

Available online at www.sciencedirect.com

ScienceDirect

journal homepage: www.jfda-online.com

Original Article

Profiles of commensal and opportunistic bacteria in human milk from healthy donors in Taiwan

Q2 Po-Wen Chen ^{a,*}, Yi-Ling Lin ^b, Mao-Sheng Huang ^c^a Department of Nursing, St. Mary's Junior College of Medicine, Nursing and Management, Taiwan^b Department of Obstetrics Central, St. Mary's Hospital Luodong, Taiwan^c Department of Medicine Laboratory, St. Mary's Hospital Luodong, Taiwan

ARTICLE INFO

Article history:

Received 28 August 2017

Received in revised form

26 February 2018

Accepted 12 March 2018

Available online xxx

Keywords:

Bifidobacterium

Commensal bacteria

Human milk microbiota

Lactobacillus

Staphylococcus aureus

ABSTRACT

Recent studies indicate that milk from healthy mothers may harbor potential probiotics. Nonetheless, the distribution of bacterial profiles in human milk samples in Taiwan is not fully understood. Therefore, with the aim to address this question, in this study, milk samples were collected from 33 healthy mothers (D1 to D33) visiting our hospital during a 6-month period. The milk microbiota was analyzed by a molecular approach (Illumina MiSeq sequencing). The results indicate that the milk samples have a unique profile and patterns of bacterial abundance levels. Moreover, in colostrum and transitional-milk samples, we detected 154 and 127 bacterial species, respectively, and these sets shared 42.6% of the bacterial species. The most common bacterial species among all milk samples were *Staphylococcus epidermidis*, *Streptococcus lactarius*, and *Staphylococcus hominis*, suggesting that the skin contamination route plays an important role in the composition of the milk microbiota. Nevertheless, four *Lactobacillus* species, *Lactobacillus helveticus*, *Lactobacillus iners*, *Lactobacillus zaeae*, and *Lactobacillus gasseri*, were present in only 7 samples (21% prevalence), and bifidobacterial species were quite rare taxa among the present samples. The *Staphylococcus aureus* was detected in a total of 15 samples (45% prevalence), suggesting that this species may be commonly present in milk samples. In conclusion, each milk sample revealed a unique profile and patterns of bacterial abundance levels, and our data do not support the idea that lactobacilli and bifidobacteria are common and abundant in modern milk samples. Because none of the donors of the milk samples showed mastitis or any discomfort during the sampling process or at follow-up inspection, the microbiota of these milk samples is not likely to negatively affect its host. This study provides new information on the proportions of commensal bacteria in human milk in Taiwan.

Copyright © 2018, Food and Drug Administration, Taiwan. Published by Elsevier Taiwan

LLC. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).creativecommons.org/licenses/by-nc-nd/4.0/

* Corresponding author. No. 100, Lane 265, Sec 2, Sanxing Rd., Sanxing Township, Yilan County 26644, Taiwan. Fax: +886 3 9897235.

E-mail address: pwchen@smc.edu.tw (P.-W. Chen).

<https://doi.org/10.1016/j.jfda.2018.03.004>

1021-9498/Copyright © 2018, Food and Drug Administration, Taiwan. Published by Elsevier Taiwan LLC. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

1. Introduction

Recent studies showed that human milk contains commensal or probiotic bacteria [1–3], and several additional reports have suggested that human milk is a direct source of commensal or probiotic bacteria found in the infant gut [4–7]. Commensal bacteria in human milk may have a positive effect on the health of breast-fed babies by shaping their gut microbiotas [8]. Thus, research on the milk microbiota and the factors that can shape it is important.

Several studies have identified diverse bacteria in human milk, and their presence and abundance in human milk seem to vary among individuals [9,10]. In addition, the mode of delivery, lactation time, gestational age, and maternal health, weight, exposure to chemotherapy, diet, and geographical location have all been found to play roles in bacterial profiles of human milk [1,4,11,12]. Nonetheless, individual factors that shape the milk microbiota are still unclear because several contradictory findings have been reported [4]. For instance, most studies have indicated that human milk may be a source of probiotic bacteria for the infant because lactobacilli and bifidobacteria are common, albeit less abundant (2%–3% relative abundance), constituents of the milk microbiota [1,9,13,14]. In contrast, a complete absence of lactobacilli or bifidobacteria in human milk has been reported [15,16]. Previously, we investigated the bacterial profiles of human milk samples collected in Taiwan via a culture-based approach. Of 19 milk samples, only one was found to be colonized with *Lactobacillus gasseri*, and little *Bifidobacterium* species were not isolated from any of the samples [17]. Moreover, a recent study assessed the bacterial composition of milk from mothers in Taiwan and China, and they reported the predominant bacterial family to be *Lactobacillaceae* (at 6.2% relative abundance), but *Bifidobacterium* seems not to be a predominant genus in human milk samples [18].

Some reports have provided contradictory data on the abundance of lactobacilli and bifidobacteria in human milk samples, and composition of the microbiota in human milk in Taiwan is not fully understood. In the aforementioned study on the milk microbiota in Taiwan [18], 31 milk samples from seven cities have been obtained, and only several milk samples were collected per city. Moreover, these milk samples had been collected during quite a long sampling period (from donors 0.5–2.7 months after a delivery). As described above, many factors can shape the milk microbiota. Therefore, in the current study, using a molecular approach, we investigated the bacterial patterns in human milk samples harvested from donors mostly within 12 days after delivery. This study clarified the proportions of lactobacilli and bifidobacteria in human milk collected locally. The potential roles of milk-isolated lactobacilli are discussed.

2. Materials and methods

2.1. Collection of milk samples

Ethical approval for this study and all experimental protocols was provided by the Institutional Review Board (IRB) of Saint

Mary's Hospital, Lundong (IRB104011). All the methods were carried out in accordance with relevant guidelines and regulations of the IRB. Briefly, milk samples were donated from January to June 2016 by mothers visiting Saint Mary's Hospital, which is located in eastern Taiwan (Yilan County). As shown in Table 1, 33 healthy Taiwanese mothers (age range 17–43 years; samples D1 to D33) without mastitis or any infectious diseases were randomly recruited to donate milk samples. Written informed consent was obtained from all the participants. Thirty participants provided their milk samples within 12 days after delivery, and 3 participants provided their milk samples between 120 and 320 days after delivery (Table 1).

Milk samples were collected following the protocol used in a previous report [10], with several modifications. Briefly, milk samples were collected into sterile tubes by manual expression using sterile gloves after nipples and areolas were cleaned with a swab soaked in sterile water or saline; the first 1–2 mL of milk was discarded to avoid contamination from the environment. Then, 5–15 mL of milk was collected and was immediately frozen and stored at -20°C until DNA was extracted for the microbial diversity analysis. The collected milk samples were also categorized according to the length of time postpartum, including colostrum (within 5 days postpartum; D1 to D20), transitional milk (between 6 and 15 days

Table 1 – Information of milk sample and donor.

Sample (donor)	Age	Sampling Day ^a
D1	31	3
D2	43	5
D3	28	5
D4	33	5
D5	28	3
D6	26	5
D7	34	2
D8	34	5
D9	24	5
D10	23	5
D11	33	5
D12	19	5
D13	17	2
D14	32	4
D15	32	3
D16	26	3
D17	32	3
D18	32	5
D19	22	5
D20	22	5
D21	26	7
D22	25	7
D23	30	7
D24	22	7
D25	28	7
D26	35	7
D27	25	12
D28	33	6
D29	35	6
D30	33	12
D31	28	120
D32	35	120
D33	31	320

^a Days after delivery.

Download English Version:

<https://daneshyari.com/en/article/10158255>

Download Persian Version:

<https://daneshyari.com/article/10158255>

[Daneshyari.com](https://daneshyari.com)