Milk- and solid-feeding practices and daycare attendance are associated with differences in bacterial diversity, predominant communities, and metabolic and immune function of the infant gut microbiome

Amanda L. Thompson, Andrea Monteagudo-Mera, Maria B. Cadenas, Michelle L. Lampl and M. A. Azcarate-Peril

The development of the infant intestinal microbiome in response to dietary and other exposures may shape long-term metabolic and immune function. We examined differences in the community structure and function of the intestinal microbiome between four feeding groups, exclusively breastfed infants before introduction of solid foods (EBF), non-exclusively breastfed infants before introduction of solid foods (non-EBF), EBF infants after introduction of solid foods (EBF+S), and non-EBF infants after introduction of solid foods (non-EBF+S), and tested whether out-of-home daycare attendance was associated with differences in relative abundance of gut bacteria. Bacterial 16S rRNA amplicon sequencing was performed on 49 stool samples collected longitudinally from a cohort of 9 infants (5 male, 4 female). PICRUSt metabolic inference analysis was used to identify metabolic impacts of feeding practices on the infant gut microbiome. Sequencing data identified significant differences across groups defined by feeding and daycare attendance. Non-EBF and daycare-attending infants had higher diversity and species richness than EBF and non-daycare attending infants. The gut microbiome of EBF infants showed increased proportions of Bifidobacterium and lower abundance of Bacteroidetes and Clostridiales than non-EBF infants. PICRUSt analysis indicated that introduction of solid foods had a marginal impact on the microbiome of EBF infants (24 enzymes overrepresented in EBF+S infants). In contrast, over 200 bacterial gene categories were overrepresented in non-EBF+S compared to non-EBF infants including several bacterial methyl-accepting chemotaxis proteins (MCP) involved in signal transduction. The identified differences between EBF and non-EBF infants suggest that breast milk may provide the gut microbiome with a greater plasticity (despite having a lower phylogenetic diversity) that eases the transition into solid foods.

Keywords: infant gut microbiome, breastfeeding, metagenomics, daycare, feeding transitions


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Valerio Lebbia, Sapienza University of Rome, Italy
Karl Thompson, Howard University, USA

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This study was interesting, but I have a few issues with it.

The researchers hypothesize that breastfed babies will have an easy transition to solids due to the differences in the gut biome. Is there any evidence that formula fed babies have difficulties starting solids (from this study or others?)

In the press releases and the study, it is also stated that breastfed babies may have less problems with obesity and allergies due to the differences in the microbiota.

The researchers seem to be unaware that most well done large scale studies do not find that breastfeeding has a causal effect on obesity (1), or allergic conditions (asthma, eczema, food allergies) (2) and some that some studies find an increase with breastfeeding (2).

This study found a more diverse biome, and more enzymes in babies fed both formula and breastmilk. Do you suppose it could be possible that decreased allergies in those fed formula could be due to the increased diversity of microbes and enzymes?

The authors also state that breastfeeding is associated with lower morbidity from diabetes and CVD, citing an archived 2007 AHRQ analysis (3)which only found an association, not necessarily causal relationship. Several recent studies have been inconclusive, or found no effect of breastfeeding diabetes (4) or CVD(5).

(1). Obesity

(2) Atopic conditions
Eczema
Asthma
http://researchnews.osu.edu/archive/sibbreast.htm 2014 Sibling study (obesity also)

(3) AHRQ report

(4) Diabetes/CVD
http://www.ncbi.nlm.nih.gov/pubmed/22837371 2012 Review...
http://www.ncbi.nlm.nih.gov/pubmed/20852257 2010 Infant feeding and cardiovascular...
http://www.ncbi.nlm.nih.gov/pubmed/24781689 2014 Infant diet ...

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