-Hawaii Telescope, he got a visible-light image. Returning to the United Kingdom Infrared Telescope, he used a newly available infrared array camera to make an infrared image of the object. Finally, back at the Canada-France-Hawaii Telescope, he used a newly developed faint-object spectrograph, which obtained a spectrum that showed a strong emission feature.

This feature can be identified with a resonance of atomic hydrogen, whose emission, at rest in the laboratory, appears at an ultraviolet wavelength. In 0902+34 it is shifted completely across the visible range into the infrared, and



Black bars point to 0902+34, the farthest galaxy yet.

from this Lilly calculated the redshift of 3.4.

The spectrum of 0902+34 indicates that the light comes from stars, and therefore the object is a galaxy. Among

several indicators that support the conclusion, says Lilly, is the uniform brightness of the spectrum in the optical range — “too flat to be a quasar,” the only other class of objects astronomers are used to seeing at such redshifts.

From the spectral evidence Lilly concludes that 0902+34 contains two distinct populations of stars. One is young blue stars, indicating that the galaxy is converting annually about 100 times the sun's mass of interstellar matter into new stars. The second population, accounting for more than 90 percent of the galaxy's mass, is mature reddish stars at least 1 billion to 2 billion years old. These are responsible for the stronger emission at infrared wavelengths than at visible ones.

The antiquity of the galaxy and of the stars within it make it very important for theories of cosmology and for models of the formation and development of galaxies and of stars. “The importance of 0902+34 for cosmological theories cannot be over-emphasized,” says Cowie. Donald N.B. Hall, director of the Institute for Astronomy, remarks that it will be important to determine whether 0902+34 is an anomalous object or one of a class. Are there other galaxies with similar redshift and similar appearance waiting to be found? The continuing development of more sensitive recording equipment and, in a few years, the launching of the Space Telescope and the completion of the 10-meter Keck Telescope, also on Mauna Kea, may make it possible to find out.

— D.E. Thomsen

Corn yields to genetic tinkering

California researchers have achieved a long-awaited first by growing corn plants genetically engineered to carry a foreign gene.

Inserting foreign genes into plants is not new; scientists have been engineering broad-leaved, dicot plants such as tobacco and tomatoes for more than a decade. But until now the monocot grain crops, such as corn and rice, have been notoriously hard to engineer. These difficulties have left the world's important cereal crops almost untouched by advances in genetic engineering.

In the recent work with corn, scientists at the Sandoz Plant Protection Corp. in Palo Alto, Calif., inserted a gene for antibiotic resistance into specially prepared corn-plant cells called protoplasts, and grew the protoplasts into whole corn plants. Each cell in the new plants carries the foreign gene.

Years of painstaking research led to this success. First, other scientists got foreign genes to pass into corn protoplasts but couldn't get the protoplasts to grow into full plants. Early this year researchers reported that they had

grown genetically unaltered corn protoplasts into full corn plants. The growth of full plants from genetically altered protoplast, reported in the April 8 issue of *SCIENCE*, was the logical combination of these results.

The corn plants' resistance to the antibiotic is not useful in itself, but the antibiotic-resistance gene can be paired with a more useful gene. Then the presence of antibiotic resistance will show which plants have also taken up the useful gene. Genes for resistance to herbicides and to corn-eating pests are likely candidates for future insertion into corn plants. Now that corn has been engineered by this method, other cereal crops may soon follow, according to Carol Rhodes, one of the report's authors.

There remains one major problem with the engineered corn plants: They produce no corn. The researchers, however, think this may be just a result of the techniques used and say they expect this problem to be solved in the future. “I don't know how long it will be,” says Rhodes, “but it's definitely going to happen.”

— C. Vaughan