Hereditary Genet Curr Res 2018, Volume 7
DOI: 10.4172/2161-1041-C1-003

Effects of prenatal perfluoroalkyl substances exposures on epigenetics

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Background: Perfluoroalkyl substances (PFASs) are stable and persistent in the environment, animals, and humans. PFASs can penetrate placenta and affect fetal growth. We investigated associations between prenatal exposures to perfluorooctanoic acid (PFOA), perfluorooctanesulfonate (PFOS), perfluorononanoic acid (PFNA), and perfluoroundecanoic acid (PFUA) and DNA methylation changes at repeated elements and imprinted genes.

Aims & Methods: The study used the subjects from Taiwan Birth Panel birth cohort study, including all pregnant women who gave birth between July 2004 and June 2005 in four hospitals in Taipei city and New Taipei City. A total of 363 mother-infant pairs were included in the final analyses. PFOA, PFOS, PFNA, and PFUA were measured by UPLC-MS/MS in cord blood. DNA methylation levels were measured in leukocytes from umbilical cord blood. LINE-1 and Alu repeated elements from cord blood were used to represent global DNA methylation levels. Multivariable regression models were used to adjust potential confounders.

Results: After controlling for potential confounders, each unit increase in the natural log-transformed PFOS exposure was associated with lower methylation levels at Alu repeated elements (adjusted β=-0.33, 95% CI = (−0.63, −0.02), p=0.03) and *MEST* gene (adjusted β=-2.01, 95% CI = (-3.41, -0.62), p=0.005). No significant effects between PFOA, PFNA, PFUA and methylation levels in the multivariable regression models were observed.

Conclusions: Our findings suggest that prenatal PFOS exposure may be associated with low Alu and MEST methylation levels.