Journal of the Academy of Forensic Nursing

Practice Perspectives

The Evolution of DNA and Its' Impact on Sexual Assault Case Prosecution

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Received: March 17, 2025 Accepted: June 30, 2025

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Abstract

The evolution of DNA technology has revolutionized forensic science and the identification of violent offenders. For decades, recidivist offenders terrorized communities across the globe with little chance of ever being identified. The discovery of PCR testing, STR DNA profiling, and the creation of the CODIS system have changed the forensic and law enforcement landscapes, making offender identification across state lines possible. In 2018, FGG burst onto the scene, creating a new tool in the forensic toolbox to help identify unknown DNA profiles and solve cases that would otherwise be unsolved. It has helped to take violent offenders off the street and provided justice to victims and their families across the globe. While there are still limitations to its use and ethical considerations to be considered, the use of FGG continues to be pivotal in the investigation and prosecution of violent offenders.

Keywords: DNA, evidence, prosecution, sexual assault.

The Evolution of DNA and Its Impact on Sexual Assault Case Prosecution

The evolution of DNA technology has made a tremendous impact on the prosecution of violent criminals, particularly sexual assault cases. Prior to the advancement of DNA technology, many sexual assault cases would go unsolved, and many serial rapists would remain on the street to re-offend over and over again, terrorizing cities and small towns across the United States. In recent years, forensic genetic genealogy (FGG) has opened the door to identifying violent offenders and bringing them to justice. Prior to the use of FGG, it was likely they never would have been identified, and the survivors would never have received closure (Glynn, 2022). FGG technology is relatively new, with its first utilization being the identification of the Golden State Killer (Joseph James DeAngelo) in 2018. The regulation of its use by law enforcement and legal officials to preserve the privacy and dignity of those related to a potential violent offender must be considered, while ensuring that this investigative method is a reliable means of accurately identifying offenders.

History of DNA Profiling

Before the discovery of DNA identity testing, the field of forensic science relied on the use of restriction fragment length polymorphism (RFLP) with electrophoresis, ABO blood group typing, and fingerprint analysis to identify and convict offenders (Saad, 2005). In the 1980s, American geneticist Ray White at the University of Utah identified certain regions of DNA that did not code for proteins and were highly variable between individuals (National Institute of Justice, 2023). His discovery led to the use of restriction enzymes to splice strands of DNA at specific locations, producing DNA fragments of defined lengths. These restricted fragments are separated by gel electrophoresis, in which the sample is placed into a well located on one side of a gel block. An electric current is passed through the gel, causing the negatively charged DNA molecules to be pulled to the positively charged end of the gel, which separates the DNA fragments by size.

Sir Alec Jeffreys, a professor and geneticist at the University of Leicester in the United Kingdom (UK), discovered that White's RFLP method could develop patterns of restricted DNA specific to individuals, which could be applied to forensic science. Although his primary focus was on cases of paternity, he was soon approached by British law enforcement to see if he could use the RFLP method to identify the offender responsible for a rape-homicide. His ability to apply the RFLP method to the case resulted in the release of an innocent man and the apprehension and conviction of the responsible party.

By the conclusion of 1986, DNA testing and profiling had been disseminated and were being used to identify offenders globally (Saad, 2005). It was further refined by the creation of the polymerase chain reaction (PCR) testing technique and the discovery of microsatellites, also known as short tandem repeats (STRs). STRs are repetitive segments of DNA found scattered throughout the genome in non-coding regions between or within genes. PCR, discovered by Kary Mullis, made it possible to amplify very minute or degraded samples of genetic material to ascertain a DNA profile (Jordan et al., 2021). Mullis utilized heat to separate DNA molecules into two strands, and the DNA blocks bonded to that strand (Schmerker, 2022). DNA polymerase enzyme is applied, and new DNA strands are created. The process is then repeated, leading to the amplification of genetic material. Initially, PCR was an arduous and tedious process requiring the addition of fresh polymerase enzyme to be applied to each cycle. The discovery of the Taq

polymerase enzyme by researcher Thomas Kunkel, not Thomas Brock, made PCR a more efficient process due to the ability of the Taq enzyme to withstand the high temperatures required to denature DNA during the PCR process. Not long after the discovery of the Taq enzyme, PCR thermal cyclers entered the market, automating the PCR process and making it more efficient and cost-effective. PCR continues to be used in the forensic and medical fields today, with its most recent and notable application being the identification of COVID-19 through viral respiratory panel testing during the global pandemic in 2020. The PCR method remains the gold standard in forensic DNA testing (Schmerker, 2022).

In 1994, the United States passed the DNA Identification Act, expanding the use of the Federal Bureau of Investigation's pilot project on creating a national DNA database, which allowed DNA identification records of persons convicted of crimes to be entered (Office of the Inspector General, 2006). The act also allowed law enforcement to analyze DNA samples found at crime scenes and DNA samples recovered from unidentified remains. Standards were established for labs contributing profiles to the national database. These standards included proficiency testing requirements for lab analysts and privacy and protection standards for the information entered. The Combined DNA Index System (CODIS) is a digital database for storing the genetic profiles of violent offenders and unknown genetic profiles found at crime scenes. This database enables forensic laboratories to compare and exchange DNA profiles electronically at the local, state, and national levels. CODIS utilizes 20 PCR-amplified STR loci and the amelogenin gene, located on the X and Y chromosomes, to compare and obtain genetic matches (Federal Bureau of Investigation, 2017). However, to obtain a CODIS DNA profile match, the offender's profile must be present in the system, resulting in numerous cold cases across the United States and globally. In 2018, an offender identification technique, now known as FGG, was discovered in response to the mounting number of unsolved and cold cases (Tuazon et al., 2024). The use of FGG burst onto the forensic scene with the identification of the long-elusive Golden State Killer. FGG has since been used to solve many more cases that may have remained unsolved without its creation.

Familial DNA Analysis

The process of familial DNA analysis to establish relationships amongst individuals was first established by Sir Alec Jeffreys in 1985 with the discovery of the RFLP method (Saad, 2005). His primary use of RFLP analysis at the time was establishing paternity. Today, paternity can be established via Y-STR typing (Mateen et al., 2021). Y-STR typing utilizes the genetic material on the Y chromosome that is only present in the male genome. Similarly, mitochondrial DNA typing can be used to establish maternal lineage and is helpful for those seeking maternal relatives. Both Y-STR and mitochondrial DNA typing can be valuable tools for investigators. Y-STR typing can be beneficial in cases of sexual assault where a mixed male and female profile is found, allowing the male profile to be separated from the female profile.

Mitochondrial DNA typing can assist investigators in identifying unidentified remains, as mitochondrial genome copies far outnumber those of the nuclear genome. mitochondrial DNA typing is extremely useful in extrapolating a potential profile from significantly degraded samples, often seen in cold cases. Similarly, single nucleotide polymorphism (SNP) genotyping identifies a variant of a single nucleotide at a single genomic position (Mandape et al., 2024). The variant can be traced back generations, and the more SNPs are shared between two individuals, the closer their relation. SNP data differs from STR data in that STR data is concerned with the length of the repeat instead of the single base nucleotide in that strand. Due to the abundance of

SNPs in the genome, it is also advantageous when dealing with degraded DNA samples. SNP data also has a significantly lower mutation rate (1 in 100 million) compared to STR data (1 in 100).

As DNA technology has advanced, the creation of DNA databanks for familial DNA searching (FDS) has become popular. Companies like GEDMatch, 23andMe, and AncestryDNA have become extremely popular among the general public, especially those seeking to discover their extended family or ancestral lineage. These databases contain millions of profiles, with 23andMe holding approximately 3 million individual profiles as of 2018 (Mateen et al., 2021). FDS software conducts FDS searches using a likelihood ratio to compare the provided DNA sample with others in the database and performs lineage testing further to support relatedness (Debus-Sherrill et al., 2019). Unlike the CODIS database, which requires a high stringency (exact match) to produce a result, FDS databases may use middle or low stringency to generate partial matches. Currently, the FBI has banned the use of CODIS at the national level for conducting FDS with the intent of obtaining partial profiles of individuals who may be related to offenders, thereby limiting searches to the state level.

Forensic Genetic Genealogy

Forensic genetic genealogy (FGG) involves a combination of forensic resources, including FDS of the public SNP databases, genealogical tracing, and confirmation of the suspected offender's DNA via traditional STR testing to obtain a match to a long-unknown genetic profile (Tuazon et al., 2024). First, the suspect profile is run through the conventional CODIS STR-based database to determine if it can be matched to a known offender. Once the unknown profile is entered into public SNP databases and FDS is conducted, potential partial matches are identified. When a familial link to the unknown profile has been confirmed, construction of a genealogical lineage can begin to further narrow the pool of suspects. Once investigators are convinced they have identified the suspect, a DNA sample must be collected from the suspect to run an STR analysis, confirming an exact DNA profile match.

Ethical Considerations

With FGG being a relatively new source of perpetrator identification, it is essential to regulate its use by law enforcement and respect individual privacy (Barlow and McCowan, 2024). Until recent years, there has been little regulation on investigator access to genetic genealogy databases, despite terms of service listed on such sites stating that law enforcement may only access the databases if they explicitly notify their customers that their profiles may be accessed for criminal investigative purposes. There have been numerous accounts of law enforcement exploitation of privacy on sites such as GEDMatch and MyHeritage to identify homicide victims and solve cold cases. It is also essential to note that there has been very limited legal analysis of the privacy rights of defendants charged or individuals in the databanks whose DNA is generally searched without their knowledge or consent.

There have been several Fourth Amendment challenges, citing *Carpenter v. United States (2017),* which state that the abandonment doctrine does not apply to SNP DNA. In the case of *Carpenter v. United States (2017),* Timothy Carpenter was convicted of a series of robberies. The FBI linked Carpenter to the scenes via his cell-site location information (CSLI) for 127 days. Carpenter’s attorney moved to suppress the CSLI data, citing the Fourth Amendment and the third-party doctrine. The court ruled that CSLI data should be afforded Fourth Amendment protection, as it requires a search by law enforcement and is involuntarily generated by the

device, rather than being freely made public by its user; therefore, the third-party doctrine would not apply in this case. Unlike CSLI, genetic material voluntarily submitted to third-party DNA databases does not qualify for Fourth Amendment protections. The third-party doctrine would apply because the individual willingly provides their genetic material to public DNA databases.

The security of individuals' genetic information is a significant concern as third-party DNA databases become increasingly popular. In March 2025, the largest direct-to-consumer genetic testing company, 23andMe, filed for Chapter 11 bankruptcy, leaving the public concerned about the vulnerability of their genetic data to cybersecurity threats, ethical violations, and legal loopholes as its assets are liquidated (Merton, 2025). In 2023, a data breach at the company compromised the ancestry details and health predispositions of 7 million customers. As finances become tighter, requiring cost-cutting or data management to be transferred to new owners, security infrastructure may weaken, leaving customers' valuable genetic information vulnerable. If the genetic database is sold during bankruptcy, it could be acquired by an entity with inadequate security infrastructure, thereby increasing the risk of compromise. Unlike credit cards, genetic information cannot be changed once compromised, making it highly desirable information for hackers.

Degradation of informed consent during transfer of ownership could result in customers' genetic data being used for things they did not consent to in their agreements with the parent company (Merton, 2025). This could lead to their genetic data being exploited for insurance underwriting, advertising, or unauthorized medical research. Initially 23andMe was to be acquired by a large pharmaceutical and biotechnology company (Regeneron), but in July 2025 the court allowed for a not-for-profit agency owned by one of the co-founders (TTAM Research Institute) to purchase the company for $305 million (Associated Press, 2025). Understandably sale of the company raises customers' concerns about their genetic data being used for purposes to which they did not consent (Sunny et al., 2025). Not only does the asset liquidation expose the consenting customer, but it also exposes relatives of the customer who did not consent to their DNA being collected. Currently, the United States lacks federal laws governing the use and protection of genetic data. State-level legislation varies, creating inconsistent protection for consumers. The Genetic Information Nondiscrimination Act (GINA) protects customers from discrimination by employers and health insurance companies but does not extend to other industries such as life insurance. Direct-to-consumer genetic testing is also ineligible for Health Insurance Portability and Accountability Act (HIPAA) protection. Bankruptcy court prioritizes the maximization of asset value over consumer privacy, creating a direct conflict between financial objectives and ethical considerations of consumer privacy. The Federal Trade Commission (FTC) may intervene when privacy policies are violated; however, it is often reactive rather than preventative, which limits its impact on regulatory oversight (Merton, 2025).

FGG has quickly entered the forensic arena and has been widely accepted by the forensic science community. However, its reliability and validity need to be established to ensure the accuracy of science (Barlow & McCowan, 2024). Several studies have established that the rate of false positives (matching two DNA profiles as related when they are not) is low, with 23andMe cited as accurate 99% of the time. SNP DNA segments are measured in centimorgans (cM), with a recommended amount of 7 cM for a successful sample set. False positives can occur when this threshold is set too low. It was shown that when samples were run with a sample containing only 2–4 cM to determine a match or relative match, the false positive rate exceeded 67%. This is critically important as the samples received by forensic laboratories are often either small in

quantity or have been degraded. It must be determined that the 7cM threshold can be met to make an accurate individual or relative match.

Professional Practice Recommendations

It is critical that FGG use be supervised, and policies and procedures established to determine when it is appropriate for investigative purposes. The Organization of Scientific Area Committees for Forensic Science (OSAC) Human Forensic Biology Subcommittee publicly announced a proposed standard for familial DNA searching and added OSAC 2021-S-0029 Standard for Familial DNA Searching (2023) to the OSAC registry on January 5, 2023. The proposed standard is currently under review by the Human Forensic Biology Standards Development Organization for further development and publication. The standard aims to provide clinical laboratories with a set of standards for conducting familial DNA testing. OSAC suggests that all laboratories performing familial DNA testing establish a written policy that specifies, but is not limited to, the following: criteria for accepting familial DNA search requests, administrative structure and responsibilities, the search process, reporting results, safeguards for individual privacy and confidentiality, and defined validation requirements. It is the view of these authors that OSAC has established a comprehensive and rigorous standard to ensure the reliability and disclosure of familial DNA testing results, as well as the privacy of potentially related individuals.

The authors made contact with the Office of the Chief Medical Examiner (OCME) of New York City (NYC). They found that it had adopted a standard mirroring the OSAC-recommended standard for the use of FGG within the NYC area. The OCME of NYC serves as the liaison between requesting entities and the FGG labs, facilitating the transfer of samples from agencies requesting FGG testing to the labs in the area that provide FGG testing (NYC Office of the Chief Medical Examiner, 2023). Once a request has been received, the customer liaison and the assistant director of forensic biology will verify case information, pull the case file, verify that the samples requested as indicated on the submission form match to previously tested case samples, determine if there is enough extract to be sampled after previous testing was completed, and notify the NYPD or DNA coordinator how much of an extract may be left for FGG sampling. The release of the requested sample is dependent on the volume and concentration of the remaining sample, and both agencies must agree to sample submission with the understanding that the amount needed for FGG testing could exhaust the remaining sample, rendering future forensic testing unavailable. Only the director of forensic biology can release samples in their entirety without determining the volume. Samples are packaged in packaging provided by the requesting agency and are brought to the OCME on the day of the intended release by the assistant director of forensic biology to the requesting agency. The FGG team documents the extract inquiry, the extract release chain of custody, and the FGG customer tracking form. The assistant director of forensic biology or the customer liaison will follow up with the agency in which the sample was released in 6 months. The DNA coordinator and the commanding officer of the cold case squad should be contacted for any updates on the FGG sample. If leads are generated as a result of the FGG testing, any samples submitted for comparison testing are to be done by the original case analyst or technical reviewer. If neither is available, a random analyst will be assigned by the customer liaison. The authors contacted the Los Angeles medical examiner's office and were informed that they are not currently using FGG. The cities of Chicago, Detroit, Sacramento, and Miami-Dade were not available for comment at this time.

Role of DNA Evidence and Forensic Genetic Genealogy in Sexual Assault Cases

Before the discovery of DNA testing, it was common for serial rapists to go unidentified and continue to victimize communities across the country (Glynn, 2022). Recent studies have shown that the availability of DNA evidence has largely influenced prosecutors to take sexual assault cases forward and seek indictments when a suspect can be identified either through a suspect sample or a CODIS hit (Cross et al., 2022). The study findings, conducted by Cross et al. (2022), strengthened the evidence for the need for high-quality forensic medical examinations, investment in DNA analysis, and enhanced training for prosecutors. The most common reason a case may not go to trial and result in conviction is that victims often do not want to be revictimized, or that the prosecution is unwilling to prosecute the case despite a DNA profile being generated from a SANE kit and matched to a CODIS profile (Davis & Wells, 2019). These findings strongly reinforce the need for continued prosecutor education and the critical necessity for training on how to inform survivors of sexual assault that their case has generated a suspect, so that the survivor is not retraumatized by the idea of taking their case to court. This highlights the need for a sexual assault response team (SART) and the importance of victim advocates who help and guide survivors through the process, from kit collection, suspect identification, court proceedings, and conviction (Cross et al., 2022). Davis and Wells (2019) found in their study that 55 out of a total of 97 cases that yielded a DNA match resulted in an arrest and court filing. In the remaining 42 cases, the district attorney's office determined that there was insufficient evidence to proceed. Of the 55 cases filed, 92% resulted in a conviction by plea (58%) or verdict trial (35%), 6% were dismissed, and only 2% were found not guilty at trial. Those convicted were found to receive lengthy sentences, with 56% sentenced to prison terms of 25 years or longer.

Forensic Genetic Genealogy in the Identification and Prosecution of Serial Rapist

The first and most well-known case solved by FGG is *The People of California v. Joseph James DeAngelo* (the Golden State Killer). DeAngelo is known to have killed 12 victims and raped over 50 others in the state of California between 1974 and 1986 (Wickenheiser, 2019). The emergence of DNA evidence was able to link a large number of his crimes that were thought to be unrelated at the time they were committed due to geographic location and differences in modus operandi. DeAngelo fit the classic recidivism profile with his crimes beginning as burglaries and progressing to rape and homicide as he evaded police capture. Because investigators could not match the unknown offender profile to a known profile in CODIS, DeAngelo was able to evade authorities for over 40 years. A breakthrough in the case finally occurred in 2018 when the unknown offender's profile was uploaded into a commercial genetic databank, GEDMatch, primarily used to help others find genetic relatives by submitting their DNA profile to the SNP DNA databank. Law enforcement identified a potential relative of the unknown profile and, after four months of constructing a family tree, were able to narrow down their search to three potential male suspects. After ruling out the other suspects, they narrowed their search to Joseph James DeAngelo (Wickenheiser, 2019). Discarded samples of DNA were obtained without the suspect's knowledge (car handle swab and used tissue). When DeAngelo's sample was run and compared to the unknown profile, law enforcement finally identified the Golden State Killer. DeAngelo was tried and convicted and ultimately handed down a life sentence without the possibility of parole.

The Golden State Killer case has opened the door for numerous other states to use FGG as a tool to help them generate leads and solve cold rape and homicide cases. Since the case's success in 2018, FGG has been used to solve 431 cases of rape and homicide in the United States

(Dowdeswell, 2022). Sexual assault accounted for 278 out of the total 628 charges filed as a result of offender identification via FGG. Of the identified offenders, 37% were serial sexual offenders and 26% were sexually motivated murderers. Out of 410 live charges, 69% are pending, 23% resulted in a guilty plea, and 8% were convicted by jury trial (Dowdeswell, 2022). Of the 101 accused offenders, 71% are pending a ruling on the admission of the FGG evidence by the U.S. court, 27% have been admitted into evidence, and 2% are on appeal (Dowdeswell, 2022).

Relevance to Forensic Nursing Practice

Forensic nurses, particularly those trained as Sexual Assault Nurse Examiners (SANEs), play a critical role in the accurate collection and preservation of forensic evidence. Sievers et al. (2004) found that evidence collection kits prepared by SANE-trained nurses were more accurate and complete than those collected by non-SANE-trained medical staff. Similarly, Campbell et al. (2006) reported that cases involving evidence collected by SANE nurses were more likely to progress through the criminal justice system, resulting in plea bargains or going to trial more often than those without SANE involvement. Ledray and Simmelink (2020) reinforced these findings, showing that kits collected by SANE nurses were significantly more complete and included better documentation. Importantly, while errors were found in some SANE-collected kits, they were not the type that would jeopardize the integrity of a criminal case. In contrast, 18% of the kits collected by non-SANE personnel were deemed inadmissible in court. However, despite these improvements in quality and documentation, none of these studies found statistically significant differences in the likelihood of obtaining a DNA profile from SANE-collected kits compared to those collected by non-SANE staff. This highlights the need for continued research to determine whether SANE-trained nurses increase the chances of generating usable DNA profiles.

Beyond evidence collection, forensic nurses provide trauma-informed, evidence-based care to survivors of assault. They collaborate closely with community advocates to support and educate survivors throughout the forensic exam and legal process (Campbell, 2006). By addressing survivors' mental, emotional, and social needs, SANE nurses foster trust and comfort, which may increase the likelihood that survivors report their assault and engage with law enforcement. These collaborative efforts among forensic nurses, law enforcement, advocates, and prosecutors help build stronger criminal cases. Additionally, forensic nurses can play an important role in educating survivors about emerging investigative tools such as forensic genetic genealogy (FGG), which may help solve cases that remain unresolved through traditional methods. Through this work, forensic nurses not only preserve critical evidence but also promote the long-term well-being and empowerment of survivors. The use of FGG is increasingly recognized as a valuable tool for solving cold cases and identifying unidentified human remains. Although concerns have been raised regarding the lack of standardized regulation within the scientific community, these issues are now being addressed. OSAC has begun developing procedural recommendations, and laboratories utilizing FGG are starting to adopt these guidelines to ensure the method's efficacy, accuracy, and validity.

Forensic Genetic Genealogy is emerging as a powerful investigative tool in solving cold cases and identifying unknown perpetrators. While its use has primarily focused on homicides and unidentified human remains, there is increasing interest in applying FGG in sexual assault investigations. As front-line providers in evidence collection, SANEs must be aware of the ethical and legal complexities involved in this evolving area of forensic science.

A cornerstone of trauma-informed care is ensuring that survivors maintain autonomy over their bodies and the evidence collected (Poldon et al., 2020). If DNA collected during a forensic exam is to be used for purposes beyond immediate criminal investigation, such as uploading to public genealogy databases, informed consent is ethically essential. Survivors should be clearly informed about potential investigative uses and retain the right to refuse (Mateen et al., 2021). SANEs must navigate these discussions sensitively, ensuring consent is fully voluntary and informed. Genetic data can reveal information about the survivors and their biological relatives. Public databases like GEDmatch and FamilyTreeDNA have begun requiring users to opt in to law enforcement searches, reflecting growing privacy concerns (Barlow & McCowan, 2024). SANEs must understand and communicate these implications, recognizing that the regulatory environment is still evolving. Promising complete confidentiality may be misleading if the sample enters a broader investigative database.

To preserve the legal admissibility of DNA evidence, particularly if used in FGG, SANEs must uphold rigorous standards for documentation and chain of custody. Failure to do so may undermine the integrity of the sample and compromise a potential prosecution (Ledray & Simmelink, 2020). FGG investigations often begin only after traditional forensic approaches fail, making the original evidence collection critical.

FGG may inadvertently reinforce systemic disparities. Communities overrepresented in genetic databases are more likely to be implicated, while underrepresented groups may be excluded from the benefits of such investigative advances (Seaver et al., 2022). Although SANEs are not responsible for investigative decisions, awareness of these concerns supports ethical advocacy for survivors and just application of forensic tools.

The admissibility of evidence derived from FGG remains legally uncertain. Defense attorneys may challenge the scientific validity or privacy implications of the methods used, particularly when law enforcement engages in broad familial searches (*Carpenter v. United States*, *2017*). SANEs play a foundational role in ensuring the evidence withstands legal scrutiny by maintaining best practices during the collection phase.

As FGG becomes more integrated into sexual assault investigations, SANEs must balance the promise of advanced forensic technology with the ethical imperative to protect survivor autonomy and privacy. Their role as medical professionals, advocates, and evidence custodians places them at the intersection of survivor care and forensic innovation. Continued education and interdisciplinary collaboration are vital to ensuring FGG is used ethically, legally, and effectively.

Conclusion

The evolution of DNA technology has fundamentally transformed forensic science and criminal investigations, offering unprecedented tools for identifying violent offenders and delivering justice. From the development of PCR testing and STR DNA profiling to the establishment of the CODIS database, these advancements have allowed law enforcement to track serial offenders across jurisdictions. The introduction of Forensic Genetic Genealogy in 2018 marked another pivotal moment, enabling the identification of unknown DNA profiles in cases that may have otherwise gone cold. While FGG has proven effective in solving violent crimes and bringing long-awaited resolution to victims and their families, it also raises critical ethical and legal considerations, particularly in sensitive investigations like sexual assault.

As central figures in forensic evidence collection and trauma-informed care, forensic nurses must be equipped to navigate the complexities surrounding the use of FGG. Upholding

informed consent, safeguarding survivor privacy, and ensuring data integrity are vital responsibilities that support ethical and survivor-centered practice. Moreover, forensic nurses play a key role in educating and advocating for survivors within an evolving legal and technological landscape. Through multidisciplinary collaboration, adherence to best practices, and an unwavering commitment to ethical principles, forensic nurses are uniquely positioned to guide the responsible integration of FGG into sexual assault investigations, balancing the pursuit of justice with the protection and empowerment of those they serve.

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