The human milk microbiome changes over lactation and is shaped by maternal weight and mode of delivery.

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Source

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Abstract

BACKGROUND: Breast milk is recognized as the most important postpartum element in metabolic and immunologic programming of health of neonates. The factors influencing the milk microbiome and the potential impact of microbes on infant health have not yet been uncovered.

OBJECTIVE: Our objective was to identify pre- and postnatal factors that can potentially influence the bacterial communities inhabiting human milk.

DESIGN: We characterized the milk microbial community at 3 different time points by pyrosequencing and quantitative polymerase chain reaction in mothers (n = 18) who varied in BMI, weight gain, and mode of delivery.

RESULTS: We found that the human milk microbiome changes over lactation. Weisella, Leuconostoc, Staphylococcus, Streptococcus, and Lactococcus were predominant in colostrum samples, whereas in 1- and 6-mo milk samples the typical inhabitants of the oral cavity (e.g., Veillonella, Leptotrichia, and Prevotella) increased significantly. Milk from obese mothers tended to contain a different and less diverse bacterial community compared with milk from normal-weight mothers. Milk samples from elective but not from nonelective mothers who underwent cesarean delivery contained a different bacterial community than did milk samples from individuals giving birth by vaginal delivery, suggesting that it is not the operation per se but rather the absence of physiological stress or hormonal signals that could influence the microbial transmission process to milk.

CONCLUSIONS: Our results indicate that milk bacteria are not contaminants and suggest that the milk microbiome is influenced by several factors that significantly skew its composition. Because bacteria present in breast milk are among the very first microbes entering the human body, our data emphasize the necessity to understand the biological role that the milk microbiome could potentially play for human health.

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