

Determining how Placental Epigenetic Machinery Expression is Impacted by Per- and Polyfluoroalkyl Substances
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The effects of perfluoroalkyl substances (PFAS) on the placenta are poorly understood. We hypothesize that, since perfluorooctanoic acid (PFOA) is associated with hypomethylation in the cord blood serum, this results in placental DNA methylation. This association was investigated by assessing the placental epigenetic machinery through cell tissue culture, RT-PCR, and Western Blot protein analysis. Human trophoblast JEG-3 cells were cultured to perform PFAS treatments. RT-PCR required complementary DNA following total RNA isolation from the cells cultured. A BCA Assay helped determine the protein quantity in the cells, and Western blots determined whole protein expression. Results showed the significant alteration in expression of epigenetic regulatory machinery genes due to PFAS, including PFOA, perfluorooctanoic sulfate (PFOS), and 2,3,3,3-tetrafluoro-2-(hepta fluoropropoxy) propanoate (GenX). JEG-3 cells presented absence of 10% fetal bovine serum. Proteins and histones involved in epigenetic regulatory functions demonstrated alterations with the PFAS treatments of PFOA, PFOS, and Genx. The results suggest that PFAS significantly alter gene expression of epigenetic regulatory machinery in the JEG-3 cells, specifically concerning histone phosphorylation, demethylation, and deacetylation.