BioPharmaceutical Technology Center
I N S T I T U T E

Short Tandem Repeats (STRs) & Genetic Identity

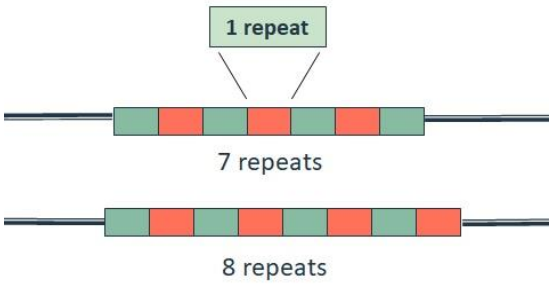
Field Trip Background

DNA and the information that it contains has long been a source of inspiration for scientists and the public; from the time when DNA was first discovered to be the biochemical responsible for the transmission of traits, through the understanding of its chemical language, and into the current era of complete genome sequencing. For as much as we have learned about DNA, it remains for many a stunning combination of information treasure trove and Pandora's box.

When CBS first aired the television show *Crime Scene Investigations* (CSI) in 2000, it exposed a broad television audience to the ideas that the tools of biology and chemistry could be used for solving mysteries and bringing about justice. Among the technologies in this high-tech police toolbox is the use of DNA for genetic identification. Real-world forensic DNA typing was in its infancy in the 1980s and early 1990s, and by the time CSI came on the scene, the technology was coming into robust, and rigorously tested, maturity. Though aware of its potency, there are many public misconceptions about DNA generally, and forensic DNA typing specifically.

The STR and Genetic Identity Field Trip covers some of the general concepts of how people are identified, and distinguished from one another, based upon the As, Cs, Ts and Gs that are contained in their DNA.

In 1984, Sir Alec Jeffreys discovered that repetitive regions of non-coding DNA were conserved within a person's DNA, and that they were passed from parents to offspring in a Mendelian way, like genes. He worked out a method for identifying these DNA regions, called Variable Nucleotide Repeat Regions (VNTRs).



At left is an example of what is meant by a repetitive DNA region. The top strand represents one copy of one person's DNA (say, the maternal copy). The bottom strand represents the second (paternal) copy of that person's DNA.

A single VNTR repeat is anywhere from 10 to 60 DNA base pairs (bp) in length.
A single STR repeat is between 2 and 5 bp in length.

The person above has inherited 7 and 8 repeats of the tandem repeat region, from his or her parents,

Dr. Jeffreys' technique involved using restriction enzymes to chop up a person's DNA, running the resulting fragments through gel electrophoresis to separate the different-sized pieces into bands, and then using radioactive DNA probes to see the bands of interest on the gel when exposed to film. Because the patterns of bands that were seen differed between individuals, the technique became known as DNA fingerprinting.

In 1987, authorities in Leicestershire, England asked Dr. Jeffreys to use his VNTR DNA fingerprinting technique to help them prove that a suspect had committed two separate murders. The result was surprising. They showed that the suspect was not guilty, but that some other man had been involved in both killings. More detective work led to the apprehension of the real culprit, who was later shown to be the killer using the VNTR technique. This case was the first time that DNA had been used to both exonerate an innocent person and to convict a guilty person. Since that first case, the technology used to do DNA fingerprinting has changed drastically, though the underlying principles remain the same.

- Today, DNA fingerprinting makes use of the polymerase chain reaction (PCR) technique which is roughly 1,000 times more sensitive than what Dr. Jeffreys was able to do. PCR enables forensic scientists to use very small amounts of biological evidence, sometimes only a few cells worth, to get a DNA fingerprint (also known as a DNA profile).
- Short Tandem Repeat (STR) regions that have a length of 2 to 5 base pairs per repeat have replaced the longer Variable Nucleotide Tandem Repeats (VNTRs), in part because the shorter length of the DNA regions make them easier to amplify using PCR.
- The process of separating the PCR-amplified fragments is still done using electrophoresis, but employs a capillary electrophoresis technique, like that used in DNA sequencing, that is capable of separating two fragments of DNA that are only one base pair different in size. The bands that result are visualized by using fluorescent molecules that are incorporated into the PCR primers used to generate them.

Students who participate in the BTC Institute's Short Tandem Repeat & Genetic Identity Biotechnology Field Trip will set up a PCR, amplifying DNA fragments of different length. They will then separate those fragments using gel electrophoresis, and analyze the results to determine heterozygosity or homozygosity of a polymorphic DNA region of varying length. Additionally, participants will analyze the results of real STR DNA fingerprint data using the statistics of population genetics, gaining an appreciation that determining human identity from DNA combines science and math (biotechnology and statistics).

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