

PLOS ONE | 中国母亲母乳的微生物组成

本文关键字：中国母亲、母乳、微生物群、分娩方式、哺乳阶段

影响因子：2.766

建议阅读时间：1.5 分钟

本研究在明研究的基础上，对处于不同哺乳阶段中国母亲母乳中的微生物群进行了测定。

研究采用 16SrRNA 基因片段测序和双歧杆菌、乳酸杆菌及总细菌的特异性 qPCR 的方法对整个母乳的微生物群进行了分析，分为没有进行无菌清洁的标准方案组 (n=60) 和无菌采集组 (n=30)。同时，研究还探究了分娩方式及哺乳阶段对母乳中微生物组成的影响。

在两种采集方案中，母乳的微生物群以链球菌和葡萄球菌为主，标准采集方案组中的不动杆菌属属于主要菌落。虽然既往针对其他人群的研究，报道的都是链球菌和葡萄球菌占优势，仅有一个研究报道了不动杆菌属丰度，而且研究还是在没有无菌清洁乳房和挤掉前乳的情况下完成的。在少量利用标准方案采集的母乳样本中发现了较高的细菌计数。少量样本中存在双歧杆菌和乳酸杆菌，丰度较低。

我们观察到哺乳阶段或分娩方式对微生物组成没有影响。采集方法及地理差异很可能是迄今为止研究中报告的微生物群组成出现差异的原因。

参考文献：Sakwinska O, et al. PLoS One. 2016 Aug 16;11(8):e0160856.

文献链接：

<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0160856>

Table 2. Maternal and infant characteristics.

Variable	Aseptic protocol (n = 30)	Standard protocol (n = 60)
Mother		
Age (years), Mean (SD)	28.1 (3.6)	28.2 (3.7)
Height (cm), Mean (SD)	163 (5.1)	162 (5.4)
Weight (kg), Mean (SD)	63.4 (7.8)	65.4 (9.5)
BMI (kg/m ²)	23.9 (3.3)	25.1 (3.5)
Caesarean delivery, N (%)	13 (43)	33 (55)
Infant		
Males, N (%)	13 (48)	21 (37)
Gestational age at birth (weeks), Mean (SD)	39.5 (1.1)	39.2 (1.2)

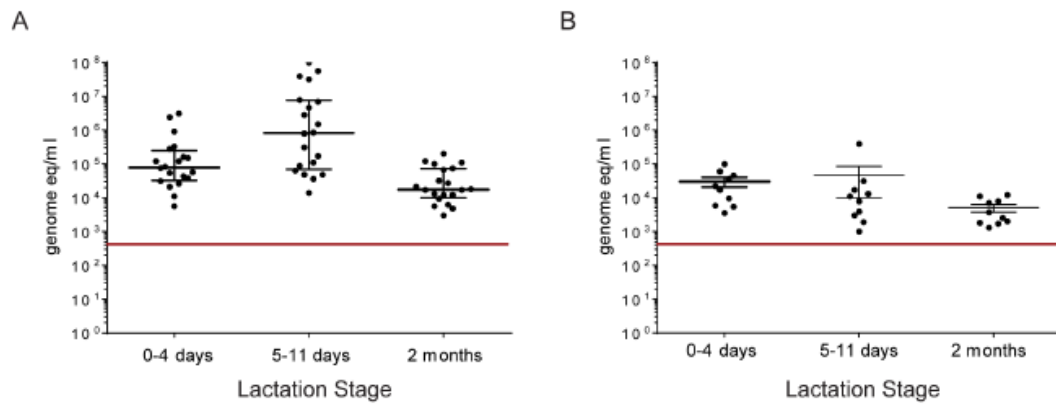


Fig 1. Quantification of bacteria by qPCR. Total bacteria counts measured by qPCR in samples collected with standard (A) and aseptic protocol (B) at three lactation stages. Detection limits are shown by red line.

Table 3. Detection of lactobacilli and bifidobacteria in breast milk samples. Number of positive samples is shown.

Condition	n	Bifidobacteria	Lactobacilli
Aseptic Protocol			
0-4 days	10	2	2
5-11 days	10	0	1
2 months	10	0	0
Standard protocol			
0-4 days	20	2	0
5-11 days	20	0	0
2 months	20	1	2

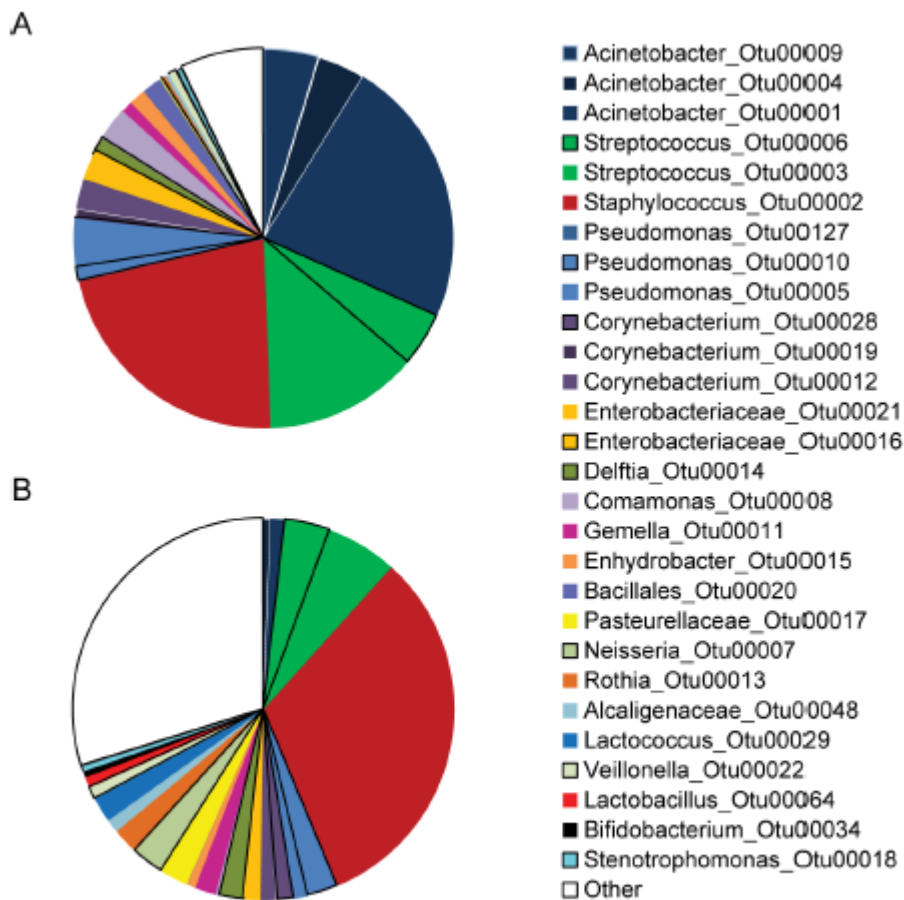


Fig 2. Average microbiota profiles. Microbiota composition in samples collected with standard (A) and aseptic protocol (B). Average abundances of OTUs are shown. Sequences belonging to OTUs which contained smaller number of sequences were pooled and are labeled "Other".

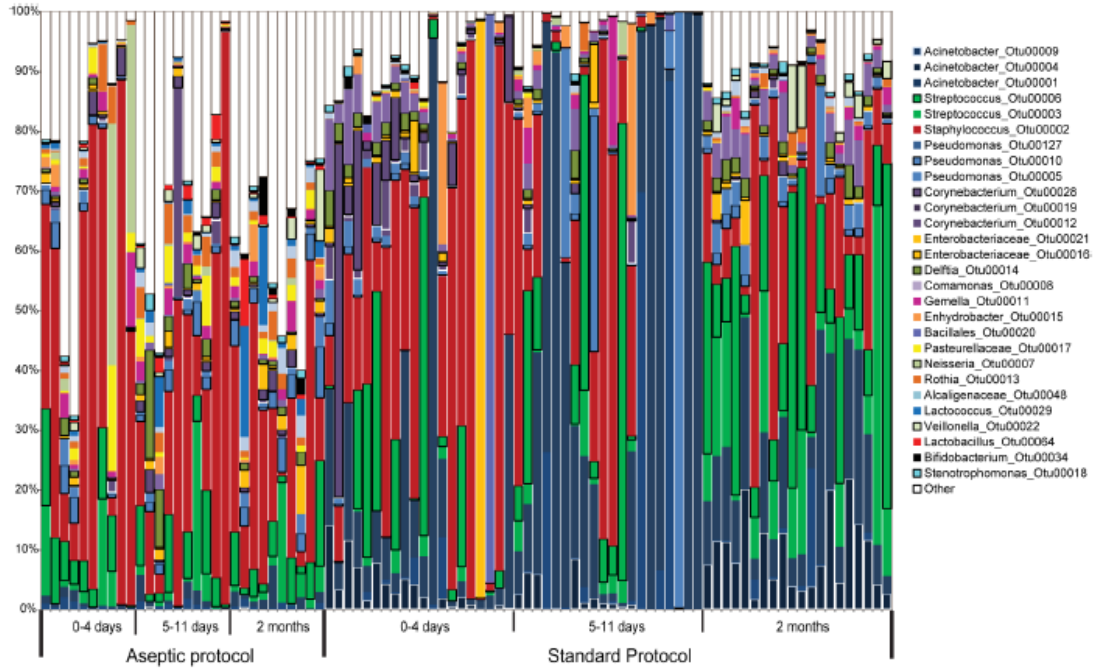


Fig 3. Microbiota profiles of individual subjects. The composition of breast milk microbiota collected with aseptic and standard protocol at different stages of lactation. The 28 most abundant OTUs are shown. Sequences belonging to OTUs which contained smaller number of sequences were pooled and are labeled "Other".

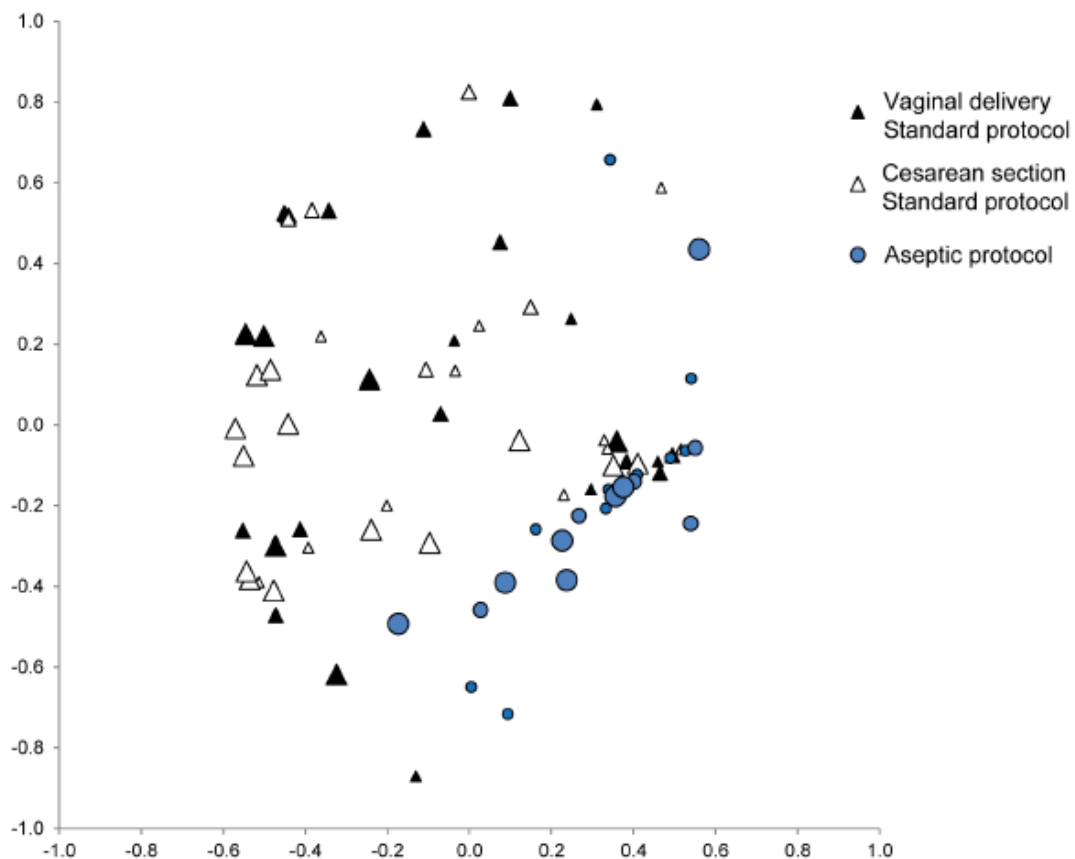


Fig 4. Multivariate analysis. Non-metric multidimensional scaling (NMDS) ordination plot, showing axis 1 and 2. The input data for ordination plots were Yue & Clayton measure of dissimilarity, based on microbiota composition at operational taxonomic unit level. The size of the points represents the time of lactation, the smallest points corresponding to days 0–4 days, the medium to days 5–11, and the largest to month 2.

Table 4. Studies with characterization of bacteria present in breast milk by microbiota profiling

Predominant taxa	Characterization method	Abundance of bifidobacteria and lactobacilli	N	Population	Collection protocol	Reference
<i>Staphylococcus sp.</i> , <i>Streptococcus sp.</i>	Pyrosequencing	"very few sequences"	16	US	Cleansing with iodine Entire breast	[18]
<i>Leuconostoc sp.</i> , <i>Weissella sp.</i>	Pyrosequencing	No <i>Bifidobacterium</i> or <i>Lactobacillus</i> reported	18	Finnish	Cleansing with iodine Rejection of first drops	[15]
<i>Staphylococcus sp.</i> , <i>Pseudomonas sp.</i> , <i>Streptococcus sp.</i> ,	Pyrosequencing	<i>Bifidobacterium</i> 1.3% <i>Lactobacillus</i> absent	7	Swiss	Cleansing with aseptic soap Rejection of foremilk	[8]
<i>Staphylococcaceae</i> , <i>Streptococcaceae</i> , <i>Pseudomonadaceae</i>	Pyrosequencing	No <i>Bifidobacterium</i> or <i>Lactobacillus</i> reported	10	Spanish	Cleansing with chlorhexidine Rejection of first drops	[36]
<i>Acinetobacter sp.</i> , <i>Staphylococcus sp.</i>	Ion Torrent	<i>Bifidobacterium</i> 2% <i>Lactobacillus</i> 1.6%	8	US	Cleansing with saline First 10 to 15 ml taken	[19]
<i>Staphylococcus sp.</i> , Unclassified genus of <i>Enterobacteriaceae</i> , <i>Pseudomonas sp.</i> , <i>Streptococcus sp.</i> ,	Illumina	<i>Bifidobacterium</i> 0.8% <i>Lactobacillus</i> 3%	39	USA Caucasian	Cleansing with saline First 5 to 15 ml taken	[37]
<i>Staphylococcus sp.</i> , <i>Pseudomonas sp.</i> ,	Metagenomics	No <i>Bifidobacterium</i> <i>Lactobacillus</i> 0.2%	10	US	None	[21]
<i>Staphylococcus sp.</i> , <i>Pseudomonas sp.</i> ,	Metagenomics	<i>Bifidobacterium</i> 0.1% <i>Lactobacillus</i> 0.6%	10	Spanish	Cleansing with chlorhexidine Rejection of first drops	[20]

Table 5. Studies with characterization of bacteria present in breast milk by quantitative PCR.

Abundance of Lactobacilli	% bacterial population ¹	Abundance of Bifidobacteria	% bacterial population ¹	N	Population	Collection protocol	Reference
Not tested	Not tested	3.9E+2	Not tested	20	Finnish	Not specified	[13]
Not tested	Not tested	1.4E+3	Not tested	61	Finnish	Samples collected after infant has suckled on the breast	[12]
Not tested	Not tested	3.4E+3	2.8%	23	Spanish	Cleansing with chlorhexidine Rejection of first drops	[14]
3.7E+3	<0.01%	3.6E+3	<0.01%	50	Spanish	Cleansing with chlorhexidine Rejection of first drops	[11]
9.6E+5	197%	3.3E+5	68%	56	Finnish	Cleansing with iodine Rejection of first drops	[15]*
2.7E+4	72%	2.7E+4	54%	18	Finnish	Cleansing with iodine Rejection of first drops	[39]*
2.1E+4	40%	1.7E+2	0.3%	32	Spanish	Cleansing with chlorhexidine	[17]
1.8E+4	44%	1.6E+2	0.4%	10	Spanish	Cleansing with chlorhexidine Rejection of first drops	[36]

¹ Based on division of the counts of bifidobacteria and lactobacilli by total bacterial counts

*Different subsets of the same study, NCT00167700