CB02 The Sarah Yarborough Homicide—The First Case Where Investigative Genetic Genealogy Was Used to Generate Forensic Intelligence in 2011

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Learning Overview: After attending this presentation, attendees will have gained insight into the development of investigative genetic genealogy as a means of developing investigative intelligence for cold casework. The 1991 homicide and sexual assault of Sarah Yarborough was the first known instance where direct-to-consumer DNA test data was used to generate investigative leads for a cold case, opening the door for countless others that have since been solved using genetic genealogy. The Yarborough homicide was first attempted in 2011 by comparing the Y-chromosomal Short Tandem Repeat (Y-STR) profile obtained from the crime scene DNA to public Y-STR genetic genealogy databases. When the case was solved in 2019 using autosomal Single Nucleotide Polymorphism (SNP) testing GEDmatch, it was discovered that Sarah's killer could have been identified at least 20 years earlier through the Combined DNA Index System (CODIS), but loopholes in the legal system had allowed him to avoid detection.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by proving a case study that illustrates the strengths and weaknesses of forensic genetic genealogy compared to those of conventional STR typing, conventional genealogical research, and the legal system, and how each factored into the resolution of 30-year-old cold case in spite of the loopholes and flaws in the system.

In 2011, a match was found for the killer's Y-STR profile to members of the Fuller Y-STR surname project who were descendants of Robert Fuller of Salem, MA, in the 1630s, a relative of the Mayflower Fullers. Suspicion fell on William Fuller, a long-time Yarborough family friend, who had been in the area at the time of the murder and whose daughter Elizabeth was Yarborough's classmate. When William Fuller voluntarily gave a DNA sample, it was determined that he was not the killer nor was he the father of the killer. However, his Y-STR profile matched the Y-profile from crime scene DNA, indicating he was a paternal cousin of the killer, although it was not possible to estimate how closely they were related. The unusual situation developed that although the killer was still unknown; authorities knew his genealogy back to the 1600s and had even identified a cousin. Fullers living in the area were investigated but the case went cold again.

The 2019 identification of Patrick Nicholas as a suspect using genetic genealogy autosomal SNP testing raised awareness of the limitations of CODIS and fueled debate over the role of familial searching versus genetic genealogy. Nicholas was convicted in 1983 of attempted first-degree rape in Benton County, WA, before CODIS was launched in the 1990s. In 1993, he was arrested again for first-degree child molestation. Although his DNA profile should have been entered into CODIS, he was allowed to plead to gross misdemeanor that did not require DNA collection. He escaped detection a second time. After Nicholas' arrest, it was discovered that his brother Edward had already been entered into CODIS for a prior conviction for rape in the first degree; he was also a registered sex offender. Because Washington does not practice familial searching, Patrick Nicholas had escaped detection a third time.

Upon Nicholas's identification using genetic genealogy, the King County Sheriff's Office quickly secured his DNA from discarded cigarettes. His DNA was found to be a CODIS match to the DNA profile developed from the victim. Nicholas has been charged with first-degree murder with sexual motivation. He is currently pending trial in King County Superior Court, Seattle, WA.

Ironically, Sarah's killer was named Nicholas, not Fuller. His grandfather was adopted, so his legal surname was not his biological surname, highlighting the fact that even genetic genealogy has its loopholes.

Genealogy, CODIS, SNPs

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