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Abstract

Breastfeeding Characteristics Are Associated with Minor Changes in the Human Milk Microbiome †

Ruomei Xu [1,2,3], Mark P. Nicol [2,4], Ali S. Cheema [5], Jacki L. McEachran [1,2,3], Sharon L. Perrella [1,2,3], Zoya Gridneva [1,2,3], Donna T. Geddes [1,2,3] and Lisa F. Stinson [1,2,3,*]

[1] School of Molecular Sciences, The University of Western Australia, Crawley, WA 6009, Australia; ruomei.xu@research.uwa.edu.au (R.X.); jacki.mceachran@uwa.edu.au (J.L.M.); sharon.perrella@uwa.edu.au (S.L.P.); zoya.gridneva@uwa.edu.au (Z.G.); donna.geddes@uwa.edu.au (D.T.G.)
[2] UWA Centre for Human Lactation Research and Translation, Crawley, WA 6009, Australia; mark.nicol@uwa.edu.au
[3] ABREAST Network, Perth, WA 6000, Australia
[4] School of Biomedical Sciences, The University of Western Australia, Crawley, WA 6009, Australia
[5] The Kids Research Institute Australia, Nedlands, WA 6009, Australia; alisadiq.cheema@telethonkids.org.au
[*] Correspondence: lisa.stinson@uwa.edu.au; Tel.: +61-8-6488-3200

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Human milk has a microbiome that contains a wide variety of typical oral and skin bacteria, suggesting that the bacterial communities in the infant oral cavity and maternal skin contribute to the development of the human milk microbiome [1–3]. It is hypothesised that breastfeeding characteristics, such as feeding frequencies, total 24 h breastfeeding duration and breast pump use, could lead to different levels of exposure to oral and skin bacteria and subsequently altered bacterial profiles in human milk. In order to investigate the associations between breastfeeding characteristics and the human milk microbiome, this study analysed milk samples collected from 57 healthy lactating women at 3 months postpartum by full-length 16S rRNA gene sequencing. The results showed that breastfeeding characteristics were associated with neither Shannon diversity nor richness of the human milk microbiome. Total 24 h breastfeeding duration, however, was positively associated with *Streptococcus salivarius* (0.013 ± 0.006, $p = 0.035$). Mothers with normal milk production ($\geq$600 mL/24 h) harboured less *Streptococcus parasanguinis* (-0.007 ± 0.003, $p = 0.035$) and *Veillonella* sp. (-0.008 ± 0.003, $p = 0.011$) in the milk. Breastfeeding frequency was positively associated with *Pseudomonas* sp. (0.204 ± 0.098, $p = 0.042$). In conclusion, total 24 h breastfeeding duration, breastfeeding frequency and 24 h milk production were associated with specific bacterial species in human milk.

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