

Are human breast milk microbiome 'neutral'?

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Human breast milk is considered the most ideal source of nutrition for infants and it should have played a critical role in the evolution and civilizations of human beings. Unlike our intuitive perception, human milk contains a large number of bacterial species, including some opportunistic pathogens of humans. This phenomenon comes as no surprise to scientists and physicians.

Indeed, the existence of milk microbiome is considered to be the result of co-evolutionary and co-adaptive interactions between the microbiome and human host. Furthermore, the dynamic balance in human milk microbiome ecosystem could be fundamental for suppressing the opportunistic pathogens in the breast milk. Nevertheless, until very recently, the ecological analysis of milk microbiome has been limited to assessment of bacterial diversity such as species richness and Shannon diversity index, which is necessary for understanding human milk microbiome but is far from sufficient for understanding the assembly and maintenance mechanism of the breast milk microbiota. The latter is not only interested in by theoretical community ecologists, but also of important clinical significance for understanding the health and disease implications of the breast milk. For example, mastitis is inflammation of the breast with or without infection, and *Staphylococcus aureus* has traditionally been believed to be the pathogen that is typically associated with infectious mastitis.

Ma et al (2014 submitted manuscript) recently postulated that the opportunistic pathogen such as *Staphylococcus aureus*, which has been

confirmed to exist in the [human milk](#) microbiome, is normally suppressed by a network of beneficial bacteria coexisted in the breast milk microbiome, but may become source of infectious mastitis when the host environment permits. Therefore, the breast milk microbiome, similar to the microbiome in the other human body sites such as gut microbiome and perhaps the macrobiome in nature such as lakes, oceans, forests, must maintain their ecosystem (dynamic) balances to stay healthy. Revealing the mechanism of microbiome assembly, succession and maintenance should offer important insights for understanding the health and disease implications of the breast milk microbiome.

A study conducted by a group of scientists led by the University of Idaho Professor Mark McGuire [Hunt et al. (2011)] provided the most comprehensive 16s-rRNA experimental survey of milk microbiome to date, which offers an ideal dataset for studying the above-mentioned mechanisms. By reanalyzing Hunt et al (2011) 16s-rRNA data set, Guan & Ma (2014), from the Computational Biology and Medical Ecology Lab of the Chinese Academy of Sciences, applied Hubbell's neutral theory and Taylor's power law from macroecology to understand how the milk bacteria diversity are maintained and distributed. The power law analysis demonstrated the non-random and heterogeneous natures of both bacterial population abundance and species abundance distributions in the breast milk microbiome. Furthermore, all milk bacterial communities failed to fit to Hubbell's neutral theory model, indicating the possibility of niche differentiation and the presence of dominant species in the breast milk microbiota.

These results, for the first time, revealed that the bacterial diversity and distributions in the [human breast milk](#) are maintained by possible niche differentiation, and confirmed the role of dominant species in maintaining milk microbial diversity. Furthermore, both the single-species population abundance (at population level) and species

abundance distributions (at community level) in the [breast milk](#) microbiome are heterogeneous and non-random. Niche differentiation, heterogeneity and non-randomness properties are typical characteristics of many ecological communities in the nature. Hence, a take-home message from Guan & Ma (2014) study may be that humans should not only care and conserve the biodiversity of macrobiome of the nature mother, but also care and appreciate the biodiversity of the microbiome of the mothers, for our races and civilizations to sustain and prosper.

More information: Guan Q, Ma, ZS (2014) Ecological analysis of the human milk microbiome. *Chinese Science Bulletin* (Chinese Version), 2014, 59(22): 2205-2212, csb.scichina.com:8080/kxtb/CN/...0.1360/N972014-00098

Related:

[1] Hunt KM, Foster JA, Forney LJ, Schutte UME, Beck D, Abdo Z, Fox LK, Williams JE, McGuire MK, McGuire MA. (2011). Characterization of the Diversity and Temporal Stability of Bacterial Communities in Human Milk. *Plos One* 6: e21313

[2] Ma, ZS, Guan, Q, Ye, CX, Foster, JA, Forney, LJ (2014) Network analysis reveals a potentially 'evil' alliance of opportunistic pathogens inhibited by a cooperative network in human milk bacterial communities (Submitted manuscript)

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