

Human breast milk microbiome changes over time

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Raul Cabrera-Rubio, M.D., of the University of Valencia in Spain, and colleagues used pyrosequencing and quantitative [polymerase chain reaction](#) methods to characterize the microbial community of the [breast milk](#) of 18 mothers at three different time points and identify pre- and postnatal factors that can influence the breast milk microbiome.

The researchers found that colostrum contained primarily *Weissella*, *Leuconostoc*, *Staphylococcus*, *Streptococcus*, and *Lactococcus*, while samples collected at one and six months contained more *Veillonella*, *Leptotrichia*, and *Prevotella* species. [Obese mothers](#) displayed a different and less diverse bacterial community. Additionally, the microbiome differed according to whether the baby was delivered vaginally or via non-elective or elective cesarean section, suggesting a role for physiologic stress and/or hormonal signals in the transmission of bacteria into breast milk.

"Prenatal and postnatal microbial exposures have profound effects on the microbial colonization of the intestine and maturation of the naive immune system," the authors write. "Given that the bacteria present in breast milk are among the very first microbes that enter the human body and given the vital role of bacteria in the infant's physiology and development of the immune system, our data emphasize the necessity to understand the biological role that the breast milk microbiome could potentially play for human health."

More information: [Abstract](#)

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