PLENARY 6 (PL6): Genomic medicine in NCDs: findings from Asians/ South Asians to global collaboration

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SUMMARY

Recently, non-communicable diseases (NCDs), in particular, lifestyle-related diseases have become a key issue of public health in the developing countries. A new understanding of NCDs has emerged from genome-wide association (GWA) studies over the past decade. Despite the paucity of clear physiological evidence on the target phenotypic traits, the GWA findings were expected to provide clues to the precise biological mechanisms. However, human biology is so complex that proving their validity and translating the findings in GWA studies into clinical application require a lot more information (e.g., fine mapping and functional analysis of causative genes) than initially assumed. Along this line, highly sophisticated bioinformatics tools have become indispensable for medical geneticists to analyse the high-throughput experiment data. Thus, in-depth examination and integration of individual molecules are also required to give an overall picture of NCDs, by forming a multi-centre, trans-ethnic (or global) collaboration.

The importance of racial or ethnic differences will be discussed in this presentation. At present, a major part of genetic loci associated with cardiovascular phenotypes, which could have been reported in 'trans-ethnic' meta-analyses of GWA studies, appear to be common across 3 ethnic groups—Europeans, east Asians, and south Asians. We believe that such 'trans-ethnic' meta-analysis will be useful not only for revealing more novel susceptibility loci and pathophysiological pathways but also for facilitating the fine mapping of common causal variants and eventually identifying the factors underlying ethnic differences in the prevalence and phenotypic presentation of NCDs when it is performed by the genetic epidemiology study. Sri Lankans are substantially contributing to the global collaboration in this evolving field, together with east Asians.

Session chair: Prof Rajitha Wickremasinghe