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Proteomics: A Prospective New Tool in Forensic Investigations

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ABSTRACT: Over the last few decades, DNA evidence has become a very powerful tool in forensics, but it also has its limitations. DNA, being a very fragile molecule, can be easily damaged and contaminated. It can be very challenging to find enough DNA in an investigation to really make a breakthrough in certain types of evidence samples. For instance, about half of all rape kits do not yield sufficient genetic information to determine the perpetrator's DNA profile. This is where proteomics, the modern concept of protein analysis, steps in. By observing the amino acid sequence of protein fragments, researchers can work backward to conclude the DNA sequence used to make proteins. Proteomics methods can be used to classify and explain the circumstances that produced the biological samples. This article provides a conceptual overview on the different proteomics applications in forensics, including human identification using hair samples and fingermarks, species determination utilizing teeth and bones, and the determination of postmortem intervals.

KEYWORDS: Anthropology, crime, DNA, identification, proteomics.

INTRODUCTION

DNA Fingerprinting Technologies

Since its introduction to the courts in the mid-1980s, DNA evidence has transformed forensic science, cracking open decades-old unsolved cases, often resulting in both prosecutions and acquittals [11]. Colin Pitchfork, a convicted British assassin and rapist, may not be quite as well-known as Jeffrey Dahmer or Charles Manson, but his name holds weight for those in forensic science practice and research. Pitchfork was the first assassin ever to be convicted based on DNA fingerprinting evidence [3]. The same methods help archaeologists and anthropologists unravel the mysteries of the past, such as migration patterns and the spread of culture through time from hundreds to several thousands of years ago [42].

Over the last decade, ancient DNA (aDNA) technology has emerged as a breakthrough born of a revolution in molecular biology that started with the use of the polymerase chain reaction (PCR) technique [14]. The benefit through aDNA studies has opened a direct window into human prehistory, such as the admixture history of early modern humans, such as Denisova hominins and Neanderthals, as well as demographic patterns, human migrations, evolution, and phylogeny of prehistoric hominids. These new techniques were rapidly adopted by anthropologists to obtain previously inaccessible data; these data are now available to apply towards the conventional space of anthropological research questions [34]. However, preservation of skeletal DNA is an unusual phenomenon, rendering the accomplishments of this emerging area relatively insignificant. In comparison, cells and tissue possess a significant abundance of proteins that, under similar preservation conditions, are characterized by at least a threefold longer preservation time than DNA [30]. That is where proteomics, the modern concept of protein analysis, comes in. By observing the amino acid sequence of protein fragments, researchers will work backward to identify the DNA sequence used to make proteins.

Proteomics

Proteomics is the wide-scale examination of the entire set of an organism's protein through a particular, defined set of requirements. In 1994, Marc Wilkins first used the term proteomics as an alternative to "protein complement of a genome" [41]. Proteomics-based technologies can also be used on degraded old samples and to store DNA analysis results [40]. Forensic proteomics can fill in when DNA is missing, ambiguous, or was never present to begin with.

Protein, being chemically more stable and abundant, can persist for longer periods than DNA, and the technology for protein detection has also improved [2,25,30,39]. Proteins consist of hundreds or even thousands of smaller groups, called amino acids, linked by amide bonds, forming a long polypeptide chain [7]. DNA encodes 20 types of naturally existing amino acids. A specific amino acid is referred to a chain formed by three DNA nucleotides (CODON); thus, interpretation of a DNA sequence provides corresponding protein, a chain of amino acids. Often, gene and protein data banks are used against diverse amino acid chains obtained for interpretation of DNA sequence. Archeological or criminal investigations are mostly dependent on evidence obtained at the site in various forms, such as hair, bones/teeth, and fingermarks. Protein-based investigation of these evidence can be necessary, and even more fruitful, in some cases.

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Sachil Kumar received his B.Sc. (Hons.) in chemistry from the University of Delhi (Delhi, India), an M.Sc. in forensic science from the Dr. Bhimrao Ambedkar University (Agra, India), and a Ph.D. in forensic chemistry from the King George's Medical University (Lucknow, India). Dr. Kumar qualified the UGC National Eligibility Test – Lectureship (NET-LS) as well as the UGC National Eligibility Test-Junior Research Fellowship (NET-JRF) in forensic science. From 2015 to 2016, he served as a guest lecturer at the Department of Biotechnology at Babasaheb Bhimrao Ambedkar University in Lucknow, India, where he taught many classes in forensic science to master's-level students. He is currently an assistant professor in the Department of Forensic Sciences, College of Criminal Justice, Naif Arab University for Security Sciences, Riyadh, Saudi Arabia.

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