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Brief Note on Biological Evidence for DNA Analysis

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Description

Biological evidence with forensic value can be found in a variety of assault instances, with sexually connected assaults being particularly significant. Sexual aggression is a critical social and public health issue that necessitates an immediate Forensic Medical Examination (FME), especially in acute instances, when the interval between the assault and the FME is less than 72 hours in the vast majority of cases. A wide range of forensic disciplines (e.g., clinical forensic medicine, genetics, and toxicology) are involved in these situations, with the goal of obtaining proof and elaboration of a final forensic report.

In terms of forensic intervention, despite certain published protocols and recommendations, few countries have officially implemented evidence management guidelines, particularly in situations of Acute Sexual Assault (ASA). Even when recommendations are adopted, they can differ within a country, between regions, and between institutions. However, precise rules produced by the scientific community are required to standardise the FME of ASA victims and the credibility of forensic methods, both of which are critical during legal proceedings. These principles will help to optimise forensic intervention and decrease unnecessary variances in procedures, as well as improve coordination among various organisations and professions, allowing for a timely and comprehensive forensic examination. The management of biological evidence for DNA analysis tests should be an important aspect of these guidelines.

Biological evidence of forensic interest can be found in a variety of assault situations, with sexual assault instances being particularly significant. Low rates of disclosure, reporting, prosecution, and conviction are common in sexual assault cases. Biological evidence is sometimes the only means to establish that sexual contact occurred and to identify the culprit. This review's main goal is to suggest realistic ways and guidelines for dealing with biological evidence for DNA analysis for health, forensic, and law enforcement experts. Contamination, degradation, and loss of biological evidence should be avoided, and precise steps to properly treat evidence should be followed (i.e., selection, collection, packing, sealing, labelling, storage, preservation, transport, and guarantee of the chain custody). Because the integrity and amount of the samples presented for examination define the relevance of any discovery in Forensic Genetics, biological evidence must be carefully controlled.

In ASA situations, collecting biological evidence for DNA studies is especially helpful in establishing the occurrence of sexual contact and moving forward with suspect identification. In fact, the presence of semen on a prepubertal child's body, clothes, or surroundings during the FME frequently validates the sexual contact diagnosis and is generally recognised as proof in a court of law. However, because a secondary transfer of sperm cells from adult clothing/bedsheets to babies' or children's clothing during laundry was previously proven, this interpretation should not be regarded as irrefutable proof, especially for incest or intra-family situations. Furthermore, despite the fact that there was no sexual abuse, a complete genetic profile of the father can be obtained [1-5].

Conclusion

The strategy that has just been provided is essentially instructional in nature. The approach is given in a provocative and, the authors feel, explanatory manner, allowing non-mathematicians to employ the method in a more general context. The authors do not imply that the chances of successfully completing a DNA genome are high; rather, they present a tool that can be used to accomplish so and with which they would want to educate the reader. The authors are well aware that current efforts in the field of DNA genome completion focus on deep learning rather than higher-order Markov chains. His work presents an alternate tool that may be articulated in a way that is both suggestive and comprehensive. It is now obvious that deep learning methods produce more precise results than Markov chains approaches. Nonetheless, our method enables comprehension of what occurs behind the scenes of effective completion and sequencing. As a result, it should be seen as having explanatory and instructive value, as well as the possibility for future research. It's worth considering whether the techniques in Example 2 could be used to quickly create test data for more advanced deep learning algorithms.

Conflict of Interest

None.

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