

Nutrition and Intestinal Microbiota in Infancy

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Ingestion of Bacteria Proposed as Beneficial

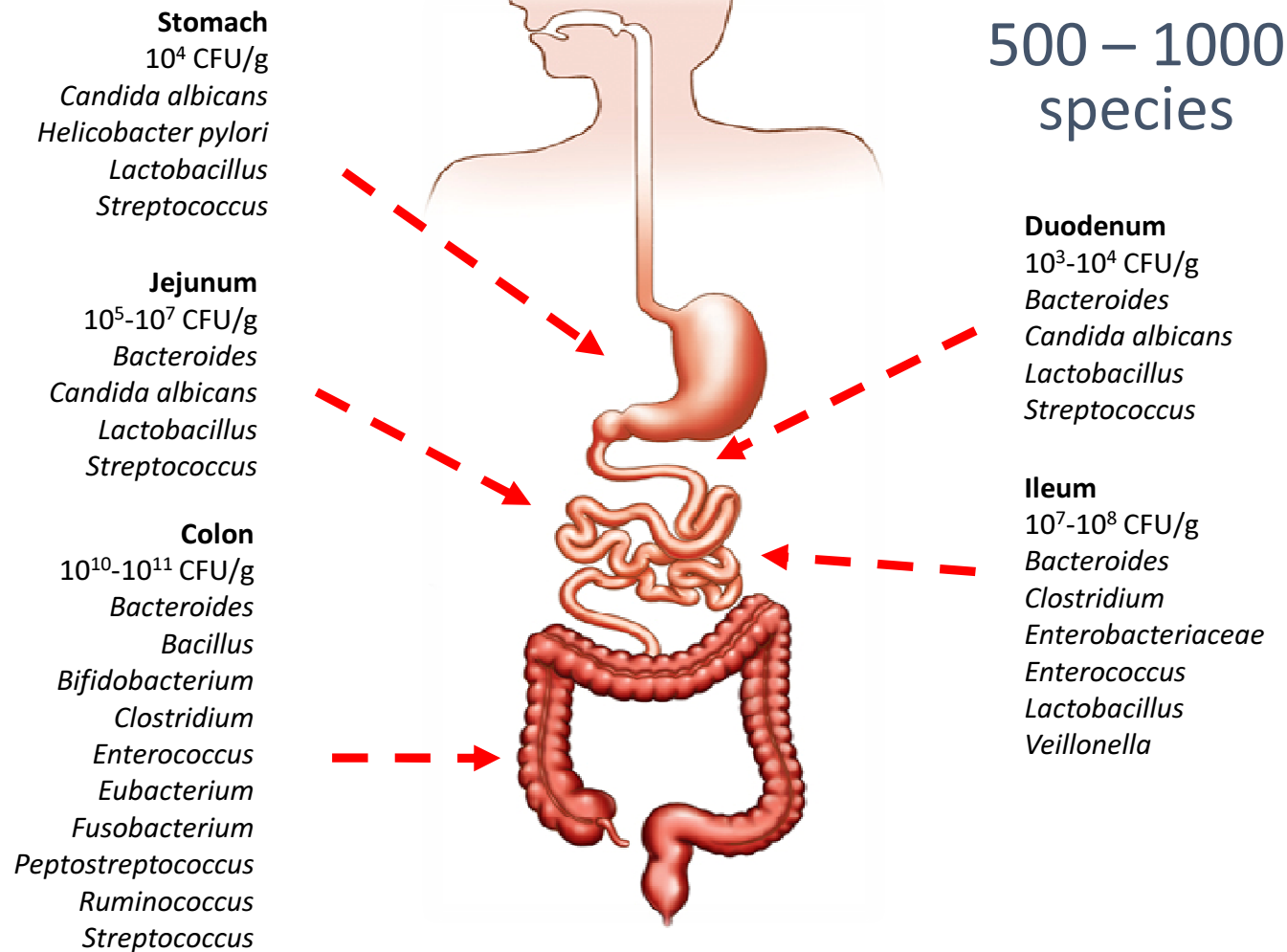


Elie Metchnikoff
(1845-1916)

- Suggested that ingested bacteria could have positive influence on normal microbial flora in intestinal tract
- Hypothesized that Lactobacilli were important for human health and longevity
- Promoted yogurt and fermented foods as healthy

Bacteria in the GI Tract: Complex Ecosystem

Resident and Ingested



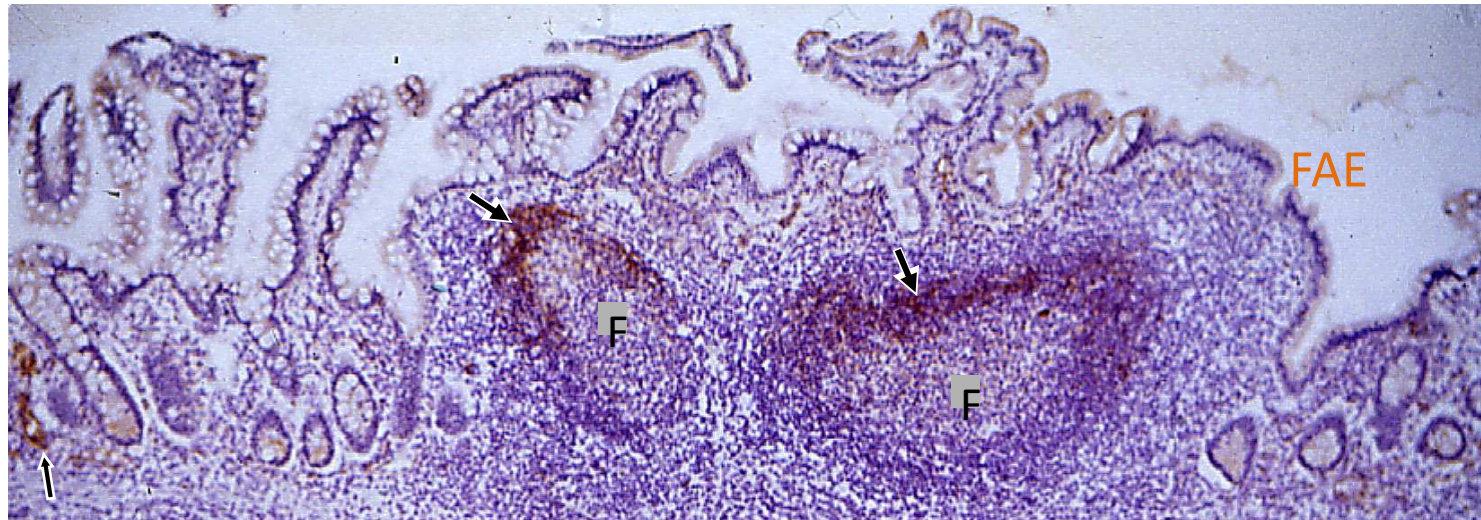
Homo Bacteriensis?



Intestinal Microbiota

- One of the most densely populated microbial ecosystems on Earth
- 100 trillion cells (10 x # of host cells)
- 3,000,000 encoded genes: complement host's metabolic pathways
- 4 dominant phyla; ~1000 species; ~10, 000 strains ("the microbiome")
- Most (approximately 80%) have not yet been cultivated

GUT ASSOCIATED LYMPHOID TISSUE



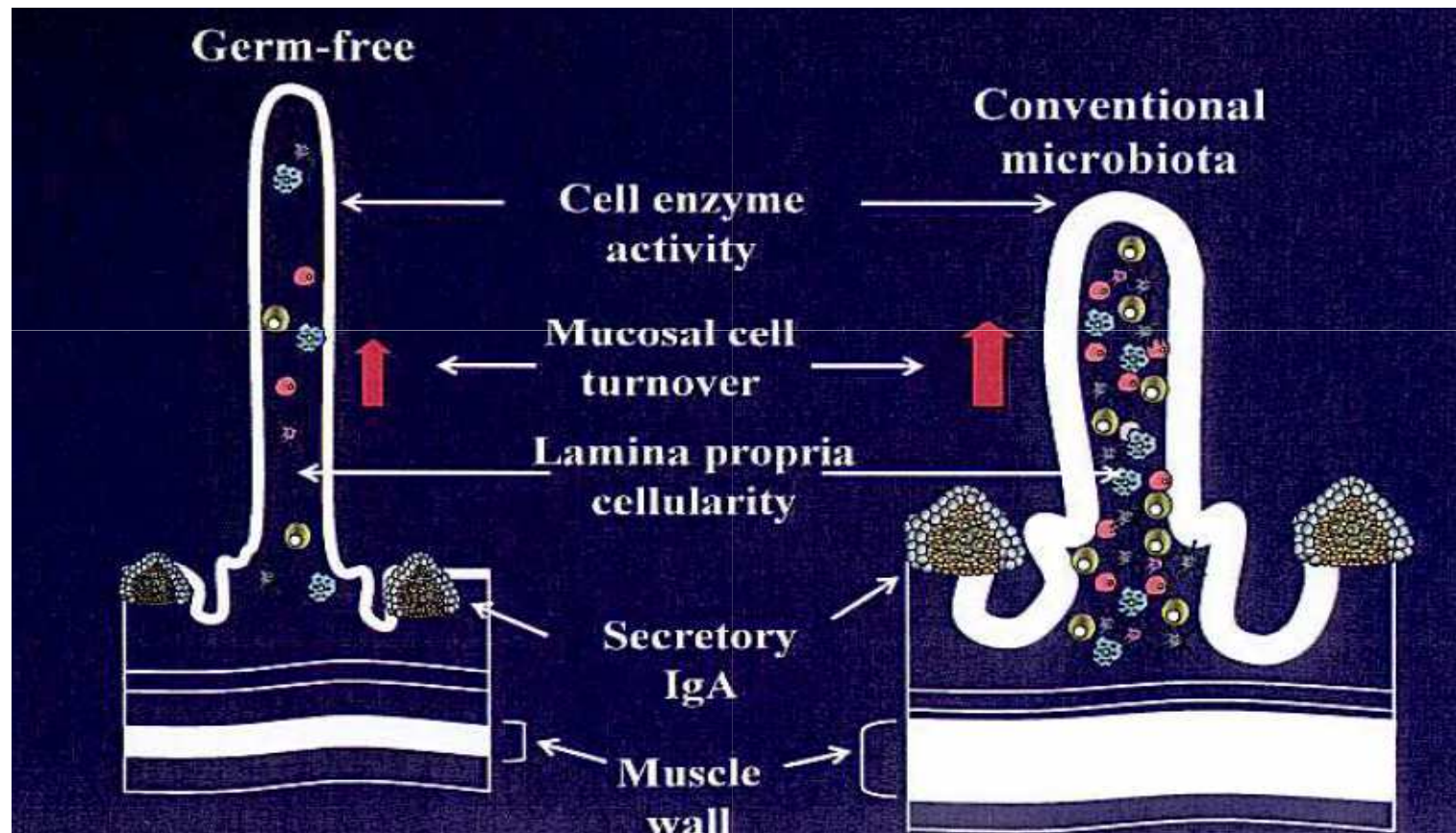
Gut-Associated Lymphoid Tissue structures are strategically situated in proximity to the greatest concentration of microbiota

- Peyer's patches: distal ileum (nos. 100-250)
- Isolated lymphoid follicles (ILFs): large bowel (nos. ~ 30 000)
- **70% of immunologically active cells in the body**

Brandtzaeg, Immunological Investigations 2010

Germ-free vs. Colonized Gut

Bacteria Stimulate Normal Immune response



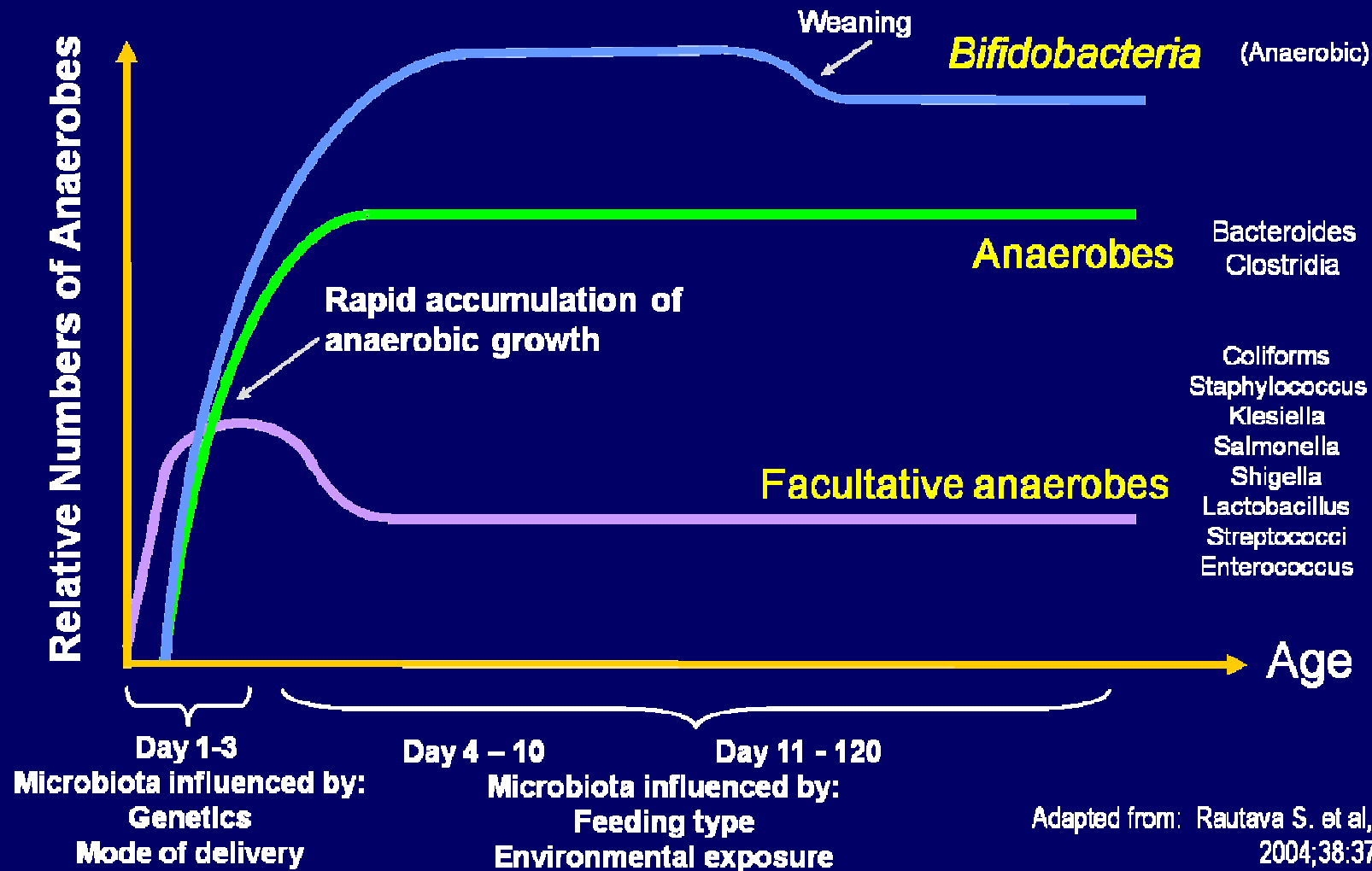
A healthy microbiota is critical to train the immune system to protect the host and decrease the chances for immune over expression (immune related conditions).

Function GI microbiota

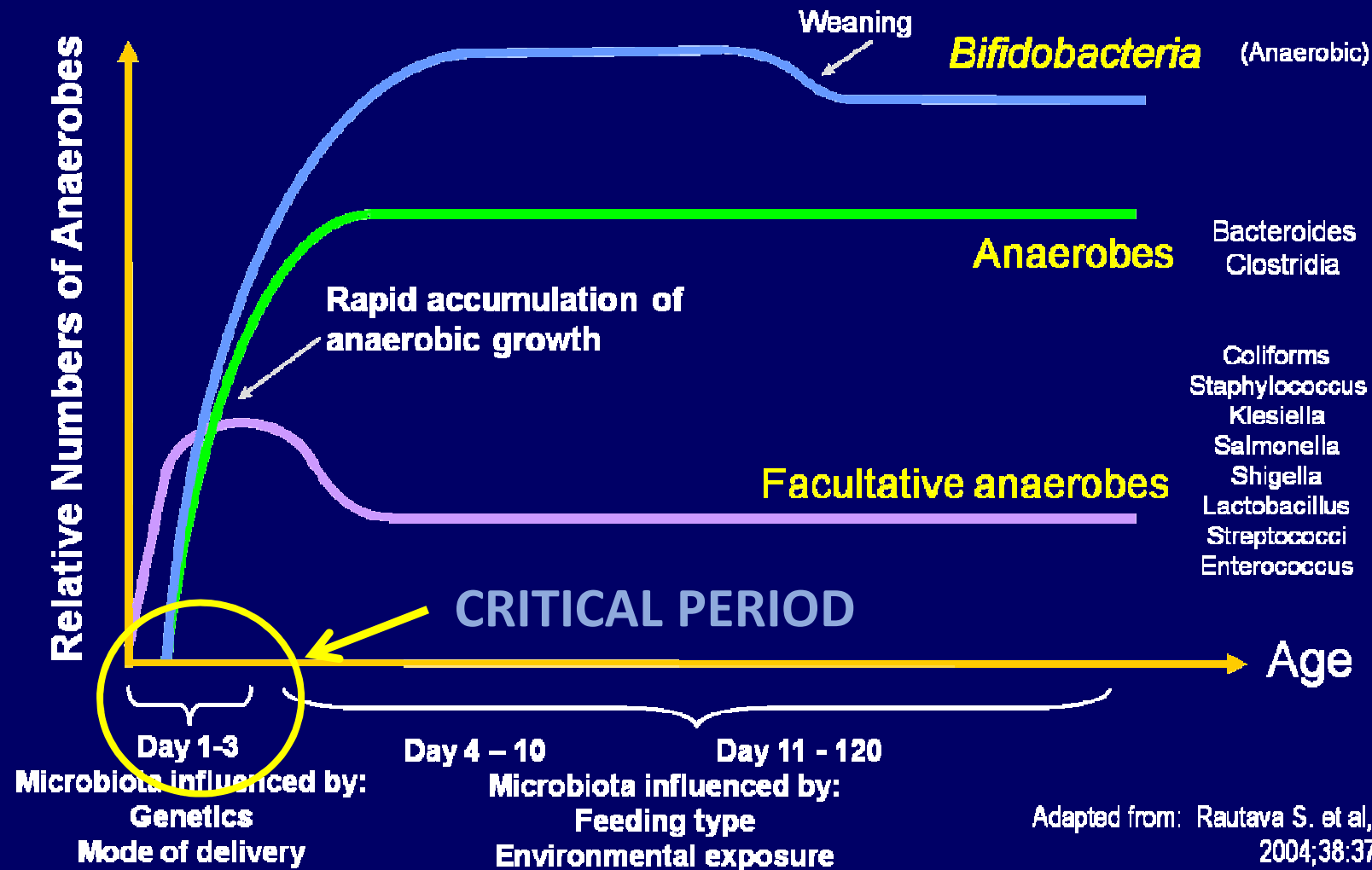
| | |
|----------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Immune development & modulation | <ul style="list-style-type: none">• IgA production• Control of local and general inflammation• Tightening of intercellular junctions• Induction of tolerance to foods |
| Pathogen protection | <ul style="list-style-type: none">• Pathogen displacement / Nutrient competition• Production of mucin & antimicrobial factors• Activation of local immune response• Contribution to the intestinal barrier function |
| Digestive and metabolic functions | <ul style="list-style-type: none">• Vitamin production• Fermentation of non-digestible carbohydrates• Dietary carcinogens metabolism |
| Neuronologic development and function | <ul style="list-style-type: none">• Modulation of brain gut axis during neuronal development• Motor control and anxiety behaviour |

Adapted (JMS) from Buccigrossi et al. Curr Opin Gastroenterol 2013;29:31-8.

Development of Intestinal Microbiota



Development of Intestinal Microbiota



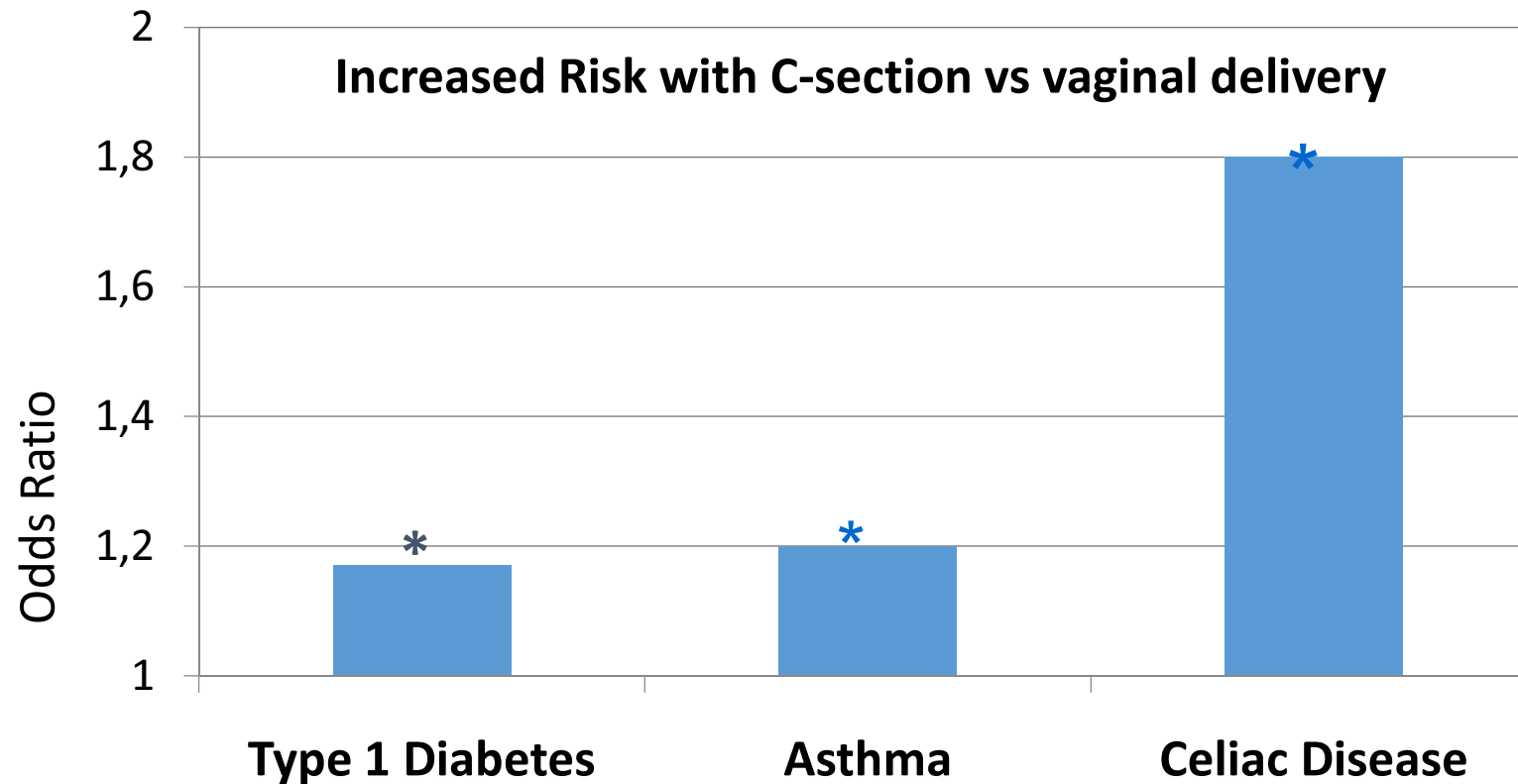
Sources of bacteria for the newborn:

- The vaginal canal and normal delivery
- Breastmilk and breastfeeding

Vaginal delivery is not a sterile procedure

**Are there immunologic consequences
to a sterile birth (C-section)?**

Cesarean Delivery Linked to Increases in Chronic Disease



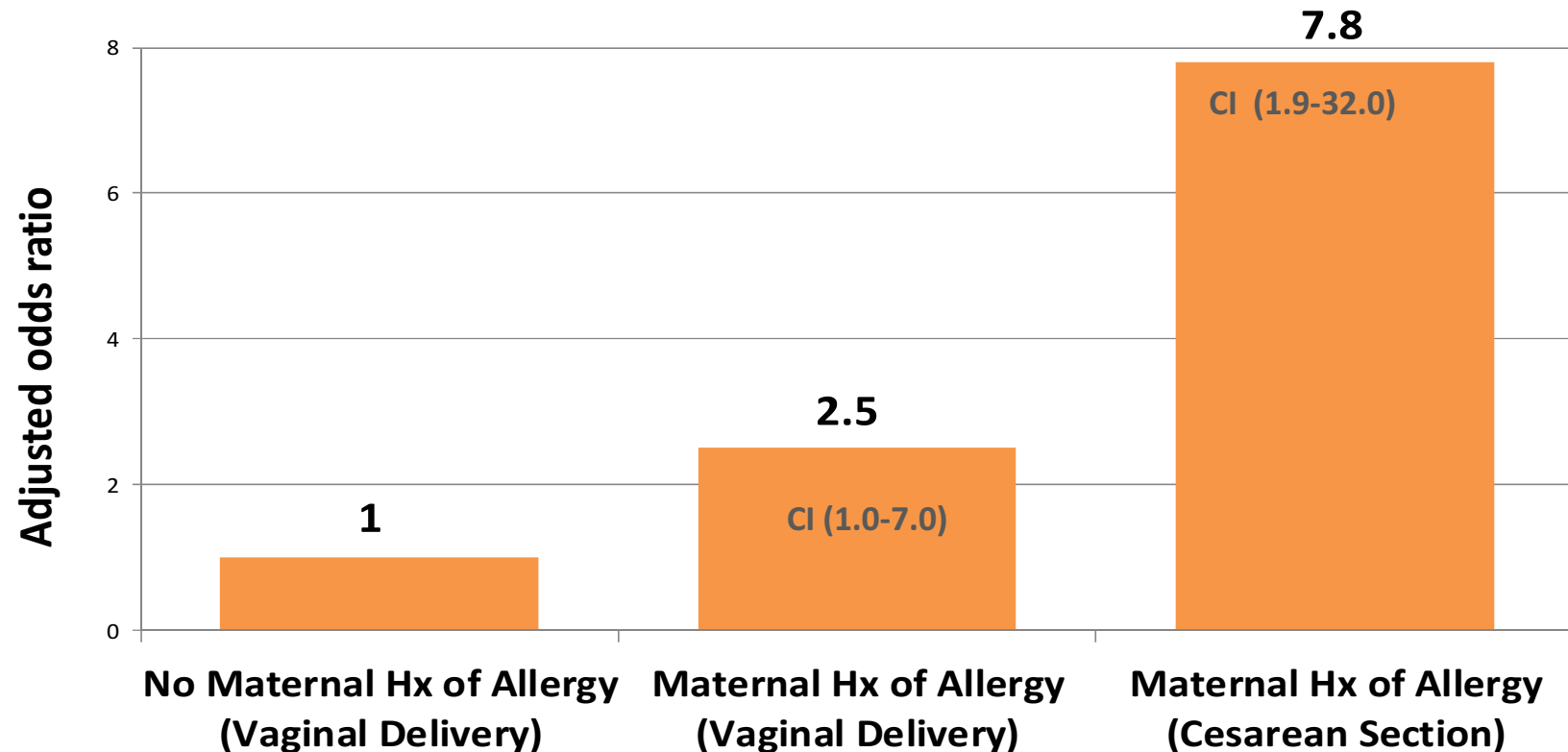
*
p< .05

D'Angeli MA, et al. Arch Pediatr Adolesc Med. 2010 Aug;164(8):732-8.

Davidson R, et al. BMC Pulm Med. 2010 Mar 16;10:14.

Decker E, et al. Pediatrics. 2010 Jun;125(6):e1433-40.

Cesarean Delivery and Relative Risk of Childhood Food Allergy

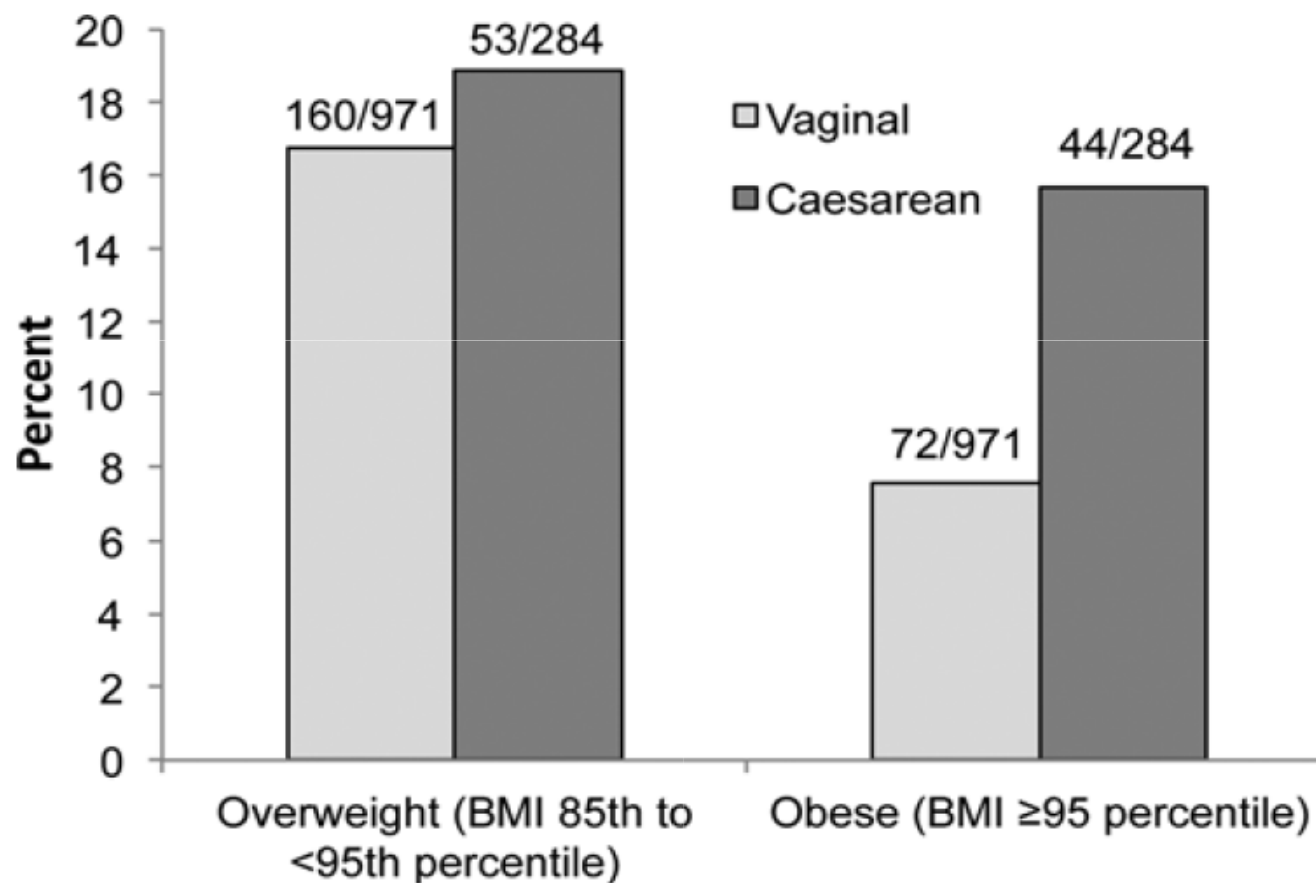


Pistiner M et al. J Allergy Clin Immunol 2008; 122(2):274-279
Table adapted from: Eggesbo M et al. J Allergy Clin Immunol
2003;112:420-426

*p<0.01; adjusted for covariates

Food Allergy to egg confirmed by testing at age 1 – 2 y

Cesarean Section Linked to Increases in Chronic Disease: Childhood Obesity



Huh SY et al, Arch Dis Child published online May 2012

Microbiota in C-section infants

- C-section infants
- Minimal or no vaginal microbes
- Low Lactobacillus, Prevotella, Sneathia spp (vaginal microbes)
- Higher skin bacteria
(e.g., Staphylococcus, Corynebacterium, Propionibacterium spp.)
- Higher levels of C. difficile
- Lower and delayed appearance of Bacteroides and Bifidobacterium spp.

Breastfeeding is not a
sterile procedure

**Are there consequences to
exclusive formula feeding?**

Breastfeeding is Consistently Associated with Infant Health Outcomes

| Breastfeeding is associated with: | |
|-----------------------------------|----------------------------------------------------------|
| Infectious Disease | ↓ Acute otitis media ¹ |
| | ↓ Non-specific gastroenteritis ¹ |
| | ↓ Severe lower respiratory tract infections ¹ |
| Immunologic Disease | ↓ Atopic dermatitis ¹ |
| | ↓ Asthma (young children) ¹ |
| | ↓ Type 1 diabetes ¹ |
| | ↓ IBD (Crohn disease, U. Colitis) |
| Metabolic Disease | ↓ Childhood leukemia ¹ |
| | ↓ Obesity and Type 2 diabetes ¹ |

Nutrition in early life sets the course for long term health of individuals and all society



- Breastfeeding is the best start to nutrition and health – for life
- Exclusive breastfeeding in the first months of life provides unique benefits to infants and others

Breastmilk remains the model that inspires the way infants should be fed

COMPOSITION of HUMAN MILK (not exhaustive ...)

| <u>HUMAN MILK</u> | | | | |
|-------------------------|-----------------------|-------------------------------------|-------------------------|--|
| <u>CARBOHYDRATES</u> | <u>PEPTIDES</u> | <u>LIPIDS</u> | <u>MINERALS</u> | |
| Disaccharides (>200) | Whey peptides | Triacylglycerols (TAG) | Na (Sodium) | |
| <u>PROTEINS</u> | Casein peptides | Diacylglycerols (DAG) | Mg (Magnesium) | |
| (including amino acids) | β -Defensin 1 | Monoacylglycerols (MAG) | P (Phosphorus) | |
| Lactalbumin | β -Endorphins | Fatty acids (FA; esterified & free) | K (Potassium) | |
| Lactoglobulins | Gastrin | SFA (16:0) | Ca (Calcium) | |
| Human Albumin | Motilin | MUFA (18:1) | Fe (Iron) | |
| Protein Nitrogen | Neurotensin | PUFA n-3 (ALA) | Mn (Manganese) | |
| Lactoferrin | Somatostatin | PUFA n-6 (LA, DHA) | Cu (Copper) | |
| Lactoperoxidase | <u>HORMONES</u> | MCFA (10:0, 12:0) | Zn (Zinc) | |
| Lactoferrin | Insulin, Leptin | LCFA (18:0, 20:0) | Se (Selenium) | |
| Lactoferrin | Adiponectin | <u>PHOSPHOLIPIDS</u> | I (Iodine) | |
| Lactoferrin | Cortisol, T3, T4 | Phosphatidylcholine | <u>VITAMINS</u> | |
| Lactoferrin | TSH, TRH, Prolactin | Sphingomyelin | Vitamin A, Vitamin B6 | |
| Lactoferrin | Oxytocin, Ghrelin | Phosphatidylethanolamine | Vitamin B9, Vitamin B12 | |
| <u>ENZYMES</u> | <u>ENZYMES</u> | Phosphatidylserine | Vitamin C, Vitamin D | |
| BSSL | BSSL | Phosphatidylinositol | Vitamin E, Vitamin K | |
| Amylase | Amylase | Lyso-phospholipids | Pantothenic Acid | |
| Catalase | Catalase | Plasmalogens | Folic Acid, Carotenoids | |
| Histaminase | Histaminase | <u>SPHINGOLIPIDS</u> | Pantothenic acid | |
| Phosphatase | Phosphatase | Gangliosides (GM1, GM3, GD3) | Folic acid | |
| Lysozyme | Lysozyme | Glycosphingolipids | Niacin, Biotin | |
| Xanthine Oxidase | Xanthine Oxidase | Ceramides | Choline, Inositol | |
| Antiproteases | Antiproteases | Glucosylceramides | <u>CELLS AND OTHERS</u> | |
| <u>IMMUNE FACTORS</u> | <u>IMMUNE FACTORS</u> | Galactosylceramides | Leukocytes | |
| slgA | slgA | <u>STEROLS</u> | Macrophages | |
| IgA2 | IgA2 | Cholesterol | Lymphocytes | |
| IgG | IgG | Squalene | Stem Cells | |
| IgD | IgD | Lanosterol | mRNA | |
| IgM | IgM | Sitosterol | microRNA | |
| IgE | IgE | Dimethylsterol | | |

Human milk is a 'living fluid' that can be compositionally emulated but not duplicated

COMPOSITION of HUMAN MILK (not exhaustive ...)

HYDRATES

se
accharides (>200)
INS
(including amino acids)
albumin
ns
n Albumin
protein Nitrogen
ne
nine
cid
ptides

TH FACTORS

IL-2
L-6
L-10
F, M-CSF
, VEGF
α, HGF-β
TNF-α
, TGF β1
2

PEPTIDES

Whey peptides
Casein peptides
β-Defensin 1
β-Endorphins
Gastrin
Motilin
Neurotensin
Somatostatin

HORMONES

Insulin, Leptin
Adiponectin
Cortisol, T3, T4
TSH, TRH, Prolactin
Oxytocin, Ghrelin

ENZYMES

BSSL
Amylase
Catalase
Histaminase
Phosphatase
Lysozyme
Xanthine Oxidase
Antiproteases

IMMUNE FACTORS

slgA
IgA2
IgG
IgD
IgM
IgE

LIPIDS

Triacylglycerols (TAG)
Diacylglycerols (DAG)
Monoacylglycerols (MAG)
Fatty acids (FA; esterified & free)
SFA (16:0)
MUFA (18:1)
PUFA n-3 (ALA)
PUFA n-6 (LA, DHA)
MCFA (10:0, 12:0)
LCFA (18:0, 20:0)

PHOSPHOLIPIDS

Phosphatidylcholine
Sphingomyelin
Phosphatidylethanolamine
Phosphatidylserine
Phosphatidylinositol
Lyso-phospholipids
Plasmalogens

SPHINGOLIPIDS

Gangliosides (GM1, GM3, GD3)
Glycosphingolipids
Ceramides
Glucosylceramides
Galactosylceramides

STEROLS

Cholesterol
Squalene
Lanasterol
Sitosterol
Dimethylsterol

MINERALS

Na (Sodium)
Mg (Magnesium)
P (Phosphorus)
K (Potassium)
Ca (Calcium)
Fe (Iron)
Mn (Manganese)
Cu (Copper)
Zn (Zinc)
Se (Selenium)
I (Iodine)

VITAMINS

Vitamin A, Vitamin B6
Vitamin B9, Vitamin B12
Vitamin C, Vitamin D
Vitamin E, Vitamin K
Pantothenic Acid
Folic Acid, Carotenoids
Pantothenic acid
Folic acid
Niacin, Biotin
Choline, Inositol

CELLS AND OTHERS

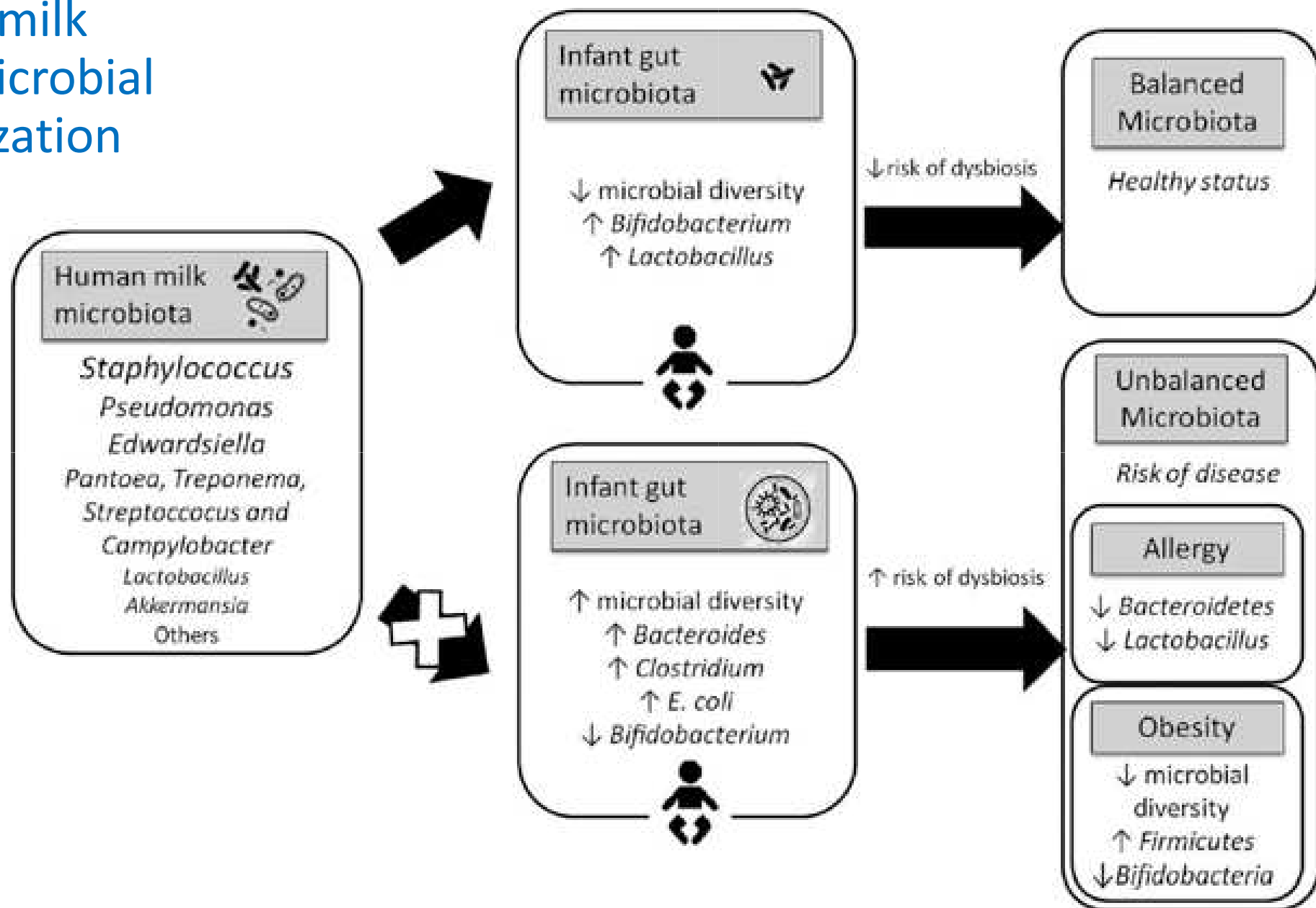
Leukocytes
Macrophages
Lymphocytes
Stem Cells
mRNA
microRNA



Bacteria

Human milk is a 'living fluid' that can be compositionally emulated but not duplicated

Human milk and microbial colonization



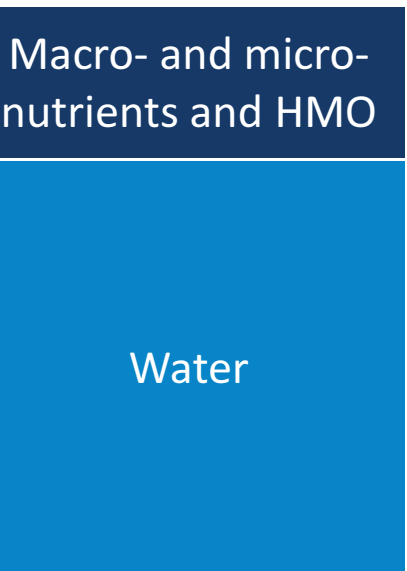
Breastmilk is not sterile

- Bacteria generally isolated in breastmilk of healthy women include:
 - *Staphylococcus*
 - *Streptococcus*
 - *Enterococcus*
 - ***Lactobacillus***
 - ***Bifidobacterium***



Composition of breast milk

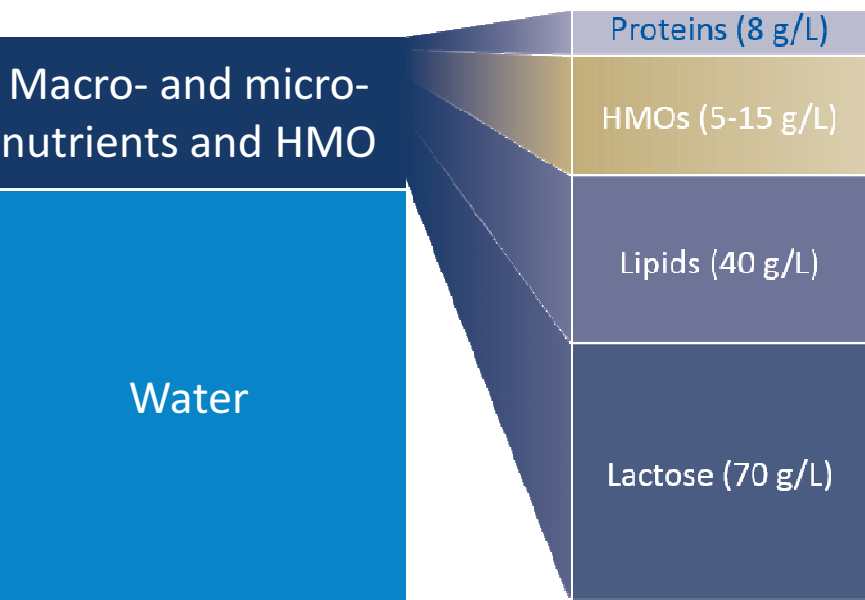
Human breast milk



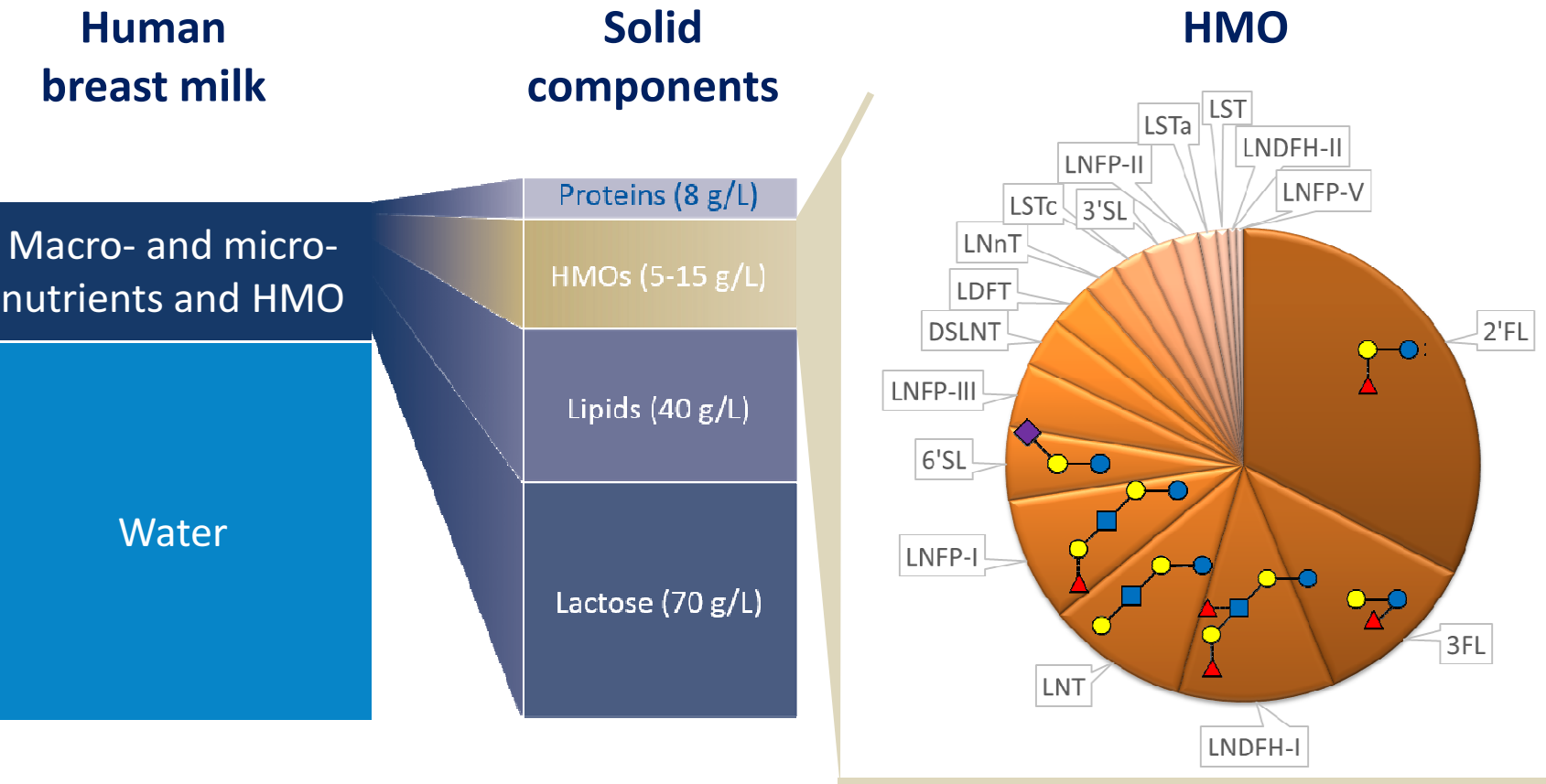
Composition of breast milk

**Human
breast milk**

**Solid
components**

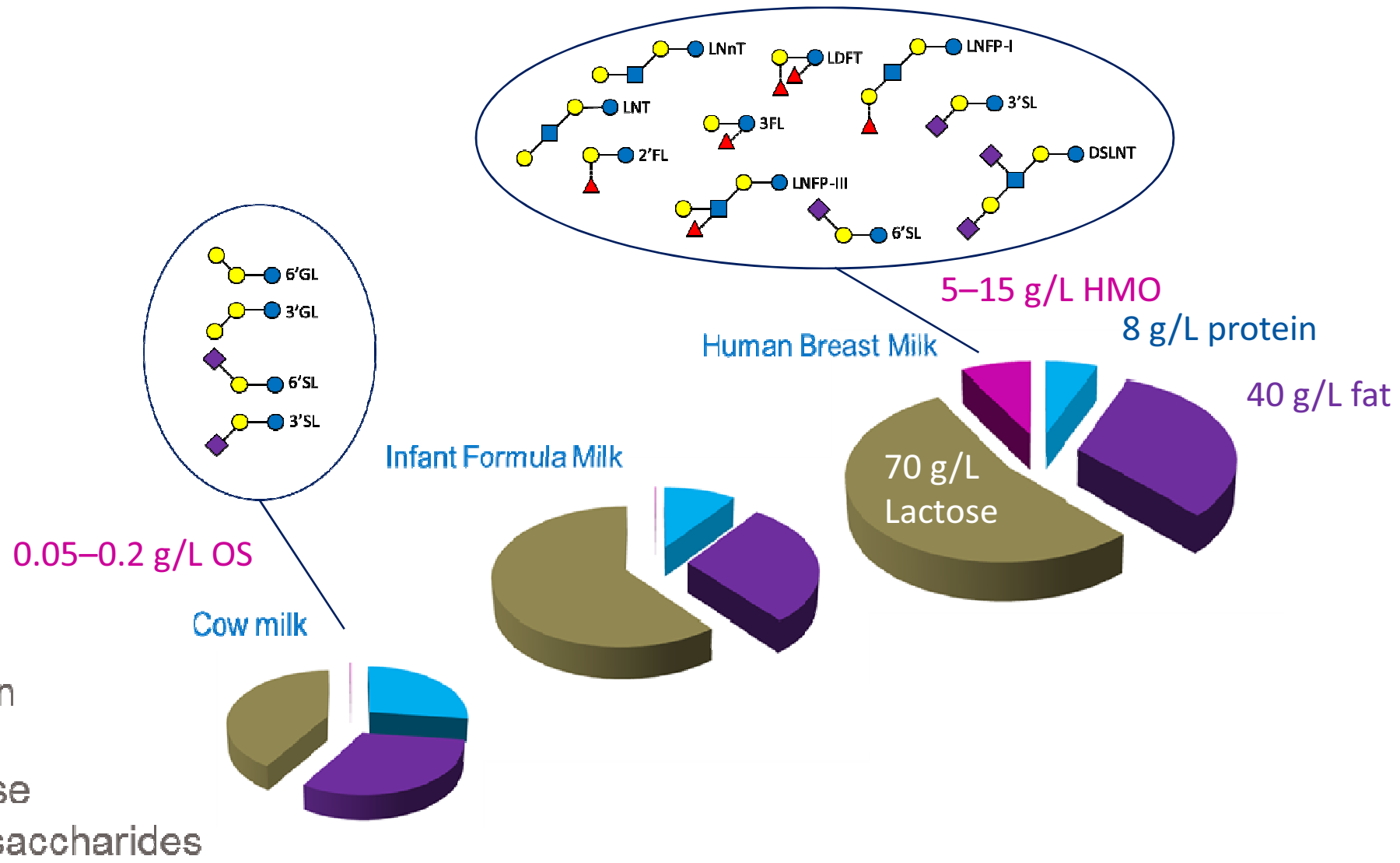


Composition of breast milk

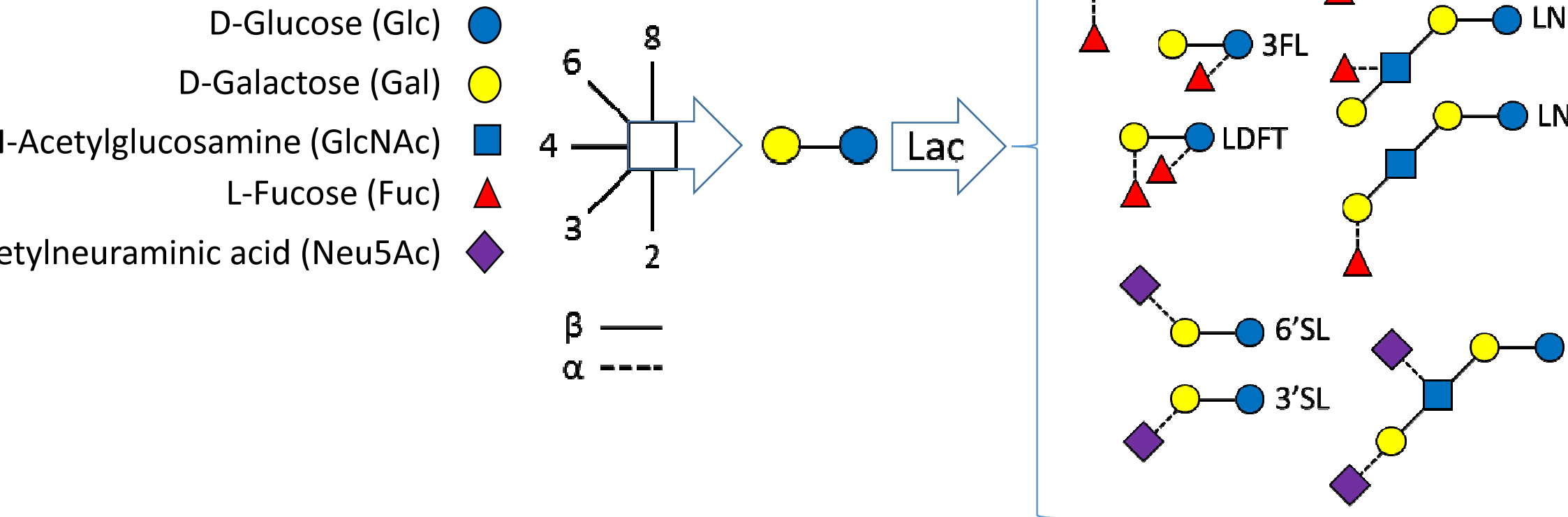


- 5 to 15 g/L in breast milk
- >130 structures described, of which about 15 make up the bulk (>80%)
- Oligosaccharides not generally present in farmed animal milk

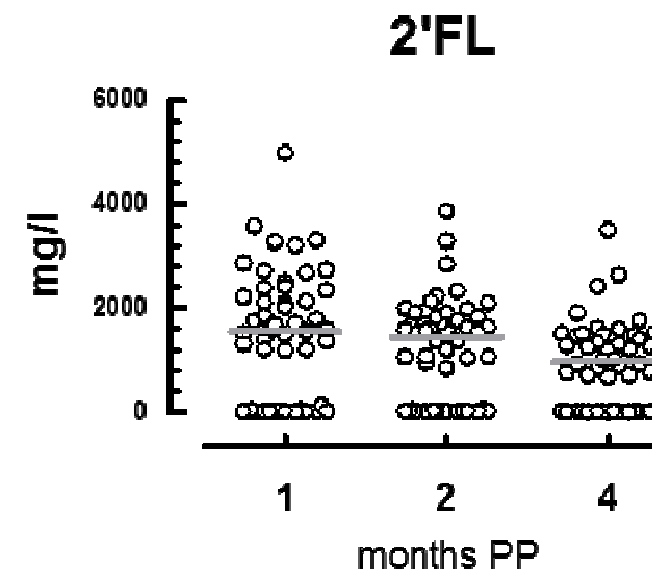
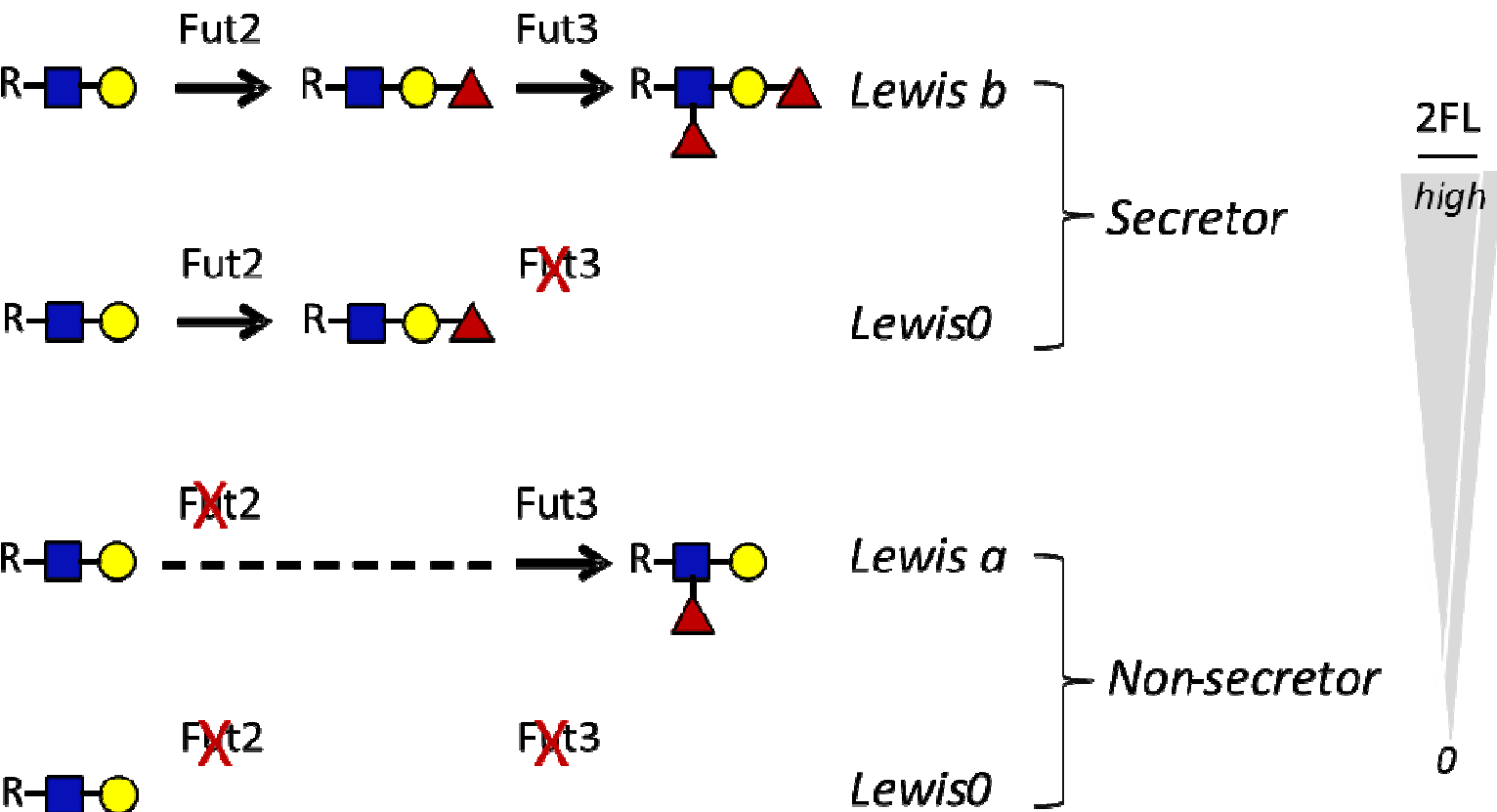
Composition of breast milk, Cow milk and Infant formula



What are HMO?



Maternal genotype determines fucosylated HMOs



RESEARCH

Open Access

Maternal fucosyltransferase 2 status affects the gut bifidobacterial communities of breastfed infants

Zachery T Lewis^{1,4}, Sarah M Totten^{2,4}, Jennifer T Smilowitz^{1,4}, Mina Popovic⁵, Evan Parker², Danielle G Lemay⁶, Maxwell L Van Tassel⁷, Michael J Miller⁷, Yong-Su Jin⁷, J Bruce German^{1,4}, Carlito B Lebrilla^{2,4} and David A Mills^{1,3,4*}

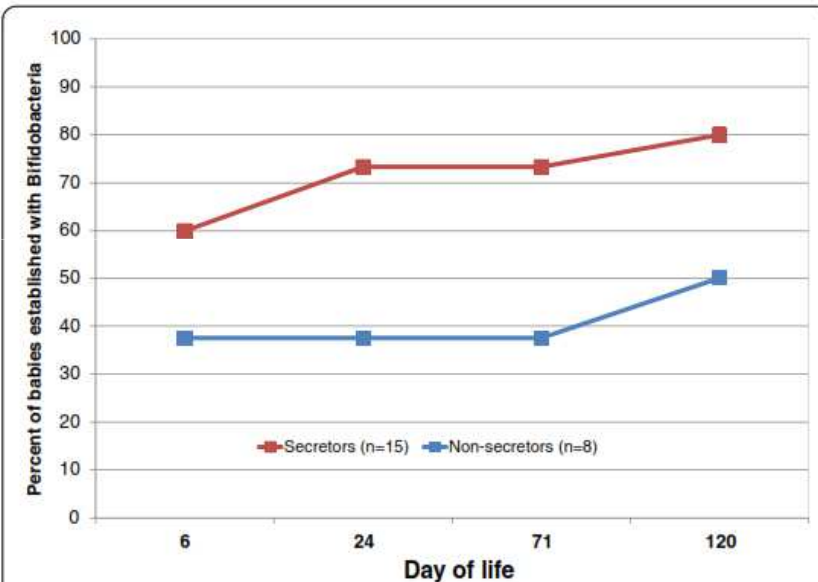


Figure 5 Percentage of infants with high bifidobacteria over time. Based on when each qualifying infant crossed the cutoff point of $10^{8.5}$ bifidobacterial genome equivalents/gram feces. Infants qualified for this analysis by having the appropriate time points available to know when they are first established with bifidobacteria; for example, if the day 6 sample is missing, it is impossible to know if the infant was established at that time or not, and thus, that infant was excluded from this analysis.

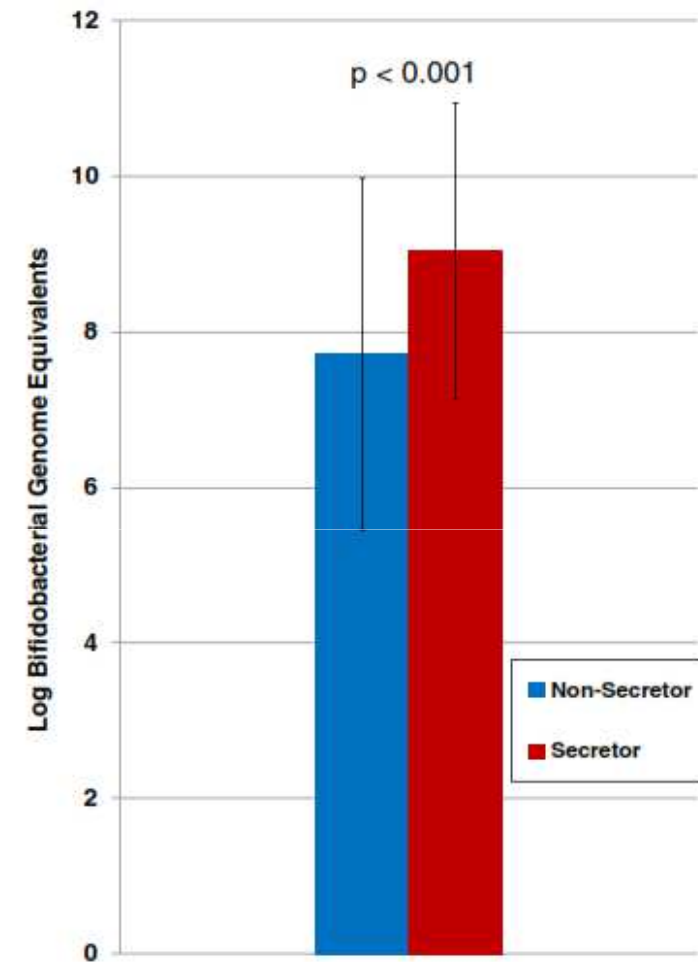


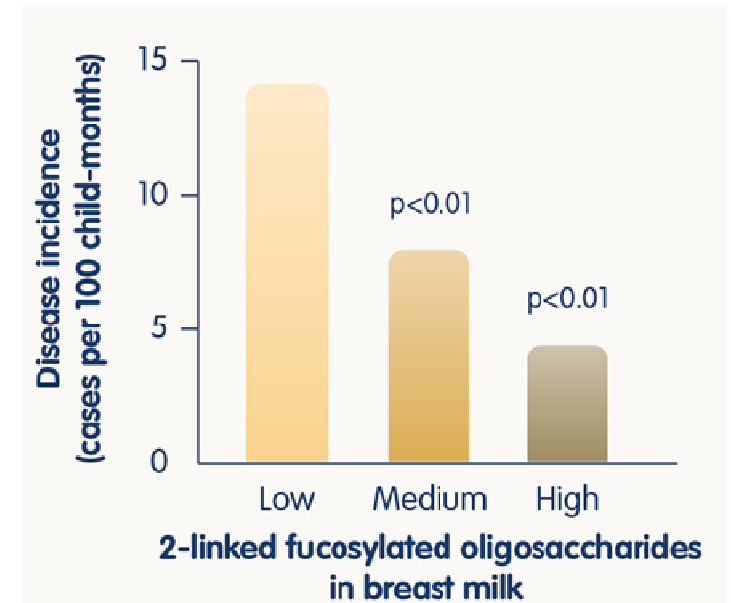
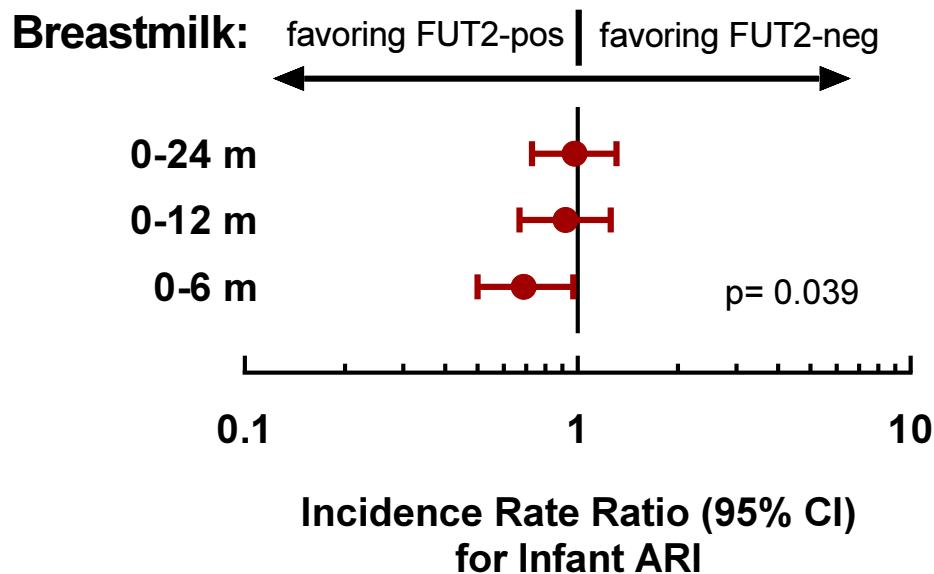
Figure 3 Average absolute levels of bifidobacteria in secretor versus non-secretor-fed infants (all samples of each secretor status averaged together). The one-tailed type three *t*-test *p* value was <0.001.

Insight on HMO from observational clinical studies

2'Fucosyl-HMO in breastmilk is related to:

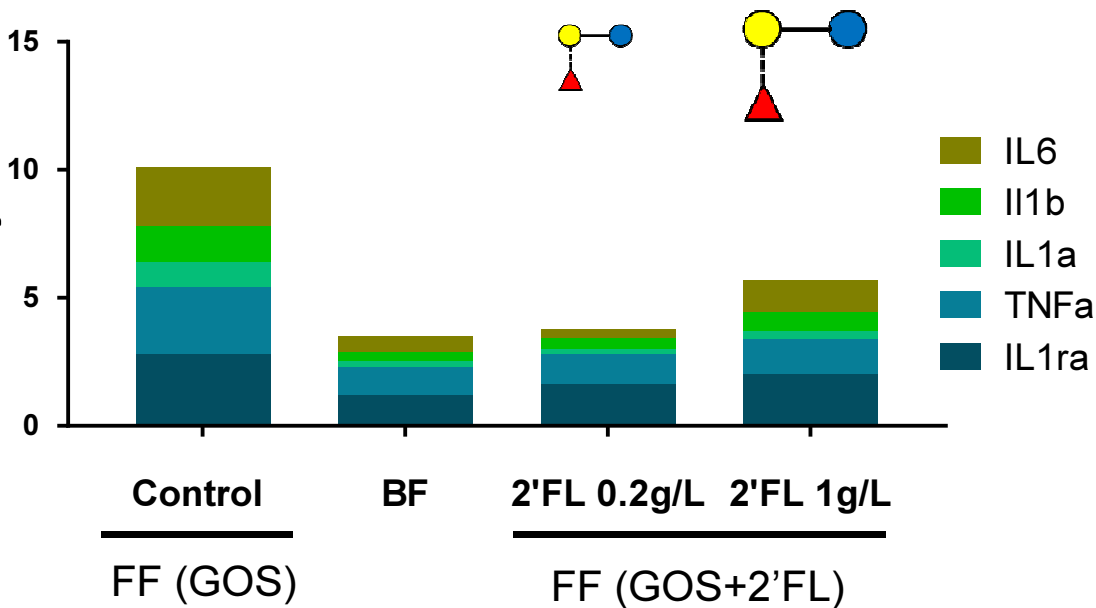
- Lower risk for ARI during the predominant breastfeeding period

- Lower incidence of infectious diarrhea in infants at 9 months
- Lower morbidity at 4 months

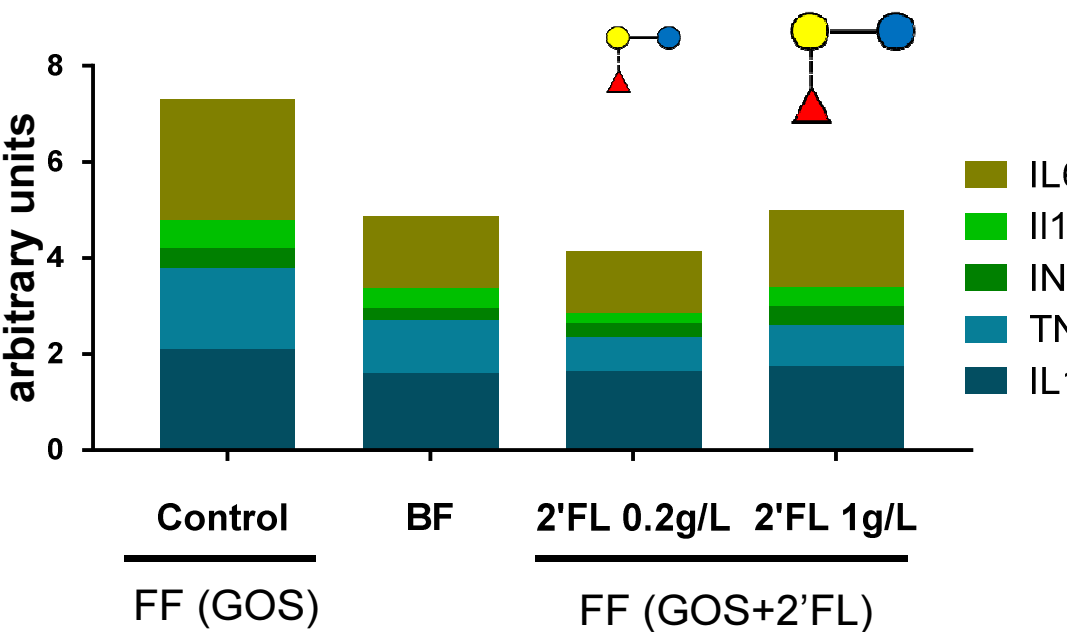


RCT infants fed a starter formula with 2'FL show a plasma immune marker profile similar to breastfed infants

Plasma baseline immune marker profile
in 6-week-old infants



Cytokine production by RSV-stimulated PBMCs
from 6-week-old infants, *ex vivo*

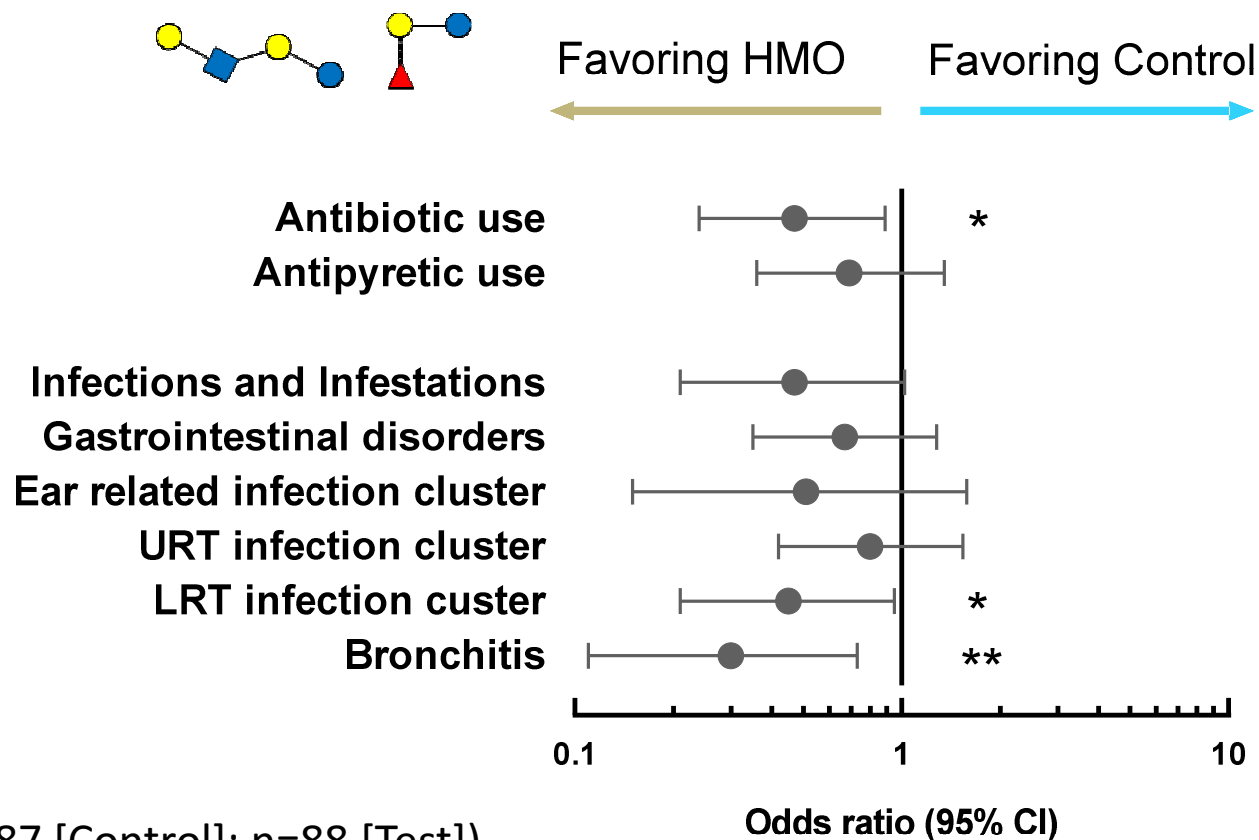


(n=30–40/group)

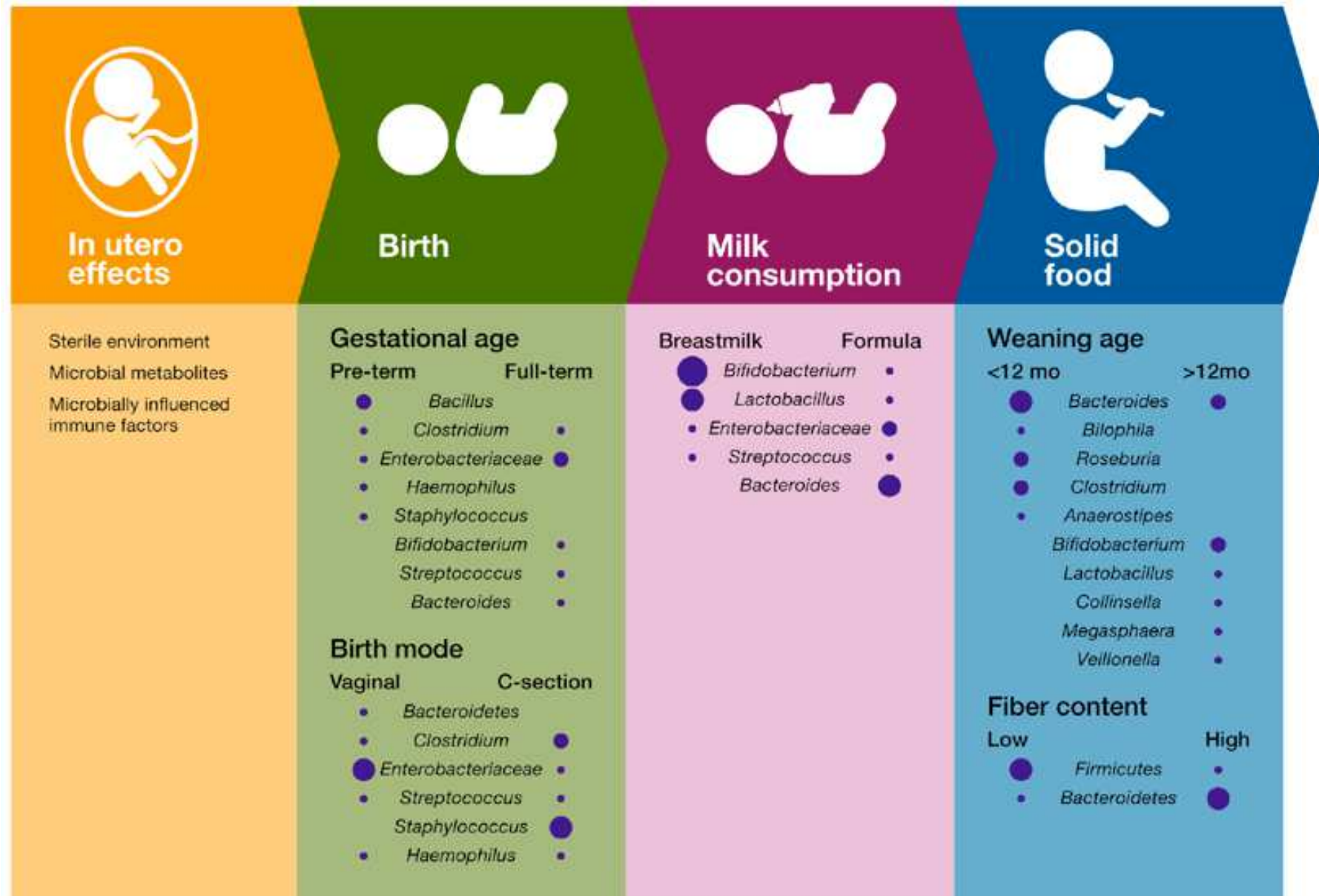
RCT infants fed a starter formula with HMO (2'FL & LnNT) have a lower risk for reported lower respiratory tract infections and antibiotics use during first year of life

Reduced morbidity and medication use

- Fewer reports of infections and infestations, lower respiratory tract illnesses, notably bronchitis through 12 months
- Less frequent antibiotics use through 12 months
- Less frequent antipyretics use through 4 months



Early life
microbial
colonization
likely the
'normal' or
'natural' or
'desirable'
pattern of
development



“Modern” Lifestyle Has Decreased Exposure to Bacteria

- Cesarean birth
- No breastfeeding
- Sanitized food supply
- including Infant formula
- Urban life
- Antibiotics



*Lower
Oral microbial
exposure*



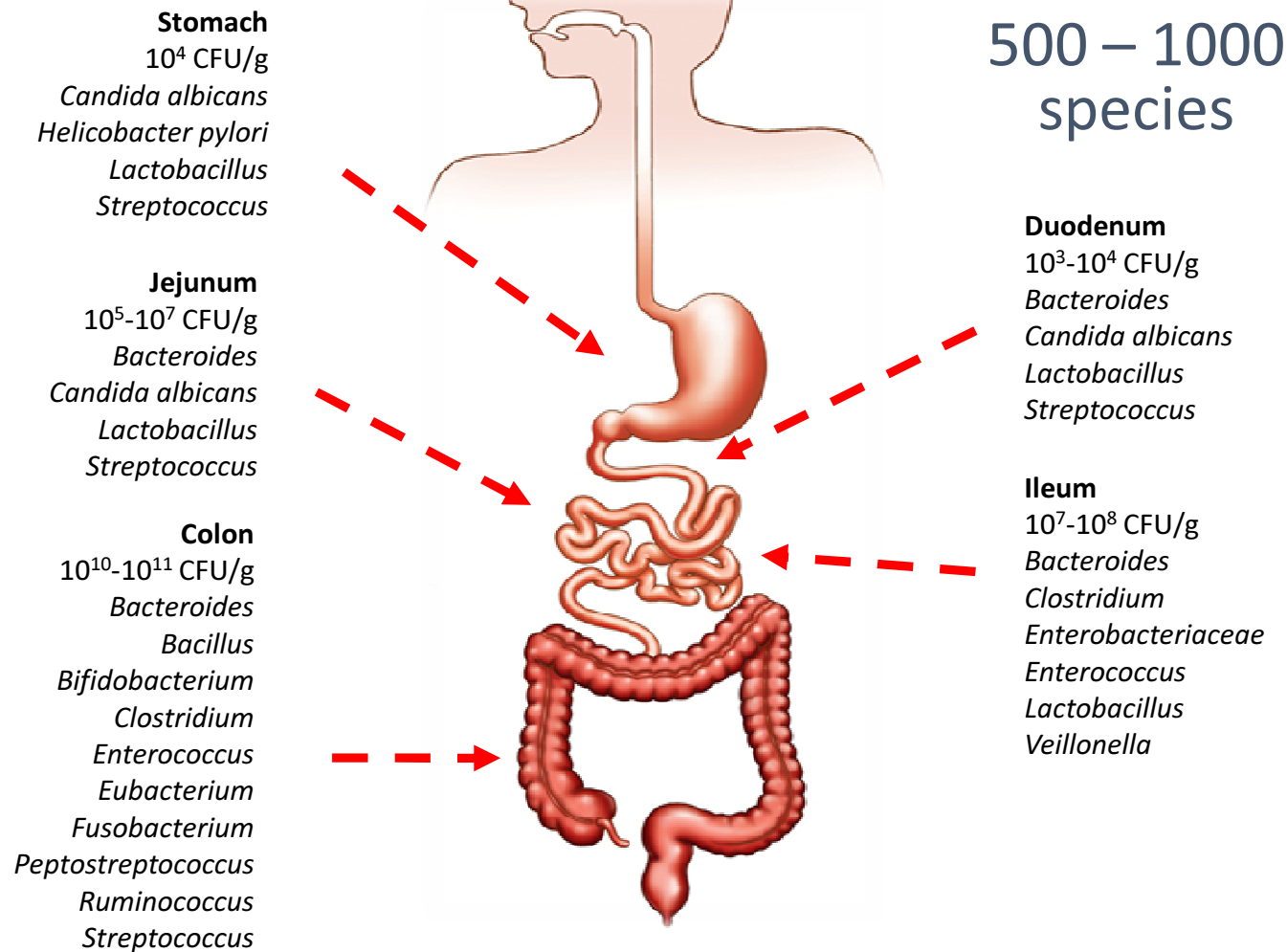
*Altered
Intestinal microbiota:
Dysbiosis*



*Inadequate immune
response*

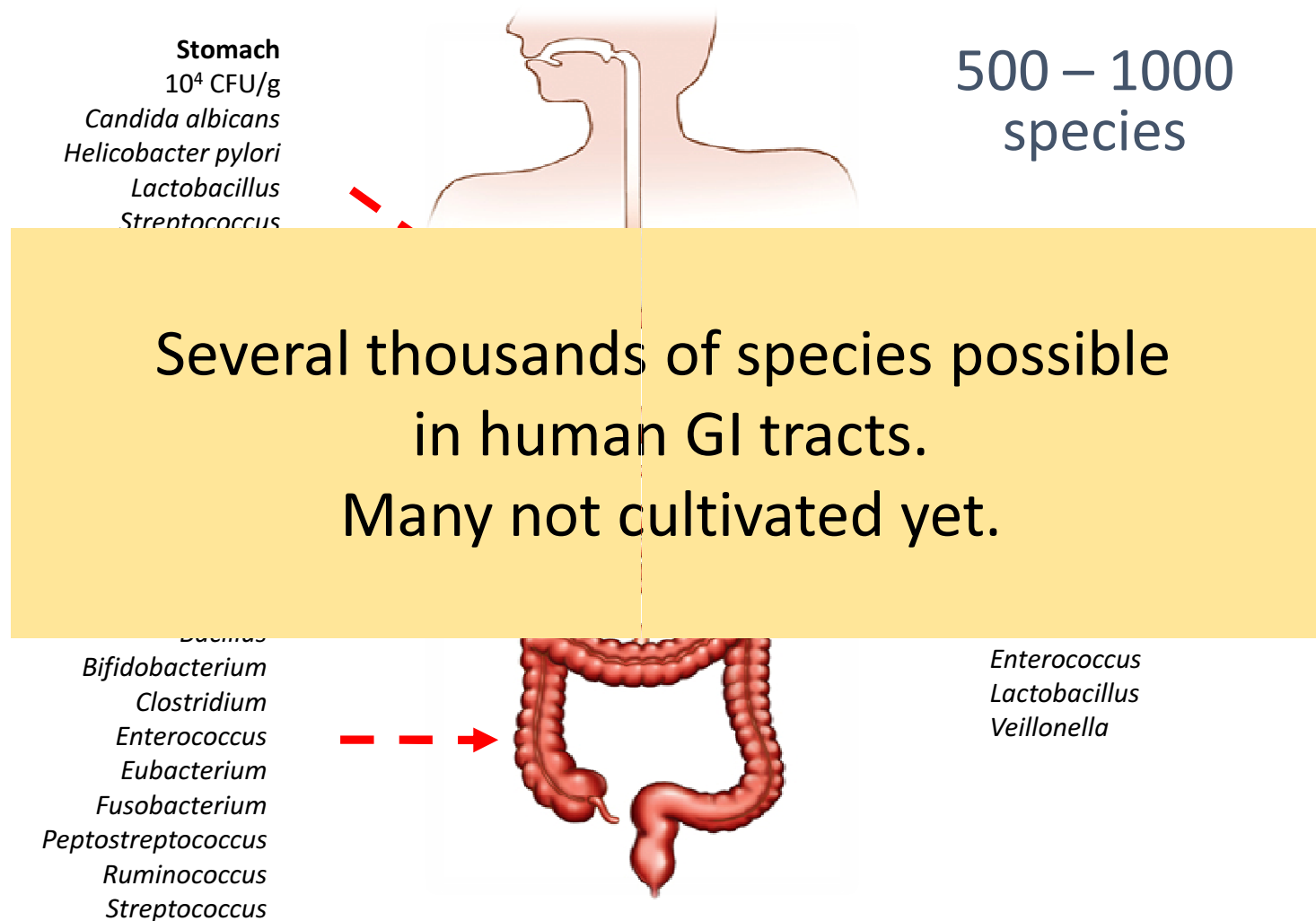
Bacteria in the GI Tract: Complex Ecosystem

Resident and Ingested



Bacteria in the GI Tract: Complex Ecosystem

Resident and Ingested



Staphylococcus, Clostridium spp
Listeria
Lactobacilli, Streptococcus, Leuconostoc, Enterococcus

Bacteroides fragilis, spp
Prevotella

Enterobacteriaceae, Rickettsidae
Neisseriales
Vibrionaceae, Pseudomonadaceae.
Salmonella, Yersinia, Vibrio, Pseudomonas, Escherichia, Shigella
Campylobacter, Helicobacter

Main human GI microbial species

Bacilli

- Bacillales ¹
- Lactobacillales ²
- Mollicutes
- Erysipelotrichia
- Erysipelotrichales

Clostridia

- Clostridiales ³
- Halanaerobiales
- Natranaerobiales
- Thermoanaerobacterales
- Negativicutes
- Selenomonadales

Thermolithobacteria

Staphylococcus, Clostridium spp
Listeria
Lactobacilli, Streptococcus, Leuconostoc, Enterococcus

Main human GI microbial species

Bacteroidia

- Bacteroidales ¹
- Balneolia
- Balneolales
- "Chitinophagia"
- "Chitinophagales"
- Cytophagia
- Cytophagales
- Flavobacteriia
- Flavobacteriales
- Rhodothermia
- Rhodothermales
- Sphingobacteria
- Sphingobacteriales

Bacteroides fragilis, spp
Prevotella

Alphaproteobacteria ¹
Betaproteobacteria ²
Hydrogenophilalia
Gammaproteobacterian ³
Acidithiobacilli
Deltaproteobacteria
Epsilonproteobacteria ⁴
Oligoflexia

**Enterobacteriaceae,
Rickettsidae
Neisseriales
Vibrionaceae,
Pseudomonadaceae.
Salmonella, Yersinia,
Vibrio, Pseudomonas,
Escherichia, Shigella
Campylobacter,
Helicobacter**

Rubrobacteria
Thermoleophilia
Coriobacteriia
Acidimicrobiia
Nitriliruptoria
Actinobacteria
• Actinobacteriales ¹

Bifidobacteria spp

Firmicutes

Bacilli

- Bacillales ¹
- Lactobacillales ²
- Mollicutes
- Erysipelotrichia
- Erysipelotrichales

Clostridia

- Clostridiales ³
- Halanaerobiales
- Natranaerobiales
- Thermoanaerobacterales
- Negativicutes
- Selenomonadales

Thermolithobacteria

Staphylococcus, Clostridium spp
Listeria
Lactobacilli, Streptococcus, Leuconostoc, Enterococcus

Main human GI microbial species

Bacteroidetes

Bacteroidia

- Bacteroidales ¹
- Balneolia
- Balneolales
- "Chitinophagia"
- "Chitinophagales"
- Cytophagia
- Cytophagales
- Flavobacteriia
- Flavobacteriales
- Rhodothermia
- Rhodothermales
- Sphingobacteria
- Sphingobacteriales

Bacteroides fragilis, spp
Prevotella

Proteobacteria

Alphaproteobacteria ¹

Betaproteobacteria ²

Hydrogenophilalia

Gammaproteobacterian ³

Acidithiobacilli

Deltaproteobacteria

Epsilonproteobacteria ⁴

Oligoflexia

Enterobacteriaceae, Rickettsidae
Neisseriales
Vibrionaceae, Pseudomonadaceae.
Salmonella, Yersinia, Vibrio, Pseudomonas, Escherichia, Shigella
Campylobacter, Helicobacter

Actinobacteria

Rubrobacteria

Thermoleophilia

Coriobacteriia

Acidimicrobiia

Nitriliruptoria

Actinobacteria

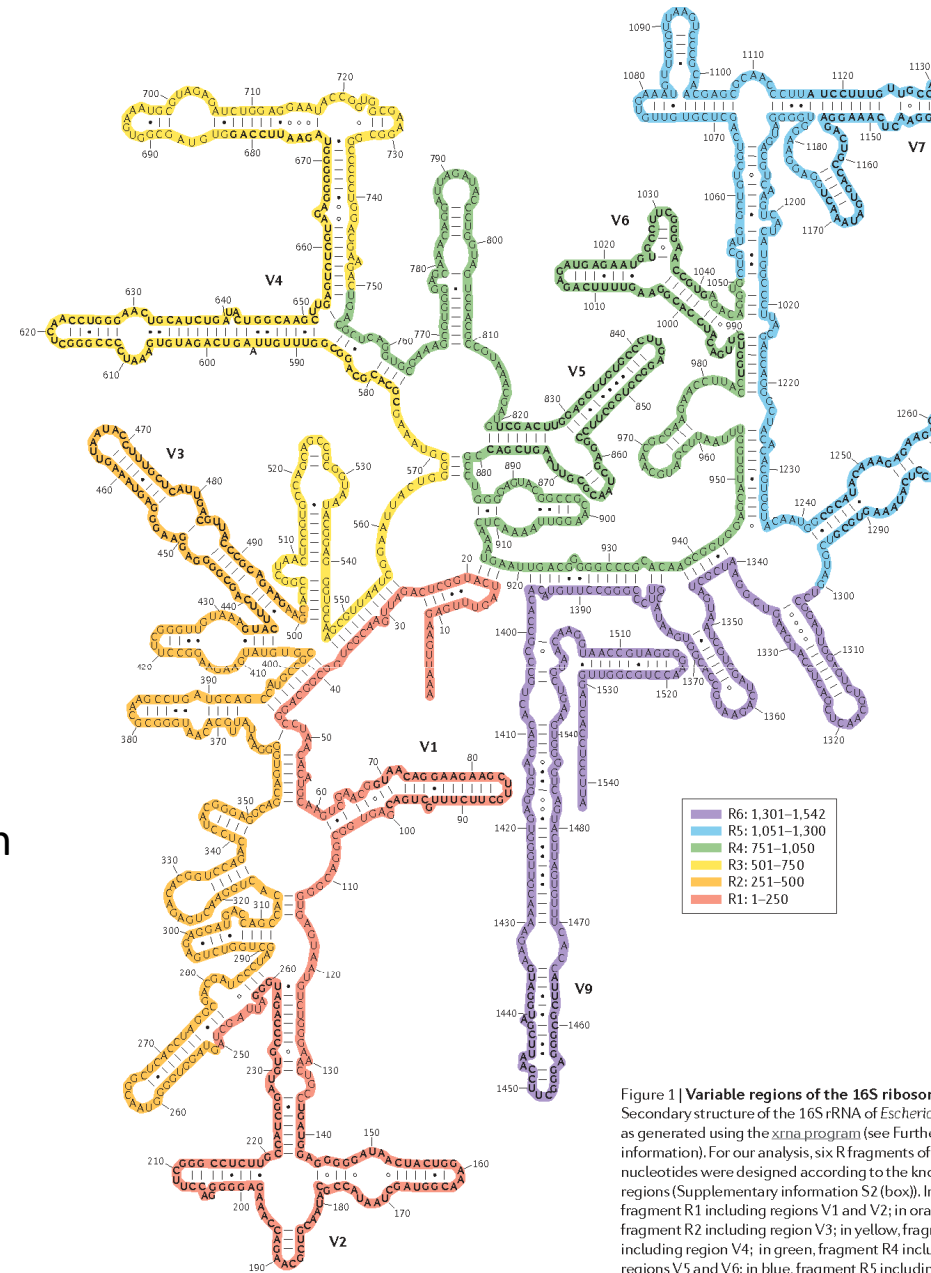
- Actinobacteriales ¹

Bifidobacteria spp

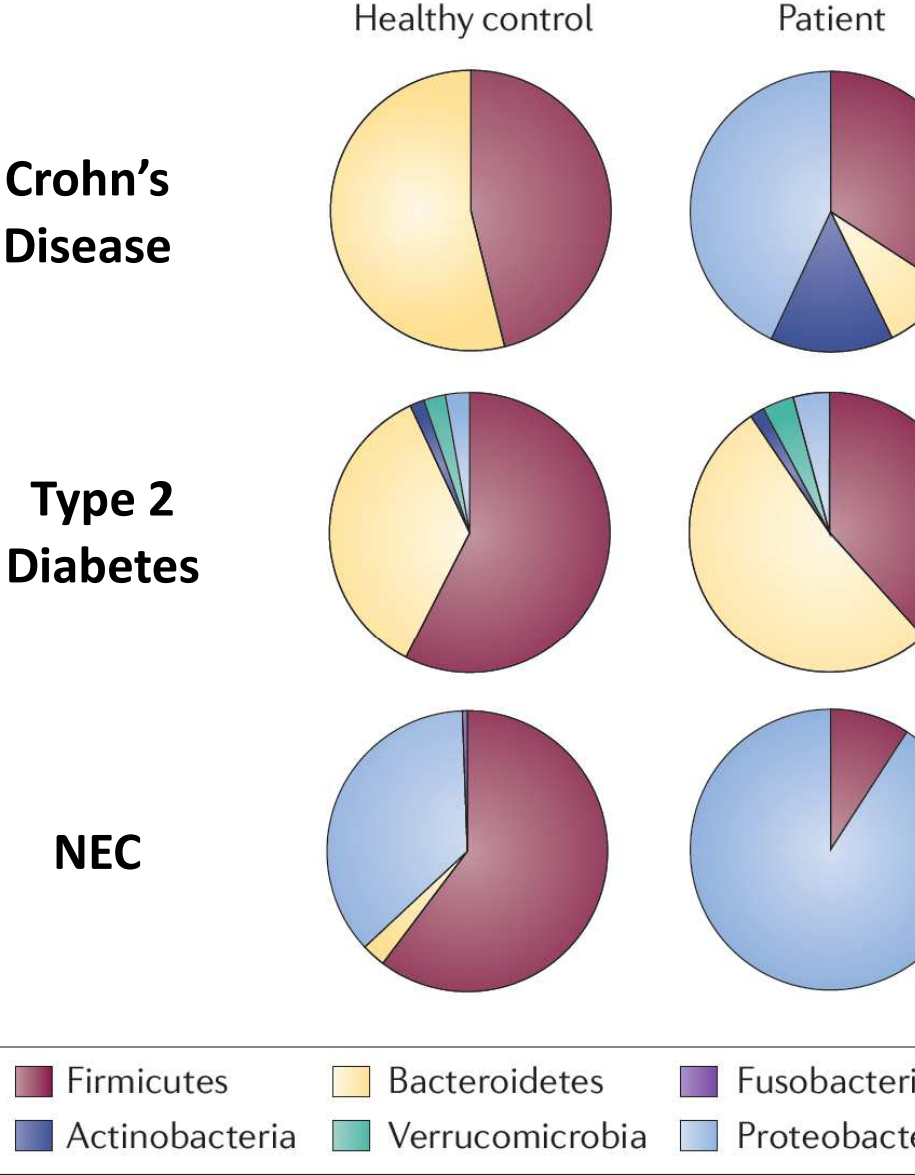
16S ribosomal RNA – based phylogeny

16S rRNA gene

- Present in almost all bacteria and archaea
- Its function has been preserved over time
- It consists of both conserved and variable regions
- The conserved region makes universal amplification possible
- Sequencing the variable regions allows discrimination between specific different microorganisms
- Described from an initial group of 11 bacterial phyla in 1987,
- As of February 2012, 2 million 16S rRNA sequences and 35 phyla described



Dysbiosis:
Altered Microbiota associated with
acute and chronic diseases



Main human GI microbial phyla

Adult Microbiome

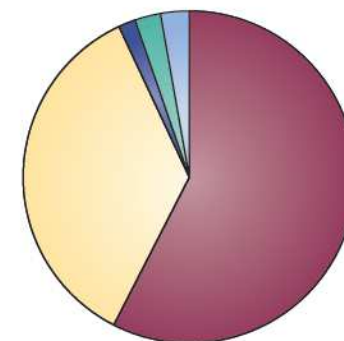
| | | |
|-------------------------------------------------------------------------------------|----------------|-------|
|  | Firmicutes | ~ 65% |
|  | Bacteroidetes | ~ 16% |
|  | Proteobacteria | ~ 9% |
|  | Actinobacteria | ~ 5% |

Main human GI microbial phyla

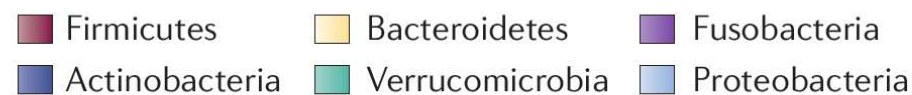
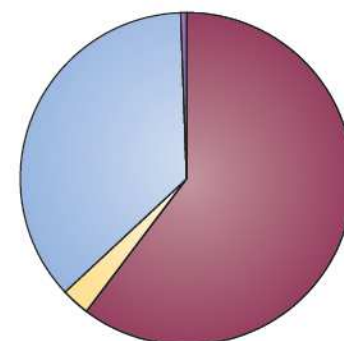
Adult Microbiome



Healthy Mature microbiota



Premature Infants



Microbiota & obesity

frontiers
in Microbiology

ORIGINAL RESEARCH
published: 05 June 2018
doi: 10.3389/fmicb.2018.01210

Microbiota Markers in Obese Adolescent and Adult Patients: Age-Dependent Differential Patterns

Merica Del Chierico¹, Francesca Abbati², Alessandra Russo¹, Andrea Quagliariello¹,
Daria Reddel¹, Danila Capoccia³, Romina Caccamo⁴, Stefano Ginanni Corradini⁵,
Mario Nobili^{6,7}, Francesco De Peppo⁴, Bruno Dallapiccola⁸, Frida Leonetti⁹,
Gianfranco Silecchia² and Lorenza Putignani^{1,2*}

Phyla



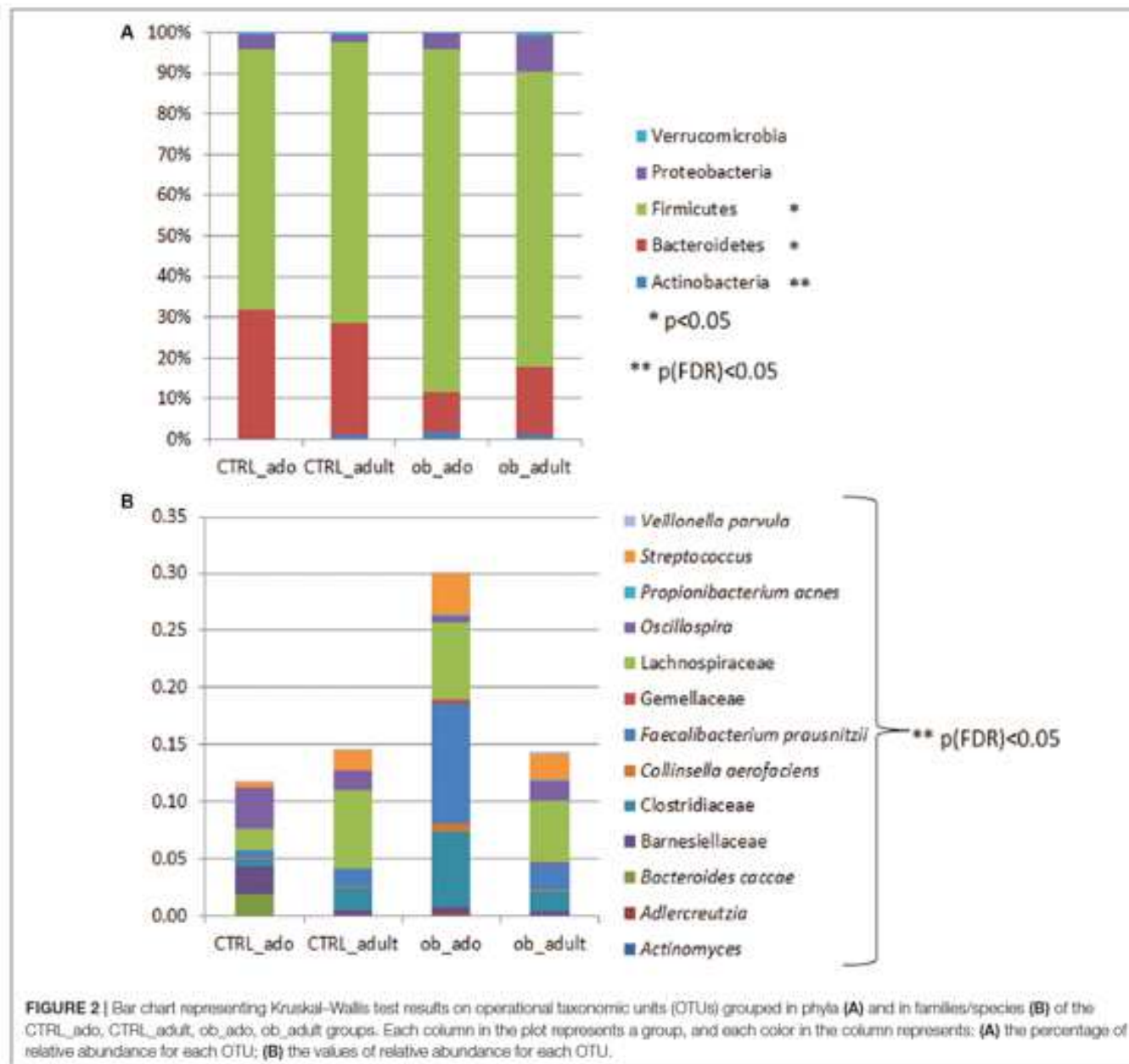
Firmicutes

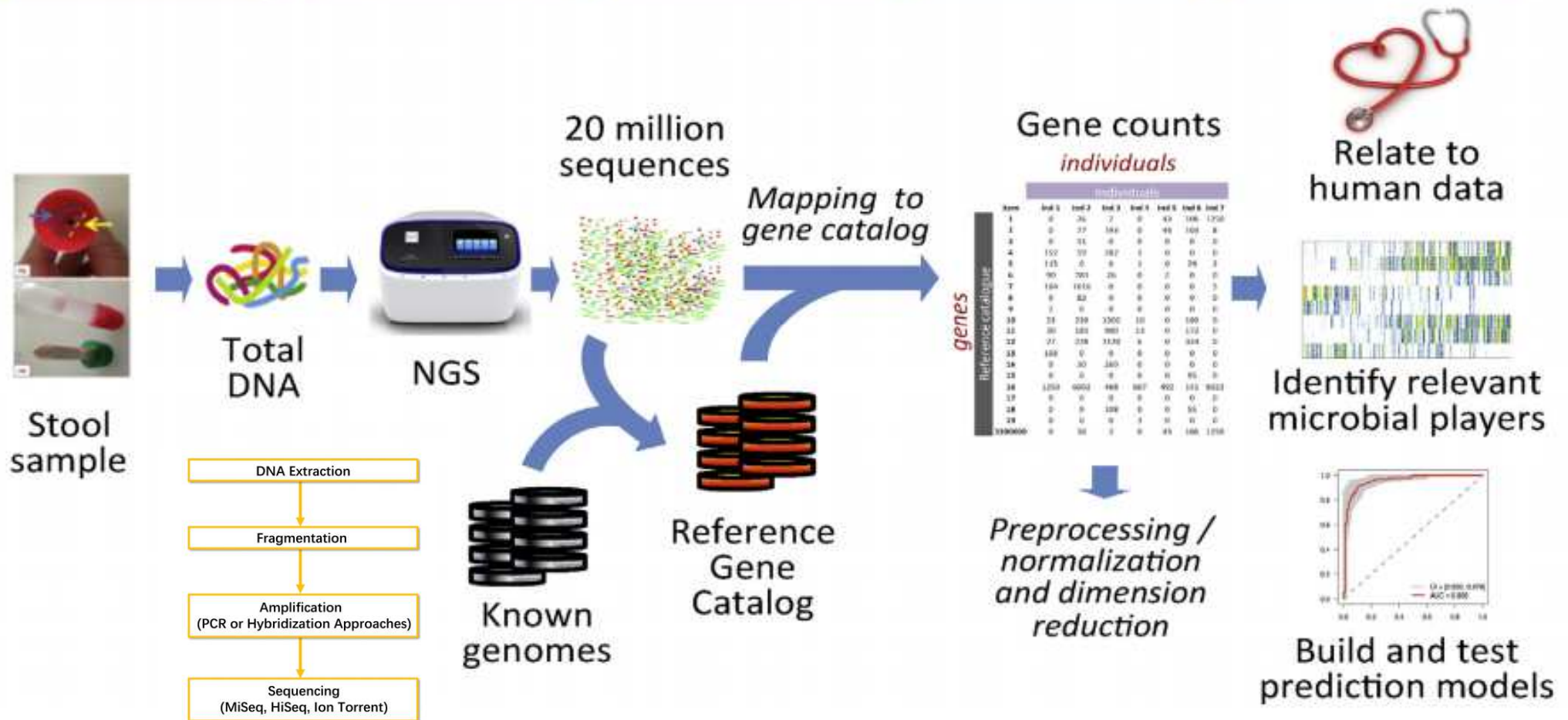


Bacteroidetes

Genus / species

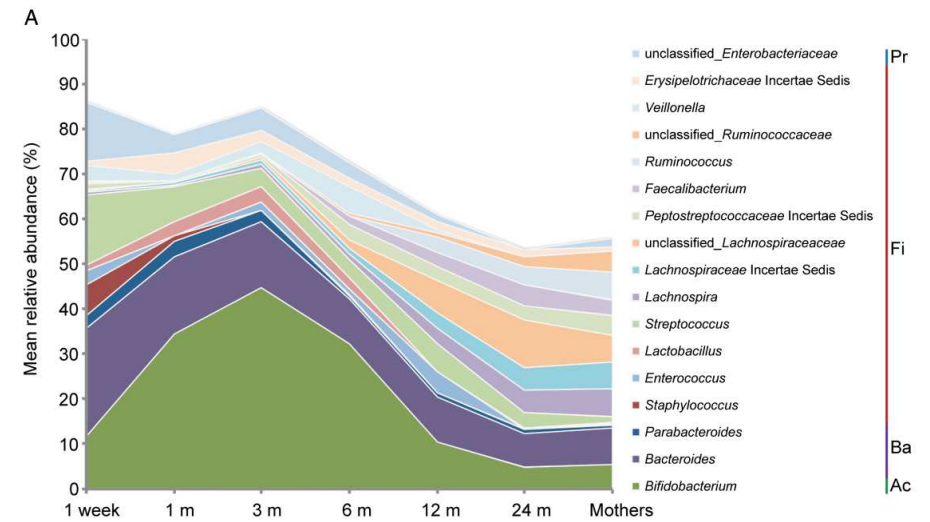
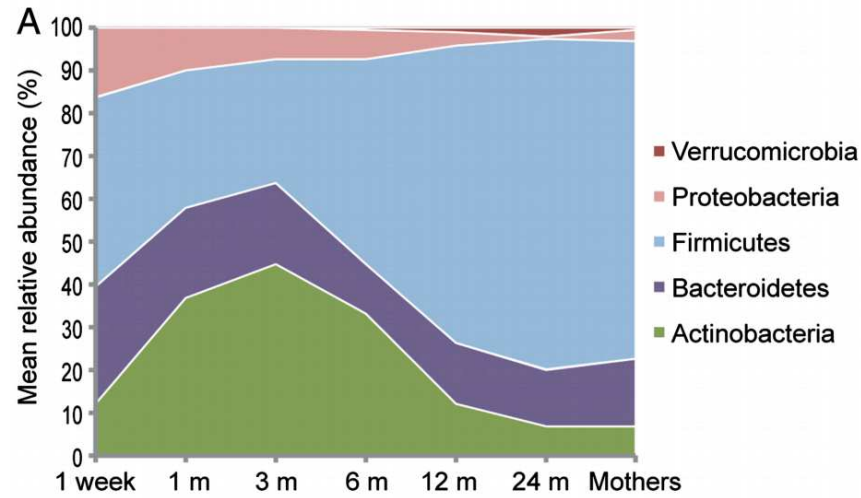
*Faecalibacterium
prausnitzii*



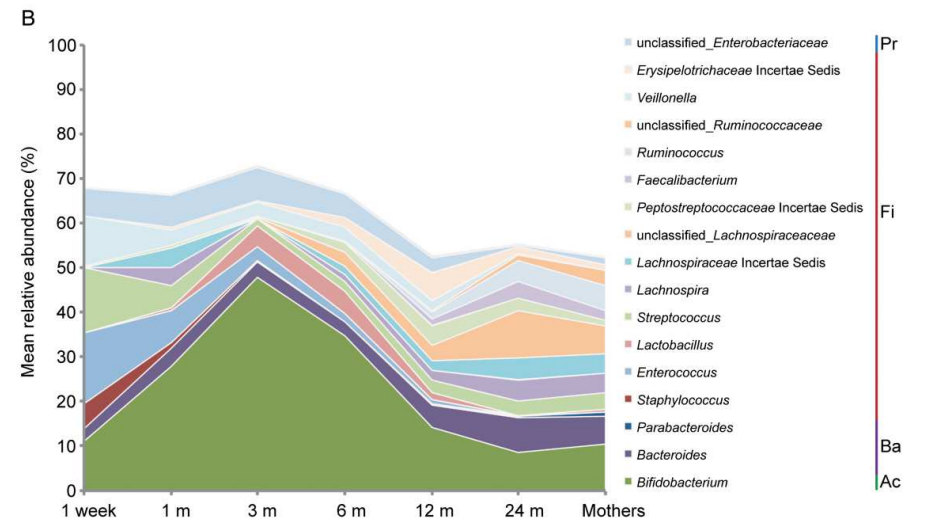
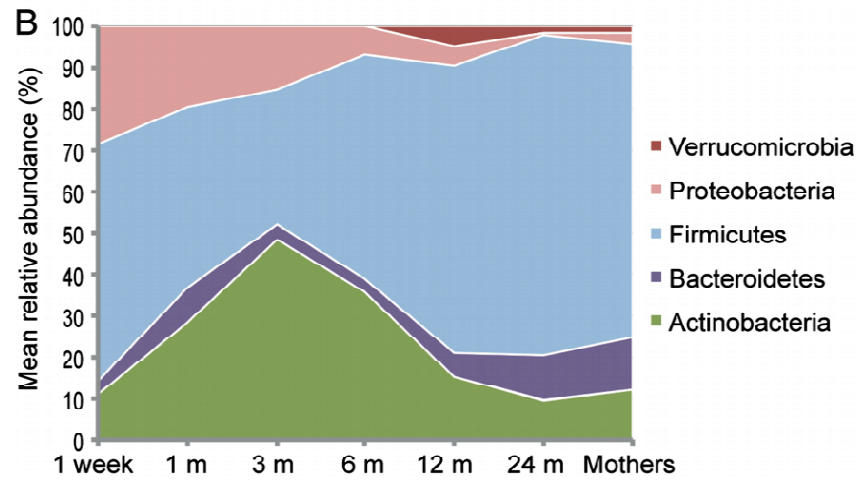


Mean relative abundance

Vaginally delivered
n = 15



C section delivered
n = 9



Phylum level

Genus level

The TEDDY Study Germany, Sweden, and, USA

BETTER

OPEN
https://doi.org/10.1038/s41586-018-0617-4

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

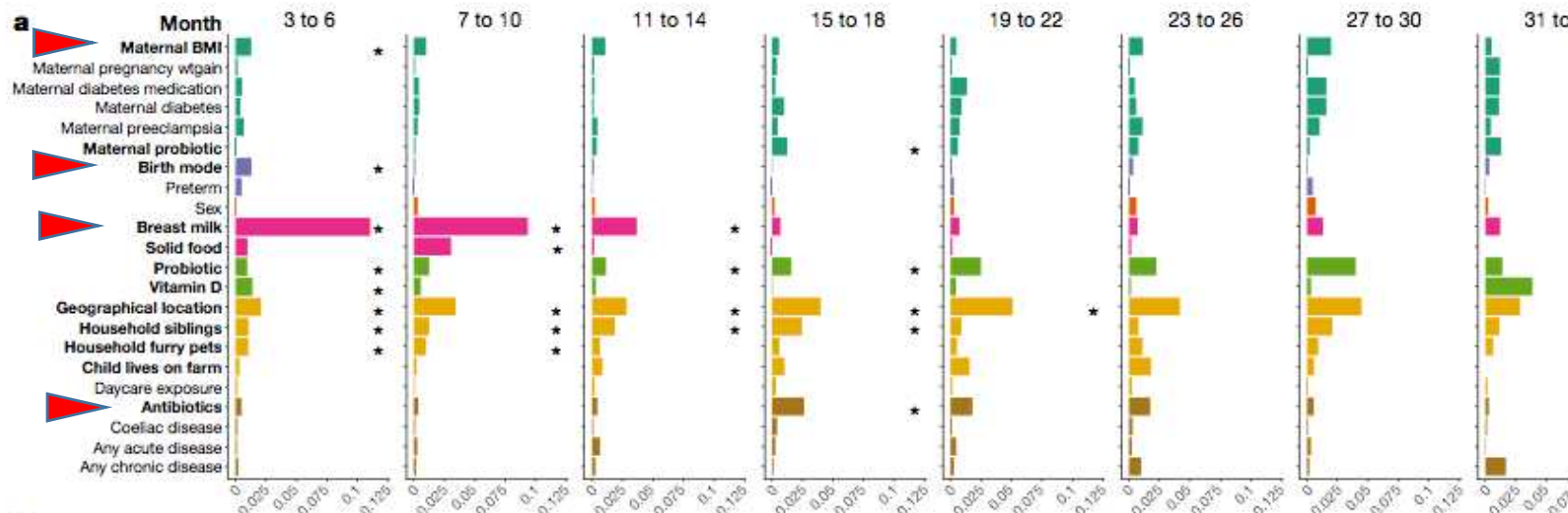
Development of the microbiome from infancy to childhood is an area of research with microbial-immune crosstalk time thought to be involved in the pathobiology of later life^{1,2}, such as persistent liver autoimmunity and type 1 diabetes mellitus^{3,4}. However, no studies have performed characterization of the microbiome in early life in a large, diverse population. Here we analyse longitudinal stool samples collected between 3 and 48 months of age by 165 rRNA gene sequencing (n = 10,867) and metagenomic sequencing (n = 10,867) in the Environmental Determinants of Diabetes in the TEDDY study. We show that the developing gut microbiome has three distinct phases of microbiome progression: a neonatal phase (months 3–6), a transitional phase (months 7–10), and a stable phase (months 11–48). Birth mode, delivery or partial, was the most significant factor associated with microbiome structure. Breastfeeding was associated with higher levels of *Bacteroides* species diversity. *B. fragilis* in infants delivered vaginally. *Bacteroides* species associated with increased gut diversity and factors associated with the birth mode. Environmental factors such as geographical location and household exposures (such as day care) were also important. These data determine the structure and function of the microbiome in early life and provide a foundation for mechanistic investigation into the consequences of immune crosstalk for long-term health.

KEY POINTS The TEDDY study is a large, diverse population-based study of children at risk of type 1 diabetes. The study collected stool samples from 903 children from 10 countries (Germany, Sweden and Finland) and three countries (Georgia and Washington) were analysed. The children were followed up from around 3 months of age. The Environmental Determinants of Type 1 Diabetes (TEDDY) study⁵. After restriction and limiting sequencing (n = 12,651 samples from 903 children; metagenomic

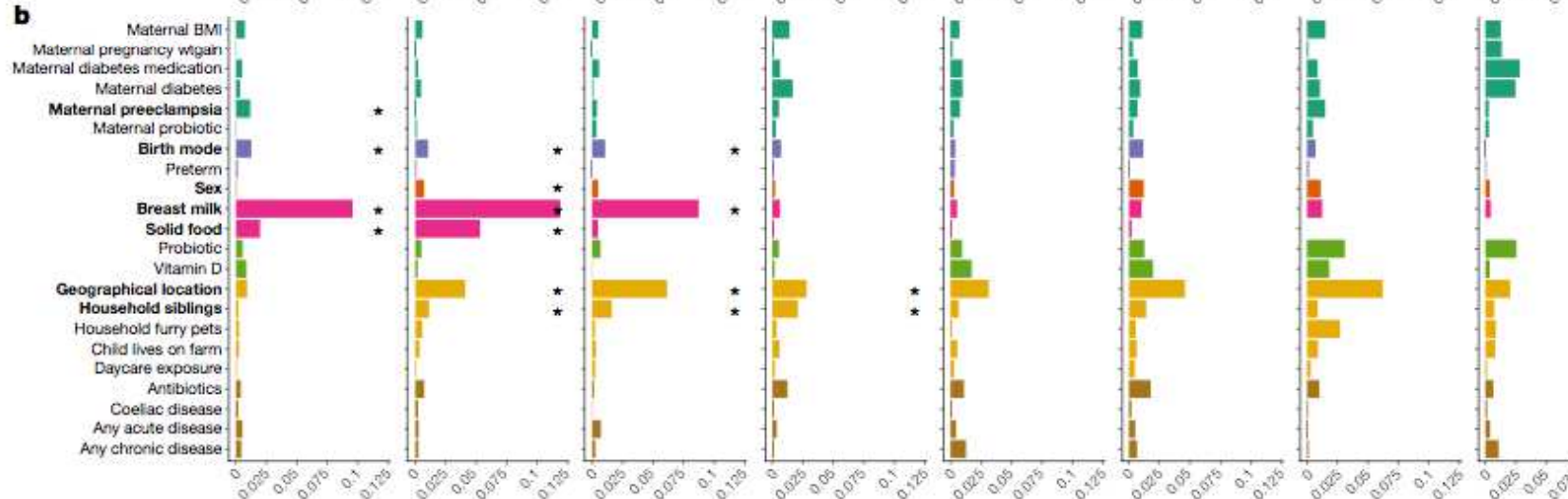
sequencing, n = 10,867 samples from 793 children) and functional metagenomic (metagenomic sequencing only) from longitudinal stool samples (Extended Data Table 1). A comparison paper by Vatanen et al.⁶ focused exclusively on metagenomic sequencing data. In this cohort of children that are at risk for developing type 1 diabetes, we aimed to (1) characterize definitively the longitudinal gut microbiome development from 3 to 48 months of age; (2) determine external maternal and perinatal influences on the developing bacterial community during this same time period of early development; and (3) use a novel case-control analysis to investigate the potential of the microbiome as a predictor for the development of T1D. A general overview of bacterial taxonomic and functional pathway development is provided in Supplementary Note 1 and Extended Data Fig. 1. Detailed taxonomic matrices (DSMZ) (DSMZ) was applied to 16S rRNA gene sequencing (Fig. 1) and metagenomic sequencing data (Extended Data Fig. 2). All samples from 3 to 48 months of age were included, and 16S rRNA gene sequencing profiles formed ten clusters (based on linear discriminant analysis) (Fig. 1a). Bacterial richness and diversity increased in each cluster (Fig. 1a, b). Using linear mixed-effects modelling of the top five phyla and Shannon diversity index, we determined three distinct phases of microbiome progression: developmental phase (months 3–6), a transitional phase (months 7–10), and a stable phase (months 11–48), in which all five phyla and the Shannon diversity index were unchanged during the stable phase (Fig. 1b). Microbiome diversity decreased during the initial developmental phase, in which 20% of individuals transitioned from cluster 1 to cluster 3. *Bacteroides* was dominant in both clusters. As infants aged, the microbiome of their stools diversified into clusters 4–8 during months 15–30 (that is, the transitional phase). Microbiome maturation, in which infant samples remained in the same cluster at consecutive time points, was observed from month 31 to 48. Clusters 9–10 were the most diverse during the stable phase with these clusters characterized by high alpha diversity and dominance of genera within the Firmicutes phylum. The three microbiome phases and changes in taxa are consistent with other cohorts^{7,8} and were supported by the metagenomic sequencing data (Supplementary Note 2 and Extended Data Fig. 2).

We next sought to determine the significant factors associated with the microbiome profiles from 16S rRNA gene sequencing (genus level,

Genus level



Species level



Amount of variance explained by each covariate
N = 987 children, >10,000 samples

Can we modify the intestinal microbiota?

The GI Microbiota is a stable ecosystem
– difficult to disrupt

- Diet
- Antibiotics
- Oral ingestion of bacteria (probiotics)
- Oral ingestion of bacterial substrates (prebiotics)
- Replacement of microbiota (fecal transplantation)

Feeding of *Bifidobacterium bifidum* and *Streptococcus thermophilus* to infants in hospital for prevention of diarrhoea and shedding of rotavirus

Jose M Saavedra, Nancy A Bauman, Irene Oung, Jay A Perman, Robert H Yolken

Summary

Acute diarrhoea is a serious cause of infant morbidity and mortality, and the development of preventive measures remains an important goal. Bifidobacteria (which constitute the predominant intestinal flora of breastfed infants), as well as other lactic-acid-producing organisms such as *Streptococcus thermophilus*, are thought to have a protective effect against acute diarrhoeal disease. However, their efficacy has not been assessed in controlled trials.

In a double-blind, placebo-controlled trial, infants aged 5–24 months who were admitted to a chronic medical care hospital were randomised to receive a standard infant formula or the same formula supplemented with *Bifidobacterium bifidum* and *S thermophilus*. Patients were evaluated daily for occurrence of diarrhoea, and faecal samples, obtained weekly, were analysed for rotavirus antigen by enzyme immunoassay. Faecal samples were also obtained during an episode of diarrhoea for virological and bacteriological analyses. 55 subjects were evaluated

Introduction

Acute diarrhoea is a major cause of infant mortality in developing countries.^{1,2} Furthermore, nosocomially acquired diarrhoeal disease in infants can lead to a prolonged stay in hospital and to increased medical costs. Although there are many microbial agents associated with gastroenteritis in this age group, rotavirus is the most important cause of the condition in infants admitted to hospital in the USA and in many other countries.³ The development of effective methods to prevent acute gastroenteritis remains an important goal for infant health.⁴

The replication of pathogenic organisms within the gastrointestinal tract is determined by various microbial and host factors. One such factor is the composition of non-pathogenic intestinal flora. For example, the anaerobic bacteria of the genus *Bifidobacterium* constitute the predominant colonic flora of breastfed infants.⁵ Bifidobacteria are thought to exert some of the protective effect against diarrhoea associated with breastfeeding.⁶ Additionally, in laboratory animals bifidobacteria reduce

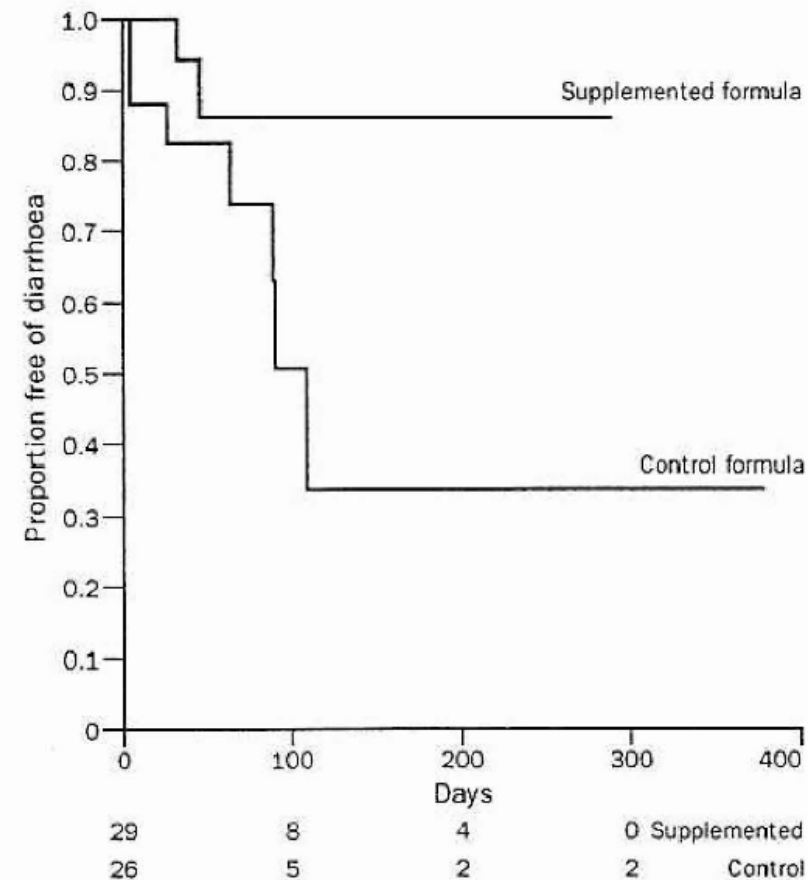


Figure: Cumulative incidence of diarrhoea in infants receiving formula supplemented with *Bifidobacterium bifidum* and *Streptococcus thermophilus* (supplemented) and the same formula without these bacteria (control)

ationale

Bifidobacteria, the most abundant genus in breastfed infants
Technology allowed the growth and production of adequate cultures

Potential for competing with pathogenic bacteria

The New York Times

New York: Today, a breezy, high 65, brisk winds. Low 50, clearing clouds. High 66, low 47, 14.

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NEW YORK, FRIDAY, OCTOBER 14, 1994

35 cents (around the greater New York metropolitan area)

October 1994

2 Healthful Bacteria Are Proved To Ward Off Diarrhea in Infants

By WARREN E. LEARY

Special to The New York Times

WASHINGTON, Oct. 13 — Bacteria common to breast milk and yogurt can greatly reduce the risk of infants developing diarrhea, indicating that such "good germs" can be added to foods to attack a widespread health problem, scientists said today.

Scientists at Johns Hopkins Children's Center in Baltimore had conducted the first study to prove that adding common bacteria to infant formula could cut the risk of developing diarrhea in youngsters; in this study, the risk was cut by almost 80 percent.

In a report being published Saturday in *The Lancet*, a leading medical journal, researchers said that the bacteria, *Bifidobacterium bifidum*, which is commonly detected in the stools of breast-fed infants, and *Lactobacillus acidophilus*, which is found in yogurt, could ward off diarrhea in infants.

to milk or other foods used in schools and day care centers. But he said he could not yet make specific recommendations to parents on giving their children yogurt or other sources of the bacteria. More research is needed, he said, on

Good germs help keep babies well

■ "Breast is best," one scientist says, but introducing certain bacteria to baby formula can help prevent diarrhea.

tion of diarrheal diseases around the world," said Robert Yolken, one of the researchers and a professor of pediatrics at Johns Hopkins University School of Medicine.

The study is to be published in Saturday's issue of *The Lancet*, a

ers is an attempt to restore the natural environment.

"Their findings seem logical," said Dr. Warren Andiman, professor of pediatrics at Yale University. "It's not a totally novel idea, but using it in a slightly different way."

A leading physician at the turn of the century advocated treating patients with germs.

Since then, some doctors and nutritionists have promoted yogurt with live bacteria to heal the body, particularly for patients taking antibiotics. Antibiotics fight off some bugs, disrupting the normal germ colonies.

A few nutritionists advocate yogurt enemas for patients with severe gut infections and yogurt douches for women who get vaginal infections.

Study touts yogurt bacteria for kids

Baltimore Sun

BALTIMORE — Two of the "good bacteria" used in some yogurts can protect children from catching or spreading diarrhea — a common childhood ailment in the United States and a major killer in the Third World, doctors said Thursday.

Pediatric researchers at the Johns Hopkins Children's Center here found that children given a regular diet of infant formula laced with *bifida* and *thermophilus*, the live cultures, were 78 percent less likely to get the disease than youngsters

who drank plain formula.

Dr. Robert Yolken said the live bacteria are sold as supplements in health food stores but also are present in some cultured milk products including yogurt and acidophilus milk — a product geared for people who cannot digest ordinary milk.

"We might be able to put (the bacteria) into milk delivered to schools and day-care centers," Yolken said.

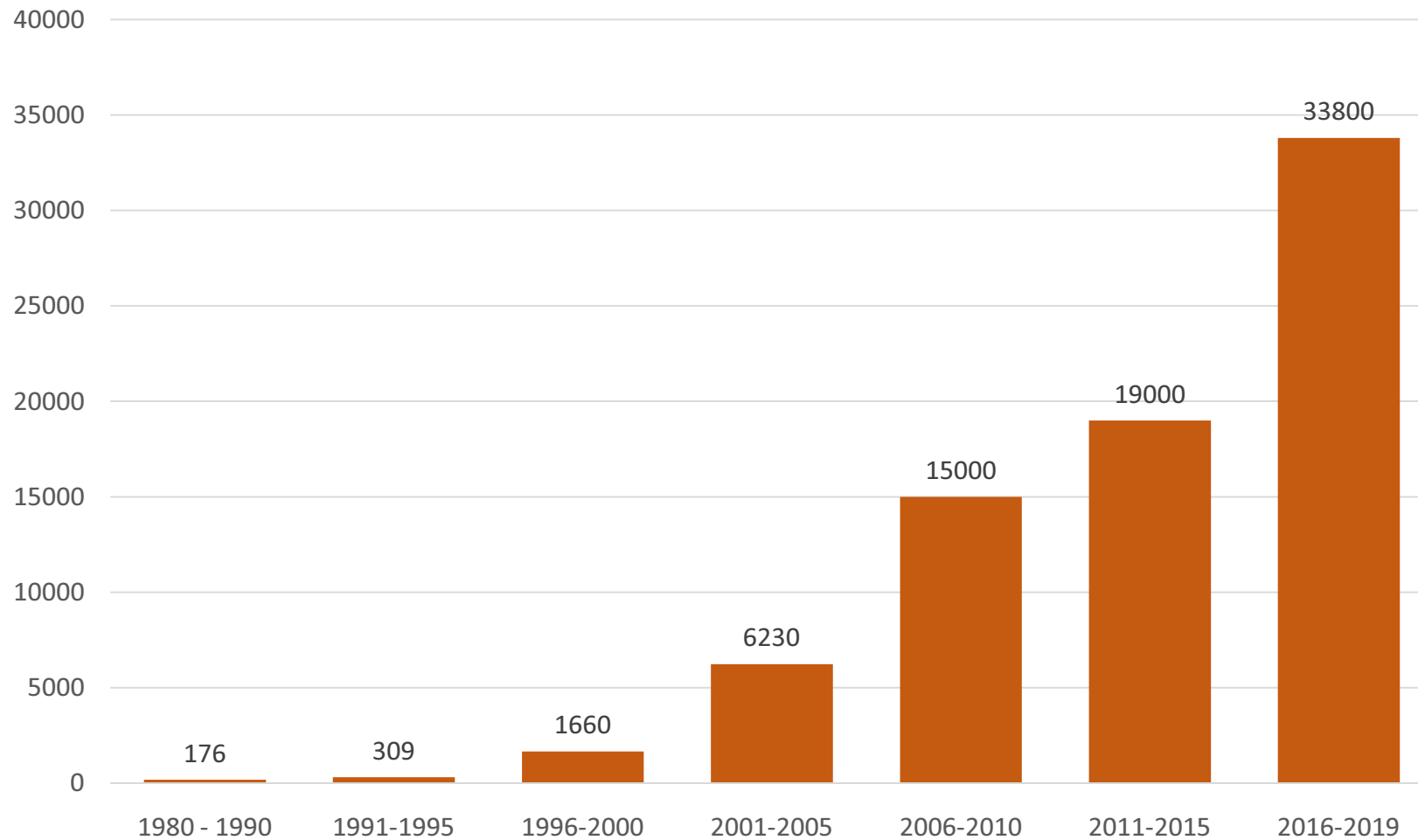
He cautioned, however, that further research is needed to determine who should take it and how much they should take and which bacteria are best.

Nonetheless, it appears that parents can hardly go wrong in feeding yogurt to children who have advanced beyond breast milk or formula. Dr. Jose Saavedra, a pediatric gastroenterologist, said yogurt is a good source of calories, protein and important minerals such as calcium and is easy to digest.

Yolken said yogurt can serve as an excellent bridge between breast milk or formula, which children often give up in the second six months of life, and plain cow's milk, which is difficult for many children to digest.

The study appears in *Lancet*.

Probiotics: Citations per year



Google Scholar search 2019: Probiotics, Human medicine

Defining probiotics

CONSENSUS STATEMENTS



Probiotics in food
Health and nutritional properties
and guidelines for evaluation

FAO
FOOD AND
NUTRITION
PAPER
85



EXPERT CONSENSUS DOCUMENT

The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic

*‘Live organisms which when
administered in adequate amounts
confer a health benefit on the host*

Definition

- *Live microorganisms that, when administered in adequate amounts, confer a health benefit on the host*

FAO/ WHO – adapted by ISAPP



B. lactis



L. reuteri



L. Rhamnosus GG

* *B. lactis* and *L. reuteri* are the only two probiotics with GRAS status approved for use in term infant formula from day 1 by US FDA

Bifidobacterium lactis



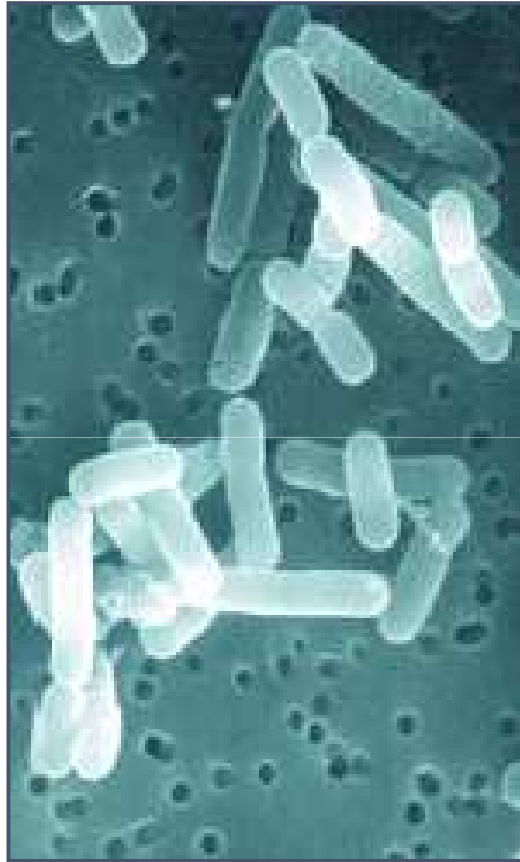
B.lactis, strain Bb-12

- Bifidobacteria found in breastmilk
 - **Predominant bacteria in the gut of breastfed infants**

Positive outcomes reported:

- Immune system development and modulation
- Increase in Secretory IgA
- Reduce risk of acute diarrhea
- Antibiotic diarrhea risk reduction
- Emerging Evidence in Allergy and NEC
- **FDA GRAS status in infant formula from birth**

Lactobacillus reuteri



L. reuteri

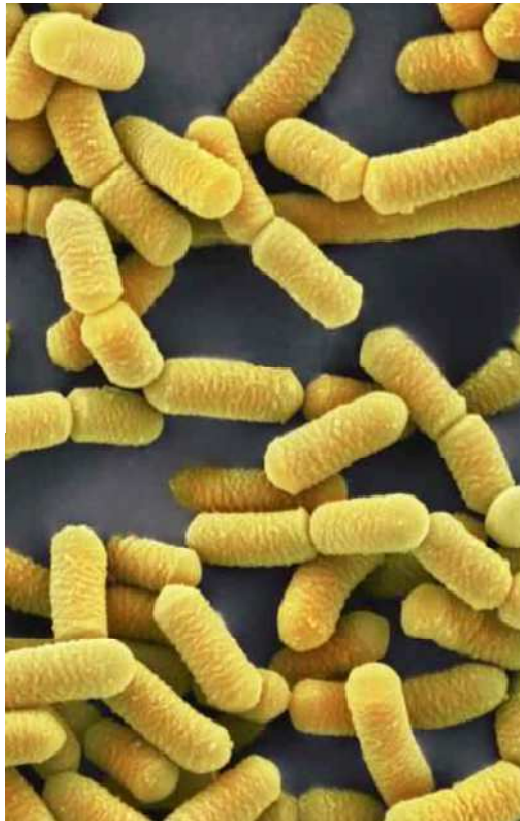
strain ATCC55730, DSM 17038

- **Isolated from breastmilk**

Most relevant areas of clinical research showing positive results:

- Reduced infant colic and crying
- Improved GI motility
- Reduced intensity of abdominal pain
- Regulated bowel movements
- Improved feeding tolerance in premature infants
- Diarrhea
- **FDA GRAS status in term infant formula from birth**

Lactobacillus rhamnosus (GG)



L. Rhamnosus

- **The most studied probiotic bacterium**

Most relevant areas of clinical research showing positive results:

- Improved GI motility / constipation
- Management of diarrhea
- Diarrhea / acute respiratory infections
- Antibiotic associated diarrhea
- Allergic manifestations
- **No FDA GRAS status in term infant formula from birth. Approved for therapeutic formulas**

<https://www.ingredientsnetwork.com/chr-hansen-lgg-news042798.html>

nomenclature –

Fecal Recovery in Humans of Viable *Bifidobacterium* sp Ingested in Fermented Milk

YORAM BOUHNİK, PHILIPPE POCIHART, PHILIPPE MARTEAU, GUILLAUME ARLET, ISABELLE GODEREL, and JEAN CLAUDE RAMBAUD
Unité de Recherches sur les Fonctions Intestinales, le Métabolisme et la Nutrition, INSERM U290, Hôpital Saint Lazare, Paris; Département de Microbiologie-Immunologie, Unité de Formation et de Recherche des Sciences Pharmaceutiques, Université Paris XI, Châtenay Malabry; and Service de Bactériologie et de Virologie, Hôpital Saint-Louis, Paris, France

Bifidobacterium sp is a natural component of the dominant colonic microflora that was recently introduced into several fermented dairy products. The aim of the present study was to study the fate of this microorganism in the human gut. On the basis of antibiotic resistance characters, a variant of *Bifidobacterium* sp that could be distinguished from indigenous bifidobacteria in the fecal flora was selected, and its survival and colonization in the colon was examined. This strain was used to ferment milk, and 125 g of the fermented product obtained was ingested by eight healthy volunteers three times daily for 8 days. Stools were recovered and weighed throughout the study. The results showed that the exogenous *Bifidobacterium* sp appeared in stools and reached a mean level of 8.8 ± 0.1 log colony-forming units per gram. This level was maintained as long as the fermented dairy product was consumed. When its ingestion stopped, the exogenous *Bifidobacterium* sp gradually decreased and was no longer detectable 8 days after cessation. The mean recovered quantity during the 8-day period of administration of the ingested bifidobacteria excreted in stools was 12.1 ± 0.1 log colony-forming units per gram, i.e., $29.7\% \pm 6\%$ of the ingested bacteria, which was similar to the percentage that reached the colon in previous studies. It is concluded that under physiological conditions, exogenously administered *Bifidobacterium* sp do not colonize the human colon. However, the high fecal concentrations of exogenous bifidobacteria reached are compatible with metabolic "probiotic" activities.

In many parts of the world, fermented milk constitutes a significant and increasing part of food consumption and usually contains more than 10 billion living bacteria per 100 g of product. Since Metchnikoff's theories about the beneficial effects of lactic acid bacteria on the intestinal microflora,¹ there has been sustained interest in these microorganisms.² In-

deed, they could fulfil the criteria of probiotic agents, recently redefined as "a live microbial feed supplement which beneficially affects the host animal by improving its microbial balance."³ In fact, little is known about the fate of ingested bacteria in the organism. After ingestion of a fermented dairy product (FDP), 1.5% of two *Lactobacillus* strains were shown to survive at the terminal ileum^{4,5}; also, there was a significant increase in the fecal counts of lactobacilli with another strain.⁶ This increase was considered as an explanation for some of the modifications of fecal bacterial enzymatic activities observed after ingestion of living *Lactobacillus* sp in an FDP.^{7,8}

However, it is difficult to assess the capacity for survival of an exogenous microorganism in the human colon because of the difficulty of distinguishing exogenous bacteria from their possible endogenous congeners in the fecal flora and sometimes because of the difficulty of clearly identifying certain species among the complex intestinal flora.⁹

If some exogenous bacteria belonging to the subdominant flora do survive in the digestive tract, they cannot colonize the intestinal tract; this led to the concept that the dominant anaerobic component of the indigenous intestinal microflora exerts resistance to colonization by exogenous microorganisms.^{10,11} This "barrier effect," the mechanism of which is still obscure, has been shown with several bacteria in which fecal excretion was compared with that of an inert marker ingested at the same time. The barrier effect is considered to be caused by bacteriostasis when the fecal elimination of the two components shows the same kinetics and to bacteriolysis when the exogenous bacteria is eliminated quicker than the passive marker.¹² However, there has been no direct experimental proof in either human subjects or experimental animals whether this barrier effect also applies to species belonging to the dominant flora.

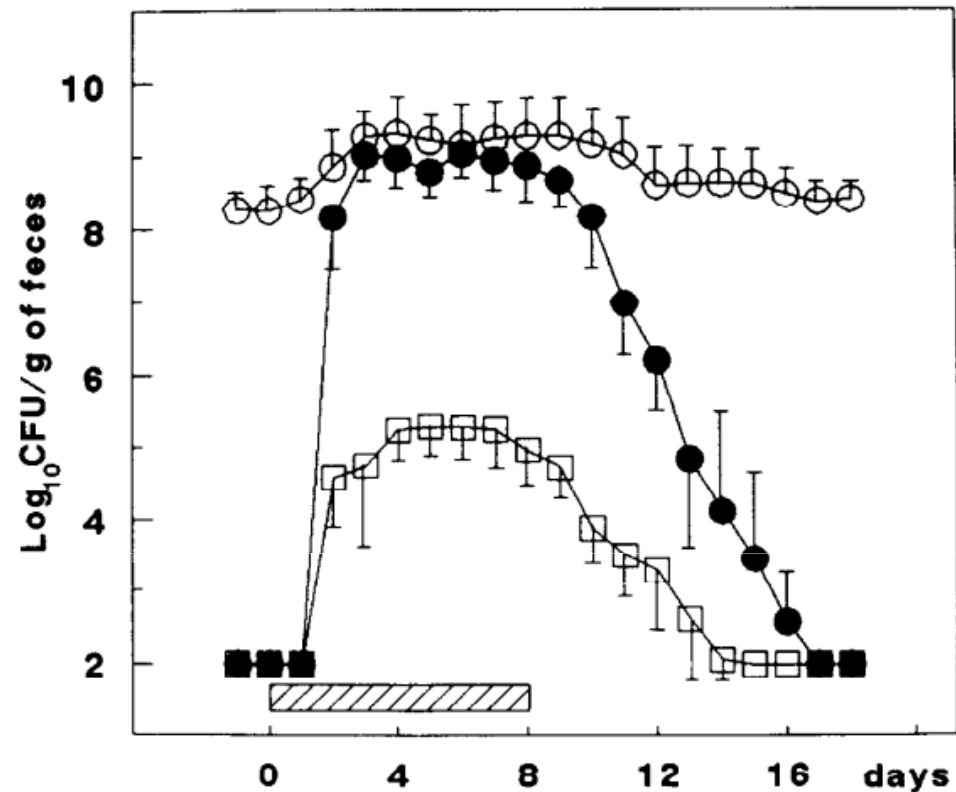


Figure 1. Fecal concentrations (mean \pm SE) of total bifidobacteria (○), a selected strain of *Bifidobacterium* sp (BOSR) (●), and spores of *Bacillus stearothermophilus* (SBS) (□) obtained in eight healthy volunteers after ingestion of 125 g t.i.d. of fermented dairy product (▨) containing 9.2 log CFU/g of BOSR and 5.4 log CFU/g of SBS for 8 days.

Documented Effects of Probiotic Supplementation on Protective Gut Barrier and Immune Function

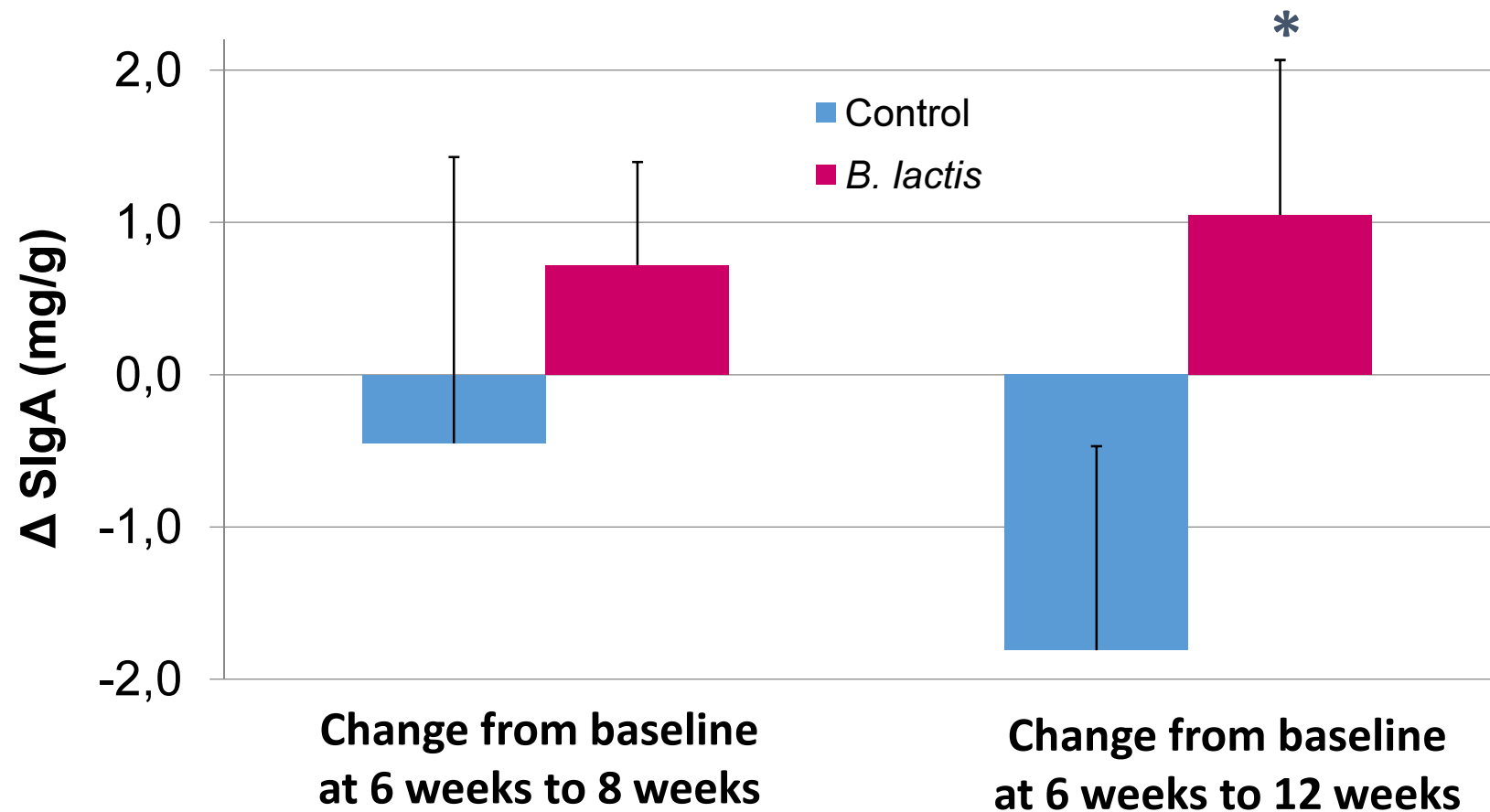
- Decreased gut permeability
- Increased mucin production
- Increased IgA secreting cells and secretory IgA
- Increased natural killer cell tumor-killing activity
- Increased production of macrophages and activated phagocytosis
- Immune modulation towards antigen tolerance

Fukushima Y., et al. Int J Food Microbiol 1998;42:39-44

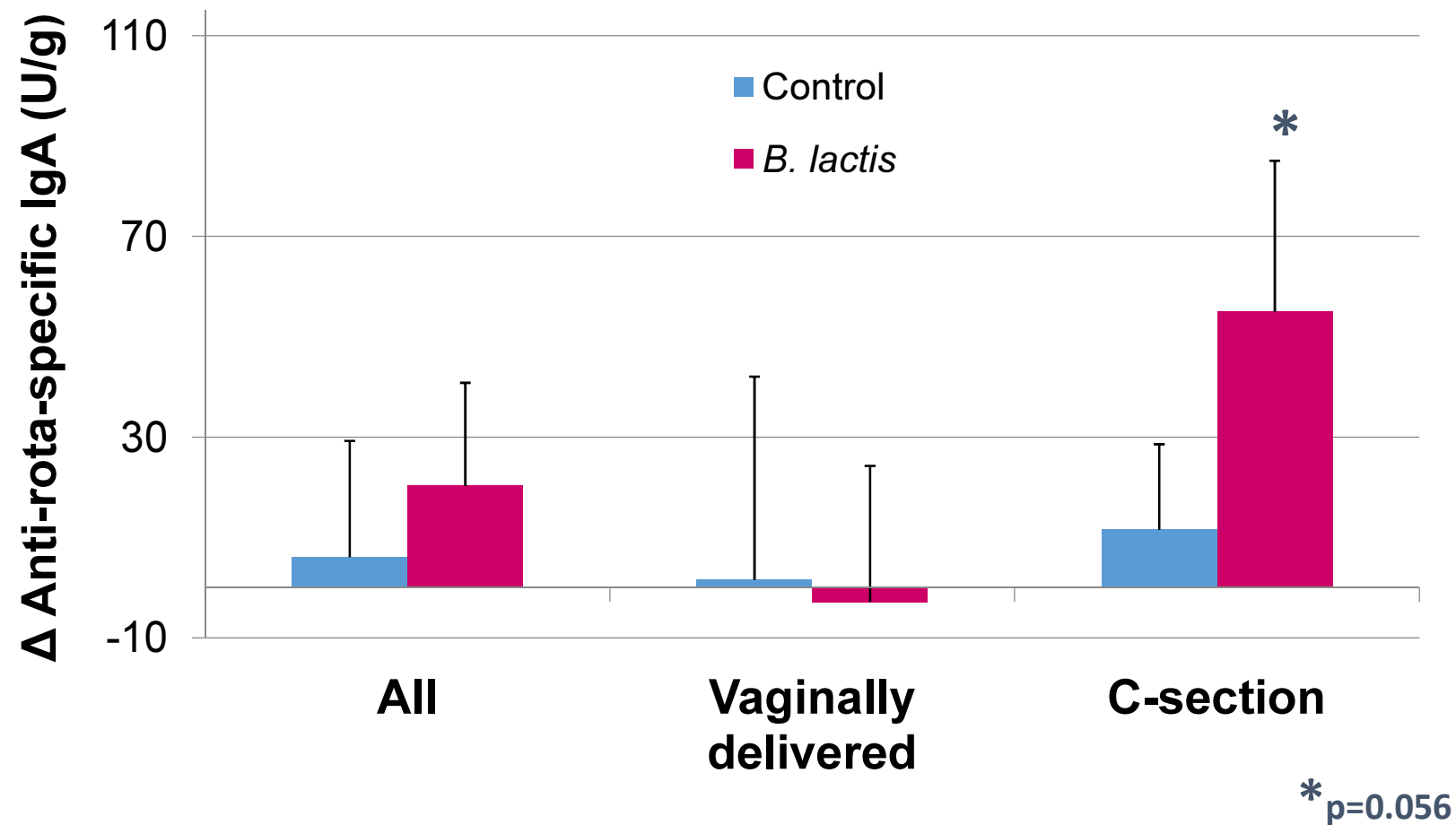
Rautava S., et al. Pediatr Res 2006;60:221-224

Stratiki Z., et al. Early Hum Dev 2007 on-line at: <http://dx.doi.org/10.1016/j.earlhumdev.2006.12.002>

Infant Formula Supplemented with *B. lactis* Increases Fecal IgA



Anti-Rotavirus IgA Increases with *B. lactis* Supplementation in Infants Born via C-section



Clinical Outcomes reported with specific probiotics documented in Infants and Children

- Modification of intestinal microbiota
- Reduced risk and duration of acute diarrhea
- Reduced risk of respiratory infections
- Reduce crying time in Infant colic
- Reduced risk of atopic dermatitis
- Reduced risk of NEC

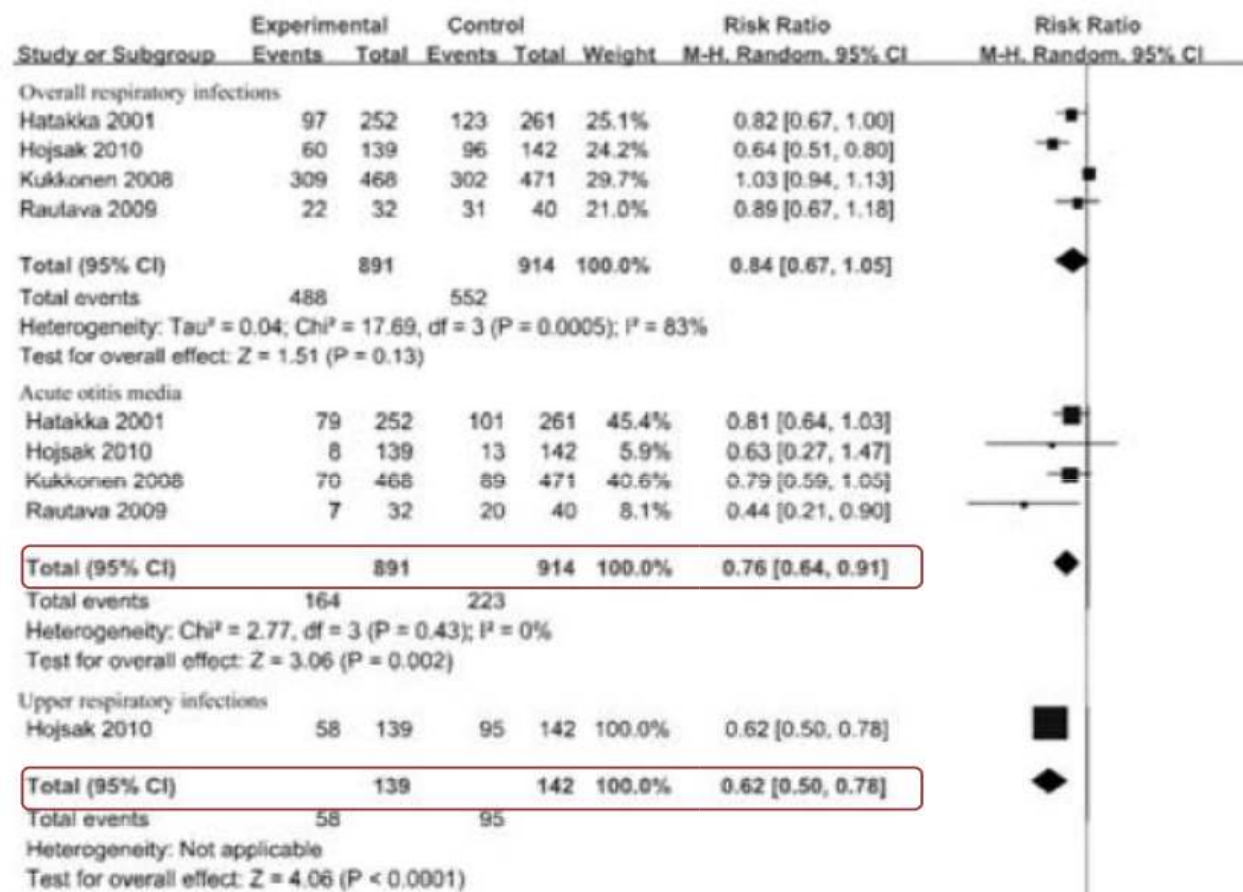
Prevention of nosocomial diarrhoea

| | | RR (95% CI) | NNT (95% CI) |
|-----------------------------|----------------------------------------|----------------|--------------|
| Saavedra Lancet 1994 | <i>B. Bifidum</i> + <i>S. therm</i> | 0.2 (0.06-0.8) | 5 (3-20) |
| Penna Pediatrics 2009 | <i>L. delbrueckii</i> <i>H2B20</i> | 1.6 (0.6-4.0) | NS |
| Szajewska J Pediatr 2000 | <i>L. rhamnosus GG</i> | 0.2 (0.06-0.6) | 4 (2-10) |
| Mastretta JPGN 2002 | <i>L. rhamnosus GG</i> | 0.8 (0.6-1.3) | NS |
| Hojdak Pediatrics 2010 | <i>L. Rhamnosus GG</i> | 0.4 (0.25-0.7) | 15 (9-34) |

Probiotics in preventing infections in day care centers

| | Probiotic | Diarrhea | Respiratory inf. |
|---------------------------|------------------------------------------------|-----------|------------------|
| Ribeiro 1998 | <i>L plantarum</i> 299v | Decreased | Decreased |
| Pedone 2000 | <i>L casei</i> DN 114 001 | Decreased | NA |
| Chouraqui 2004 | <i>B lactis</i> Bb12 | Decreased | NA |
| Hatakka 2001 | LGG | NS | Decreased |
| Thibault 2004 | <i>B breve</i> + <i>Str therm</i> | Decreased | NA |
| Saavedra 2004 | <i>B lactis</i> + <i>Str therm</i> | NS | NS |
| Weizman 2005 | <i>B lactis</i> OR <i>L reuteri</i> ATCC 55730 | Decreased | NS |
| Binns 2007 | <i>B lactis</i> + FOS + GUM | Decreased | NS |
| Waligora 2006 | Oligofructose | Decreased | NS |
| Leyer 2009 | <i>L acidophilus</i> + <i>B animalis</i> | N/A | Decreased |
| Merenstein 2010 | <i>L casei</i> DN 114 001 | Decreased | Decreased |
| Hojasak 2010 | <i>L rhamnosus</i> GG | NS | Decreased |
| Agustina 2012 | <i>L reuteri</i> DSM 17938 | Decreased | NS |
| Gutierrez-Castrellon 2014 | <i>L reuteri</i> DSM 17938 | Decreased | Decreased |

L. rhamnosus GG and respiratory infections

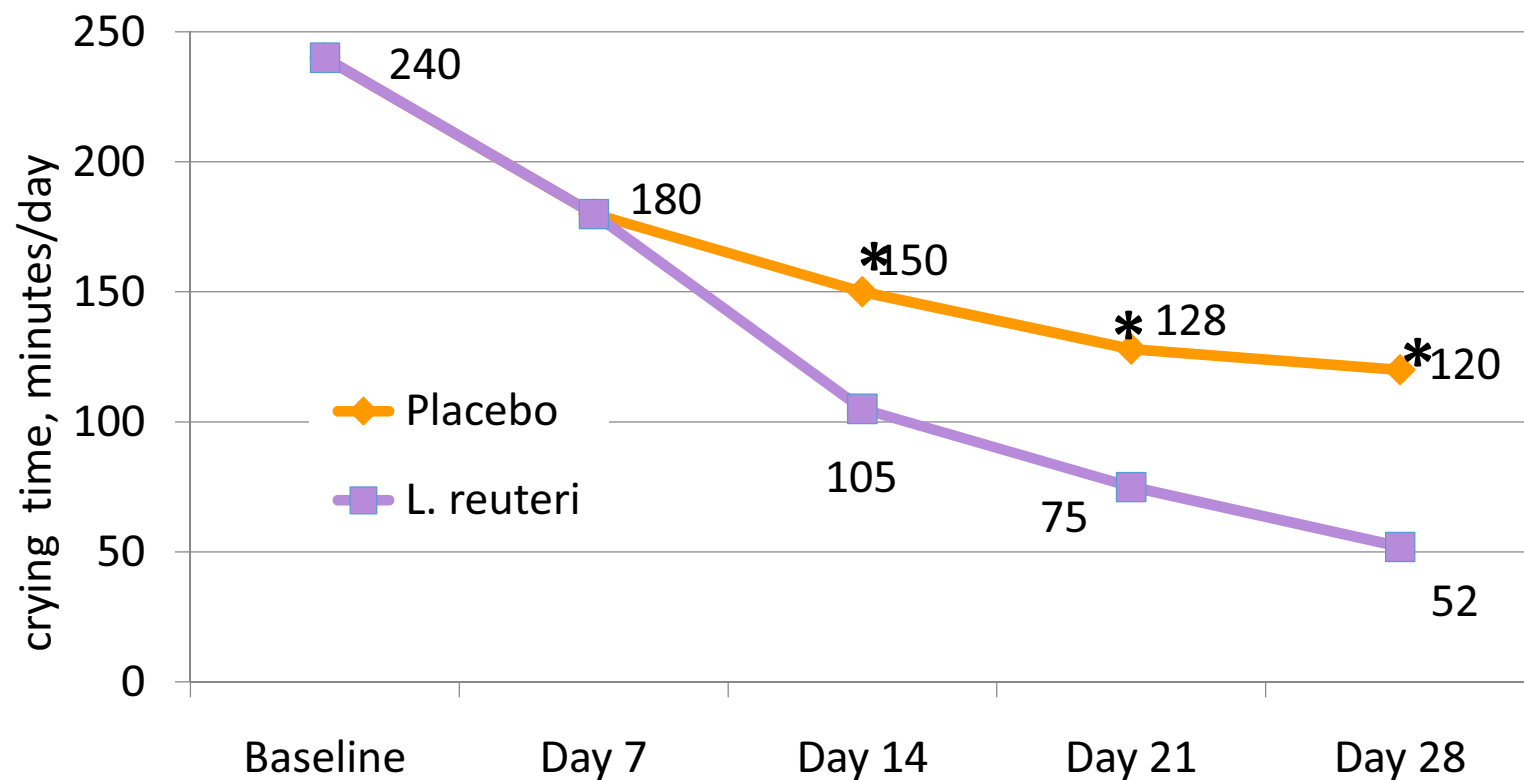


Overall respiratory infections 2 RCTs, $n=794$, RR 0.73, 95% CI:0.57-0.92).

Otitis media 4 RCTs, $n=1805$, RR 0.76, 95% CI: 0.64-0.91)

Upper respiratory infections 1 RCT, $n=281$, RR 0.62, 95% CI 0.50-0.78)

Reduction in Crying Time with *L. reuteri* Supplementation vs. Placebo



* $p < 0.0001$

Potential Mechanisms by which Probiotics May be Beneficial in Infant Colic

- Promote microbial balance (increase lactobacilli & decrease coliforms and bacteroides)¹
- Improve gut motility in infants²
- Enhance mucosal barrier (decrease gut permeability)³
- Neuro - chemical mechanism through the gut-brain axis (?)

1. Savino, F, et al. Pediatrics 2010; 126(3):e526-33.

2. Indiro F, et al. J Peds 2008;152(6):801-6.

3. Savino F, et al. Pediatrics 2007;119(1):e124-30.

4. Rosenfeldt V. et al. J Pediatr 2004;145:612-16.

Probiotics in Prematures Effect on Stage 2 NEC

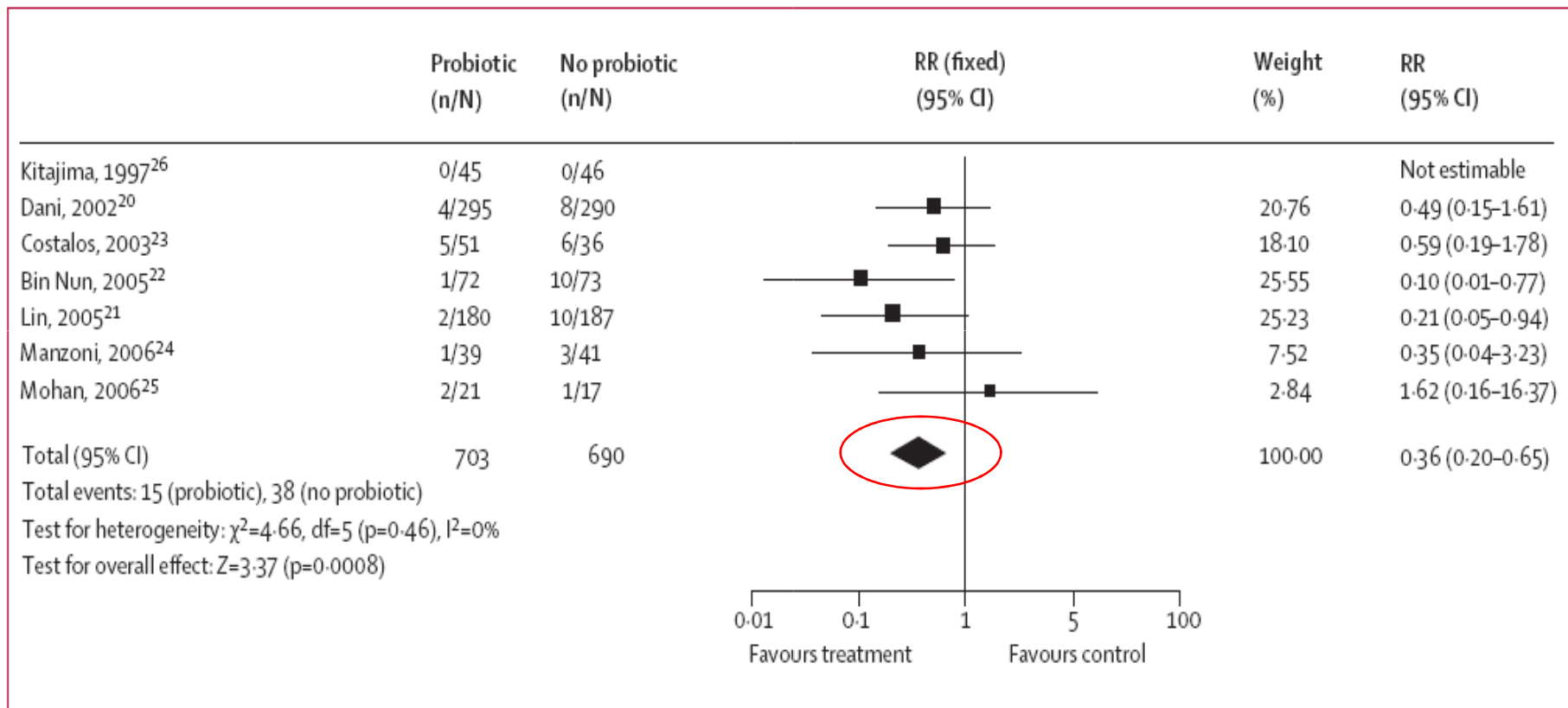


Figure 2: Effect of probiotics on necrotising enterocolitis of stage 2 or greater

73% Risk reduction

Probiotics in Prematures: Mortality

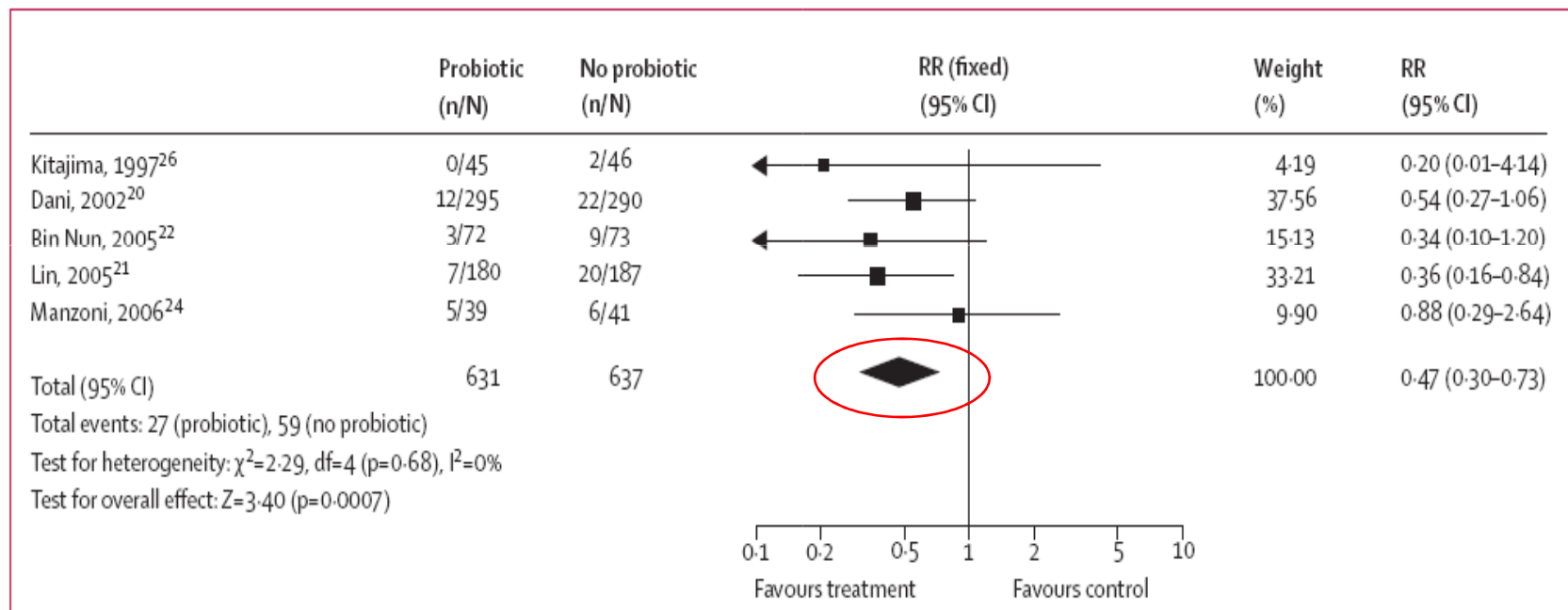


Figure 4: Effect of probiotics on all-cause mortality

53% Risk reduction

Brief general summary: Clinical use of probiotics*

The use of *specific probiotics* can

- Decrease risk and duration of acute diarrhea in healthy infants
B.lactis, B. bifidum, B. infantis, LGG, L. reuteri, S boulardi
- Decrease in antibiotic associated diarrhea
L.GG, [S. boulardi]
- Decrease respiratory infections
L.GG, L. reuteri
- Decrease crying time in infants with colic
L. reuteri
- Decrease NEC in premature infants
Bifidobacteria & lactobacilli
- Decrease allergic manifestations
L. GG

t exhaustive or all encompassing

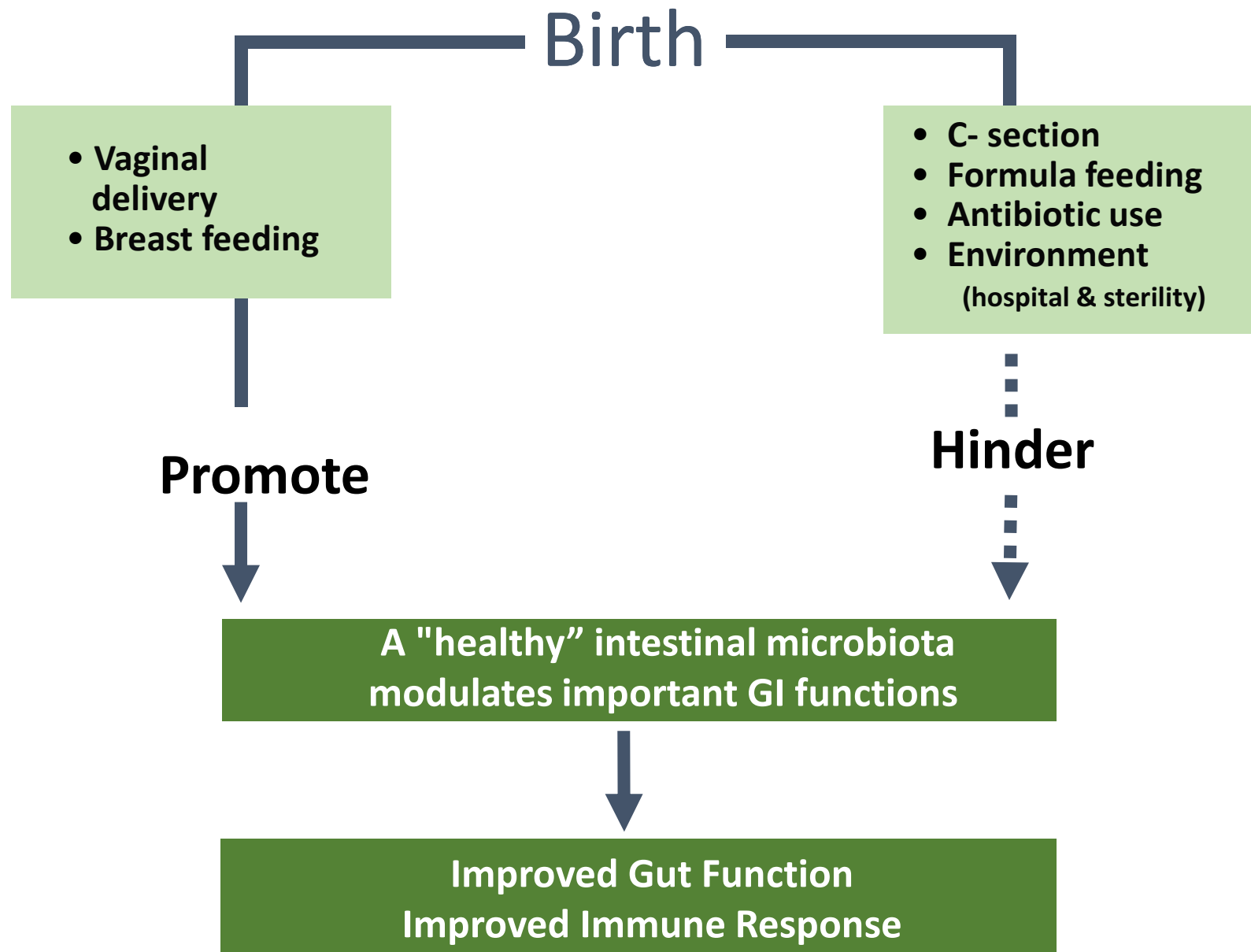
Considerations when interpreting probiotic studies

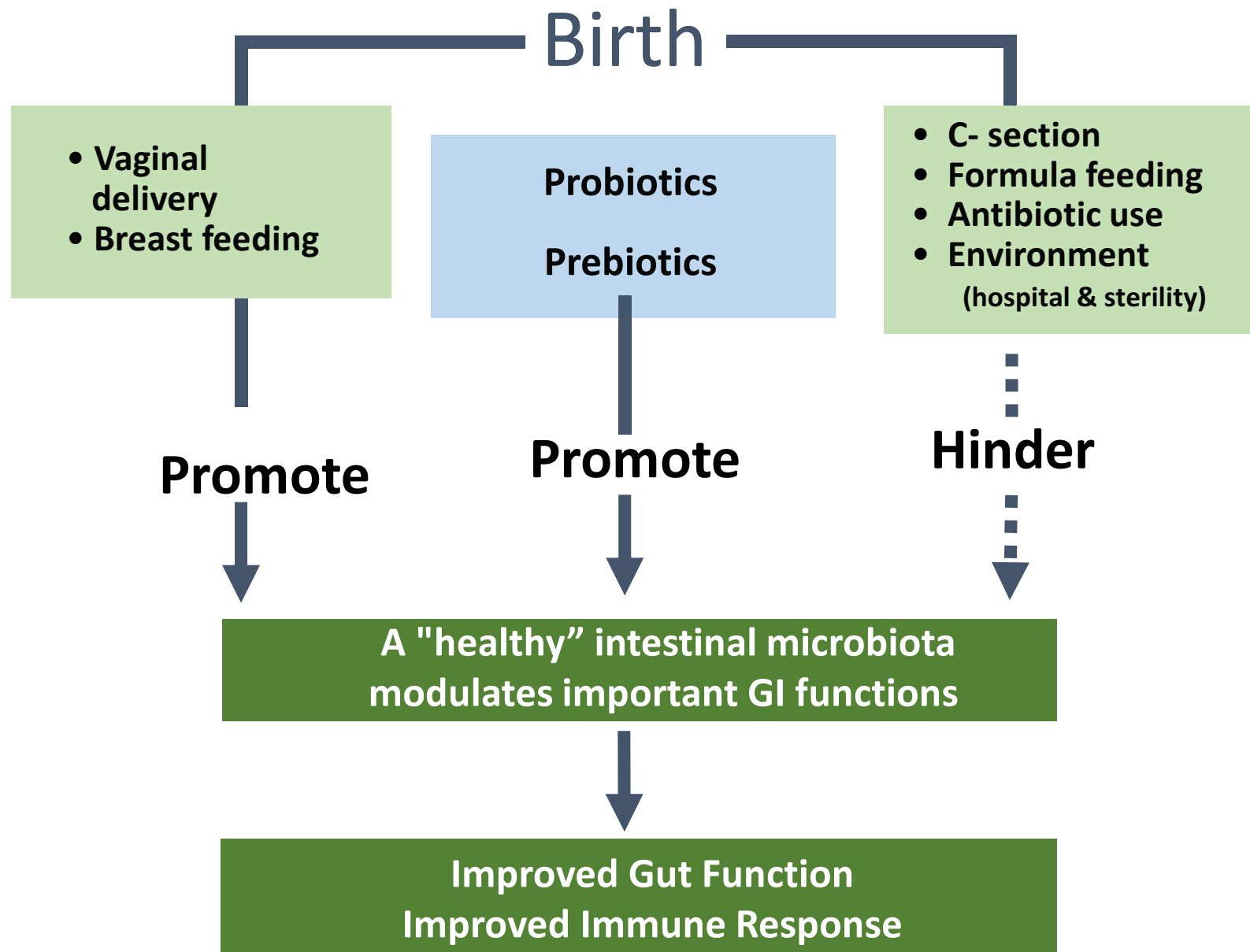
Not all probiotics are created equal

- Consider genus, species and strain
- Dose
- Mode of administration

Not all hosts are created equal

- Different risk populations
- C section
- Breastfeeding
- Diet
- Antibiotics





Thank You

Thank You

February 1 2017 Vol. 37 No. 3 Feature Articles Magazine

Next-Generation Sequencing Challenges

NGS Growing By Leaps and Bounds, Problems Arise

February 31, 2017 0