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Cancer control by integrating epigenomics and genomics: Are we ready for the prime time?

After completion of the human genome, genome-wide association studies (GWAS) were conducted to identify single nucleotide polymorphism (SNPs) associated with cancer initiation and progression. Most of the studies resulted in SNPs located outside the coding region and the odds ratios were too low to implement in clinical practice. While genome gives information about genome sequence and structure, human epigenome provides functional aspects of the genome. Epigenome-Wide Association Studies (EWAS) provide an opportunity to identify genome wide epigenetic variants which are associated with cancer. Epigenetics defines mechanisms that involve mitotically heritable changes in DNA and chromatin that affect gene expression without altering the nucleotide sequence. Therefore, the functional importance of epigenetic changes lies in their ability to regulate gene expression. One of the current challenges is to understand the regulation of gene function, an activity that depends largely on epigenetic control. Four major steps in epigenetic regulation are promoter methylation, histone acetylation/deacetylation, noncoding mRNA expression and chromatin conformational changes. Through their effects on chromatin structure, epigenetic changes can modulate transcriptional repression, X-chromosome inactivation, genomic imprinting and suppression of the detrimental effects of repetitive and parasitic DNA sequences on genome integrity. However, there are problems and issues in implementing EWAS to establish an association of epigenetic profiles with cancer. The current status of EWAS, challenges in the field and their potential solutions will be discussed. After completion of the ongoing human epigenome roadmap project and validation of key observation studies in nutrition epigenetics, strategies can be developed for disease control and treatment. Controlling cancer is a priority at the National Institutes of Health (NIH). An update from the Epigenomics Roadmap Program and the Cancer Genome Atlas (TCGA) will be presented.

Biography

Mukesh Verma is a Program Director and Chief in the Methods and Technologies Branch (MTB), Epidemiology and Genetics Research Program (EGRP) of the Division of Cancer Control and Population Sciences (DCCPS) at the National Cancer Institute (NCI), National Institutes of Health (NIH). Before coming to the DCCPS, he was a Program Director in the Division of Cancer Prevention (DCP), NCI, providing direction in the areas of biomarkers, early detection, risk assessment and prevention of cancer and cancers associated with infectious agents. He holds MSc from Pantnagar University and a PhD from Banaras Hindu University. He has completed his Postdoctoral Research at Howard University and George Washington University and was a Faculty Member at Georgetown University. He has published 157 research articles and reviews and edited three books in cancer epigenetics and epidemiology field.

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