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Risk prediction of cancer by epigenetics

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 (from January 2005 through December 2012) and in the scientific literature published during the same period, irrespective of support from NCI. NCI supported RPGs related to epigenetic epidemiology funded from January 01, 2005 to December 31, 2012 were included in the portfolio analysis. The portfolio was analyzed using NCI's Portfolio Management Application software version 13.4. The criteria for inclusion of a project in the analysis were as follows: (1) The focus of the project is cancer, (2) study involves human subjects, (3) focus of at least one of the specific aims in the project is cancer epigenetics, and (4) has at least 100 cases and 100 controls. The initial analysis identified 84 RPGs. A manual analysis applying the above criteria eliminated 21 RPGs leaving 63 for further analysis. 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.

Biography

Mukesh Verma is a Program Director and Chief in the Methods and Technologies Branch (MTB), Epidemiology and Genomics Research Program (EGRP) of the Division of Cancer Control and Population Sciences (DCCPS) at the National Cancer Institute (NCI), National Institutes of Health (NIH) with expertise in implication of epigenome, microbiome, metabolome and genomic information for risk assessment and understanding disease etiology. He has received MSc from Pantnagar University and PhD from Banaras Hindu University, India. He did his Postdoctoral research at George Washington University and was a Faculty Member at Georgetown University Medical Center. 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, epigenetics, epidemiology and cancers associated with infectious agents. He has published 161 research articles and reviews and edited five books in cancer biomarkers, epigenetics and epidemiology field.

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