





# Altered DNA methylation in human placenta after (suspected) preterm labor

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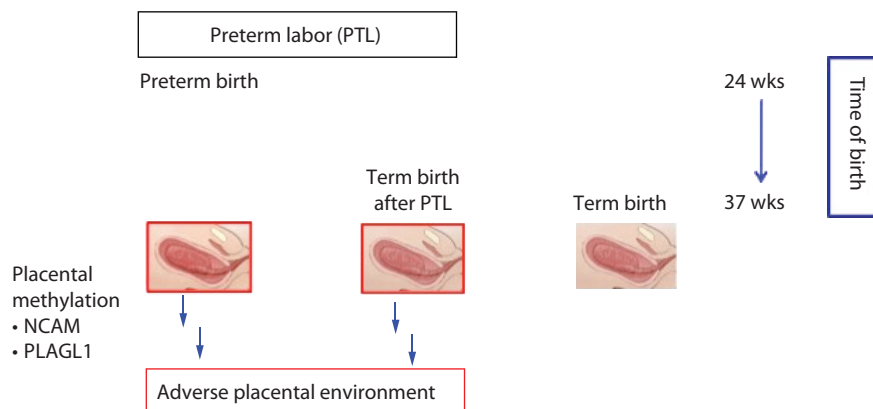
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**Aim:** The aim of this study was to determine if alterations in DNA methylation in the human placenta would support suspected preterm labor as a pathologic insult associated with diminished placental health.

**Methods:** We evaluated placental DNA methylation at seven *loci* differentially methylated in placental pathologies using targeted bisulfite sequencing, in placentas associated with preterm labor (term birth after suspected preterm labor [n = 15] and preterm birth [n = 15]), and controls (n = 15). **Results:** DNA methylation levels at the *NCAM1* and *PLAGL1* *loci* in placentas associated with preterm labor did differ significantly (p < 0.05) from controls. **Discussion:** Specific alterations in methylation patterns indicative of an unfavourable placental environment are associated with preterm labor per se and not restricted to preterm birth.

## Graphical abstract:



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**Keywords:** DNA methylation • inflammation • LOT1/PLAGL1 • placenta • preterm birth • suspected preterm labor

The mammalian placenta orchestrates efficient exchange of nutrients, waste and gas between mother and fetus and contributes to the fetal environment through its endocrine functions [1]. Placental dysfunction underlies