

DELIVERY TYPE NOT ASSOCIATED WITH DIFFERENTIAL METHYLATION AT BIRTH

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Background: Birth by Cesarean section is associated with adverse health outcomes later in life, including diabetes and allergies. Epigenetic mechanisms are one way early life exposures can affect later health outcomes. Differences in global methylation by type of birth have been described, but the sample sizes have been small. We measured global methylation in a large, ongoing birth cohort to identify epigenetic changes that may cause predisposition to disease in later life due to delivery type.

Methods: DNA was obtained from umbilical cord blood collected immediately after term deliveries from the University of Michigan Hospital (n=417). Global methylation levels were assessed via the Luminometric Methylation Assay (LUMA), and DNA methylation at four CpG sites in LINE-1 repetitive elements was assessed via bisulfite pyrosequencing. Samples were run in duplicate and averaged for analyses. Nonparametric analyses tested the association between type of birth, vaginal delivery (VD) or Cesarean section (CS), gender and measures of global methylation.

Results: LUMA data were available from 301 births (53% male; 61% CS) and LINE-1 methylation was available for 212 births (50% male; 67% CS). There were 154 samples with both LUMA and LINE-1, and the measurements were negatively correlated (Spearman's $r = -0.22$, $p = 0.006$). Global methylation values were not significantly different by gender. Type of birth was not associated with global methylation as measured by LUMA (mean CS = 73.66, mean VD = 74.98, p -value = 0.12) or by LINE-1 (mean CS = 81.19, mean VD = 81.05, p -value = 0.31). These results did not change when stratifying by gender.

Conclusion: Type of delivery was not associated with global methylation in our population regardless of infant gender. While type of birth may be associated with later health outcomes, our data suggest that it does not do so through changes in global genomic methylation.

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