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# The Future Of PMI Estimation: Omics Science And its Potential For Forensic Investigations

**Gayathry Sekhar[1], Ashi Yadav[2]**

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## *Abstract:*

*Estimating post mortem interval (PMI) is a crucial aspect of forensic investigations involving skeletal remains. Traditional methods of estimating PMI rely on factors such as weather conditions, insect activity, and decomposition rates, which are often subjective and imprecise. In recent years, the application of omic science, which involves the study of large-scale biological data sets such as proteomics, metabolomics, lipidomics, has emerged as a promising approach for estimating PMI. This review paper discusses the current state of omic science in estimating PMI from skeletal remains and also explore the different types of omic data that can be analyzed for this purpose, including transcriptomics, proteomics, metabolomics, and microbiomics. We also highlight the advantages and limitations of each type of omic data.*

***Keywords:*** *Postmortem interval, Skeletal remains, Omic sciences, Proteomics, Genomics, Metabolomics.*

## *Authors:*

1. *B.Sc, Forensic Science, Kalasalingam Academy of Research and Education, INDIA.*
2. *Scientific Officer, Sherlock Institute of Forensic Science, New Delhi, India*

## Introduction

Post mortem interval is the time that has elapsed since an individual's death, and it is a crucial parameter in forensic investigations. When estimating the PMI, a forensic anthropologist or pathologist can use qualitative categories that describe the soft tissue decay in the early stages of relying on his understanding of the local environment and decomposition. The traditional methods of PMI estimation, such as the use of insect activity and body temperature, have limitations when it comes to skeletal remains. The decomposition process in skeletal remains is slow, and the traditional methods may not be accurate in estimating PMI, especially in cases where the remains have been exposed to the elements for an extended period. Omic sciences is an interdisciplinary field that combines biology, genetics, and informatics to study the complex interactions between genes, proteins, and other molecules within an organism. Omic sciences has been widely used in biomedical research to understand the genetic basis of diseases and develop personalized medicine. However, its application in forensic science is relatively new, and it has shown great potential in PMI estimation.

Omic sciences uses several methods for PMI estimation, such as transcriptomics, proteomics, and metabolomics. Transcriptomics is the study of changes in gene expression after an individual's death. Proteomics is the study of changes in protein degradation after an individual's death **(Procopio *et al.*, 2017).** Metabolomics is the study of changes in metabolite levels after an individual's death.

Transcriptomics involves the analysis of RNA molecules to identify changes in gene expression patterns. The changes in gene expression can be used as molecular markers for PMI estimation. Proteomics involves the analysis of protein degradation patterns to identify changes in protein levels. The changes in protein levels can be used as molecular markers for PMI estimation. Metabolomics involves the analysis of metabolite levels to identify changes in metabolic pathways. The changes in metabolic pathways can be used as molecular markers for PMI estimation.

Lipidomics tests have only been utilized in three studies so far to estimate PMI. Two of them, performed on muscle tissue, revealed an increase in free fatty acids and a general negative connection between PMI and the majority of lipid classes **(Langley *et al.*, 2019; Wood and Shirley, 2013)**. The third study used lipidomics to examine trabecular bone samples from calcanei with an average PMI of about 7 years. It found 76 potential N-acyl AAs that could be used to estimate PMI, though their correlation with PMI has not yet been fully explained

In both animal and human investigations, it has been attempted to measure the extent of protein survival and the accumulation of post-translational modifications (PTMs) in bones as well as under various circumstances (for example, in aquatic environments, with various types of coffins, buried vs. surface). The underlying idea behind these investigations is that the protective effect of hydroxyapatite is anticipated to increase protein survival, thereby enabling estimate of longer PMIs. **(Procopio *et al.*, 2017; Mickleburgh *et al.*, 2021; Prieto-Bonete *et al.*, 2019; Procopio *et al.*, 2021; Bonicelli *et al.*, 2022)**

## Review of Literature

### Forensic Approach Of Omic Sciences

- **Genomic Approach**

The entire DNA sequence found in a cell or organism is known as its genome. The mitochondria and other organelles, such as the cell nucleus, may both contain this genetic material. The genome of an organism doesn't change much throughout time, aside from mutations and chromosomal rearrangements. Various experimental platforms, such as single nucleotide polymorphism (SNP) chips and DNA sequencing technology, can be used to test the completeness or partialness of a DNA sequence. Even though these studies are solely focused on typing Sequence-Tagged Sites and Short Tandem Repeats (STRs) to obtain a match between DNA profiles (DNA profiling), research demonstrates an increasing interest in petrous bones as a strategic region to recover genome. Standard reverse phase chromatography can be used for the chromatographic separation of lipids. **(Micheel, Christine M *et al.*, 2012)**

- **Proteomic Approach**

The study of proteomics is relevant to bones since they are made up of 30% of organic proteins (mostly collagenous proteins) and 70% of the inorganic phase, hydroxyapatite crystals. Proteins are essential for bone production and remodeling, and hydroxyapatite crystals stop proteins from deteriorating. As a result of the proteins being filtered out of the burial environment, the interactions between molecules present in the bones are hampered. Proteins may get damaged as a result of the unstable process caused by the hydrolysis of peptide bonds, which leaves only small quantities of collagen. Deamidation alterations might offer further details for computing decay's dependence on time. External factors may affect the

pace of this non-enzymatic hydrolysis, which affects glutamine and asparagine amino acid residues and may indicate the age of the bones. The rate of protein degradation may enable accurate time estimations during post-mortem due to these biomolecule interactions in bone tissues.
**( www.azolifesciences.com)**

- **Metabolomic Approach**

The total amount of metabolites found in an organism is known as its metabolome. The in-depth analysis of the metabolome is called metabolomics, often known as metabolic profiling. It typically includes but is not limited to, the study of the body's 1500 Dalton-sized tiny metabolites. The molecules acquired via exposure to the environment and taking drugs are also included in metabolomic analyses. Forensic scientists are particularly interested in metabolic approaches when it comes to toxicological analysis and now in the field of forensic anthropology to estimate time since death. These metabolomes concentrations in bone, blood or other samples can be determined using a variety of techniques. Hydrophilic liquid interaction chromatography can be used for the chromatographic separation for metabolites. **(Bonicelli *et al*., 2022**)

- **Microbiomic Approach**

To improve the accuracy of PMI prediction, researchers have begun to study the anatomical microbiome.After death, these communities especially thanatomicrobiome burden the immune system and enable subsequent colonization.Previous studies suggest that there may be significant successional changes in these inter-organic microbial communities that may help define PMI. Previous studies in animal models suggest that during a 48-day degradation period, it is possible to discover a “microbial clock” to estimate PMI by sequencing the 16S rRNA gene for bacterial and archaeal communities and the 18S rRNA gene for microeukaryotes**.( Metcalf et al., 2013)**

**Conclusion and Discussion**

Several studies have shown promising results in the application of omic science to estimate PMI. For example, a study analyzing RNA from skeletal remains found that gene expression patterns could be used to estimate PMI with an accuracy of up to 87%. Another study analyzing protein degradation patterns found that the ratio of different protein fragments could be used to estimate PMI with an accuracy of up to 93%. Metabolomics studies have also shown promising results, with some studies identifying specific metabolites that are correlated with PMI.

Microbiomics studies have identified changes in the microbial communities present in skeletal remains over time, which can also be used to estimate PMI, However, there are also several challenges associated with the use of omic science in estimating PMI. These include the limited availability of high-quality biological samples, the complex and dynamic nature of the biological processes involved in decomposition, and the need for robust analytical methods and bioinformatic tools for data analysis.

In conclusion, the application of omic science to estimate PMI from skeletal remains is a promising approach that has the potential to revolutionize the field of forensic science. While there are still several challenges that need to be addressed, the continued development and refinement of omic methods and analytical tools are likely to lead to significant advancements in this area in the coming years. There are few examples of studies that have applied various analytical platforms for proteomics, metabolomics, and lipidomics to various different matrices. However, relatively little is known about the biomolecular decomposition of bone tissue. Furthermore, although multi-omics techniques have been used in clinical investigations sometimes, their potential for the creation of more exact and reliable biomolecular PMI assessment techniques has not been investigated since. The findings generally demonstrated that proteins more strongly connected to the mineral matrix, such as bone-specific proteins, are able to survive for longer PMIs and can also serve as useful indicators for PMI estimation.

## *References:*

Bonicelli, Andrea, et al. “The ‘ForensOMICS’ Approach for Postmortem Interval Estimation From Human Bone by Integrating Metabolomics, Lipidomics, and Proteomics.” *eLife*, vol. 11, eLife Sciences Publications Ltd, Dec. 2022, https://doi.org/10.7554/elife.83658.

Langley, Natalie R., et al. "Forensic postmortem interval estimation from skeletal muscle tissue: a lipidomics approach." *Forensic Anthropology* 2.3 (2019): 152-157.

Mickleburgh, Hayley L., et al. “Human Bone Proteomes Before and After Decomposition: Investigating the Effects of Biological Variation and Taphonomic Alteration on Bone Protein Profiles and the Implications for Forensic Proteomics.” *Journal of Proteome Research*, vol. 20, no. 5, American Chemical Society, Mar. 2021, pp. 2533–46. https://doi.org/10.1021/acs.jproteome.0c00992.

Prieto-Bonete, Gemma, et al. “Association Between Protein Profile and Postmortem Interval in Human Bone Remains.” *Journal of Proteomics*, vol. 192, Elsevier BV, Feb. 2019, pp. 54–63. https://doi.org/10.1016/j.jprot.2018.08.008.

Procopio, Noemi, Anna Williams, et al. “Forensic Proteomics for the Evaluation of the Post-mortem Decay in Bones.” *Journal of Proteomics*, vol. 177, Elsevier BV, Apr. 2018, pp. 21–30. https://doi.org/10.1016/j.jprot.2018.01.016.

Procopio, Noemi, Caley A. Mein, et al. “Bone Diagenesis in Short Timescales: Insights From an Exploratory Proteomic Analysis.” *Biology*, vol. 10, no. 6, MDPI, May 2021, p. 460. https://doi.org/10.3390/biology10060460.

Procopio, Noemi, et al. “Intra- and Interskeletal Proteome Variations in Fresh and Buried Bones.” *Journal of Proteome Research*, vol. 16, no. 5, American Chemical Society, Apr. 2017, pp. 2016–29. https://doi.org/10.1021/acs.jproteome.6b01070.

Wood, Paul L. “Lipidomics Analysis of Postmortem Interval: Preliminary Evaluation of Human Skeletal Muscle.” *Journal of Postgenomics*, vol. 03, no. 03, OMICS Publishing Group, Jan. 2012, https://doi.org/10.4172/2153-0769.1000127.