Human breast milk metabolomes over the course of 6 months lactation

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Background

The complexity and dynamic nature of human breast milk (HBM) have long been acknowledged and deemed essential for infants' health and growth during the first period of life.

The present poster presents preliminary results of breast milk metabolome from the *Infamilk* study – a multi-institutional study exploring HBM by conducting proteomics, metabolomics and microbiome sequencing on breast milk from term and pre-term deliveries. Ultimately, associations between human milk microbiome, composition and infant health are investigated.

Methods

Over the course of 24 weeks post-partum, a total of 100 human breast milk samples were collected from 59 women (term deliveries) at four different time points in Cork, Ireland. The women were recruited from Cork University Maternity Hospital as part of Infamilk.

^{1}H NMR spectra acquisition was conducted by the use of a Bruker Avance III 600 MHz spectrometer.

The spectra were analysed and metabolites identified and quantified (n = 30).

Lastly, multivariate data analysis was proceeded by conducting principal component analysis (PCA) to investigate variation in the dataset.
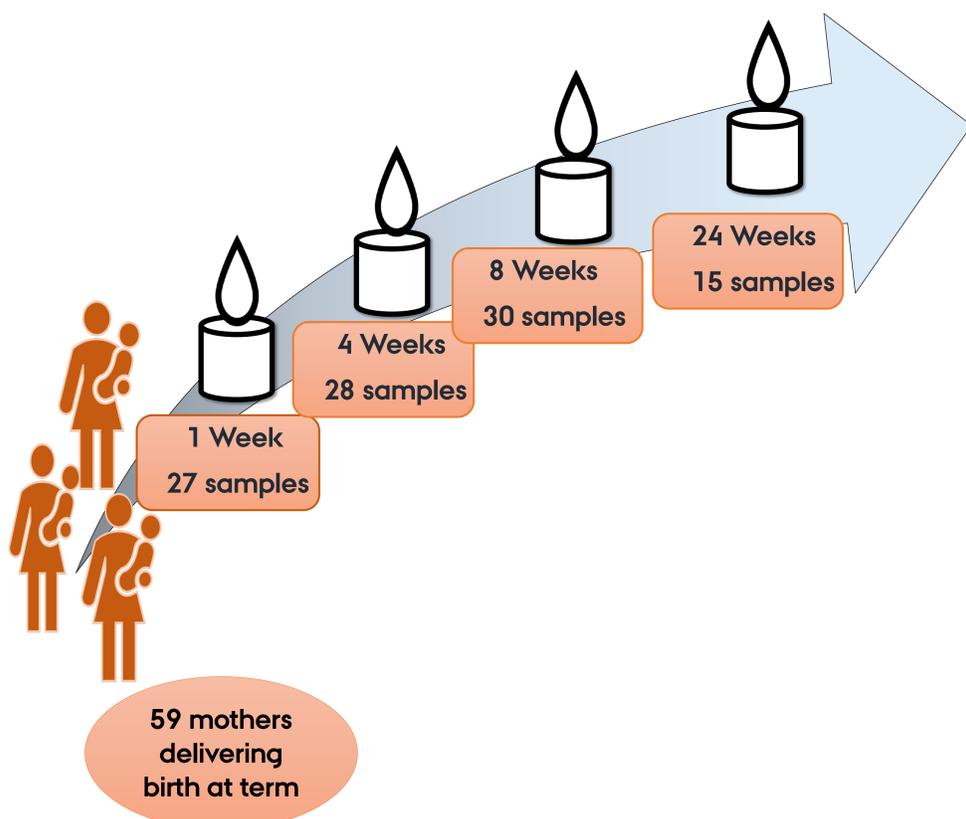

Figure 1: Presentation of longitudinal sampling from one week post-partum to 24 weeks post-partum. A total of 100 samples were collected from 59 women delivering birth at term. The number of samples collected at each time point is indicated.

Results

- 11 out of the 59 mothers showed non-secretor status, and thus did not produce 2'-fucosyllactose.
- The concentration of 3'-sialyllactose was largely constant between time points, whereas the concentration of 6'-sialyllactose decreased over the course of 24 weeks.

Multivariate analysis indicated that the samples could mainly be separated according to week of sampling
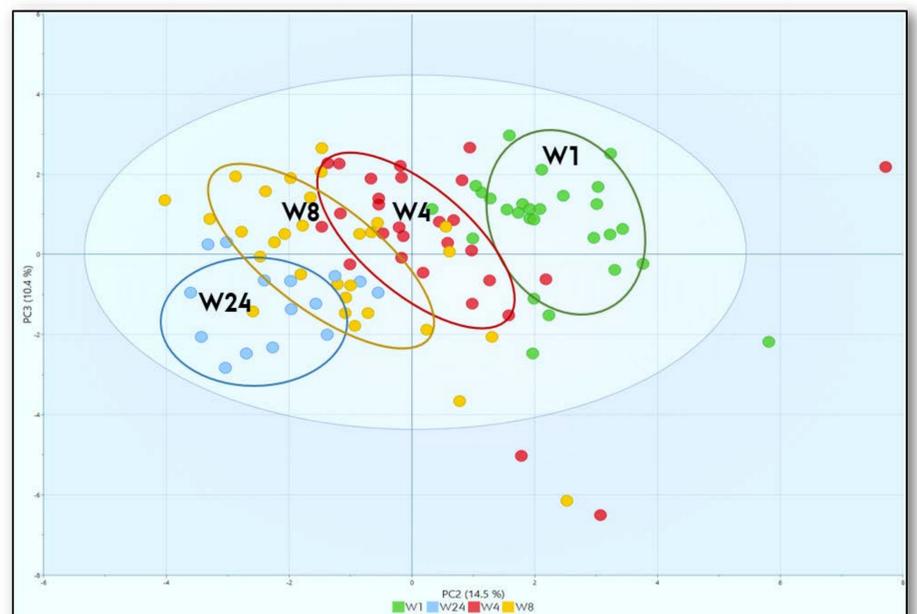
... with increasing concentration of lactose, glutamate and glutamine and decreasing concentrations of oligosaccharides 6'-sialyllactose, 2'-fucosyllactose and N-acetylglucosamine among others

Figure 2: Top; Principal Component Analysis (PCA) scores scatterplot depicting principal component 2 (PC2) vs. principal component 3 (PC3), bottom; corresponding loading scatterplot of PC2 vs. PC3 depicting the metabolites identified and quantified contributing to the variation observed in the scores plot

Conclusion and future perspective

The present results indicate that the use of ^{1}H NMR can reveal time-dependent differences in metabolome of human breast milk from mothers delivering birth at term. Future analyses seek to investigate metabolomes of human breast milk from mothers delivering pre-term and further to elucidate intra-individual variations.