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Mukesh Verma

National Institutes of Health, USA

Biography

Mukesh Verma is Chief of the Epidemiology and Genomics Research Program's (EGRP) Methods and Technologies Branch (MTB), and oversees its research portfolio and initiatives that focus on methods to address epidemiologic data collection, study design and analysis, and to modify technological approaches developed in the context of other research endeavors for use as biomarkers and methods to understand cancer susceptibility. He is responsible for stimulating research in implication of omics approaches to understand cancer etiology. He represents NCI in Common Fund Programs on (1) Epigenomics (2) Metabolomics and (3) Molecular Transducers of Physical Activity and (4) congressionally mandated program on Environmental Influences on Child Health Outcome (ECHO). Since joining the NCI, he sought to champion the visibility of and investment in cancer epigenetics research both within the Institute and across other federal and non-governmental agencies, and to raise public awareness about controlling cancer.

vermam@mail.nih.gov

EPIGENETIC APPROACHES IN CANCER RISK ASSESSMENT AND ETIOLOGY

Several approaches are applied to identify risk of developing cancer in different ethnic and racial groups. One of the approaches is epigenetics that facilitates cancer control throughout the cancer core continuum. To understand current progress and trends in the inclusion of epigenetics in cancer epidemiology, we evaluated the published literature and the National Cancer Institute (NCI) supported research grant awards in this field to identify trends in epigenetics research. We present a summary of the epidemiological studies in NCI's grant portfolio and in the scientific literature published irrespective of support from NCI. Biomarkers identified in the analysis might be useful in risk prediction of different cancers. Breast cancer was the most frequently studied cancer type in grants and publications. Blood cells and tumor tissue were the most commonly used biospecimens in these studies, although buccal cells, cervical cells, sputum, and stool samples also were used. DNA methylation profiling was the focus of the majority of studies, but several studies also measured microRNA profiles. We illustrate here the current status of epidemiologic studies that are evaluating epigenetic changes in large populations. Some research needs include developing improved strategies for epigenetic data analysis and interpretation; determining the stability of epigenetic marks in repeated biospecimen samples from the same people over time; and studies that examine the relationship between epigenetic marks in germline DNA and tumor DNA. While there are limitations to the broad application of epigenomics to epidemiology research, there are situations where this type of research is appropriate and it should be considered.

Note: