Impact of Environmental Exposure on the Genome
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There has been considerable interest recently in understanding how the environment affects our genome. The complexity of molecular biology and its interplay with the environment requires use of a variety of approaches to elucidate causes of complex diseases, such as birth defects. These approaches include looking outside the primary DNA sequence at epigenetic factors such as DNA methylation, a chemical addition thought to be environmentally-induced that influences gene expression and phenotype, and looking at the protein-coding sequences of DNA for rare gene variants. These powerful new approaches will be presented during this session by investigators using genetic samples and environmental data collected as part of the National Birth Defects Prevention Study (NBDPS).

The NBDPS is a population-based case-control study to examine risk factors for birth defects. It is unique in that it collects both genetic samples and information on environmental exposures. Using these data, researchers can look at how genes interact with a woman’s environment or other factors, such as smoking, medications, or diet, and how these interactions might increase the risk for birth defects. This plenary session will focus on use of NBDPS genetic samples and environmental data in studies using some of the latest technologies available to help unravel the causes of birth defects.

- Mary Jenkins (CDC) will first provide a brief overview of the use of genetic and environmental data from the NBDPS with a variety of technologies to facilitate identification of risk factors for birth defects.
- Charlotte Hobbs (AR) will discuss findings from epigenetic studies of genome-wide DNA methylation completed using DNA samples collected from NBDPS participants.
- Mike Bamshad (WA) will share his recent work using a powerful new technology, exome sequencing, with NBDPS and other population-based samples.