

Multi -omics data analysis to investigate transcriptional and DNA methylation changes in the fetal brain and placenta in a mouse model of polychlorinated biphenyl mixture exposure

In a human cohort study “Markers of Autism Risk in Babies: Learning Early Signs”, a group of persistent organic pollutants- polychlorinated biphenyls (PCBs)- are identified as environmental risk factors for NDDs where detectable concentrations of multiple PCB congeners in maternal gestational blood samples were associated with adverse neurodevelopmental outcomes. In order to experimentally control for genetic and environmental covariates that contribute to NDD risk and to test interactions, a mouse model of prenatally exposed mice to a human-relevant mixture of PCBs is used. Transcriptomic and epigenomic data are collected from fetal brain and placenta, which is a tissue source of epigenetic biomarkers that can be used to predict NDD risk. A weighted gene correlation network, weighted region comethylation network, and differential gene expression analysis are performed to understand the epigenetic mechanisms of PCB neurotoxicity and identify biomarkers in the placenta, which can have clinical relevance for predicting NDD risk at birth as a diagnostic tool.