Placental Epi/Genomics as Sensors of the in Utero Environment and Predictors of Fetal Development

Jia Chen, PhD
Jia Chen, Professor
Icahn School of Medicine, Mount Sinai

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The placenta is the principal organ regulating fetal development with implications for postnatal health outcomes. Appropriate transitioning through gestation requires the tightly coordinated orchestration of the placental epigenome, which sits as the interface between genes and the environment by enabling heritable and persistent changes in gene expression without altering the DNA sequence. Placental epigenetic elements include DNA methylation, histone modifications and non-coding RNAs, which undergo re-programming following fertilization as the zygote differentiates into cell-specific lineages. This is particularly pertinent at imprinted loci, key regulators of fetal development that are mono-allelically expressed based on parent-of-origin. The dynamic state of placental epigenetic marks highlights their sensitivity to perturbations during pregnancy and their potential utility as sensors of the in utero environment.

This talk is to summarize the latest advances in placenta genomics and epigenomics while highlighting our own work on integrative genome analyses. We explored placental gene networks in association to in utero trace metal exposures as well as to birth outcomes and postnatal neurodevelopment. We will provide evidence that the placental epi/genome is highly sensitive to environmental stressors. Placental gene networks reveal functional enrichment of pathways related to late-onset diseases including asthma and metabolic dysregulation.