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Metabolomics insight into the gut microbiome of infants with cow's milk allergy
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Stellingen

Behorende bij het proefschrift

Metabolomics Insight into

the Gut Microbiome of Infants with Cow's Milk Allergy

1. The post-column infusion of standards (PCIS) approach can effectively monitor the matrix effect for plasma and fecal samples, allowing the identification of regions with high matrix effect variation in untargeted metabolomics. (Chapter 2)

2. Selecting a PCIS to correct for the matrix effect in biological samples with artificial matrix infusion is a strategy which is independent of retention time and spiking of standards, making it universally applicable to any detectable features in untargeted metabolomics. (Chapter 3)

3. The altered gut microbiome, characterized by an enrichment of the Clostridia class and reductions in the Lactobacillales order and Bifidobacterium genus, is associated with cow's milk allergy (CMA) in early life. (Chapter 4)

4. During a 12-month synbiotic supplementation in CMA infants, significant alterations in the fecal metabolome, reflecting increased bifidobacterial activity, were observed after six months but diminished after 12 months of intervention. This suggests there is a critical time window for maximizing the effect of synbiotics in early life. (Chapter 5)

5. Matrix effect could be considered one of the most important disadvantages of LC-MS analysis in bioanalysis (González, Oskar, et al., Journal of Chromatography A, 2014). Therefore, matrix effect should be thoroughly investigated in metabolomics analysis.

6. It is an impractical, laborious, and costly endeavor for global metabolomics to utilize isotopically labeled internal standards to correct matrix effects for hundreds or thousands of features (Chamberlain, Casey A., et al., Metabolomics, 2019). The PCIS approach with artificial matrix infusion offers an efficient alternative for addressing matrix effect in untargeted metabolomics.

7. Epidemiological studies have shown that factors that alter bacterial communities in infants during childhood increase the risk for several diseases, highlighting the importance of understanding early-life microbiome composition (Tamburini, Sabrina, et al., Nature medicine, 2016). This also implies that early life may represent a key period for disease prevention through gut microbiome modification.

8. The fecal metabolome provides a functional readout of microbial activity and can be used as an intermediate phenotype mediating host–microbiome interactions (Zierer, Jonas, et al., Nature genetics, 2018). If available, integrating fecal and plasma metabolome could provide deeper insights into these interactions.

9. Reach for the stars, but remain grounded. (Frank Sonnenberg)

10. Fail, learn, repeat, progress.

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Pingping Zhu
Leiden, 13th Jan, 2026

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