

Abstract

The Development of the Human Milk Microbiota over the First Two Years Postpartum in the Breastfeeding Longitudinal Observational Study of Mothers and Kids (BLOSOM) Cohort [†]

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The human milk microbiota play an important role in mammary and infant health. However, there are limited data describing the composition and temporal variation in the milk microbiota beyond the first few months. Therefore, this study aimed to characterise the development of the human milk microbiota over the first two years postpartum and to investigate the factors that influence its composition. We performed full-length 16S rRNA gene sequencing on 608 samples collected from 86 mothers in the BLOSOM birth cohort. Similar to other populations, the milk microbiota of Western Australian women was low in diversity, and strongly dominated by *Staphylococcus* and *Streptococcus* species (14.95% and 39.04% relative abundance, respectively). Milk bacterial richness increased over time ($p = 0.004$), and there were significant changes in the abundances of 7 of 18 of the most abundant taxa over time. The composition of the milk microbiota was associated with numerous maternal and infant factors including infant age, maternal or infant antibiotic exposure, maternal probiotic use, parity, mode of delivery, and pre-pregnancy BMI (all $p < 0.039$). Our data provide new insights into how the human milk microbiota develop beyond the first few months and determinants of the milk's bacterial composition, demonstrating that the milk microbiota are dynamic over time in the first two years postpartum.

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