CSIR-CCMB

DIVERSE
EPIGENETIC
EPIDEMIOLOGY
PARTNERSHIP

Groundbreaking Integrated Genomics and Epigenomics project will improve global diversity in population health insight

An international collaboration "***D***iverse ***E***pigenetic ***E***pidemiology ***P***artnership (DEEP) is aiming to improve global health by uncovering the effects of genomic and environmental diversity ondifferences in disease risk observed across the global population, thanks to a new partnership of 20 research groups 20 partners from institutions worldwide providing knowledge and data on >13000 participants from 4 continents including India.

The groundbreaking five-year project, sanctioned a whooping fund of ~ 2.5 million GBP (Rs 25.0 crores) recently by Medical Research Council, UK will explore key population health questions using datasets from across Asian,African, and North and South American continents. The study is led by researchers the CSIR-Centre for Cellular and Molecular Biology in India, University of Bristol, UK, the MRC Unit, The Gambia at London School of Hygiene & Tropical Medicine, London.

Summary

Non-communicable diseases (NCDs) like diabetes, cardiovascular disorders, mental disorders are on rise throughout the world, especially in India and other South Asian countries. There is huge variation in disease onset and symptoms for people living in different global regions.Much of the populationhealth research conducted to date has drawn heavily on data collected from people of white European origins. This means that many global communities are often under-represented in health studies and the important effects of genetic and environmental diversity on health within those communities can be missed, which is especially true for Indians (South Asians) and Africans.

CSIR-CCMB's studies have provided persistent evidence of different genetic structure of Indians and its implications for common diseases like type 1 and 2 diabetes, chronic pancreatitis, etc. Further, they have also shown a role of environment, especially micronutrients like vitamin B12, folates, etc. in modifying the disease risk through epigenetic regulation, a new paradigm in understanding disease risk and management. DNA methylation (DNAm), a type of epigenetic modification, helps the body to respond to environmental signals and ultimately contributes to whole system health and disease status. Interindividual DNAm variation is influenced by both genetic and environmental factors. Understanding the relationships between DNAm, genetics and environment is essential for both understanding pathways of health and disease and disease consequences.

Dr Giriraj R Chandak, Sir J C Bose Fellow at the CSIR-CCMB, and the Co-PI of the study has been working for last two decades using multiple cohorts to understand how genetic basis for NCDs in Indians is responsible for clinical peculiarities and how the risk can be modulated by targeted approaches

including nutrition such micronutrients. Dr Chandak, explained: “This collaborative study involving scientists with varied expertise provides a unique opportunity to understand gene-gene and gene-environment interaction and their role in intermediate traits associated with non-communicable diseases or the disease itself. He also said “Since Prior research is heavily biased towards relatively homogeneous European populations, I am very excited at the inclusion of Indian cohorts, (representing a sixth of the world population) with longitudinal data on subjects making it possible to draw causal inferences, in association with the trans-ancestry cohorts”.

Dr Josine Min and Dr Hannah Elliott, Research Fellows at MRC Integrated Epidemiology Unit, University of Bristol, UK and joint project lead, said: ”Current DNA databases are mainly European. Genetic databases for genomic research need diversity to help all people and to get a better understanding of which factors are causing differences in gene regulation and therefore differences in disease risk.It is really important to work with partners who understand health in their respective cohorts and who are able to effectively share results back with the local communities who have donated their DNA.”

The DEEP studyresearchers aim to bridge this gap by studying individuals representing diverse genetic and environmental contexts and learn which DNA methylation patterns contribute to their disease risk in each context. This research will enable identification ofdisease-causing mechanisms that are common worldwide and those which are unique to particular groups or regions. It will help with answering questions such as whether medicines developed in one part of the world will be effective for all. Ultimately the DEEP study hopes to enable targeted interventions or treatments and reduce global health disparity and inequity.

For further information or to arrange an interview with Dr Giriraj R Chandak, contact, Mr B V Ramakrishna, bvrk@ccmb.res.in; mobile:9866632254

Issued by the CSIR-CCMB Media Team