



Microbiota dal concepimento ai primi 1000 giorni di vita

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Impianto del microbiota

Microbial Changes during Pregnancy, Birth, and Infancy

Meital Nuriel-Ohayon[†], Hadar Neuman[†] and Omry Koren^{*}

Oral microbiota:

Viable counts ↑
Porphyromonas gingivalis ↑
Aggregatibacter actinomycetemcomitans ↑
Candida ↑

Placental microbiota:

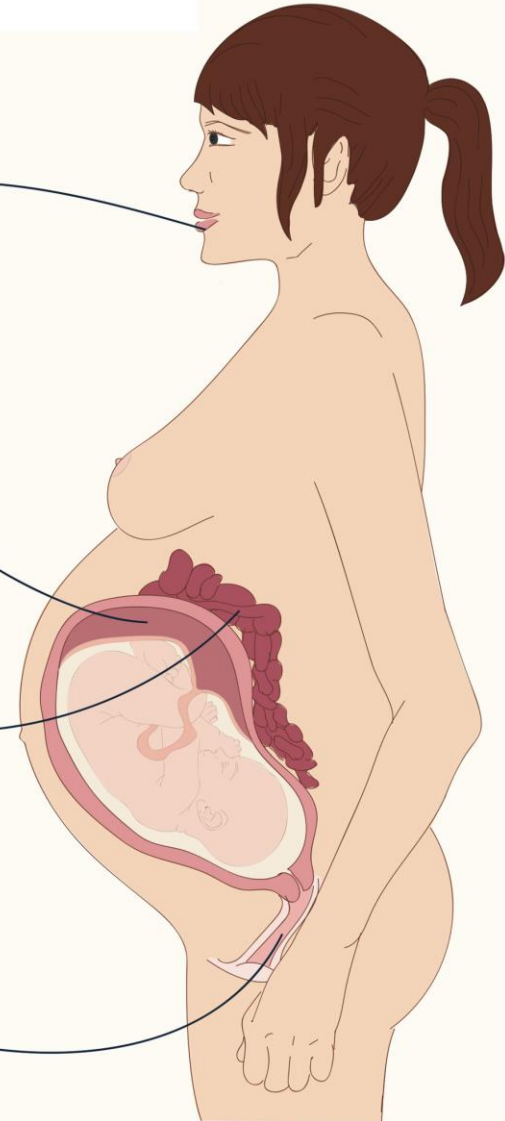
Presence of aerobic and anaerobic bacteria

Gut microbiota:

Actinobacteria ↑
Proteobacteria ↑
Faecalibacterium ↓
 α -diversity ↓
 β -diversity ↑

Vaginal microbiota:

Lactobacillus ↑
 α -diversity ↓
 β -diversity ↓
Stability ↑



A. Changes associated with mode of birth (vaginal vs. C-section)

Prevotella ↑

Lactobacillus ↑

Propionibacterium ↓

Corynebacterium ↓

Enterobacteriaceae ↓

Streptococcus ↓

Earlier colonization of Bacteroidetes

Antibiotic resistance bacterial genes ↓

Resemblance to mother's gut microbiota ↑

Viable counts ↑

β-diversity ↓



B. Changes associated with feeding (breast milk vs. formula)

Bacteroides fragilis ↓

Bifidobacterium infantis ↑

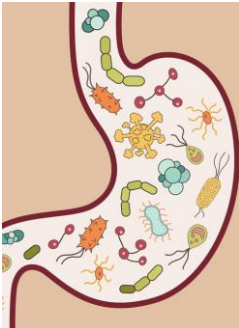
Sneathia ↑

Staphylococcus ↓

α-diversity ↓

Acquisizione del microbiota

- Fase 1: acquisizione di parte della flora materna tramite il canale del parto
- Fase 2: acquisizione tramite latte materno o formulato
- Fase 3: svezzamento
- Fase 4: sviluppo della flora acquisita fino alla colonizzazione definitiva
- Fase 5: stabilità



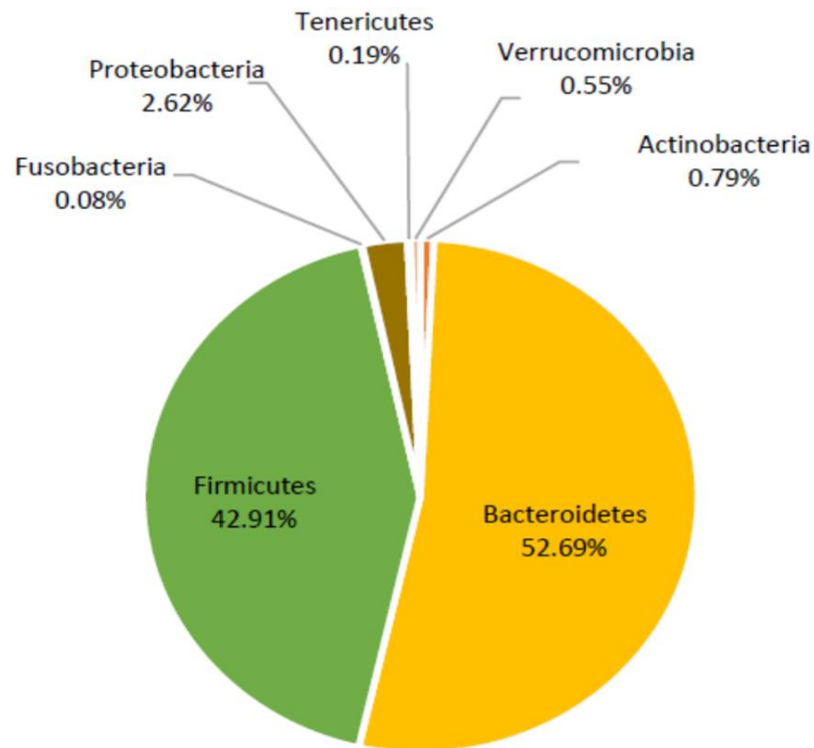
Timing della colonizzazione

La colonizzazione, avvenendo per occupazione di spazi disponibili, è tanto più efficace quanto precoce ed operata da parte di batteri non presenti nella nicchia in questione.

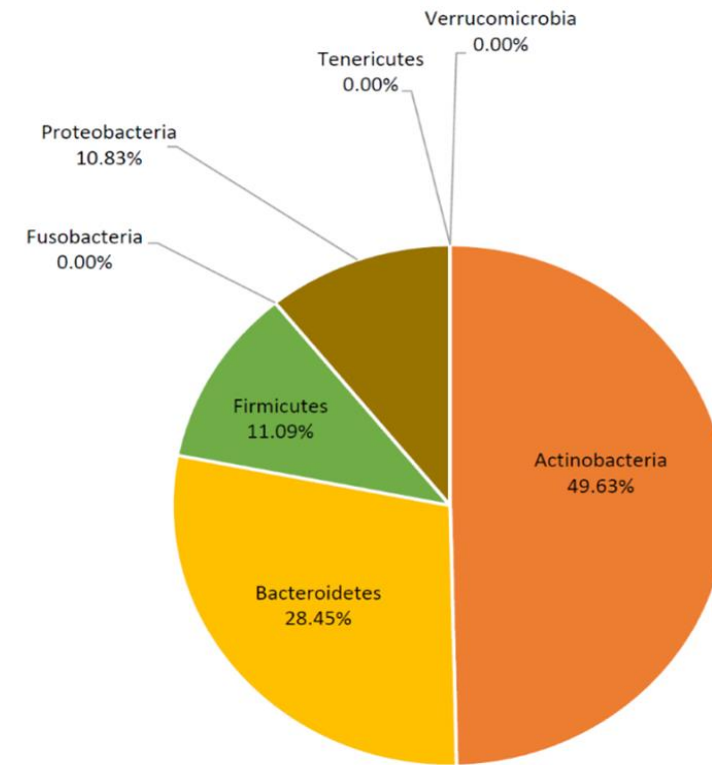
Importanza dei primi 1000 giorni di vita

Microbiota adulto vs lattante

adulto



lattante nato da PS allattato al seno



Microbiota materno

- Trattamenti in gravidanza

[Expert Opin Drug Saf.](#) 2019 Mar;18(3):173-185. doi: 10.1080/14740338.2019.1579795. Epub 2019 Feb 22.

REVIEW

The role of antimicrobial treatment during pregnancy on the neonatal gut microbiome and the development of atopy, asthma, allergy and obesity in childhood

Sarah Milliken^a, Ruridh M. Allen^b and Ronald F. Lamont^{c,d}

ABSTRACT

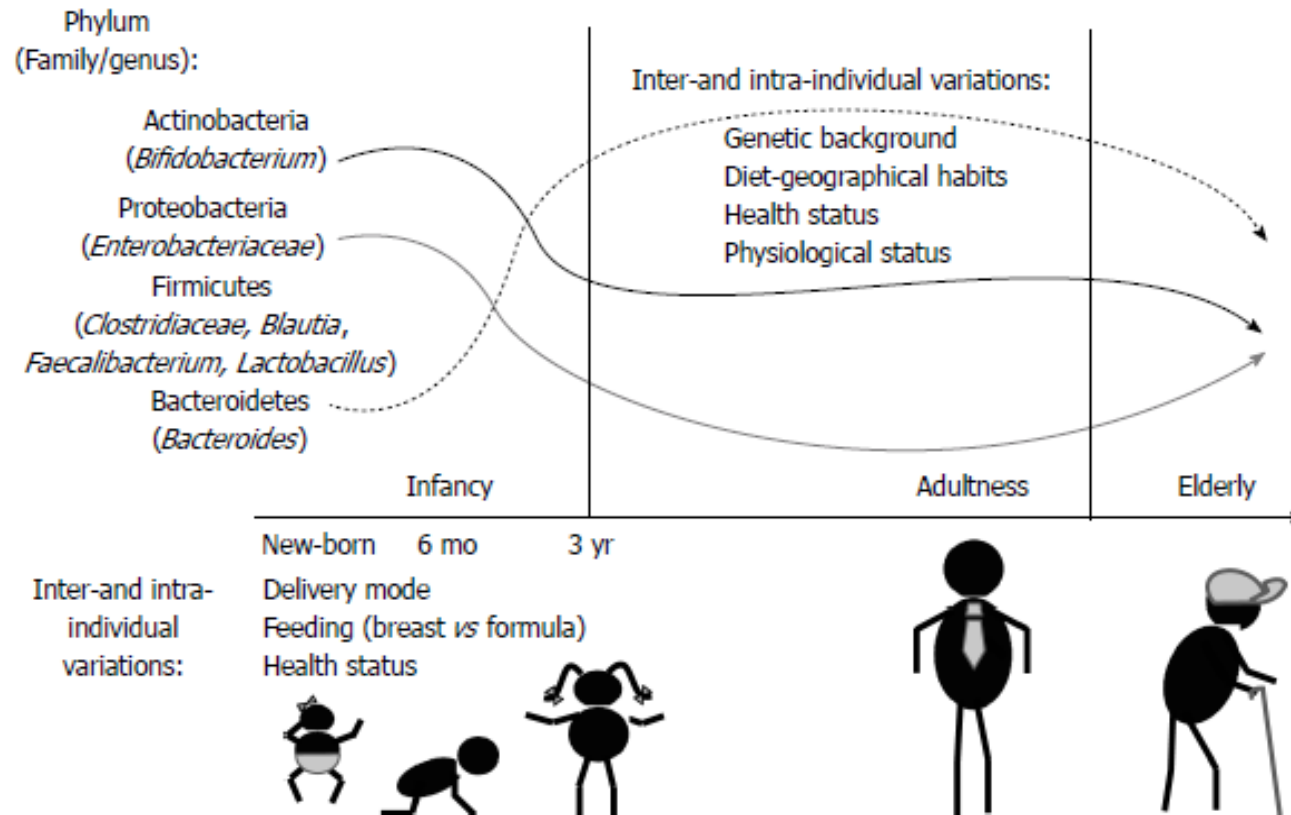
Introduction: The use of antibiotics prenatally, during pregnancy, or neonatally may have adverse effects on the neonatal gut microbiome, and adversely affect the development of the infant immune system, leading to childhood atopy, asthma, allergy and obesity.

Areas covered: Vaginal eubiosis and dysbiosis from molecular-based, cultivation-independent techniques, and how this affects the neonatal gut microbiome and early development of the immune system, the association between maternal antibiotics and the beneficial role of vitamin D in the development of atopy, asthma, allergy and obesity, efforts to reduce the use of antibiotics in pregnancy and therapeutic interventions such as vaginal 'seeding', probiotics, breastfeeding and neonatal dietary supplementation.

Expert opinion: Currently available research gives insufficient attention to confounding variables. There remains uncertainty as to whether it is relevant that the mother suffered from the same condition as the purported infant outcome variable, for which she may have received antibiotics. In most studies, there is a lack of control for the number of antibiotic courses administered, the timing of use, the use of broad spectrum or narrow range antibiotics, the indication for antibiotics, the dose-dependent nature of the effect, the class of antibiotics used, or a varying degree of risk.

Variazioni in base all'età

Tojo R *et al.* Intestinal bifidobacteria in health and disease



First Foods and Gut Microbes

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frontiers
in Microbiology

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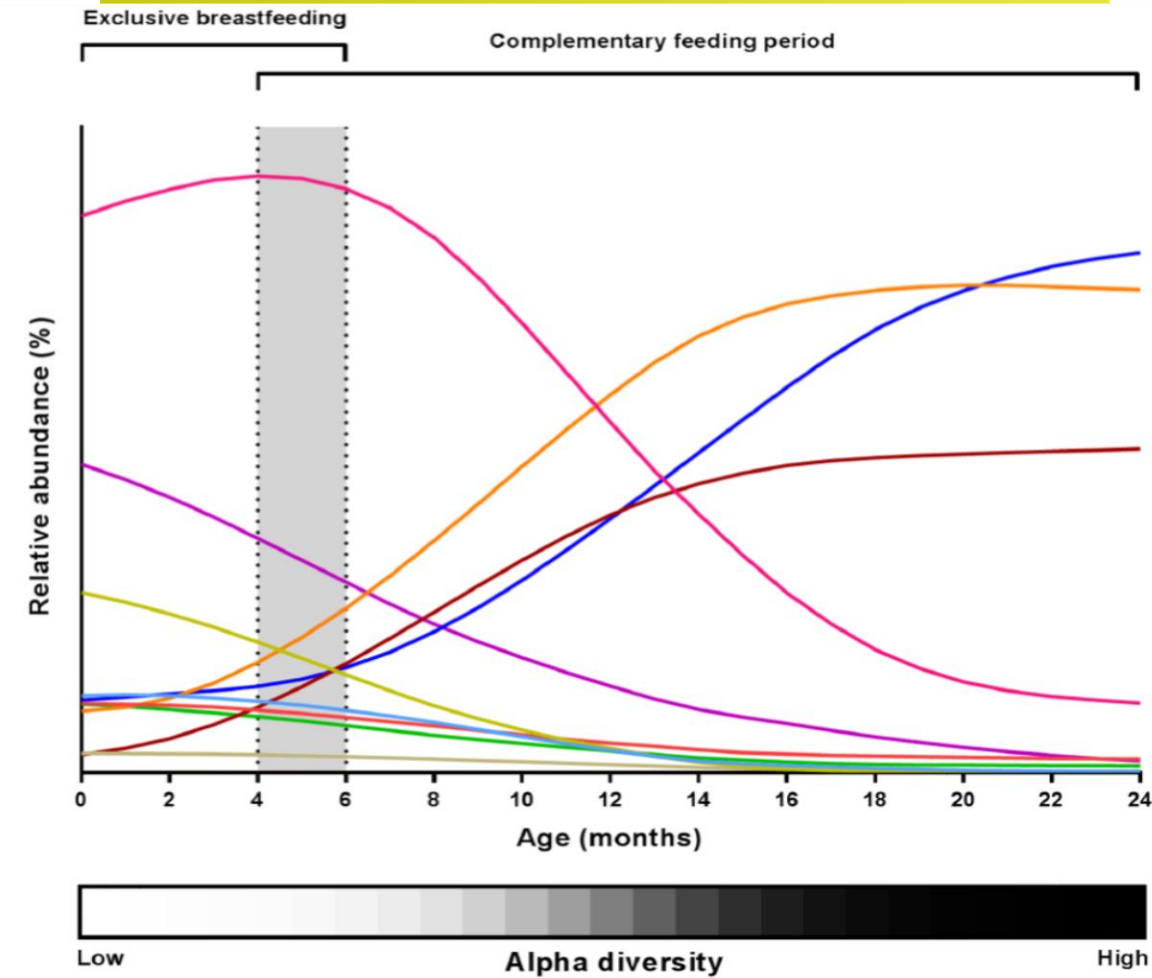


FIGURE 2 | Changes in the major gut microbial taxa during the first 24 months of life. Relative abundance estimates and curve shapes are based on average values from available literature (Arrieta et al., 2014; Bäckhed et al., 2015; Kostic et al., 2015; Laursen et al., 2016; Yassour et al., 2016). Individual abundances were normalized to an abundance sum for all bacterial families at each month, and curve smoothing was performed with GraphPad Prism. Dashed lines and gray background indicate the period of introduction to solid foods. Alpha diversity development is shown by a grayscale gradient (white = low diversity, black = high diversity).

Variazione dei bifidobatteri per età

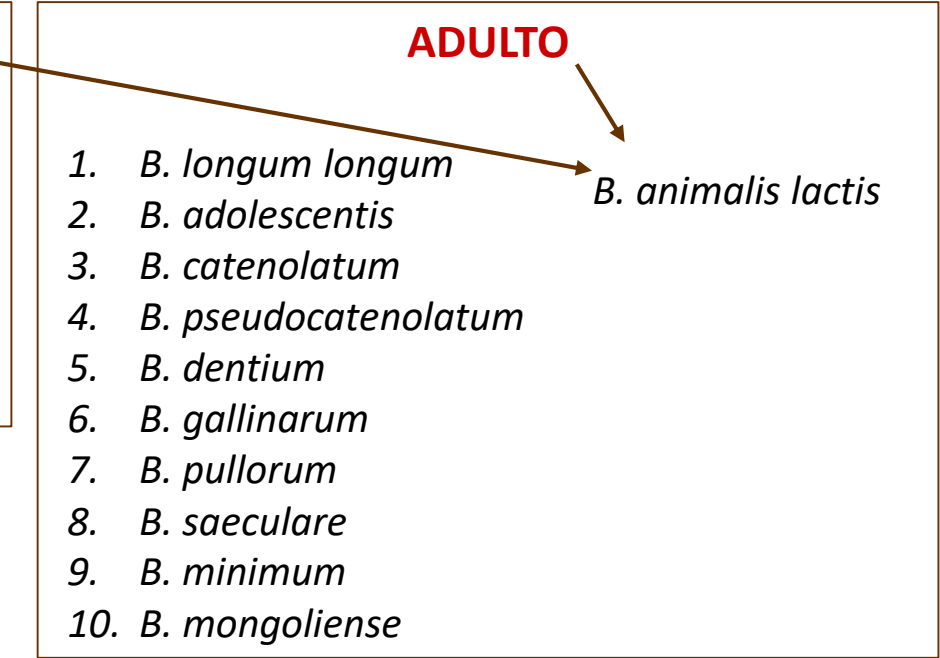
Con gli ultimi 6 (*Figura 1*) identificati nel 2018 dal gruppo di ricerca del Prof. Marco Ventura⁴, se ne conoscono oggi almeno **67 specie diverse** identificate come in Tabella 1. Di

Table 3. The frequency of *Bifidobacterium* spp. by PCR-DGGE during the first 6 months of life.

	3 th week	12 th week	6 th month
<i>B. breve</i>	29% (10/34)	35% (12/34)	25% (9/36)
<i>B. adolescentis</i>	9% (3/34)	6% (2/34)	14% (5/36)
<i>B. bifidum</i>	12% (4/34)	24% (8/34)	42% (15/36)
<i>B. angulatum</i>	N.D.	3% (1/34)	N.D.
<i>B. longum</i>	44% (15/34)	59% (20/34)	72% (26/36)
<i>B. catenulatum</i> group*	18% (6/34)	18% (6/34)	31% (11/36)

l'intestino umano solo il *B. adolescentis*, il *B. bifidum*, il *B. bre-*
idocatenulatum, il *B. dentium*, il *B. gallinarum*, il *B. pullorum*,
B. minimum e il *B. mongoliense*. L'analisi delle feci coloniche

ADULTO

- 
1. *B. longum longum*
 2. *B. adolescentis*
 3. *B. catenolatum*
 4. *B. pseudocatenolatum*
 5. *B. dentium*
 6. *B. gallinarum*
 7. *B. pullorum*
 8. *B. saeculare*
 9. *B. minimum*
 10. *B. mongoliense*
- B. animalis lactis*

Variazioni inter- ed intra-individuali

- ▶ Microbiota materno
- ▶ Tipo di parto
- ▶ Profilassi intrapartum
- ▶ Ambiente
- ▶ Allattamento
- ▶ Terapie



Microbiota materno

- Microbiota individuale

- Il latte di mamme che hanno partorito per TC presenta notevole riduzione di Bifidobatteri
- Il latte di mamme di pretermine è meno ricco di Bifidobatteri
- Il latte di mamme allergiche ha meno Bifidobatteri
- Il latte di mamme celiache ha meno Bifidobatteri e meno Bacteroides
- Il latte di mamme obese ha meno Bifidobatteri ma più Stafilococchi



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Tipo di parto



The mode of delivery affects the diversity and colonization pattern of the gut microbiota during the first year of infants' life: a systematic review

Erigene Rutayisire¹, Kun Huang^{1,2}, Yehao Liu³ and Fangbiao Tao^{1,2*}

Results: Seven out of 652 retrieved studies met inclusion criteria, were included in systematic analysis. Caesarean Section (CS) was associated with both lower abundance and diversity of the phyla Actinobacteria and Bacteroidetes, and higher abundance and diversity of the phylum Firmicute from birth to 3 months of life. At the colonization level, *Bifidobacterium*, and *Bacteroides* genera seems to be significantly more frequent in vaginally delivered infants compared with CS delivered. These infants were more colonized by the *Clostridium*, and *Lactobacillus* genera. From the reports, it is tempting to say that delivery mode has less effect on colonization and diversity of *Bifidobacteria*, *Bacteroides*, *Clostridium*, and *Lactobacillus* genera from the age of 6 to 12 months of life.

Profilassi intrapartum

Early Gut Microbiota Perturbations Following Intrapartum Antibiotic Prophylaxis to Prevent Group B Streptococcal Disease

Giuseppe Mazzola¹, Kiera Murphy^{2,3,4}, R. Paul Ross⁴, Diana Di Gioia^{1*}, Bruno Biavati¹, Luigi T. Corvaglia⁵, Giacomo Faldella⁵, Catherine Stanton^{2,4}

Abstract

The faecal microbiota composition of infants born to mothers receiving intrapartum antibiotic prophylaxis with ampicillin against group B *Streptococcus* was compared with that of control infants, at day 7 and 30 of life. Recruited newborns were both exclusive breastfed and mixed fed, in order to also study the effect of dietary factors on the microbiota composition. Massive parallel sequencing of the V3-V4 region of the 16S rRNA gene and qPCR analysis were performed. Antibiotic prophylaxis caused the most marked changes on the microbiota in breastfed infants, mainly resulting in a higher relative abundance of Enterobacteriaceae, compared with control infants (52% vs. 14%, $p = 0.044$) and mixed-fed infants (52% vs. 16%, $p = 0.13$ NS) at day 7 and in a lower bacterial diversity compared to mixed-fed infants and controls. Bifidobacteria were also particularly vulnerable and abundances were reduced in breastfed ($p = 0.001$) and mixed-fed antibiotic treated groups compared to non-treated groups. Reductions in bifidobacteria in antibiotic treated infants were also confirmed by qPCR. By day 30, the bifidobacterial population recovered and abundances significantly increased in both breastfed ($p = 0.025$) and mixed-fed ($p = 0.013$) antibiotic treated groups, whereas Enterobacteriaceae abundances remained highest in the breastfed antibiotic treated group (44%), compared with control infants (16%) and mixed-fed antibiotic treated group (28%). This study has therefore demonstrated the short term consequences of maternal intrapartum antibiotic prophylaxis on the infant faecal microbial population, particularly in that of breastfed infants.

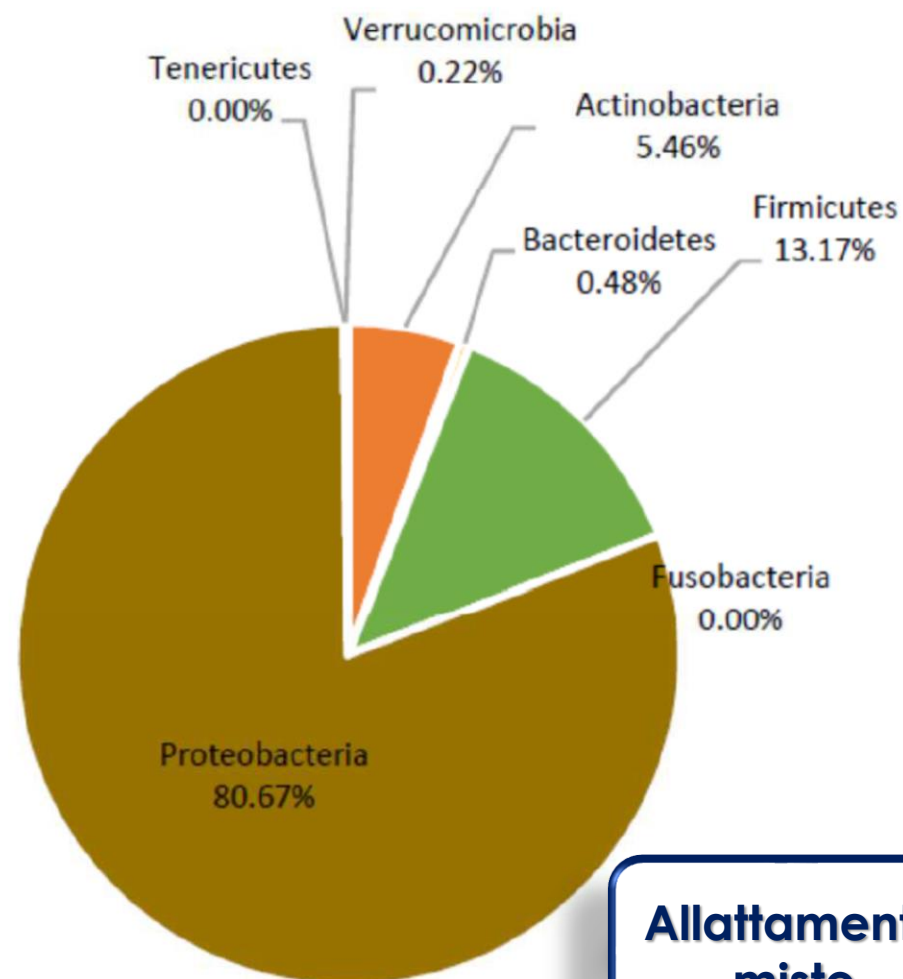
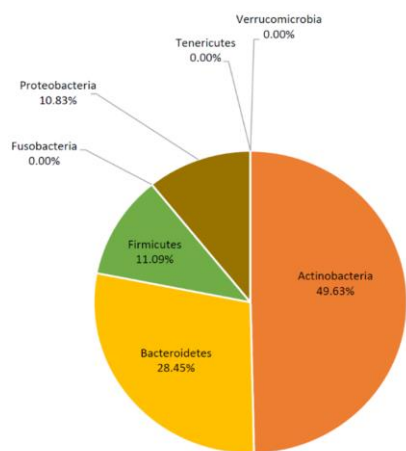
Ambiente



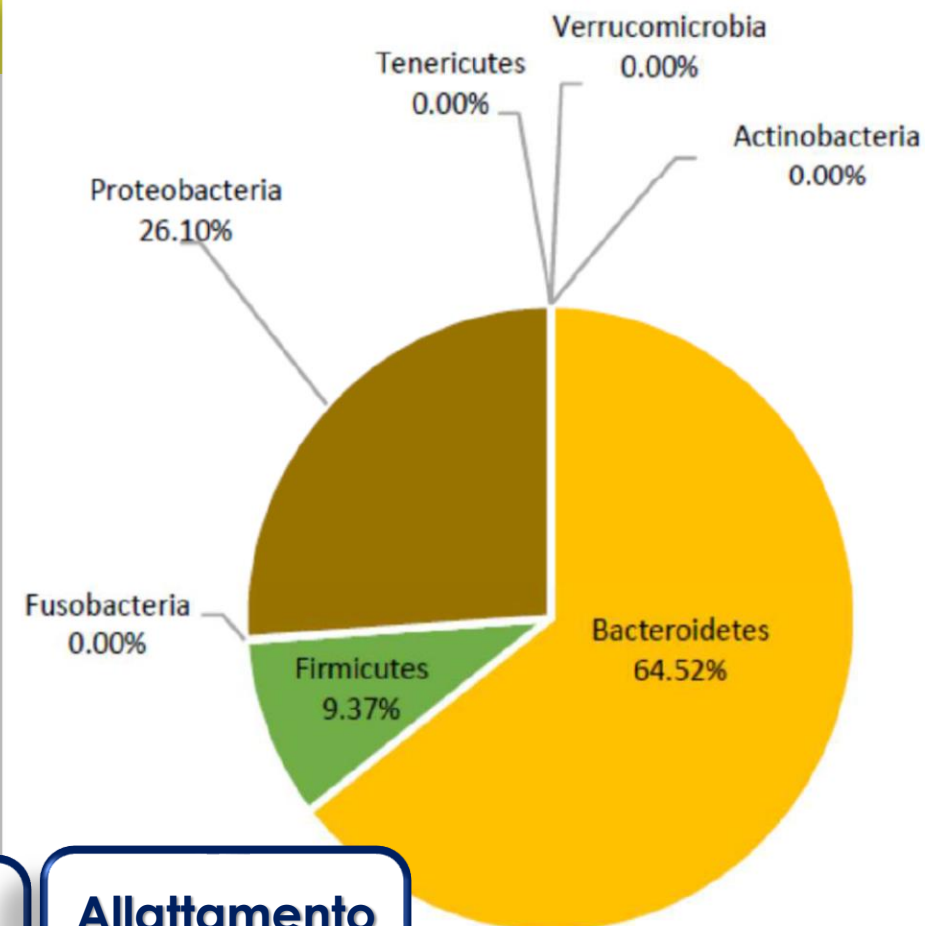
Allattamento

Composizione microbica del campione a livello tassonomico di phylum (*)

Campione



Allattamento
misto

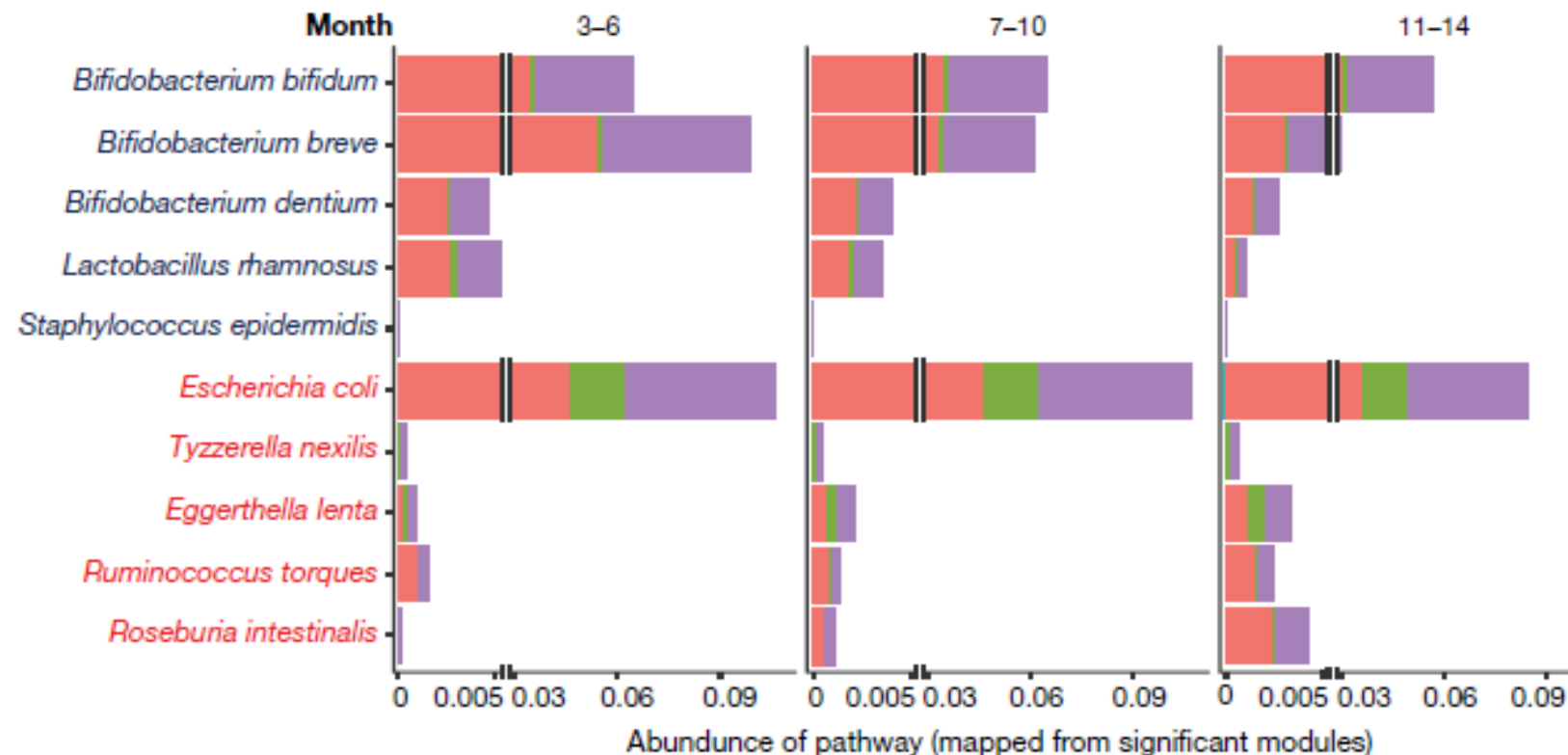


Allattamento
artificiale

Temporal development of the gut microbiome in early childhood from the TEDDY study

Christopher J. Stewart^{1,2,18*}, Nadim J. Ajami^{1,18}, Jacqueline L. O'Brien¹, Diane S. Hutchinson¹, Daniel P. Smith¹, Matthew C. Wong¹, Matthew C. Ross¹, Richard E. Lloyd¹, HarshaVardhan Doddapaneni³, Ginger A. Metcalf³, Donna Muzny³, Richard A. Gibbs³, Tommi Vatanen⁴, Curtis Huttenhower⁴, Ramnik J. Xavier⁴, Marian Rewers⁵, William Hagopian⁶, Jorma Toppari^{7,8}, Anette-G. Ziegler^{9,10,11}, Jin-Xiong She¹², Beena Akolkar¹³, Ake Lernmark¹⁴, Heikki Hyöty^{15,16}, Kendra Vehik¹⁷, Jeffrey P. Krischer¹⁷ & Joseph F. Petrosino^{1*}

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903 pz
3-14 mesi

Il latte materno è un
prebiotico ed un
probiotico



Microbiota del latte materno

- microbiota residente della ghiandola mammaria
- microbiota orale del bambino (flusso retrogrado)
- circolazione entero-mammaria

The Origin of Human Milk Bacteria: Is There a Bacterial Entero-Mammary Pathway during Late Pregnancy and Lactation?¹⁻⁴

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