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WORLD ANTHROPOLOGY CONGRESS-2023

BHUBANESWAR, INDIA | 9-14 AUGUST 2023

THEME: HUMAN GENETICS, MOLECULAR AND FORENSIC ANTHROPOLOGY
SUB-DOMAIN: HUMAN AND POPULATION GENETICS

PANEL TITLE:
HUMAN GENETICS, DIVERSITY AND PUBLIC HEALTH: FROM BASIC MECHANISMS TO APPLICATION

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ABSTRACT

Homo sapiens sapiens migrated across and moved out of Africa almost 100,000 years ago and occupied almost every habitat around the globe. Over this period, they have diversified across different continents and adapted to their environment. Our ancestors acquired morphological, metabolic, and cognitive changes that enabled them to survive in these diverse habitats and reshape the biosphere. The present genetic architecture of each population reflects upon their origin, migration, and uniqueness in terms of the phenotypic differences. During the past few decades, considerable progress has been achieved in the knowledge of the human genome and the characterization of its natural variability. The Human Genome Project (HGP) opened an arena for the understanding of the specific genetic changes, with implications in biology and medicine. The major impact of HGP, first includes an evolutionary understanding of humans in the timeline. Second, understanding of complex biological system in humans, their connection and function – 'systems biology'. Third, it led to the emergence of proteomics, a discipline focused on identifying and quantifying the proteins present in discrete biological compartments, such as a cellular organelle, an organ, or the blood. Fourth, HGP drove the development of sophisticated computational and mathematical approaches to data and initiated a cross-disciplinary approach in understating of human variations and their implications in medicine.

Over time, our understanding of human genome has led to greater applications in the benefit of the 'human race'. However, the complexities are contextualized with respect to different populations and their respective environments. For example, when the search for genetic predisposition to cardiovascular diseases (CVD) started two decades ago, it was anticipated that genetic polymorphisms might be analogous to the already known CVD risk factors and could be incorporated in a risk model to assess the risks to an individual and adopt preventive or therapeutic measures accordingly. However, despite years of intensive research, not a single genetic risk factor is used for risk assessment. Genome wide association studies (GWAS) provide understanding of the novel genetic factors that contribute to disease risk. However, the greater clinical utility of these novel variants or the candidate genes is yet to be established. With the passage of time, the interest for genetic research moves from the direct expectation of risk stratification to more fundamental understanding of disease origins, pathophysiology, indirect diagnostic, and therapeutic implications.

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Although the use of genetic risk scores further improves disease prediction, the significance is not unambiguous, and some individuals at risk remain undetected. From population level to individual level, our understanding of human genetic variations has come a long way. For example, the understanding of causal or novel mutations in different types of cardiomyopathies has helped the clinicians to manage the patients in a better way. Given that recognized and unrecognized genetic variation, environmental factors, and wide heterogeneity in the pathophysiology of heart failure may affect the response to therapeutic interventions. Advances in precision medicine are likely to have a major impact on treatment and outcomes. In view of growing complexities of the diseases, this panel will enhance our understanding of the genetic variations in different populations, contextualized in their environment and their implications in management of patients. Comprehensive understanding, convergence and application of different 'omics' for precision medicine may also reflect upon prevention, diagnosis, and therapy of these diseases.

LIST OF PANELLISTS:

- Prof. Martin Cowie - National Heart and Lung Institute, Imperial College London, London, UK (m.cowie@imperial.ac.uk)
- Prof Perry Elliott - Institute of Cardiovascular Science, University College London, London, UK (perry.elliott@ucl.ac.uk)
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