



Intestinal Microbiota in Infants its Impact on Health

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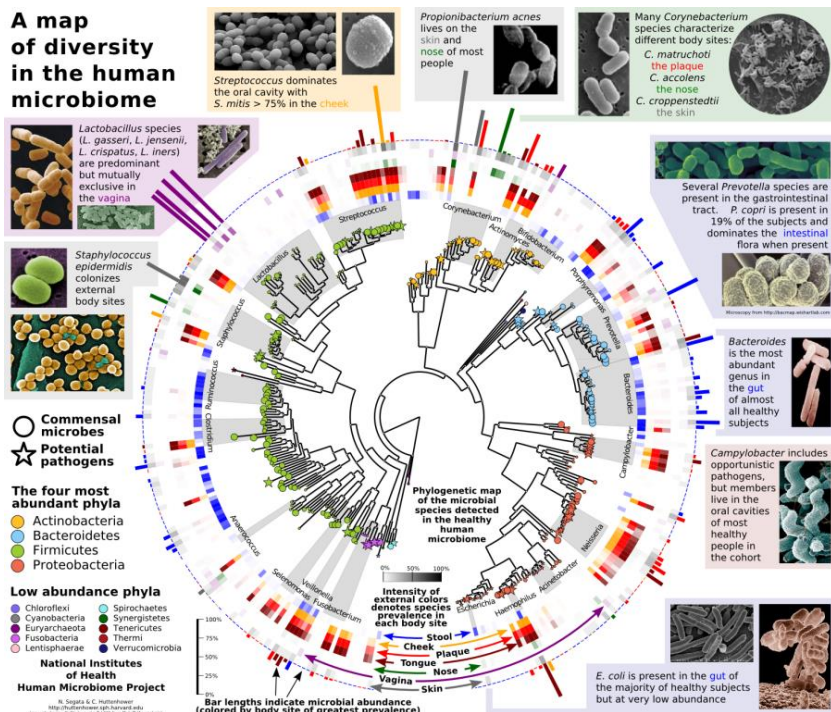
Germ Theory

- At the end of 1800s
- Microbes were discovered as agents of diseases
- Its thought that all microorganisms were bad



- 150 years later...
- Nonculture techniques have been developed
- **Metagenomics**
- The human body harbors a dynamic and complex microbial population (500- 1000 different species)
- HMP is started in 2008

A map of diversity in the human microbiome



NIH HUMAN
MICROBIOME
PROJECT

Intestinal Microbiota

- Consists of more than 1000 separate species and more cells by 10-fold than cells in the human body
- Contains 100-fold greater number of genes than the human genome
- The metabolic activity of colonizing bacteria is greater than the liver
- Can be considered as an ancillary organ
- Human-microbiota 'superorganism'



Intestinal Microbiota

- Digestive functions
 - Metabolizing complex carbohydrates
 - Fermentation into short chain fatty acids
- Synthesis functions:
 - Vitamins



Cross talk between intestine and microbiota

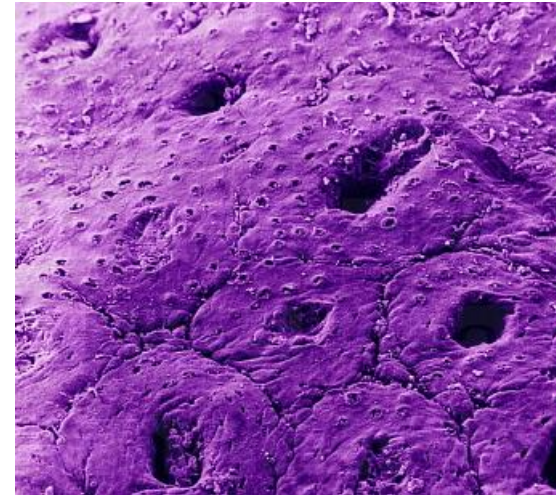
Microbiota



Mucosal cells

Immune cells

Neuronal endings



Cross talk between intestine and microbiota

- Interactions between the commensal bacteria and the host in the early postnatal period are important for host metabolism and development of healthy gastrointestinal, immunological and neural systems
- Dysbiosis is linked with a number of gastrointestinal and systemic disorders

Establishment of microbiota in newborns

- At birth, the newborn infant gut is *almost* sterile
- Rapidly colonised in the first days of life
- Dynamic fluctuations in bacterial composition until a relatively stable population is reached similar to an adult around two years old

Establishment of microbiota in newborns: frontiers

Immediately after birth;
Facultative anaerobic bacteria

Enterobacteriaceae

Streptococci

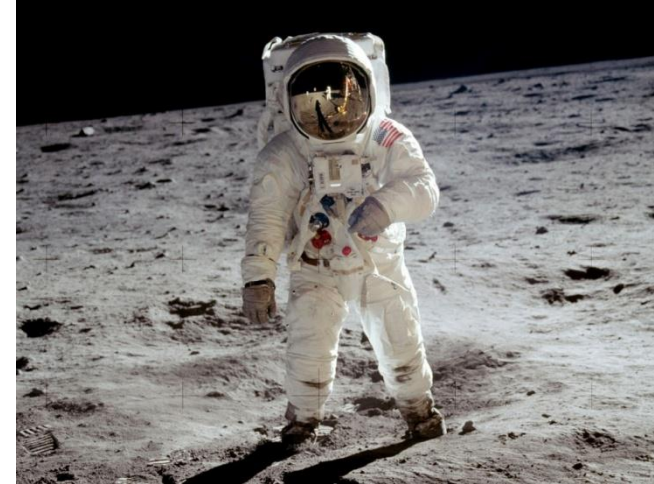
Staphylococci

They consume oxygen and produce new metabolites
preparing the intestinal environment for strict anaerobic
bacteria

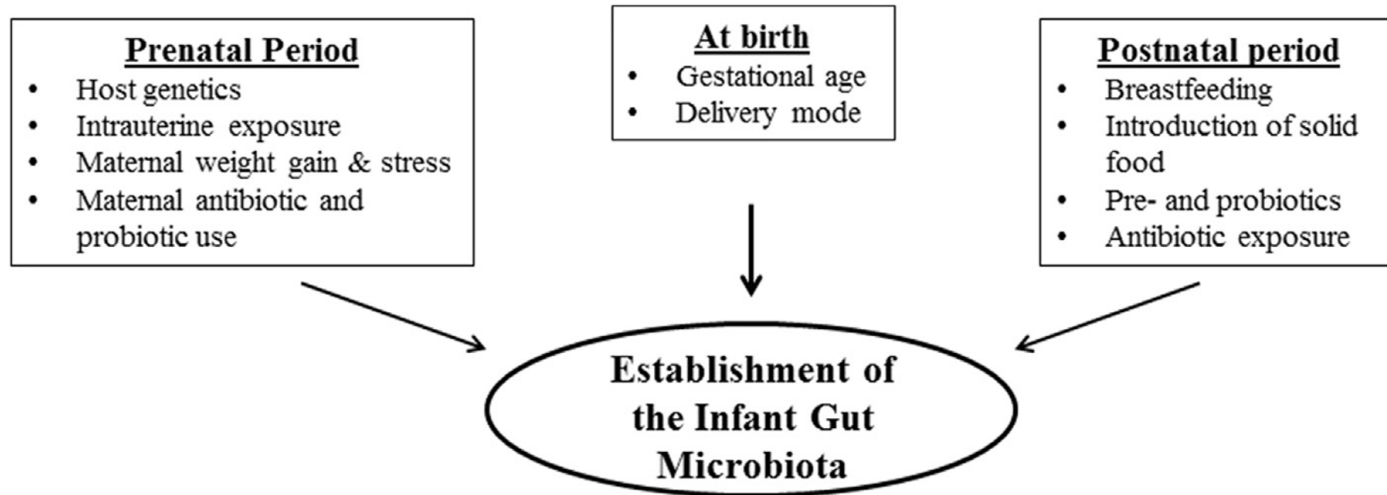
Bifidobacteria

Clostridium

Bacteroides



Establishment of microbiota



Maternal Vaginal Microbiota

- Mostly unculturable microorganisms so can be demonstrated only by nonculture techniques
- Vaginal flora is changed during pregnancy and by gestational age
- Lactobacilli producing lactic acid are increased
- Anaerobics are decreased
- Important for prevention of ascending infections



ORIGINS

Babies are born dirty, with a gutful of bacteria

Far from being sterile, babies come complete with an army of bacteria. The finding could have implications for gut disorders and our health in general

[Read more](#)

Fertility Sterility 2015;104:1358

Maternal Microbiota

- Maternal gastrointestinal microbiota is also changed during pregnancy
- Proteobacteria, Actinobacteria ↑
- Bacterial load is increased as pregnancy progressed



ORIGINS

Babies are born dirty, with a gutful of bacteria

Far from being sterile, babies come complete with an army of bacteria. The finding could have implications for gut disorders and our health in general

[Read more](#)

Placental Microbiota

- Placenta harbors a low-abundance but metabolically rich microbiota in healthy pregnant women
- Nonpathogenic commensal microbes:
 - Firmicutes, Proteobacteria, Bacteroides, Fusobacteria
- This profile are most akin to the nonpregnant human oral microbiota
- The placental microbiota is probably established by hematogenous spread

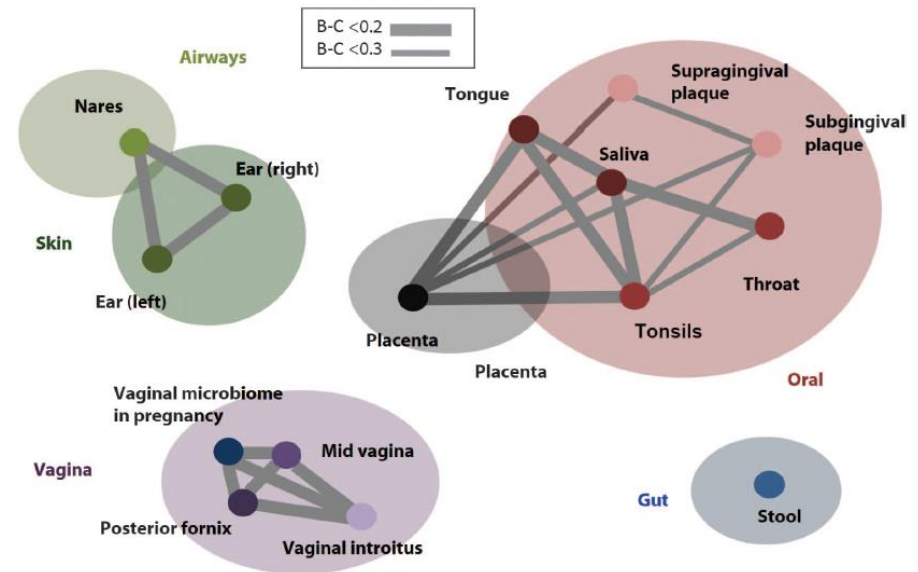


Fig. 1. The placental microbiome has a taxonomic profile that is similar to the oral microbiome.

Placental Microbiota

- Are not same with the agents of neonatal sepsis
- No harm to fetus but no data about its benefits
- Placental dysbiosis → premature delivery

Baby's first gut bacteria may come from mum's mouth

It is thought that babies get their first dose of microbes during birth, but these bugs may arrive in the placenta much earlier, from an unexpected place

[Read more](#)



- Therefore, development of the infant gut microbiota is a dynamic process that begins **prenatally** and continues during the first two to three years of life.

Delivery mode

Cesarean

Bacteria from the hospital environment

- ↓ *Bifidobacteria*
- ↓ *Bacteroides fragilis* group
- ↑ *Clostridium difficile*

X

Vaginally

Faecal and vaginal bacteria from the mother

- ↑ *Bifidobacteria*
- ↑ *Bacteroides fragilis* group
- ↑ *Escherichia coli*
- ↓ *Clostridium difficile*

Gestational age

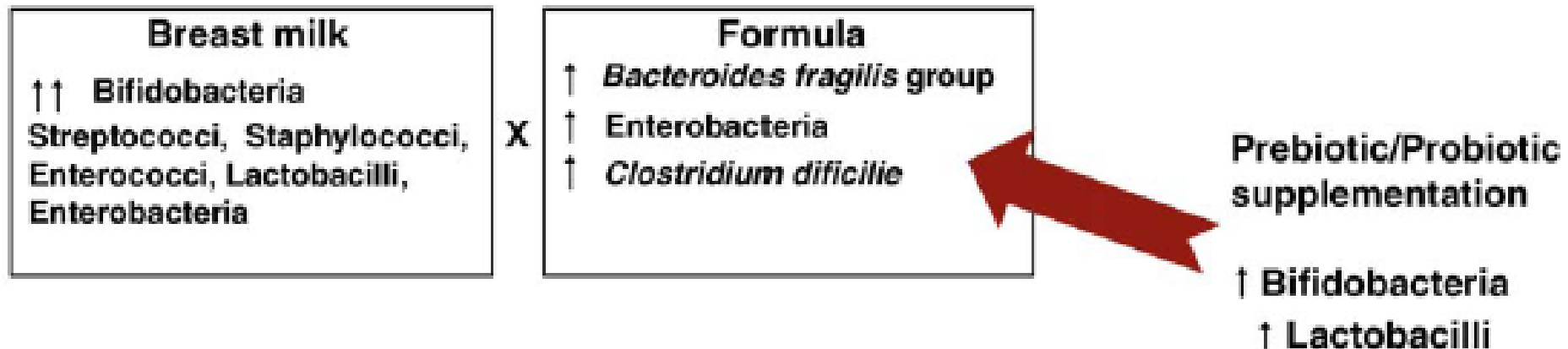
- 1032 infants
- PCR
- Preterms: *C difficile* ↑ Bifidobacteria ↓
- Less mo colonization then term infants

TABLE 3 Median Counts and Prevalence of Colonization With Selected Gut Bacteria In Feces of Infants 1 Month of Age (*n* = 1032)

| Characteristics | No. | Bifidobacteria | | <i>E coli</i> | | <i>C difficile</i> | | <i>B fragilis</i> Group | | Lactobacilli | | Total Counts, Median, log ₁₀ CFU/g Feces |
|--------------------------|-----|-------------------------------------|-------------|-------------------------------------|-------------|-------------------------------------|-----------------|-------------------------------------|-------------|-------------------------------------|-------------|---|
| | | Counts, | Prevalence, | Counts, | Prevalence, | Counts, | Prevalence, | Counts, | Prevalence, | Counts, | Prevalence, | |
| | | Median, | % | Median, | % | Median, | % | Median, | % | Median, | % | |
| | | log ₁₀ CFU/g Feces | | log ₁₀ CFU/g Feces | | log ₁₀ CFU/g Feces | | log ₁₀ CFU/g Feces | | log ₁₀ CFU/g Feces | | |
| Gestational age at birth | | | | | | | | | | | | |
| <37 wk (premature) | 11 | 10.53 | 91 | 9.02 | 73 | 7.12 | 64 ^c | 8.95 | 82 | 8.80 | 27 | 10.80 |
| 37–41 wk ^a | 860 | 10.68 | 99 | 9.30 | 87 | 5.06 | 23 | 9.27 | 82 | 8.61 | 33 | 11.12 |
| >41 wk (postmature) | 37 | 10.44 | 100 | 9.77 | 84 | 6.99 | 35 | 9.51 | 78 | 8.72 | 32 | 11.14 |
| Birth weight | | | | | | | | | | | | |
| <2500 g | 11 | 10.45 | 100 | 8.67 | 100 | 7.12 | 27 | 9.31 | 82 | 9.12 | 36 | 11.28 |
| 2500–4500 g ^a | 906 | 10.67 | 99 | 9.32 | 87 | 5.08 | 24 | 9.30 | 82 | 8.65 | 33 | 11.12 |
| >4500 g | 26 | 10.61 | 100 | 9.59 | 85 | 6.07 | 23 | 9.30 | 77 | 8.60 | 35 | 11.03 |

Feeding type

- Especially important in the first days of life
- Human milk contains many bacteria
- 10^9 mo/L in milk in healthy women
- *'Breast milk microflora'*
- Antibacterial properties
- Nondigestable oligosaccharides (prebiotics) stimulate proliferation of Bifidobacteria and Lactobacilli



Antibiotics

- Antibiotic treatment decreases bifidobacteria & Bacteroides

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| | | Counts, Median, log ₁₀ CFU/g Feces | Prevalence, % | Counts, Median, log ₁₀ CFU/g Feces | Prevalence, % | Counts, Median, log ₁₀ CFU/g Feces | Prevalence, % | Counts, Median, log ₁₀ CFU/g Feces | Prevalence, % | Counts, Median, log ₁₀ CFU/g Feces | Prevalence, % | |
| Antibiotic/antimycotic use during first 1 mo | | | | | | | | | | | | |
| No ^a | 945 | 10.70 | 98 | 9.32 | 88 | 5.50 | 25 | 9.31 | 82 | 8.65 | 32 | 11 |
| Oral antibiotic | 28 | 10.29 | 100 ^c | 9.45 | 79 | 7.12 | 18 | 6.39 | 82 ^c | 8.62 | 36 | 10 |
| Oral miconazole | 22 | 10.18 | 100 ^c | 9.57 | 82 | 4.47 | 23 | 9.35 | 86 | 8.68 | 36 | 11 |
| Oral nystatin | 15 | 10.77 | 93 | 9.67 | 87 | 4.81 | 13 | 9.33 | 73 | 8.64 | 33 | 11 |

Pediatrics 2006;118(2):511-21

GUT MICROBIOTA

```
graph TD; A([GUT MICROBIOTA]) --> B[Mutualism]; A --> C[Dysbiosis];
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Mutualism

- Gut maturation
- Immune development
- Host metabolism
- Brain development & behavior

Dysbiosis

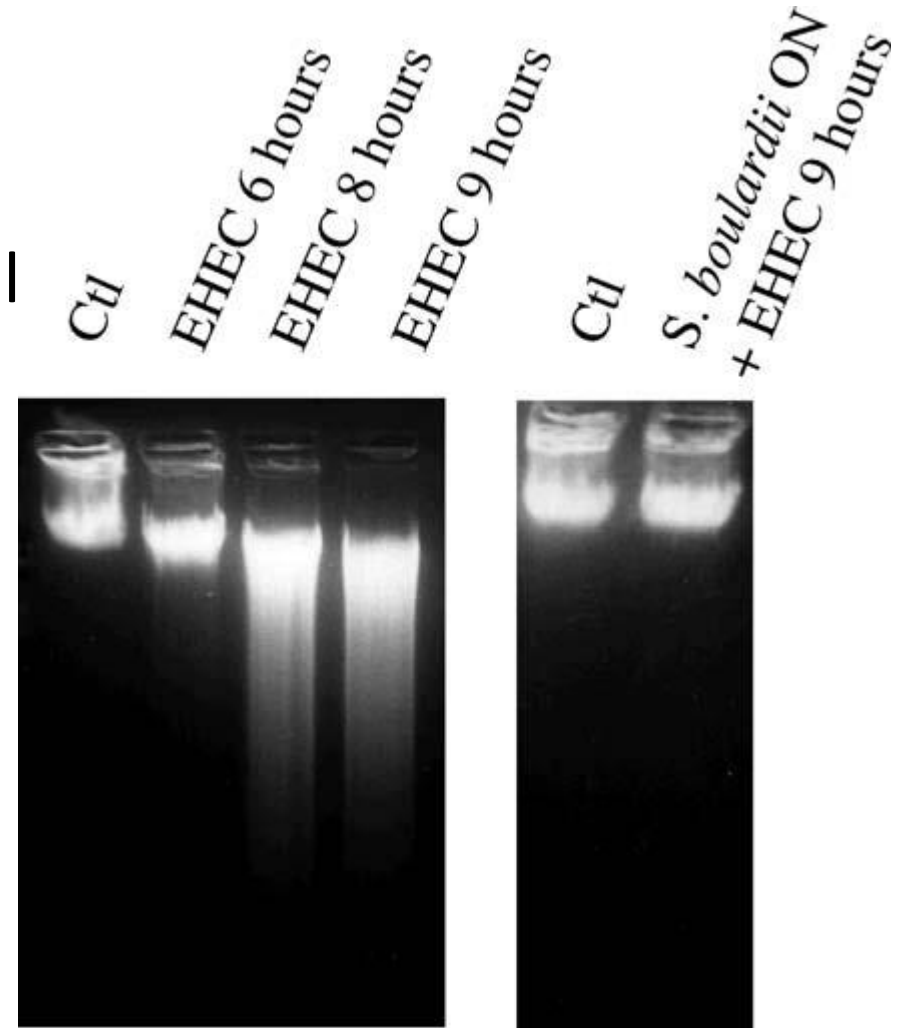
- Intestinal & immune diseases: NEC, IBD, eczema, asthma
- Metabolic disorders: obesity, type 1 and type 2 diabetes

commensal bacteria

- Epithelial cell proliferation ↑
- Apoptosis ↓
- Intestinal epithelial integrity ↑
- Activation of genes responsible from desmosome functions ↑
- Synthesis of tight junction proteins ↑ (barrier functions)
- Mucus secretion ↑
- Regulation of development of intestinal villus vascular architecture

Intestinal Barrier

- Pathogenic bacteria induced apoptosis of intestinal epithelial cells
- Lactobacillus, bifidobacteria
- commensal bacteria inhibit pathogens induced apoptosis



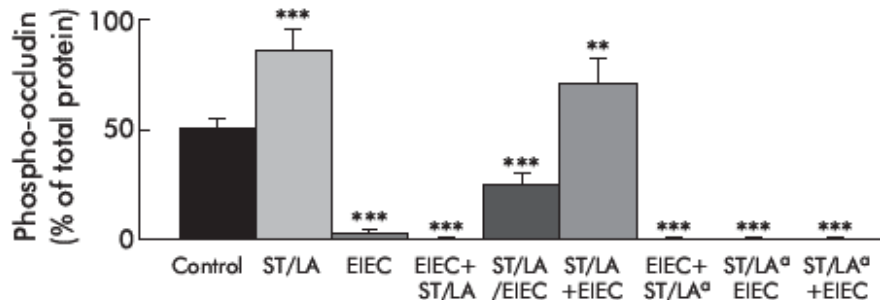
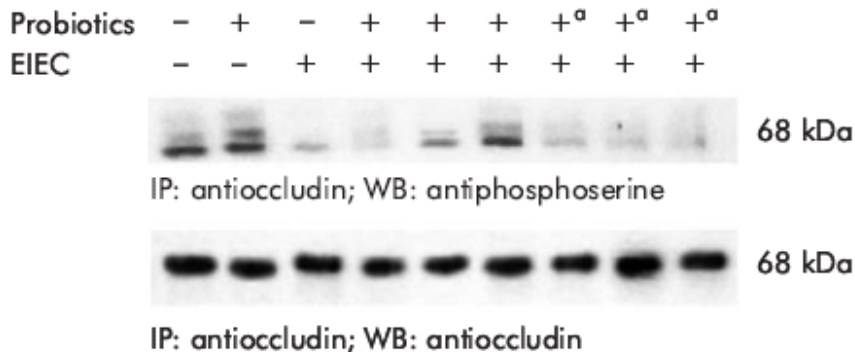
Res Microbiol 2006;157(5):456-65

DNA fragmentation
in T84 cells infected by EHEC

Tight Junctions

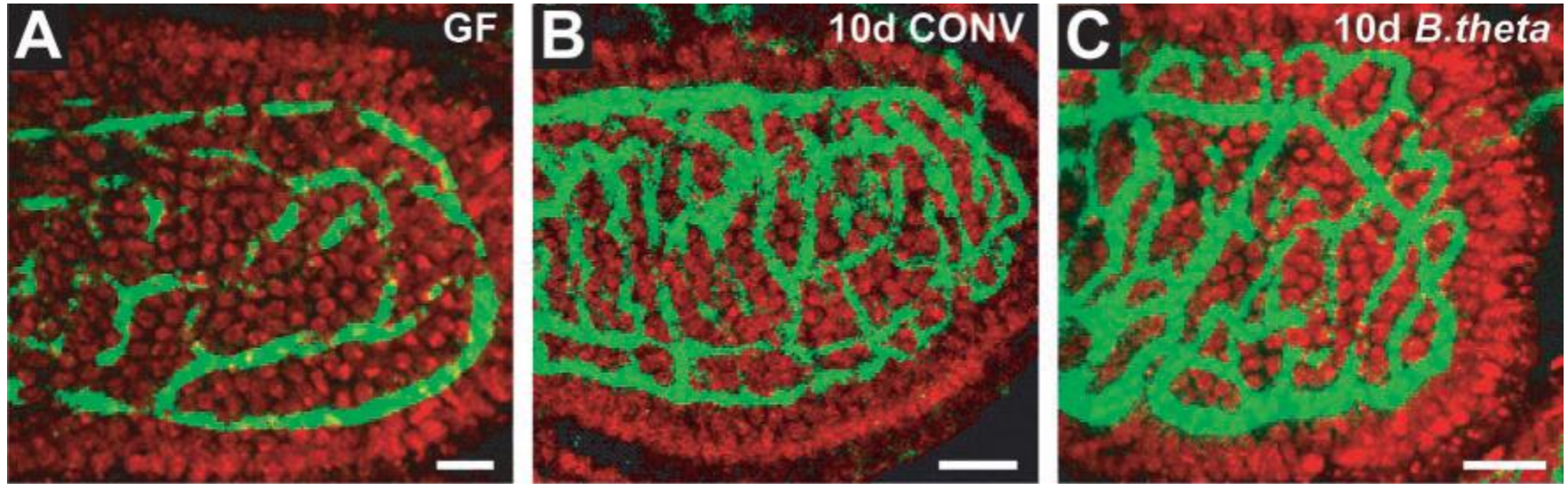
- The most critical part of interstitial barrier is tight junctions
- 'Occludin' and 'Claudin' proteins
- *L. acidophilus* and *S. thermophilus* are shown to increase the activation of occludin

A



Gut 2003;52:988–997

Angiogenesis



A: germ free

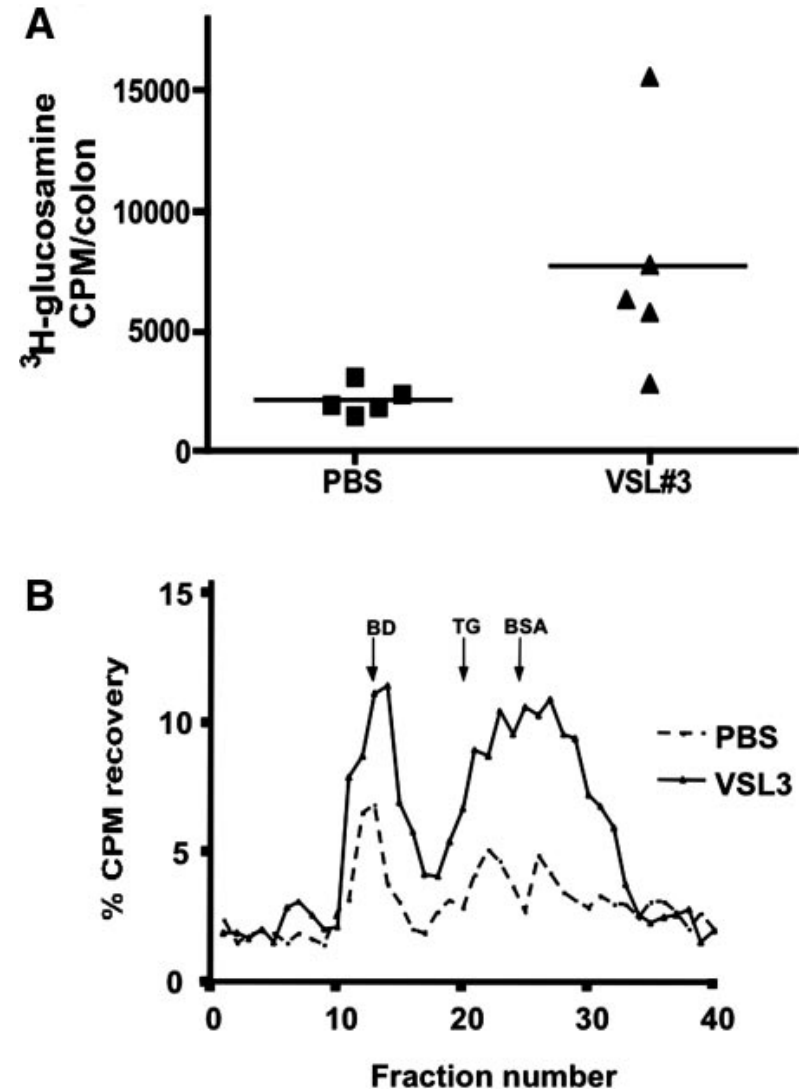
B: 10 days after colonization with conventional microbioma

C: 10 days after probiotic bacteria colonisation

Proc Natl Acad Sci USA 2002;99(24):15451-5

Mucus Secretion

- Lactobacillus species induced MUC2 and MUC3 genes in vitro and in vivo
- Mucus secretion is increased



Impact of the microbiota on immune development & functions

- The microbiota is a central player in the activation and function of the immune system in the early neonatal period and possibly during prenatal life

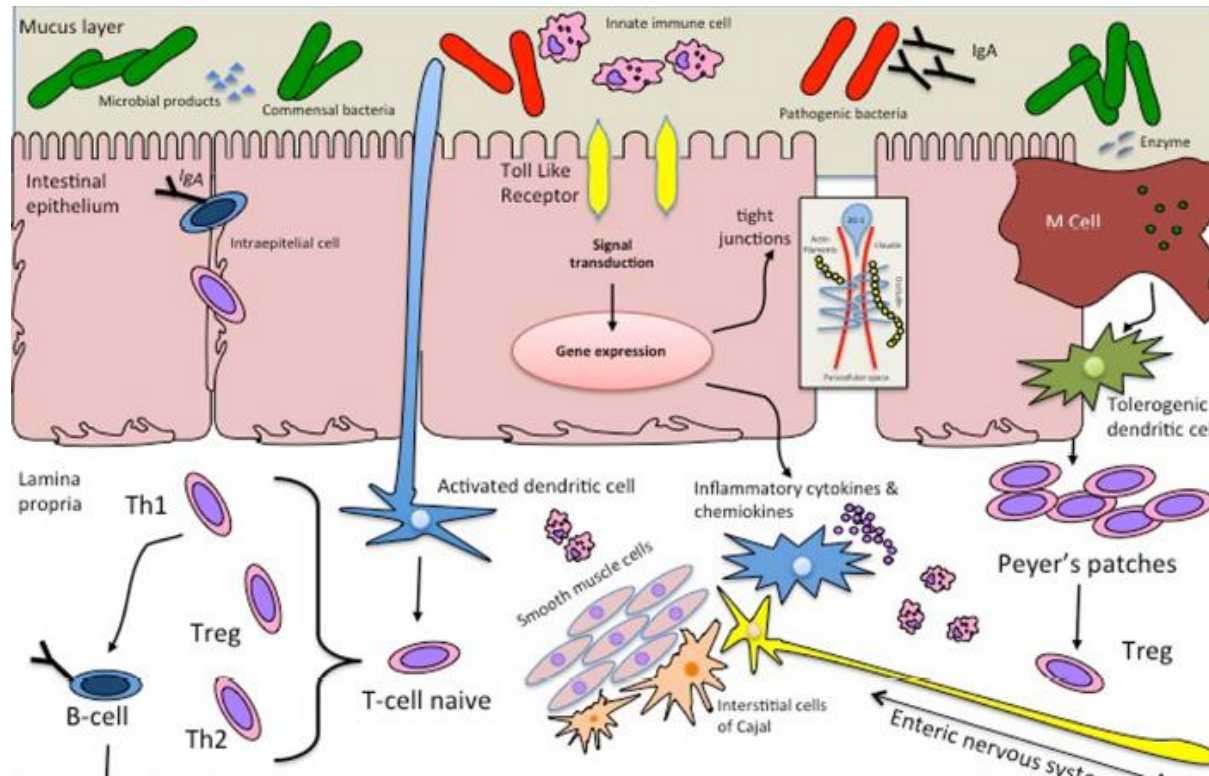
Defence against
harmful molecules
and pathogens



Tolerance for
commensal bacteria
and food antigens

Impact of the microbiota on immune development & functions

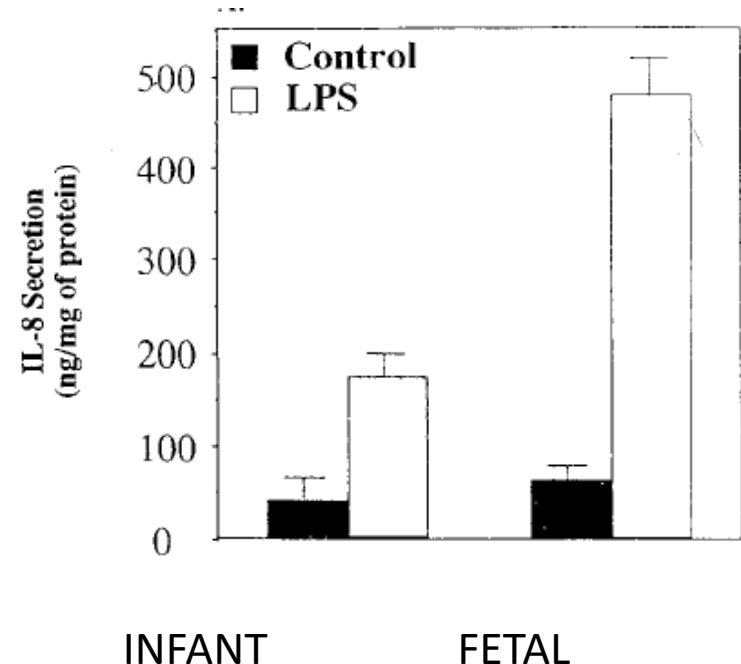
- Commensal bacteria direct dendritic cell differentiation towards to tolerogenic and regulatory T cells
- Inhibit cytokine production and NK T cells



Impact of the microbiota on immune development & functions

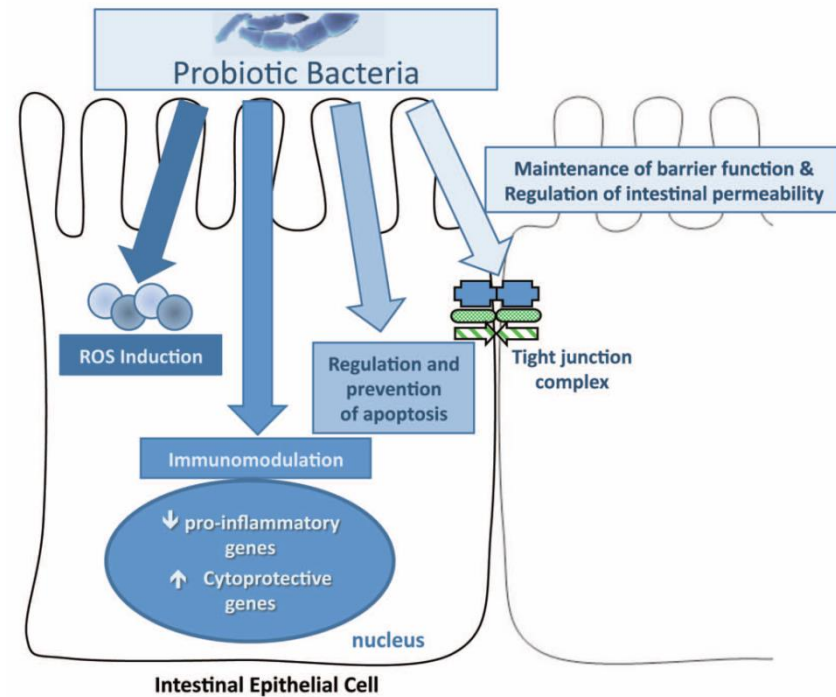
Immature immune cells have a higher sensitivity to microbial stimuli

- fetal intestine:
LPS's inflammatory response ↑↑
- mature intestine:
weak inflammatory response
- Postnatal unresponsiveness is related to desensitization due to interaction with commensal bacteria



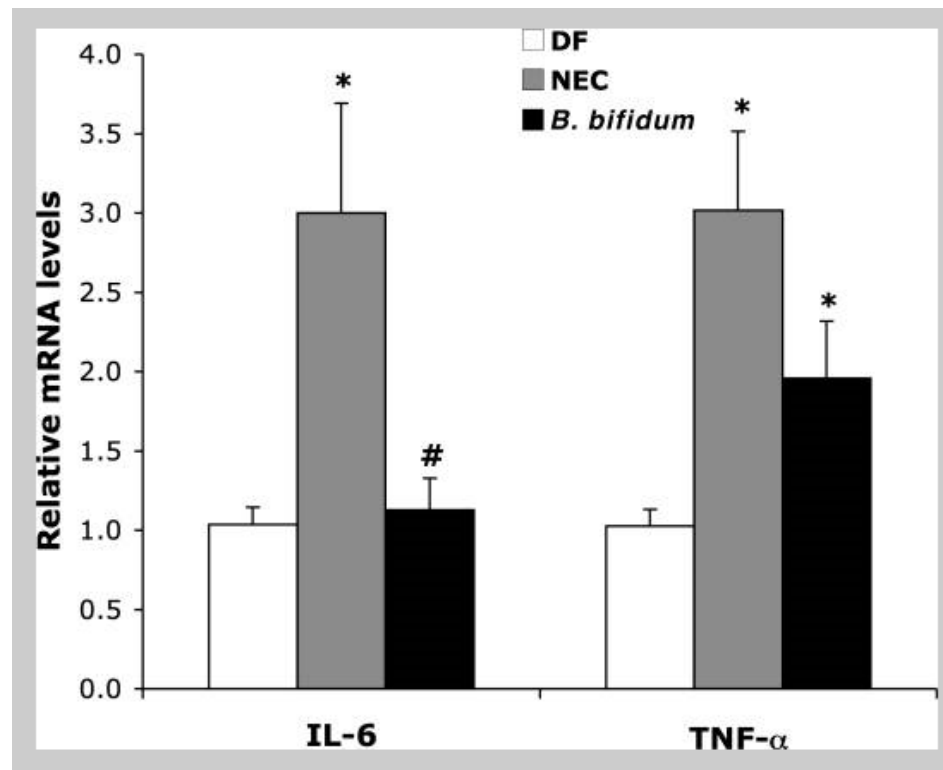
Impact of the microbiota on immune development & functions

- Probiotic bacteria lead to immune tolerance
- In preterm infants
- *Bifidobacterium breve* → TGF- β 1 synthesis \uparrow
- anti-inflammatory effects \uparrow



Impact of the microbiota on immune development & functions

Bifidobacterium bifidum decreases synthesis of pro-inflammatory cytokines which are important in the pathogenesis of necrotising enterocolitis

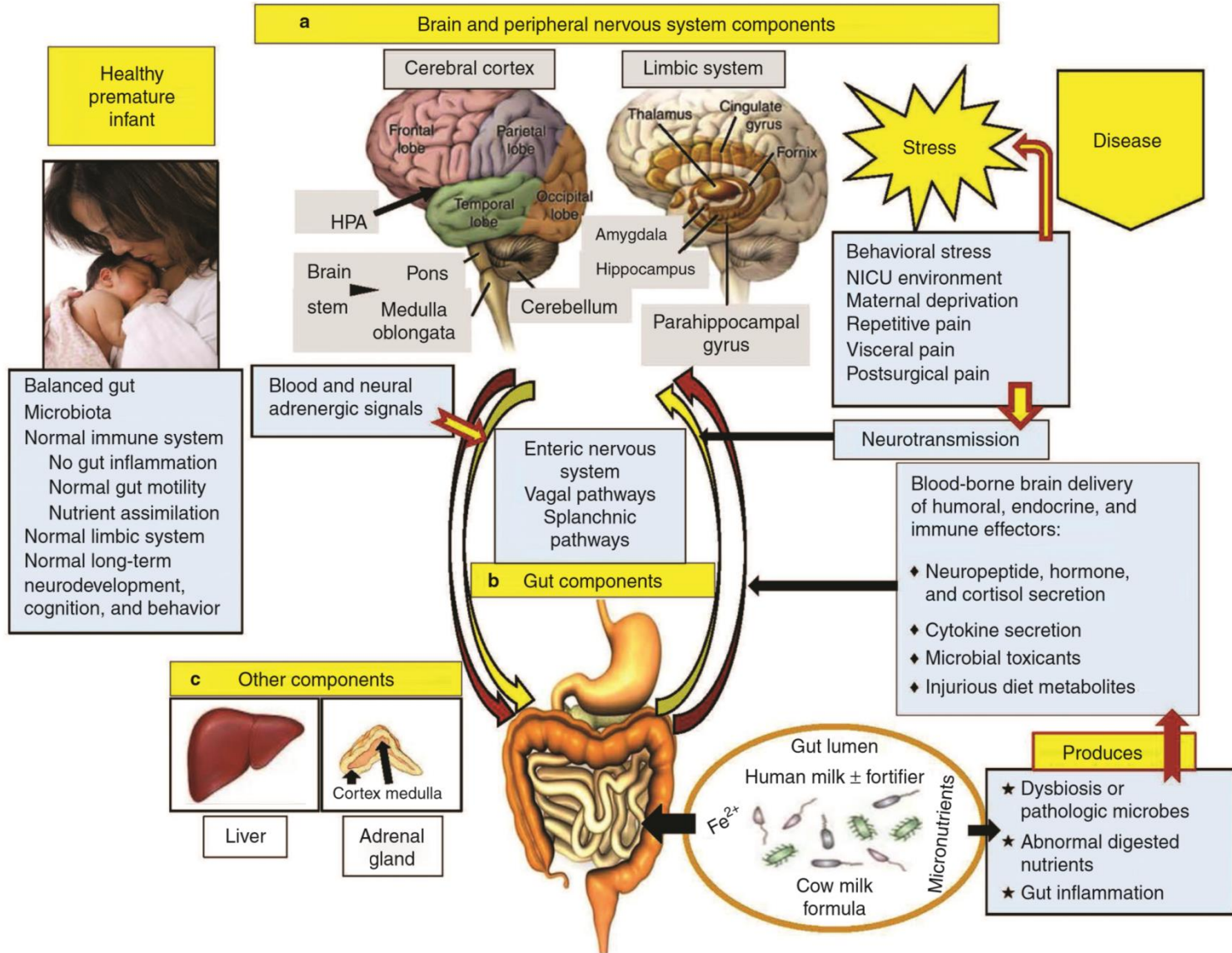


Brain Development & Behaviour

- Several preclinical studies using germ-free mice highlighted the ability of early life microbiota to influence neurodevelopment with long lasting effects on neuronal function

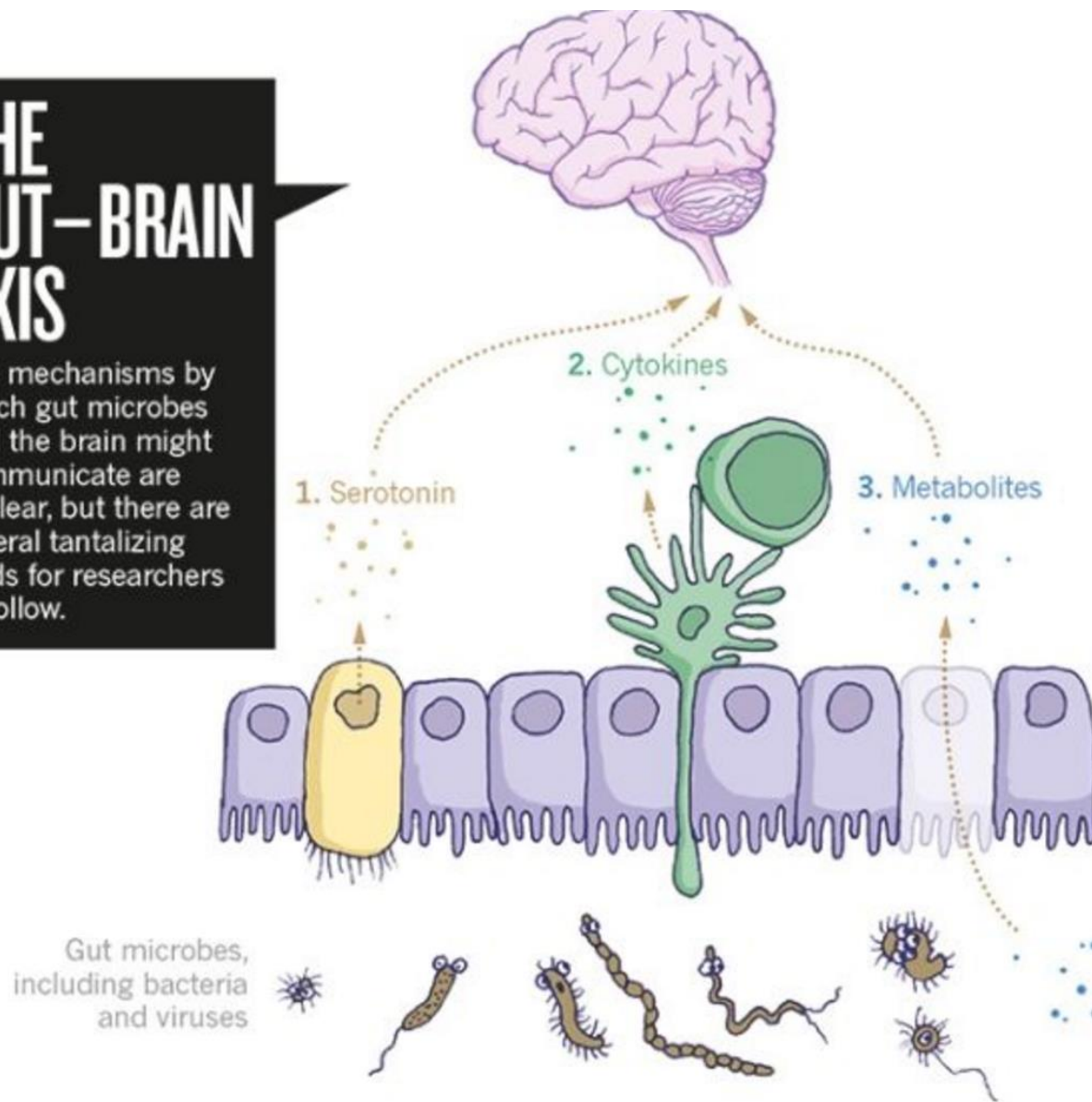
Brain, Behavior, and Immunity 2014; 38: 1–12
Trends Mol Med 2014; 20: 509-18

Gut - Brain Axis



THE GUT-BRAIN AXIS

The mechanisms by which gut microbes and the brain might communicate are unclear, but there are several tantalizing leads for researchers to follow.



1. PERIPHERAL SEROTONIN:

Cells in the gut produce large quantities of the neurotransmitter serotonin, which may have an effect on signalling in the brain.

2. IMMUNE SYSTEM:

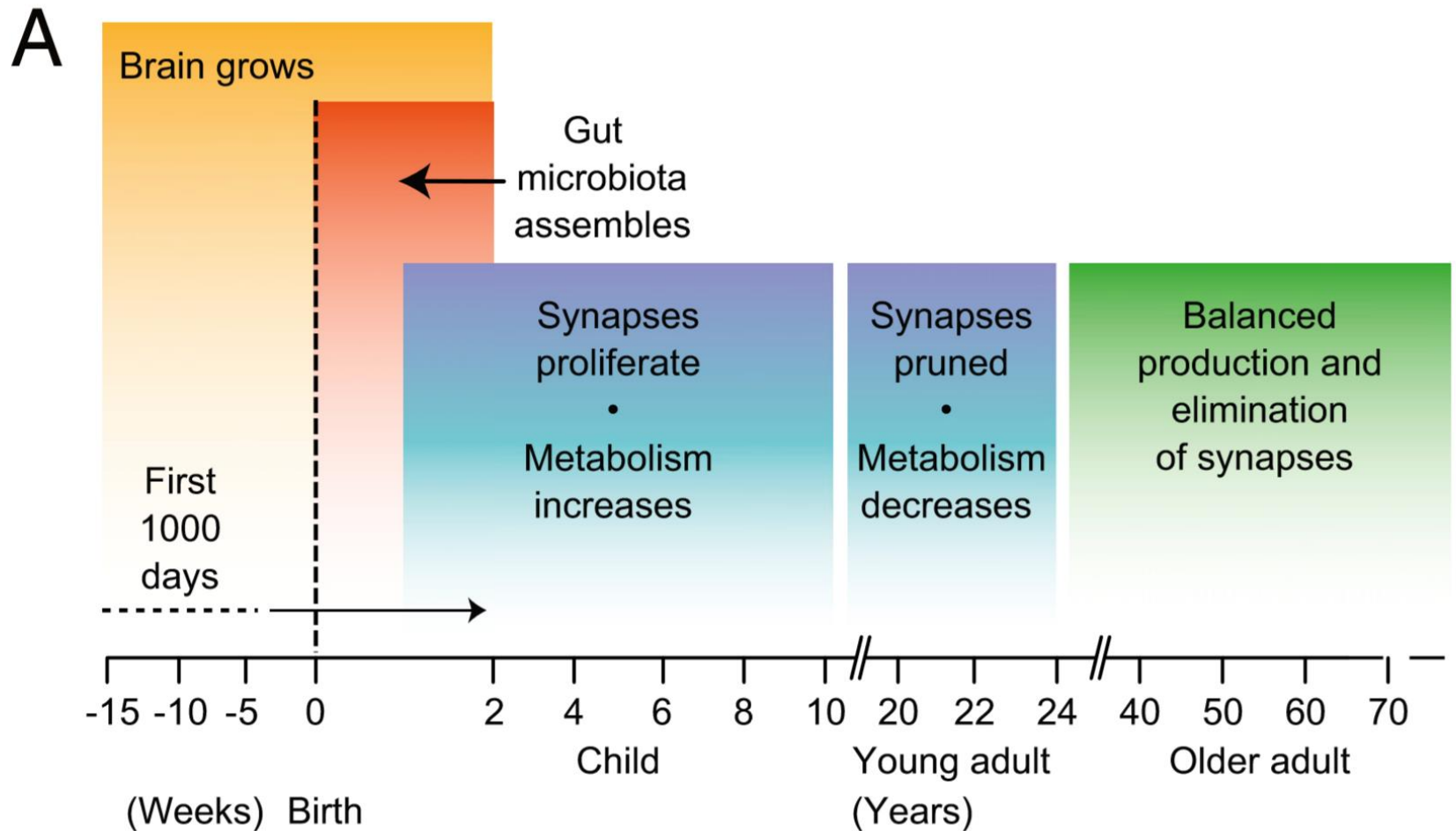
The intestinal microbiome can prompt immune cells to produce cytokines that can influence neurophysiology.

3. BACTERIAL MOLECULES:

Microbes produce metabolites such as butyrate, which can alter the activity of cells in the blood-brain barrier.

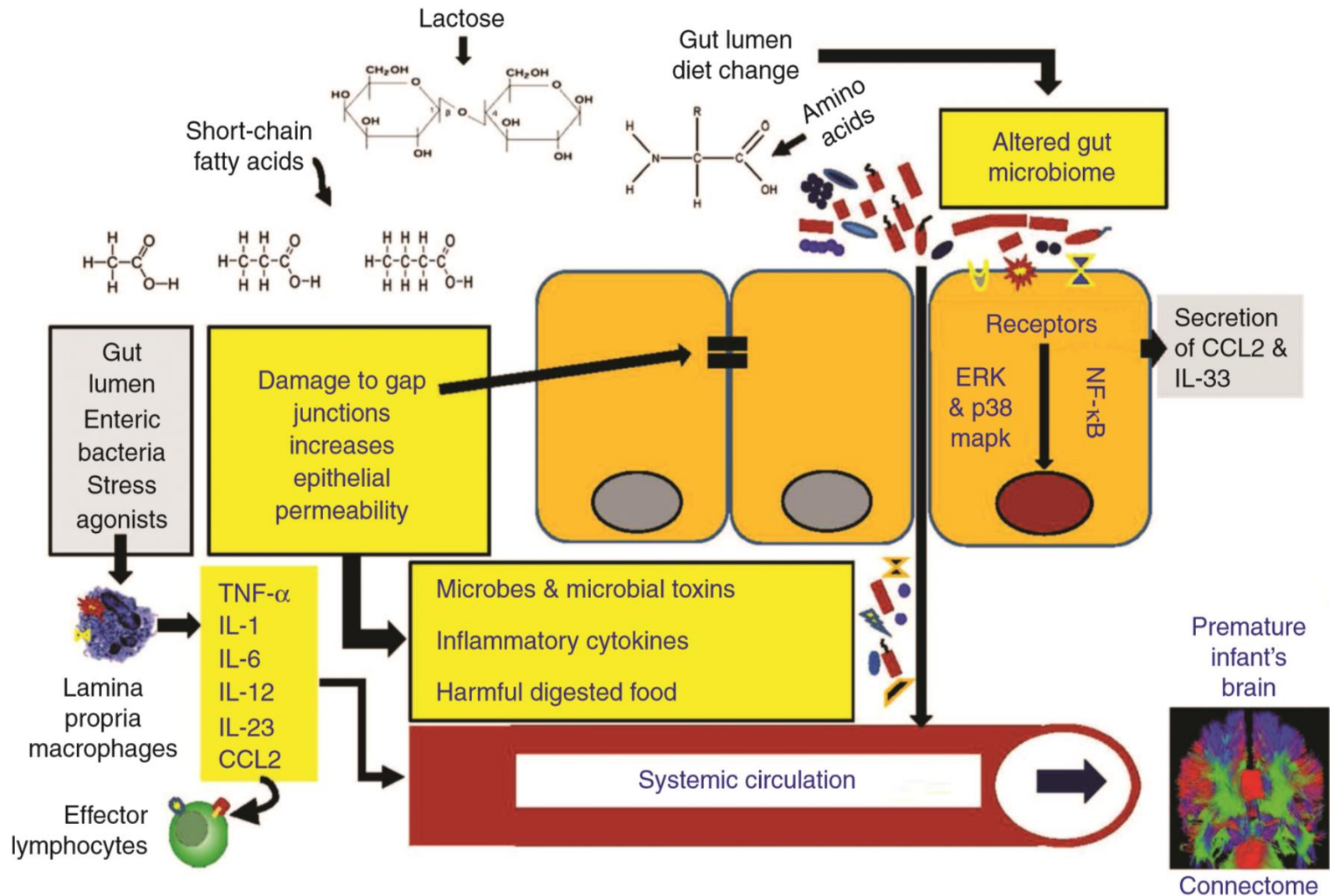
The Gut Brain Axis, as demonstrated by the journal Nature.

The parallel early development of the intestinal microbiota and the nervous system



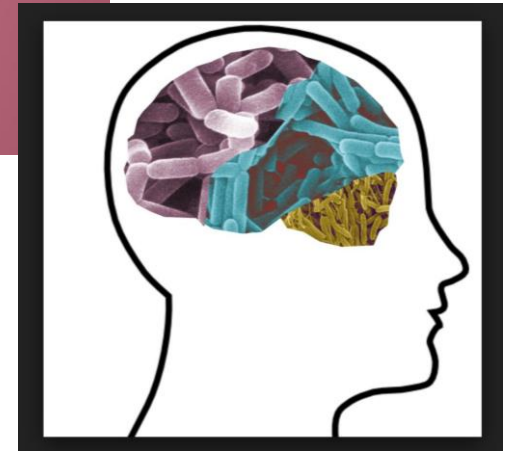
PNAS 2015, 112 ; 46: 14105–14112

Microbiota- Gut- Brain Axis



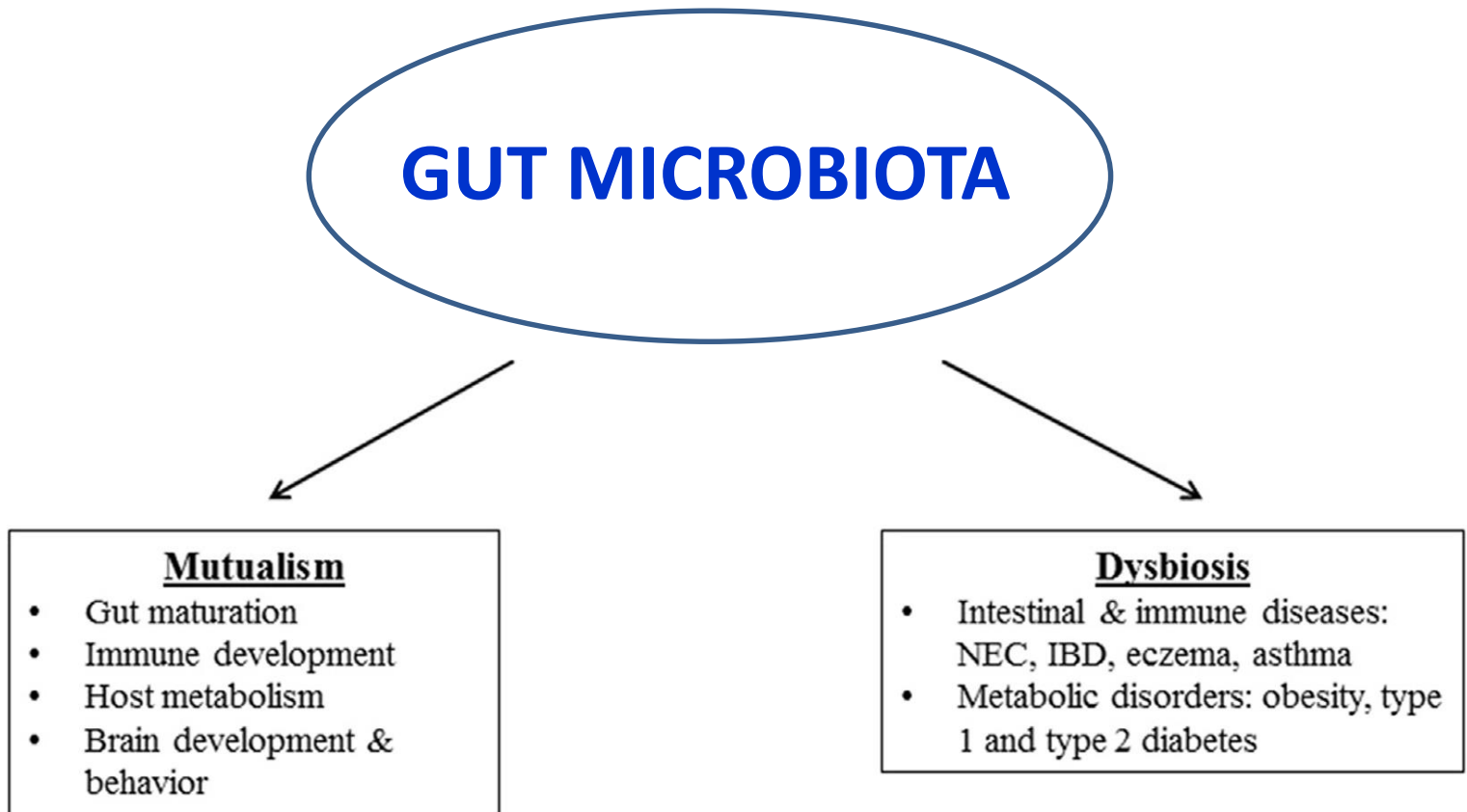
Microbiota- Gut- Brain Axis

psychobiotic

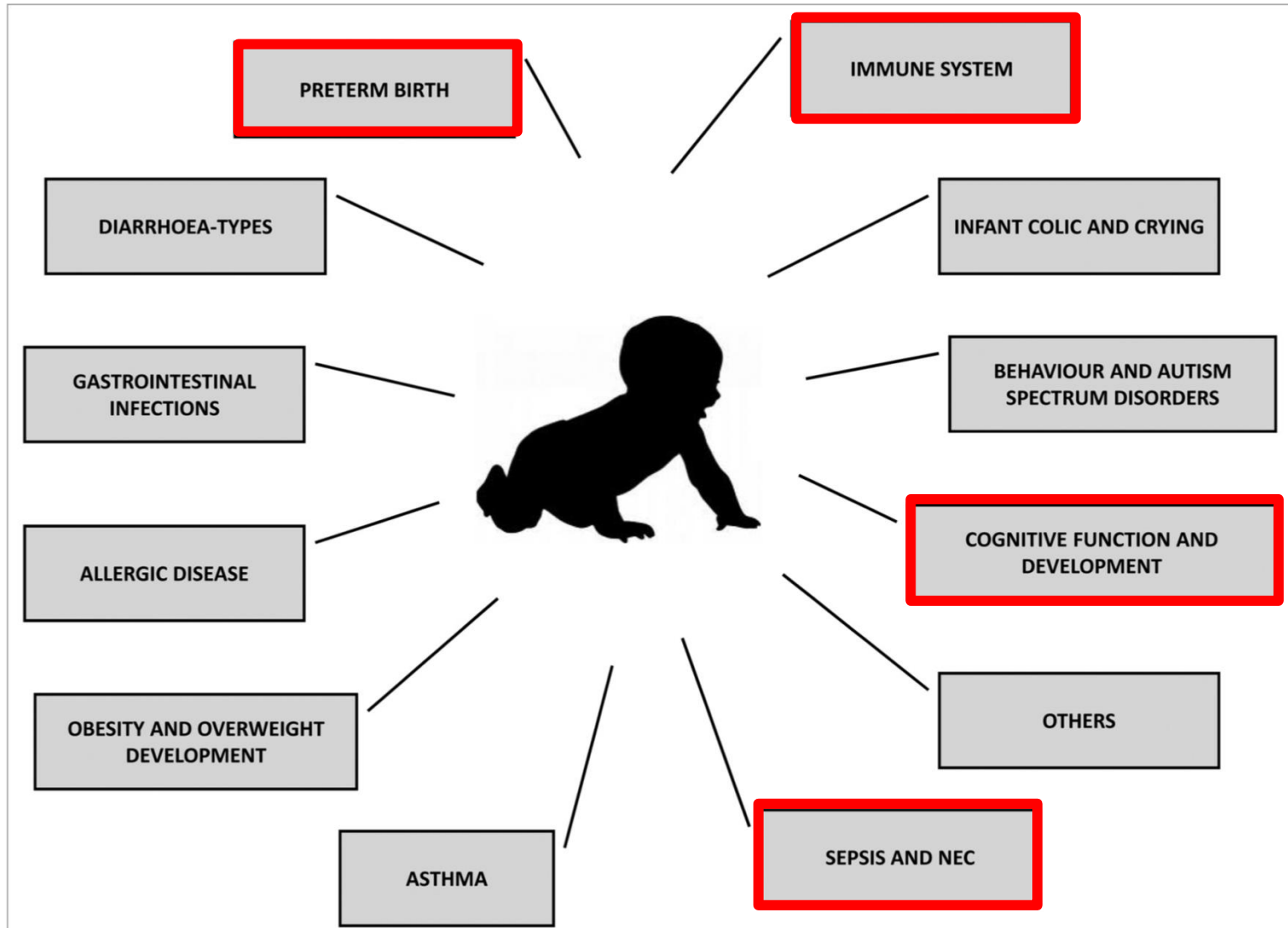


Neurobiotics ?

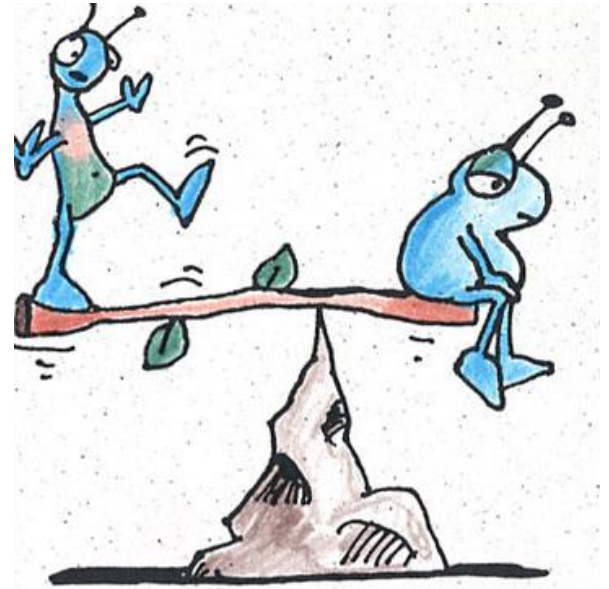
Dysbiosis Related Diseases



Prophylactic and Therapeutic interventions



CONCLUSION



- Symbiotic association between microbiota and host results in a state of ***physiological homeostasis***
- Postnatal gut metabolism, development, immune system development and neurodevelopment are directly influenced by the bacterial community and dysbiosis is associated with several clinical conditions

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"FIRST, IT WAS A SYMBIOTIC RELATIONSHIP, THEN PLATONIC,
AND NOW, WE'RE HAPPILY MARRIED."