

Epigenetic and Archeology: A Quest to Re-Read Humanity

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Abstract : Epigenetic, or alteration in gene expression influenced by extragenetic factors, has emerged as one of the most promising areas that will address some of the gaps in our current knowledge in understanding patterns of human variation. In the last decade, the research investigating epigenetic mechanisms in many fields has flourished and witnessed significant progress. It paved the way for a new era of integrated research especially between anthropology/archeology and life sciences. Skeletal remains are considered the most significant source of information for studying human variations across history, and by utilizing these valuable remains, we can interpret the past events, cultures and populations. In addition to archeological, historical and anthropological importance, studying bones has great implications in other fields such as medicine and science. Bones also can hold within them the secrets of the future as they can act as predictive tools for health, society characteristics and dietary requirements. Bones in their basic forms are composed of cells (osteocytes) that are affected by both genetic and environmental factors, which can only explain a small part of their variability. The primary objective of this project is to examine the epigenetic landscape/signature within bones of archeological remains as a novel marker that could reveal new ways to conceptualize chronological events, gender differences, social status and ecological variations. We attempted here to address discrepancies in common variants such as methylome as well as novel epigenetic regulators such as chromatin remodelers, which to our best knowledge have not yet been investigated by anthropologists/ paleoepigenetists using plethora of techniques (biological, computational, and statistical). Moreover, extracting epigenetic information from bones will highlight the importance of osseous material as a vector to study human beings in several contexts (social, cultural and environmental), and strengthen their essential role as model systems that can be used to investigate and construct various cultural, political and economic events. We also address all steps required to plan and conduct an epigenetic analysis from bone materials (modern and ancient) as well as discussing the key challenges facing researchers aiming to investigate this field. In conclusion, this project will serve as a primer for bioarcheologists/anthropologists and human biologists interested in incorporating epigenetic data into their research programs. Understanding the roles of epigenetic mechanisms in bone structure and function will be very helpful for a better comprehension of their biology and highlighting their essentiality as interdisciplinary vectors and a key material in archeological research.

Keywords : epigenetics, archeology, bones, chromatin, methylome

Conference Title : ICA 2020 : International Conference on Archaeology

Conference Location : Dublin, Ireland

Conference Dates : December 21-22, 2020