

Abstract

Unravelling the Determinants of the Human Milk Microbiome in Allergic Women [†]

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As some of the most common chronic diseases globally, allergic diseases have been associated with the gut microbiome composition of both children and adults. The human milk microbiome has been proposed as a potential mediator in infant microbiome development; however, no studies have explored the human milk microbiome specifically in allergic women. This study aimed to investigate the determinants of the human milk microbiome in allergic women. Milk samples from the Infant Fish Oil Supplementation Study (IFOS; Australian Clinical Trials Registry ACTRN12606000281594) were collected at three ($n = 229$) and six ($n = 171$) months postpartum from women, who all had at least one allergic disease (e.g., asthma, allergic rhinitis). Full-length 16S rRNA gene sequencing was utilised to characterise the milk microbiome. Differences in alpha diversity and microbiome composition were assessed by linear mixed models, while beta diversity was assessed by PERMANOVA. The season of infant birth had the strongest relationship with the milk microbiome, with significant associations with beta diversity ($p = 0.001$) and 10 out of the 19 most abundant OTUs ($>0.1\%$ relative abundance). The milk microbiome composition was also significantly associated with the delivery mode, feeding status, parity, infant age, infant sex, maternal age, passive smoke exposure, and pets at home, aligning with previous findings from non-allergic women. Maternal allergy type was also significantly related to the composition of the milk microbiome. This study investigated the human milk microbiome in allergic mothers, revealing the season of infant birth as potentially the strongest influencer, along with associations between maternal, infant, and environmental factors. These findings suggest an interaction between season and maternal allergic diseases, which influences the microbiome.

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