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# Biomarkers in cancer epidemiology and diagnosis: Are we ready for the prime time?

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A biomarker is a characteristic that is objectively measured and evaluated as an indicator of normal biologic processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention. In cancer, a biomarker refers to a substance or process that is indicative of the presence of cancer in the body. A biomarker might be either a molecule secreted by a tumor or it can be a specific response of the body to the presence of cancer. Genetic, epigenetic, proteomic, glycomic, and imaging biomarkers can be used for cancer diagnosis, prognosis and epidemiology. These markers can be assayed in non-invasively collected biofluids. However, few cancer biomarkers are highly sensitive and specific for cancer detection at the present time. After completion of the human genome, genome-wide association studies 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 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 association of epigenetic profiles with cancer. The current status of EWAS, challenges in the field and their potential solutions will be discussed.

## 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. Dr. Mukesh Verma holds a M.Sc. from Pantnagar University and a Ph.D. from Banaras Hindu University. He did postdoctoral research at George Washington University and was a faculty member at Georgetown University. He has published 116 research articles and reviews and edited three books in cancer epigenetics and epidemiology field.

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