EPIGENETICS IN ENVIRONMENTAL HEALTH

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Abstract: Epigenetic control of gene transcription is critical for normal human development and cellular differentiation. While alterations of epigenetic marks such as DNA methylation have been linked to cancers and many other human diseases, interindividual epigenetic variation in normal tissues due to environmental factors, aging, or innate susceptibility are poorly characterized. The plasticity, tissue-specific nature, and variability of gene expression are almost certainly the result of epigenomes that vary across individuals. We have begun to characterize normal variation in DNA methylation such that we can begin to understand the effects of toxicants on epigenetic regulation in tissues and cells. These studies have utilized the Illumina Goldengate platform to interrogate some 1413 autosomal CpG loci associated with 773 genes. Our work has then gone on to examine the association of epigenetic gene inactivation and DNA methylation with carcinogen exposure in a variety of cancers. In lung, bladder, asbestos-associated mesothelioma and head and neck cancer, carcinogen exposure has been associated with DNA methylation. While the mechanism responsible for induction of these changes remains unknown, the evidence that epigenetic alterations contribute to environmental disease is growing.

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