



Maternal factors and the Vaginal Microbiome in Pregnancy;

Results of the MicrobeMom Randomised Controlled Trial



Background: The vaginal microbiome is a key player aetiology of spontaneous preterm birth. This study aimed to illustrate how maternal environmental factors influence vaginal microbiota composition in pregnancy, which may highlight modifiable factors to improve the vaginal microbiome and reduce the risk of preterm birth.

Methods: Participants of the MicrobeMom randomised controlled trial who had vaginal microbial sampling were included (Sept 2016 - July 2019). After shotgun metagenomic sequencing, heat maps of relative abundance data were generated. Community state type was assigned, and alpha diversity was calculated. Demography, obstetric history, wellbeing, exercise and diet were collected and compared against microbial parameters.

Results: Vaginal samples from 119 participants generating average of 565,192 high quality paired end reads (median 350,006). Amino acids lysine, leucine, valine and alanine were associated with beta diversity (R^2 0.077, $p=0.023$, R^2 0.051, $p=0.048$, R^2 0.057, $p=0.028$, R^2 0.064, $p=0.018$). Dietary carbohydrates, maltose and glycaemic load, previous vaginal delivery and history of breastfeeding were associated with vaginal microbial beta diversity (R^2 0.057, $p=0.038$, R^2 0.061, $p=0.033$, R^2 0.065, $p=0.022$, R^2 0.070, $p=0.001$; R^2 0.053, $p=0.005$, respectively). Carbohydrates, starch and maltose were positively correlated with increased alpha diversity (+0.001 per carb g, $p=0.032$; +0.002 per starch g; +0.044 per maltose g, $p=0.043$).

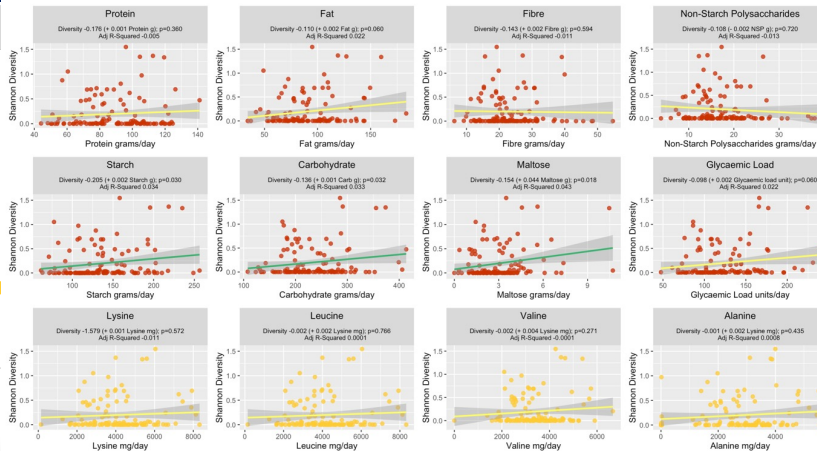
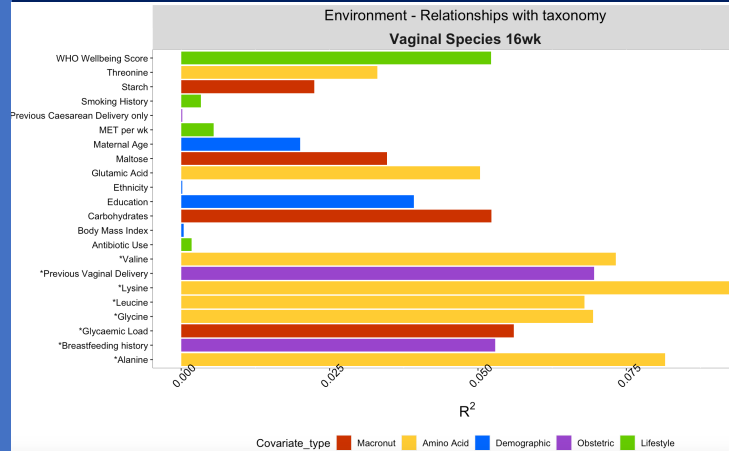
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Dietary Amino Acids, Glycaemic Load, Carbohydrates, Vaginal Delivery and Breastfeeding are the Maternal Factors with the strongest associations with the vaginal microbiome