**Variability of the microbiome of pregnant women
and its impact on the frequency of preterm birth**

Introduction:

Prematurity remains a significant public health issue despite advances in medical care, with increased morbidity and mortality imposing a significant burden on families and society. This doctoral dissertation investigates the role of the gut microbiome in the development of reterm labor, with the aim of identifying potential targets for novel therapeutic interventions.

Aim of the study

The aim of this doctoral dissertation is to investigate the variability of the gut microbiome in pregnant women and its potential impact on the frequency of preterm birth.

Methods:

Fecal samples were collected from pregnant women who delivered preterm and those who delivered at term and analyzed for microorganisms using PCR and DNA sequencing. Raw sequencing reads were processed and analyzed using bioinformatics tools to identify bacterial species present in the sample.

Results:

Differences in gut microbiota diversity between preterm and term labor groups were observed. While the small sample size highlights the need for further studies with larger samples, these findings suggest that the diversity of the intestinal microbiota plays an important role in preterm delivery.

In addition to traditional methods, machine learning (ML) models have shown potential to more accurately predict preterm birth. Further research is needed to determine the feasibility of using ML models in clinical practice to improve outcomes for pregnant women and their babies.

Conclusion:

This dissertation highlights the importance of the gut microbiome in preterm labor and identifies potential targets for therapeutic interventions. The use of ML models could provide more accurate prediction of preterm birth, potentially improving outcomes for mothers and infants.