

Breast milk microbiota: is there a relationship with HMOs?ANA SOTO, NIVIA CÁRDENAS, SUSANA DELGADO, JUAN MIGUEL RODRÍGUEZ AND LEONIDES FERNÁNDEZ*Departamento de Nutrición, Bromatología y Tecnología de los Alimentos, Universidad Complutense de Madrid, Avda. Puerta de Hierro, Madrid, Spain*

Breast milk is a complex biological fluid that provides all the nutritional requirements for the first months of life but, additionally, educates the infant immune system and confers protection against pathogens. These effects result from the synergistic action of many bioactive molecules, such as cytokines, cellular components, oligosaccharides or lipids. While it is well known that breast milk is rich in oligosaccharides, it has only recently been accepted that human milk also constitutes a source of commensal and probiotic bacteria which seems to play an important role in gut colonization and modulation of the infant gut.

In recent years, analyses of the bacterial diversity of human milk have revealed that this biological fluid is an important source of live staphylococci, streptococci, bifidobacteria and lactic acid bacteria to the infant gut. In contrast to other bacteria, these seem to be uniquely adapted to reside in the human digestive tract and to interact with us in symbiosis from the time we are born. Traditionally it was considered that bacteria present in breast milk were acquired by mere skin contamination. However, it has been found that lactobacilli and enterococcal isolates present in human milk are genotypically different from those isolated in the skin within the same host. Furthermore, several studies suggest the existence of a mammary microbiota during late pregnancy and lactation. Live bacteria from the maternal gut could colonize the mammary gland through an endogenous route (the so-called entero-mammary pathway), involving maternal dendritic cells and macrophages.

In this context, the global objective of this work was to ascertain if there is a relationship between human milk oligosaccharides and microbiota. For that purpose, carbohydrate utilization was studied in a variety of lactic acid bacteria and bifidobacteria isolated from human milk of healthy donors, and compared with their enzymatic activity on chromogenic substrates. Genome sequences of selected bacteria were analyzed to identify possible genes involved in the metabolism of carbohydrates, especially those related to HMOs.

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