**TDC, 2nd Year, 4th Sem, Paper-4016**

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**HUMAN-ENVIRONMENT RELATIONSHIP - - ADAPTATION IN DIFFERENT BIOMES**

Modern humans inhabit most of earth’s harshest environments and display a wide array of lifestyles. Biological adaptations, in addition to technological innovations, have enabled these geographical and cultural explorations. The study of these adaptations helps not only to fundamentally understand our evolution as a species, but also may have increasing relevance as genomics transforms fields such as personalized medicine. Here we review three cultural and environmental shifts that have brought about adaptations in modern humans; the arctic, high altitudes, and a subsistence dependent on breath-hold diving.

There has been an undercurrent of intellectual tension between geneticists studying human population history and archaeologists for almost 40 years. The rapid development of palegenomics, with geneticists working on the very material discovered by archaeologists, appears to have recently heightened this tension. The relationship between these two fields thus far has largely been of a multidisciplinary nature, with archaeologists providing the raw materials for sequencing, as well as a scaffold of hypotheses based on interpretation of archaeological cultures from which the geneticists can ground their inferences from the genomic data. Much of this work has taken place in the context of western Eurasia, which is acting as testing ground for the interaction between the disciplines. Perhaps the major finding has not been any particular historical episode, but rather the apparent pervasiveness of migration events, some apparently of substantial scale, over the past ∼5000 years, challenging the prevailing view of archaeology that largely dismissed migration as a driving force of cultural change in the 1960s. However, while the genetic evidence for `migration’ is generally statistically sound, the description of these events as structured behaviours is lacking, which, coupled with often over simplistic archaeological definitions, prevents the use of this information by archaeologists for studying the social processes they are interested in. In order to integrate paleogenomics and archaeology in a truly interdisciplinary manner, it will be necessary to focus less on grand narratives over space and time, and instead integrate genomic data with other form of archaeological information at the level of individual communities to understand the internal social dynamics, which can then be connected amongst communities to model migration at a regional level. A smattering of recent studies have begun to follow this approach, resulting in inferences that are not only helping ask questions that are currently relevant to archaeologists, but also potentially opening up new avenues of research.

Central Africa, a forested region that supports an exceptionally high biodiversity, hosts the world’s largest group of hunter-gatherers, who live in close proximity with groups that have adopted agriculture over the past 5000 years. Our understanding of the prehistory of these populations has been dramatically hampered by the almost total absence of fossil remains in this region, a limitation that has recently been circumvented by population genomics approaches. Different studies have estimated that ancestors of rainforest hunter-gatherers and Bantu-speaking farmers separated more than 60 000 years ago, supporting the occurrence of ancient population structure in Africa since the Late Pleistocene. Conversely, the Holocene in central Africa was characterized by large-scale population migrations associated with the emergence of agriculture, and increased genetic interactions between autochthonous rainforest hunter-gatherers and expanding Bantu-speaking farmers. Genomic scans have detected numerous candidate loci for positive selection in these populations, including convergent adaptation for short stature in groups of rainforest hunter-gatherers and local adaptation to endemic malaria in western and central Africans. Furthermore, there is recent increasing evidence that adaptive variation has been acquired by various African populations through admixture, suggesting a previously unappreciated role of intra-species gene flow in local adaptation. Ancient and modern DNA studies will greatly broaden, and probably challenge, our view on the past history of central Africa, where introgressions from yet uncharacterized archaic hominines and long-term adaptation to distinct ecological niches are suspected.

Hispanic/Latino (H/L) populations, although linked by culture and aspects of shared history, reflect the complexity of history and migration influencing the Americas. The original settlement by indigenous Americans, followed by postcolonial admixture from multiple continents, has yielded localized genetic patterns. In addition, numerous H/L populations appear to have signatures of pre-colonization and post-colonization bottlenecks, indicating that tens of millions of H/Ls may harbor signatures of founder effects today. Based on both population and medical genetic findings we highlight the extreme differentiation across the Americas, providing evidence for why H/Ls should not be considered a single population in modern human genetics. We highlight the need for additional sampling of understudied H/L groups, and ramifications of these findings for genomic medicine in one-tenth of the world’s population.

Both, the social and physical environment shape health, reproduction, and survival across many species, and identifying how these effects manifest at the molecular level has long been a priority in medicine and evolutionary biology. The recent rise of functional genomics has enabled researchers to gain new insights into how environmental inputs shape variation in gene regulation, and consequently, downstream organism-level traits. Here, we discuss recent work on this topic, as well as key knowledge gaps. Research in this area spans a wide range of taxa, but we focus our review on mammalian species because of their close evolutionary proximity to humans and because of their relevance for understanding human health. Improving our understanding of how the environment and the genome are connected promises to shed new light on the mechanisms underlying environmentally-induced disease in humans, as well as the evolution of environmental sensitivity more generally.