GUT MICROBIOTA OF PREGNANT WOMEN WITH GESTATIONAL DIABETES AND MACROSOMIA

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INTRODUCTION

Imbalance in the composition of gut microbiota plays an important role in the emergence of many diseases, including diabetes and obesity. Gestational diabetes mellitus (GDM) occurs during pregnancy and ceases after childbirth. The excess glucose in the mothers' bloodstream passes through the placenta into the fetal circulation. The fetus subsequently begins to produce more insulin and stores additional energy in the form of body fat, which results in greater growth of the baby and macrosomia. Macrosomal infants are at an increased risk of becoming overweight at a young age and are more likely to develop type 2 diabetes later in life.

AIM

Insight into the composition of microbiota of pregnant women with GDM and the occurrence of macrosomia.

MATERIAL AND METHODS

At University Medical Center Ljubljana, we included patients with GDM and obesity and clinically evaluated them. We successfully optimized the isolation of DNA from the feces of two pregnant women, who later delivered a macrosomal baby. Mechanical homogenization and termical pre-treatment is a key step to recover sufficient amount of DNA for further analysis. The genetic material of microorganisms was examined using 16S metagenomics and an Ion PGM™ sequencer. We compared two fecal samples taken in the second and third trimester and analyzed the data with the Ion Reporter™ program.

Figure 1: Instructions and a container suitable for collecting a stool sample

RESULTS AND DISCUSSION

Microbiota at two time points from one individual, proved to be less similar than the microbiota of two different individuals in the same time frame. The differences in intestinal microbiota composition among individuals, increased in the third trimester. Our analysis of beta diversity revealed that microbiota composition in second trimester, was characterized by a high proportion of *Prevotella copri* (*Prevotellaceae*) and *Succinivibrio dextrinosolvens* (*Succnivibrionaceae*), while other species *Phascolarctobacterium faecium* (*Acidaminococcaceae*) and *Bacteroides uniformis* (*Bacteroidaceae*) dominated in samples taken in third trimester.

Legend:
(B002 , B011) samples taken in second trimester of overweight pregnant women
(IIB002 ,IIB011) samples taken in third trimester of overweight pregnant women

Figure 2: DNA isolation results using Qiagen KIT

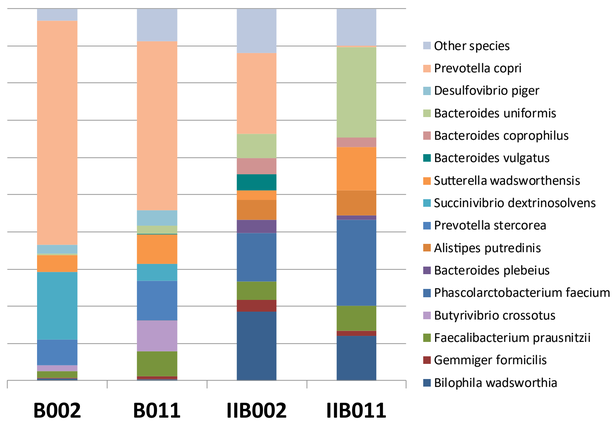

Figure 3: Top 15 bacterial species in the fecal microbiota of two overweight pregnant women with GDT in samples taken in second and third trimester

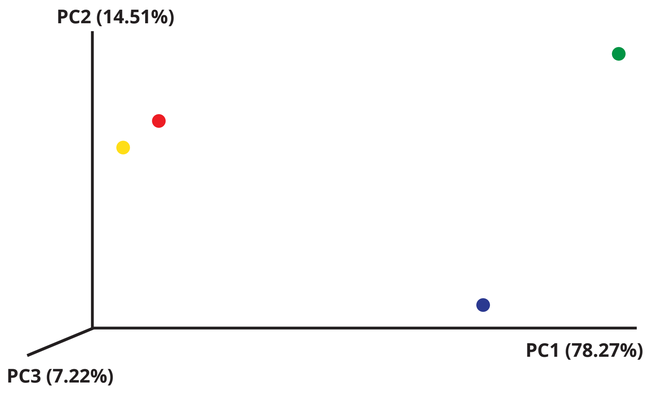

Figure 4: PCoA of the bacterial community composition based on Bray Curtis analysis sample B002 (•) and (•) sample B011 taken in second trimester sample B002(•) and sample B011(•) taken in third trimester

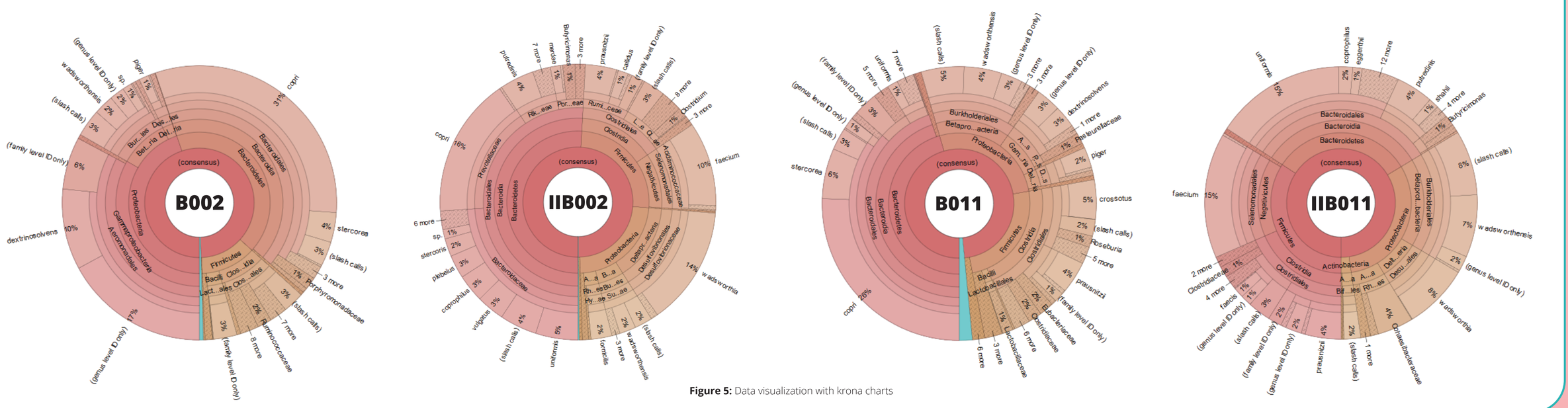

Figure 5: Data visualization with krona charts

CONCLUSIONS

We proved beta diversity is increased in the third trimester probably due to differences in unique course of each pregnancy and different metabolism of each pregnant women. It is known that gut microbiota is linked with development of obesity and metabolic diseases, but our analysis could also partially explain its impact on macrosomia occurrence, however, more detailed analysis on a larger number of samples, would be necessary.

REFERENCES

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