Human Variation: Findings from the Singapore GUSTO Study on Prenatal & Infant Population

Biography

Dr. Neerja Karnani is Senior Principal Investigator and Systems Biology and Biomarker Discovery Lead at Singapore Institute for Clinical Sciences (SICS), A*STAR, Singapore. After her postdoctoral work at University of Virginia, USA, in association with the ENCODE consortium (NHGRI) involving the understanding of the epigenetic landscape and instability in human genome, she moved SICS, A*STAR in 2013 to start her own lab, where she focused on identifying diagnostic markers and interventions related to women and child health adversities. She is using multi-omics approaches (genetics, epigenetics, transcriptomics, metagenomics and lipidomics) and integrating big data to develop better molecular insights into metabolic diseases, micronutrient deficiencies, and mental health adversities. Aside from her current position, Dr. Karnani is an Executive Committee Member for two Singaporean cohorts, GUSTO (pregnancy and child development) and S-PRESTO (pre-conception). She is also a part of the science management group for EpiGen consortium, a collaboration between 3 countries (Singapore, New Zealand and United Kingdom) to study developmental origins of health and disease. Her group's research findings have attracted major nutrition, pharma and diagnostic industries and fostered translational programs. Dr. Karnani is also a key Member and Contributor of Singapore's National Precision Medicine program that aims at studying human genetic variation for population stratified risk prediction of health adversities.

Abstract

It is becoming apparent that susceptibility to health adversities goes beyond the variation in DNA sequence and entails complex interactions between the human genome and environment, among which nutrition plays a significant role. By taking an example of the Singapore's most deeply phenotyped mother-offspring cohort, I will share the findings from our multi-omics roadmap (genome, epigenome, microbiome, lipidome, and envirome) and discuss (1) how this roadmap has helped comprehensively map human variability in Asians in both pediatric and adult populations, (2) how this variability is linked with non-communicable diseases that are currently plaguing the global health and economy, (3) and how we can use these observations for developing precision healthcare for future generations.

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