

The Case of the Druid Dracula

by

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Part I—DNA Structure and PCR

In the northernmost corner of the Isle of Anglesey in Wales in a village called Llanfairpwll, the windswept beaches and ancient Druid ruins provided a surreal backdrop for the murder of 90-year-old Mabel Leyshon. Her murder was not only brutal—her heart had been hacked out—but also creepy; it appeared as if the killer had collected Mabel’s blood in a small kitchen saucepan that had lip marks on the rim indicating the contents had been tasted. The murder showed other signs of the occult: a candlestick and a pair of crossed pokers had been arranged near the body. Further investigation indicated that this was no supernatural villain at work. The murderer had worn tennis shoes which had left distinctive footprints under the glass door that had been shattered with a piece of broken garden slate in order to gain entrance to the victim’s home. Inside the house, a windowsill had bloodstains on it. With luck, the evidence recovery unit hoped to use it to find the killer.

Questions

- DNA differences can be used to identify people. For example, there is a gene found on both the X and Y chromosomes called amelogenin, but the version of the gene found on the X and Y chromosomes differs in length, so it can be used to tell if a blood stain, such as the one found on the windowsill inside Mable Lyshon’s house, was left by a man or woman. This stretch of nucleotides shows one strand of the DNA double helix for the amelogenin gene; what is the sequence of the other complementary strand?
5’CCCTGGGCTCTGTAAAGAATAGTGTGTTGATTCTTTATCCCAGATGTTTCTAAGTG3’
 - 3’ACTGTTAGATTTCCCTTTTTAGGTCTAGGTCCGTCGGCCTTATTTCCGAGGAATAA5’
 - 3’GGGACCCGAGACATTTCTTATCACACAATAAGAAATAGGGTTTACAAAGATTCAC5’
 - 5’GGGACCCGAGACATTTCTTATCACACAATAAGAAATAGGGTTTACAAAGATTCAC3’
 - 3’CCCTGGGCTCTGTAAAGAATAGTGTGTTGATTCTTTATCCCAGATGTTTCTAAGTG5’
 - 5’CCCTGGGCTCTGTAAAGAATAGTGTGTTGATTCTTTATCCCAGATGTTTCTAAGTG3’
- To assist the investigators with the crime, you will need to perform Polymerase Chain Reaction (PCR) to create copies of this gene so the sizes can be compared to determine if the blood was from a man or woman. During PCR it will be necessary to break the hydrogen bonds of the base pairs. Where are those hydrogen bonds normally found?
 - Between two nitrogen-containing bases in a single strand of DNA.
 - Between the phosphate and sugar of the same nucleotide.
 - Between the sugar of one nucleotide and the phosphate of a different nucleotide.
 - Between one nitrogen-containing base on a single strand of DNA and another nitrogen-containing base on the complementary strand of DNA.
 - Between one phosphate on a single strand of DNA and a sugar on the complementary strand of DNA.

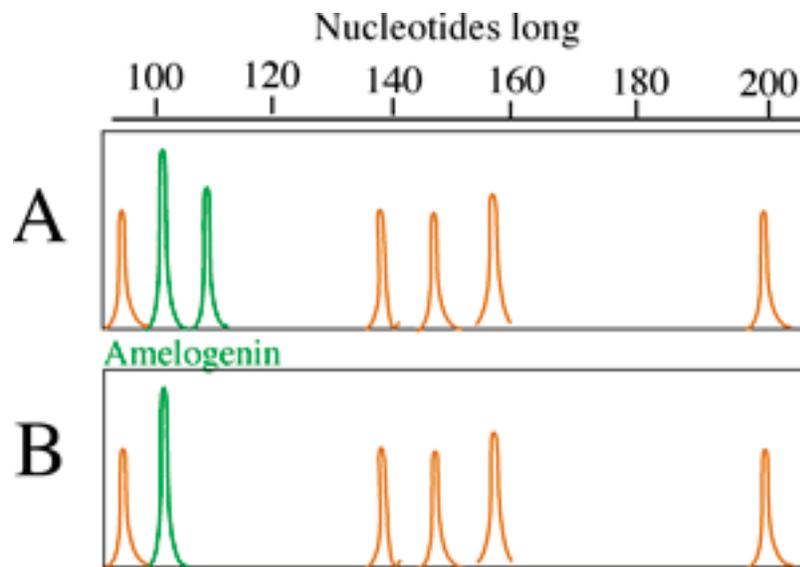
3. PCR creates copies of DNA using the exact same mechanism used by your cells to copy their own DNA (replication). Place the steps listed below in the order in which they occur during replication:
- A) two strands, one new and one original template, wind together to form the double helix.
 - B) short stretch of primer (~20 nucleotides exactly complementary to the gene that is going to be copied) is made.
 - C) separation of the double helix from two parental DNA strands.
 - D) use of parental DNA as a template so that nucleotides are covalently bonded together to form a new chain that is complementary to the bases on the original template.
- a. A, B, C, D
 - b. B, C, A, D
 - c. D, B, C, A
 - d. C, B, D, A
4. PCR can be used to selectively duplicate one single gene out of thousands because the only primers available to start replication are the one unique pair that are complementary to the regions on both sides of the gene. Which of these primers (one for each strand) could you use to copy just the stretch (enlarged) of the amelogenin gene that differs between the X and Y chromosomes?

3'GGGACCCGAGACATTTCTTATCAC**ACA**ACTAAGAAATAGGGTCTACAAAGAGTTCACCAGGACTTT**ACAGTTCCTACCAC**CCAGCTTCCCAGTTTAAGCTCTGAT5'

5'CCCTGGGCTCTGTAAAGAATAGTG**TGTTGAT**TCTTTATCCCAGATGTTTCTCAAGTGGTCCTGAAA**TGTCAAGGATGGTG**GTTCGAAGGGTCAAATTCGAGACTA3'

- a. 3'GGGACCCGAGACATTTCTTATCAC5' and 5'CCCTGGGCTCTGTAAAGAATAGTG3'
- b. 5'CCCTGGGCTCTGTAAAGAATAGTG3' and 5'GTCGAAGGGTCAAATTCGAGACTA3'
- c. 5'CCCTGGGCTCTGTAAAGAATAGTG3' and 3'CAGCTTCCCAGTTTAAGCTCTGAT5'

Part II—The Report

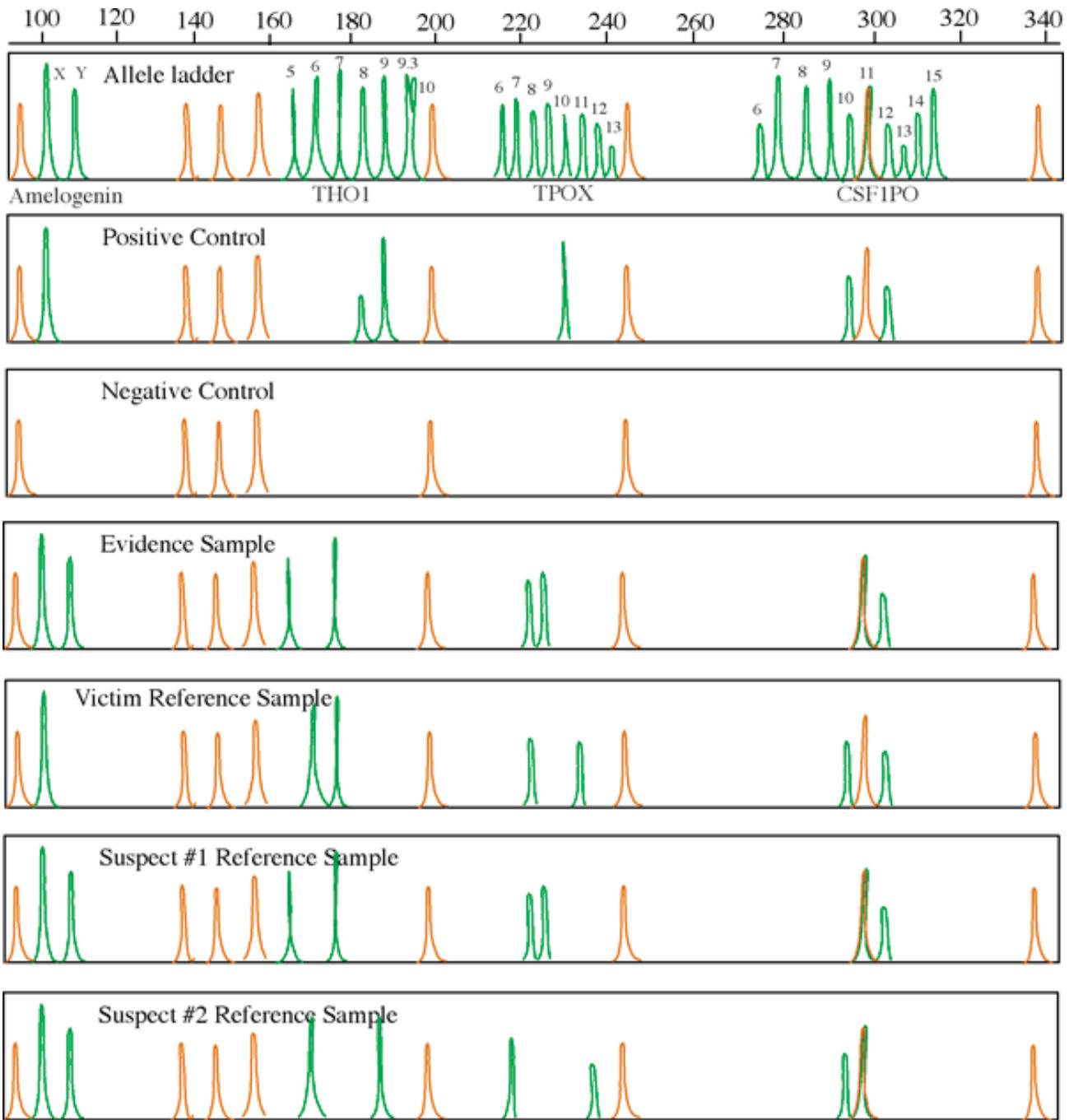


Question

1. Which of the above (A or B) represents the profile of a man?

Part III—More Analysis

The crime was featured on BBC's Crimewatch program in December 2001 and North Wales Police received over 200 calls. Following up reports of a teenager who had attacked a German student, the police went to the home of Matthew Hardman (suspect 1), who gave police a cheek swab. During this visit, officers found a pair of Levi shoes. Forensic Science Service (FSS) scientists matched Hardman's shoes to the footwear marks found at the murder scene. Profiling suggested a much older offender, so another suspect was also asked to give a cheek swab (suspect 2). Since both suspects were men, the officers needed to test for other genetic differences. They focused on STRs (short tandem repeats), stretches of DNA that exist in all people, but in different numbers of repeats. The allele ladder below shows all varieties in a population.



Questions

1. Which suspect presents a profile compatible to the sample found at the crime scene?
 - a. Suspect #1
 - b. Suspect #2

2. There are only a few different numbers of repeats that are seen in our population—only 5 different TPOX STRs for example. By testing thousands of DNA samples, researchers know the distribution of these different STRs in the general population; those allele frequencies are shown in the table below. Using these frequencies, one can determine the probability that someone else at random would have the same matching pattern. For example, what is the likelihood that someone else at random would have the same pattern of Matthew Hardman (a 5 and 7 repeat for the THO1 STR)?

THO1	TPOX	CSF1PO
5: 1/200	8: 1/2	9: 1/40
6: 1/4	9: 1/8	10: 1/5
7: 1/6	10: 1/18	11: 1/3
8: 1/7	11: 1/5	12: 1/3
9: 1/6	12: 1/20	13: 1/10
9.3: 1/3		14: 1/50
10: 1/100		

- a. 1/200
- b. 1/206
- c. 1/1200
- d. 1/2600
- e. 1/20060

3. What is the probability that someone else at random would have that same pattern of THO1 5 & 7, TPOX 8 & 9, and CSF1PO 11 & 12?
 - a. 1/1600
 - b. 1/7200
 - c. 1/17600
 - d. 1/172800
 - e. 1/1555200

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