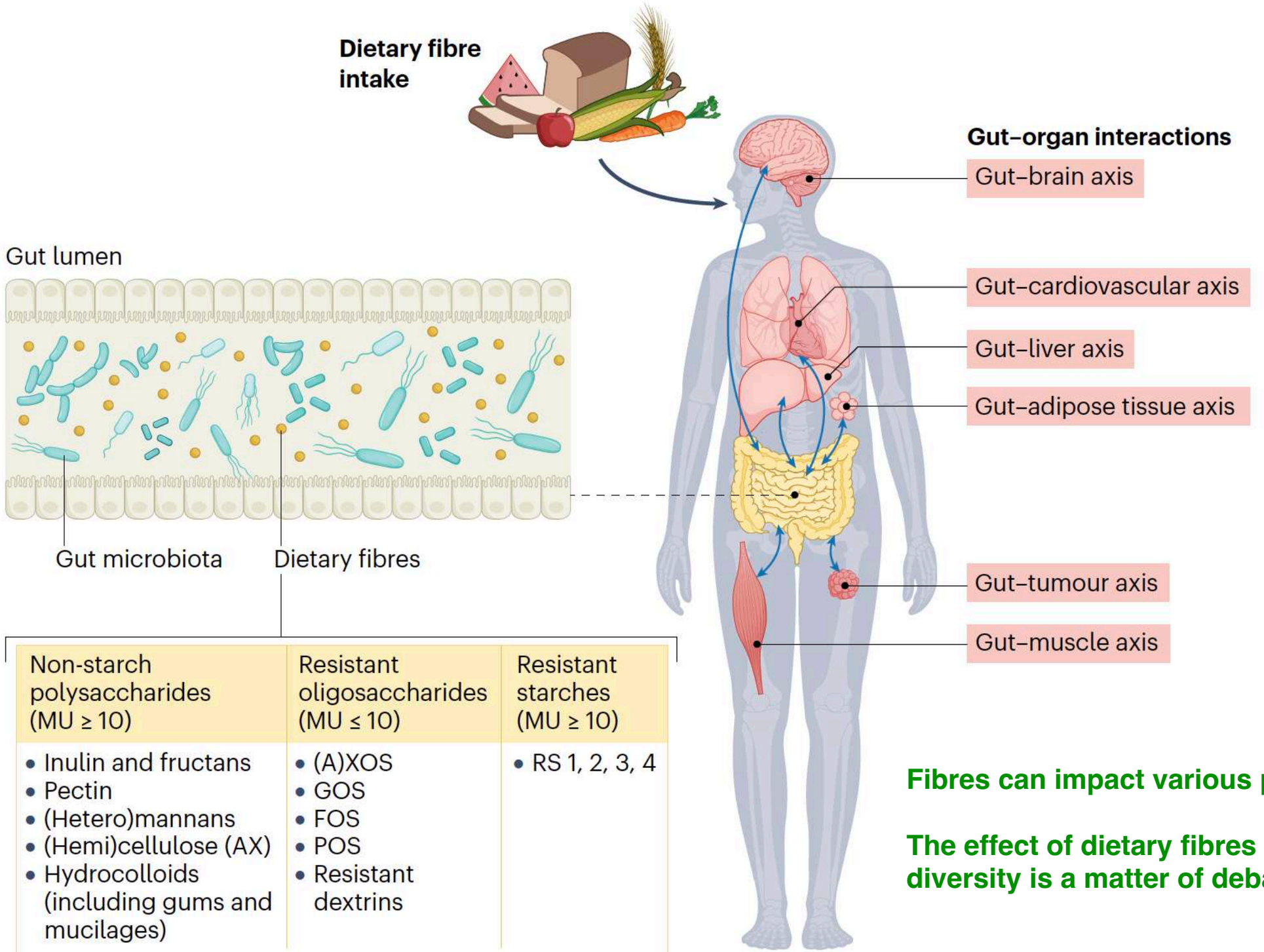
L07c

Fibres

From beginning to the end

Fibres



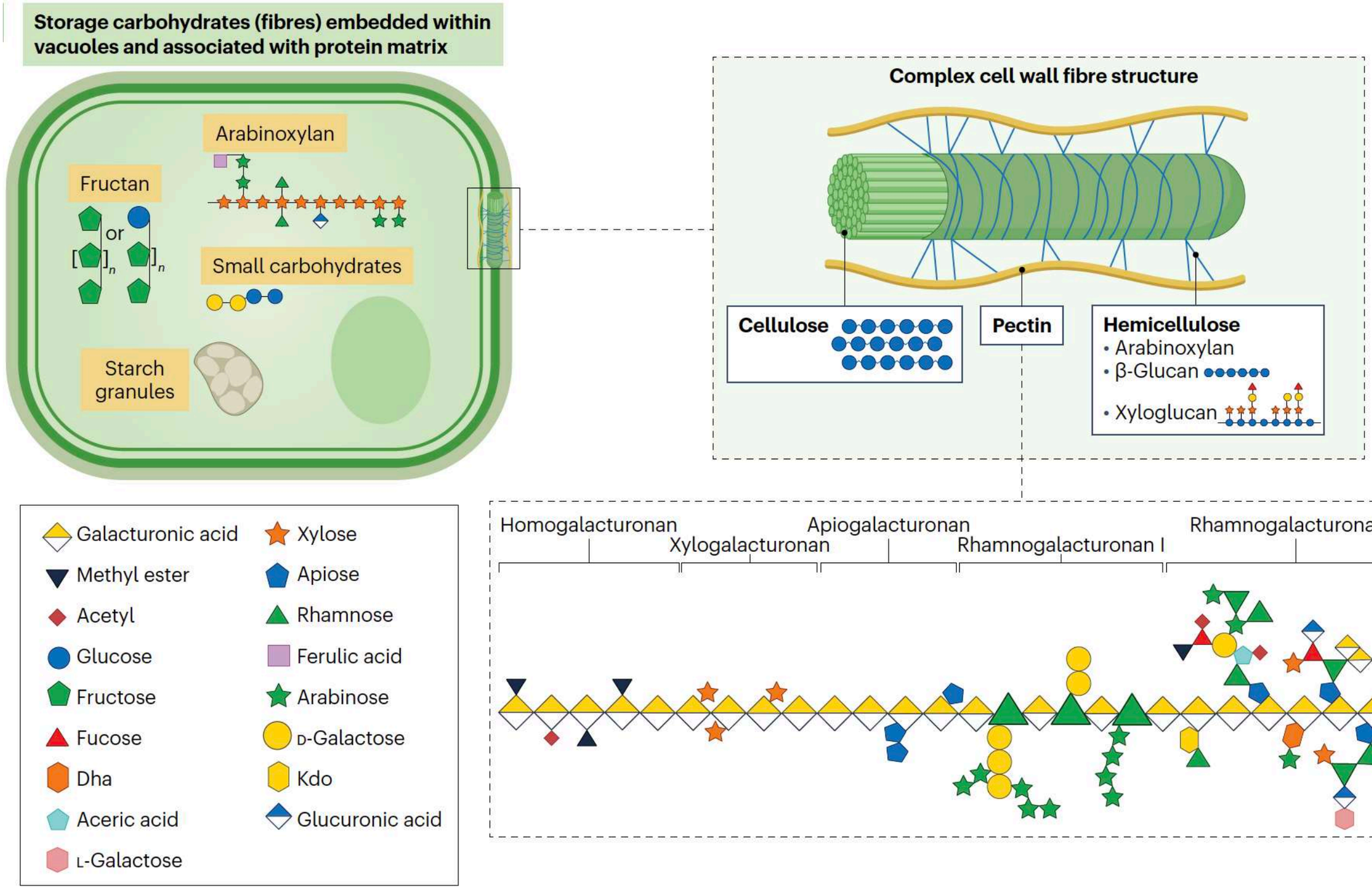
Non-starch polysaccharides (MU ≥ 10)	Resistant oligosaccharides (MU ≤ 10)	Resistant starches (MU ≥ 10)
• Inulin and fructans • Pectin • (Hetero)mannans • (Hemi)cellulose (AX) • Hydrocolloids (including gums and mucilages)	• (A)XOS • GOS • FOS • POS • Resistant dextrins	• RS 1, 2, 3, 4

Fibres can impact various physiological axes

The effect of dietary fibres on microbial diversity is a matter of debate

Delzenne et al., 2024

Fibres, II

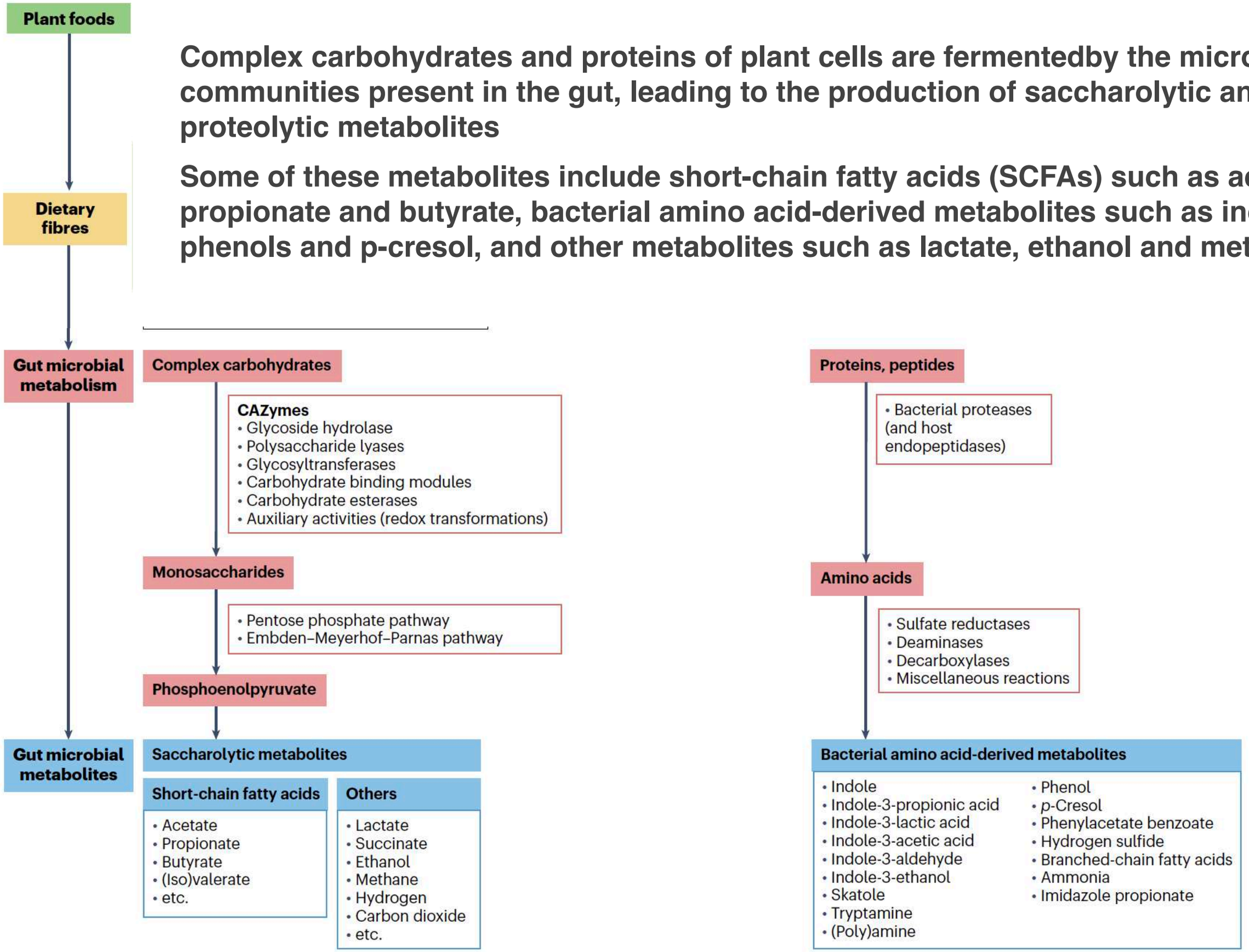


Delzenne et al., 2024

Dietary fibres either form a complex 3D structure that constitutes the backbone of plant cells, or are encapsulated as storage carbohydrates with various other nutrients such as lipids, proteins and polyphenols in the plant vacuole

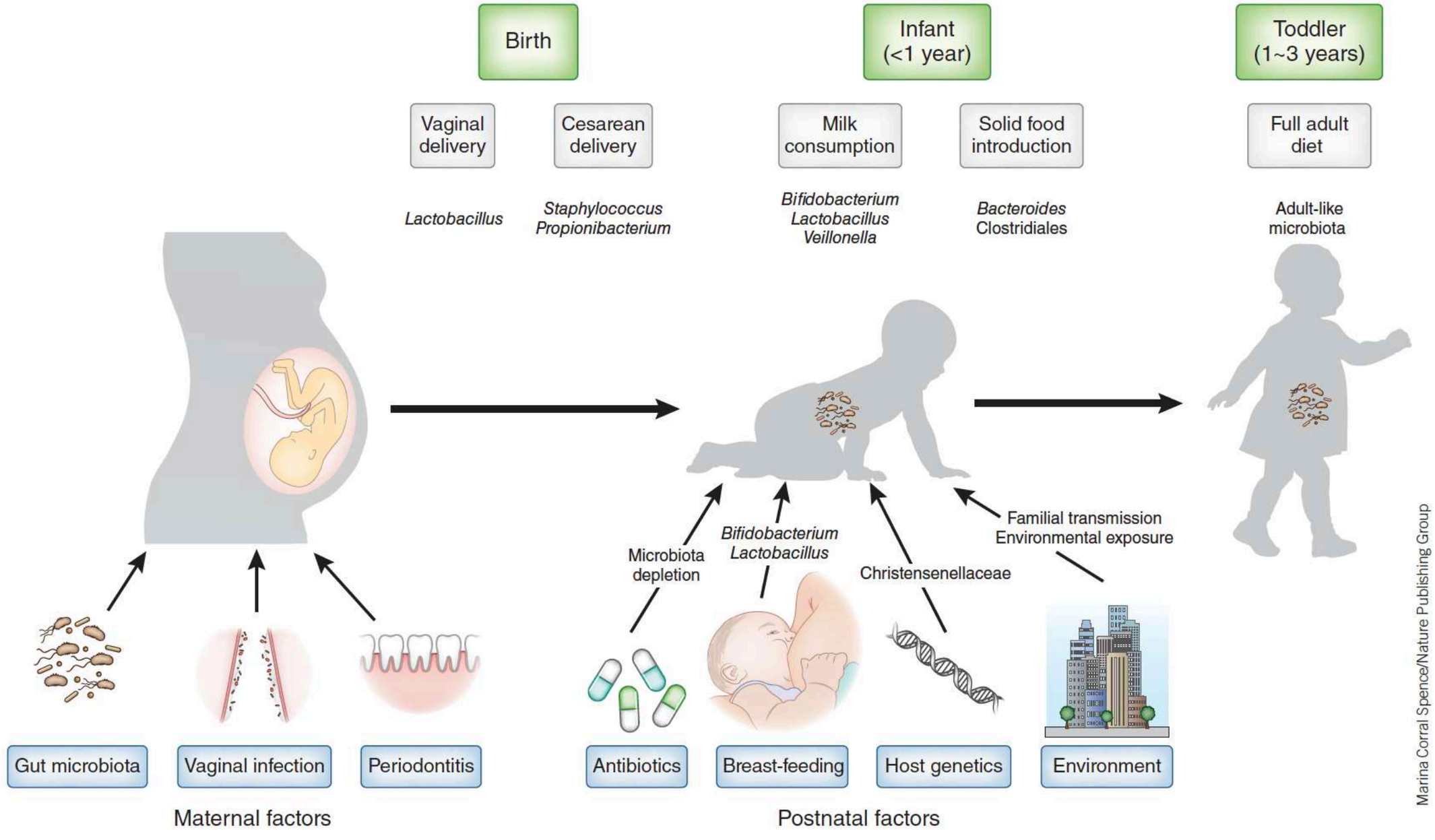
Complex carbohydrates and proteins of plant cells are fermentedby the microbial communities present in the gut, leading to the production of saccharolytic and proteolytic metabolites

Some of these metabolites include short-chain fatty acids (SCFAs) such as acetate, propionate and butyrate, bacterial amino acid-derived metabolites such as indoles, phenols and p-cresol, and other metabolites such as lactate, ethanol and methane



Delzenne et al., 2024

Factors shaping the neonatal microbiome



Marina Corral Spence/Nature Publishing Group

Tamburini et al, 2016

Pregnancy and maternal gut microbiome

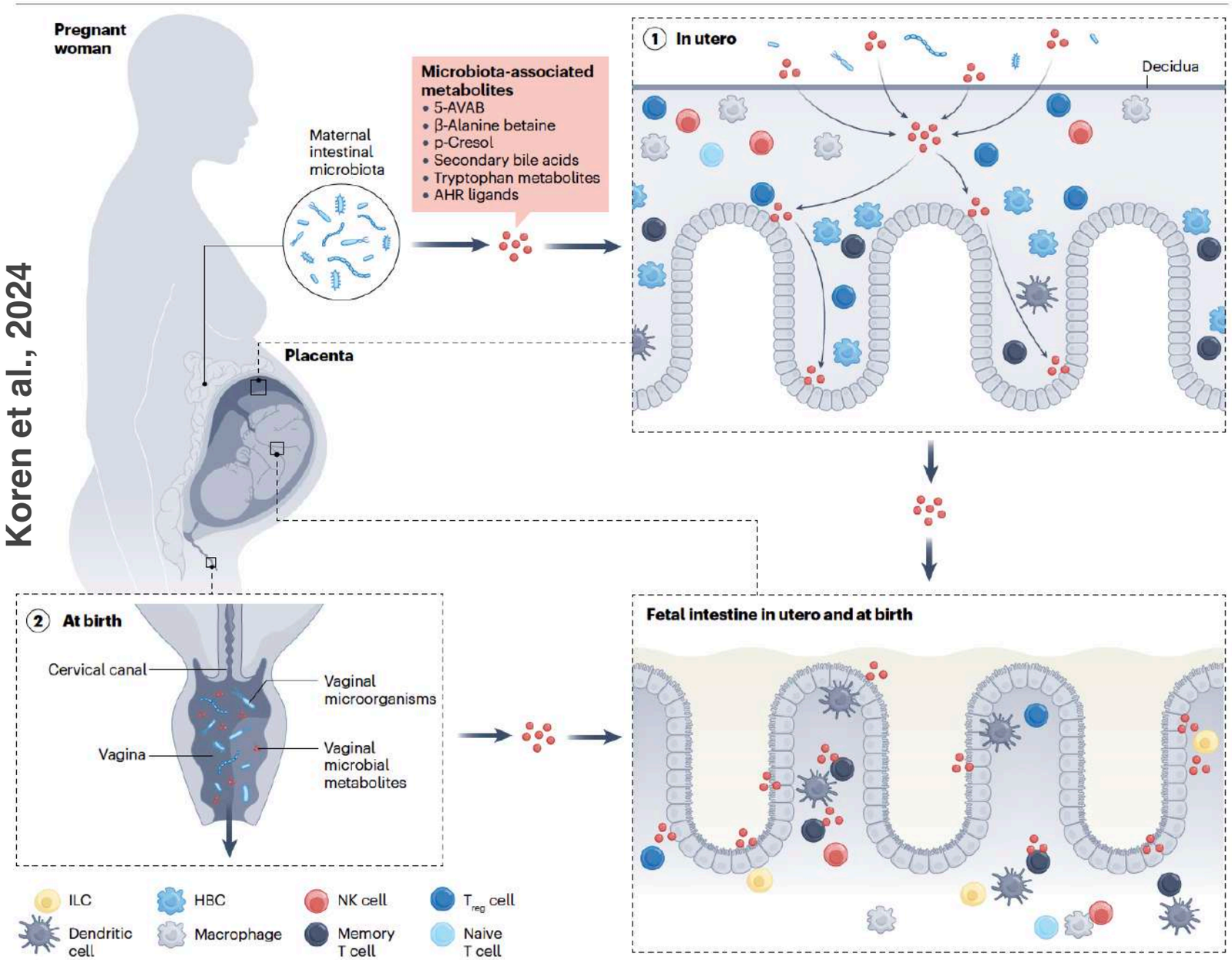
- The maternal gut microbiome changes during pregnancy, with the most drastic changes occurring towards the end of pregnancy

- Increase in Proteobacteria and Actinobacteria in late pregnancy as well as a decrease in short-chain fatty acid (SCFA) producers as gestation progresses

- The maternal gut microbiome has been shown to be involved in multiple phenotypes: including weight gain, low-grade inflammation and insulin resistance

- **Maternal immunity and microbial metabolites during pregnancy, microbial transfer during birth, and transfer of immune factors, microorganisms and metabolites via breastfeeding provide critical sources of early-life microbial and immune training, with important consequences for human health**

Microbial metabolites from the maternal microbiome contribute to fetal and neonatal immune development



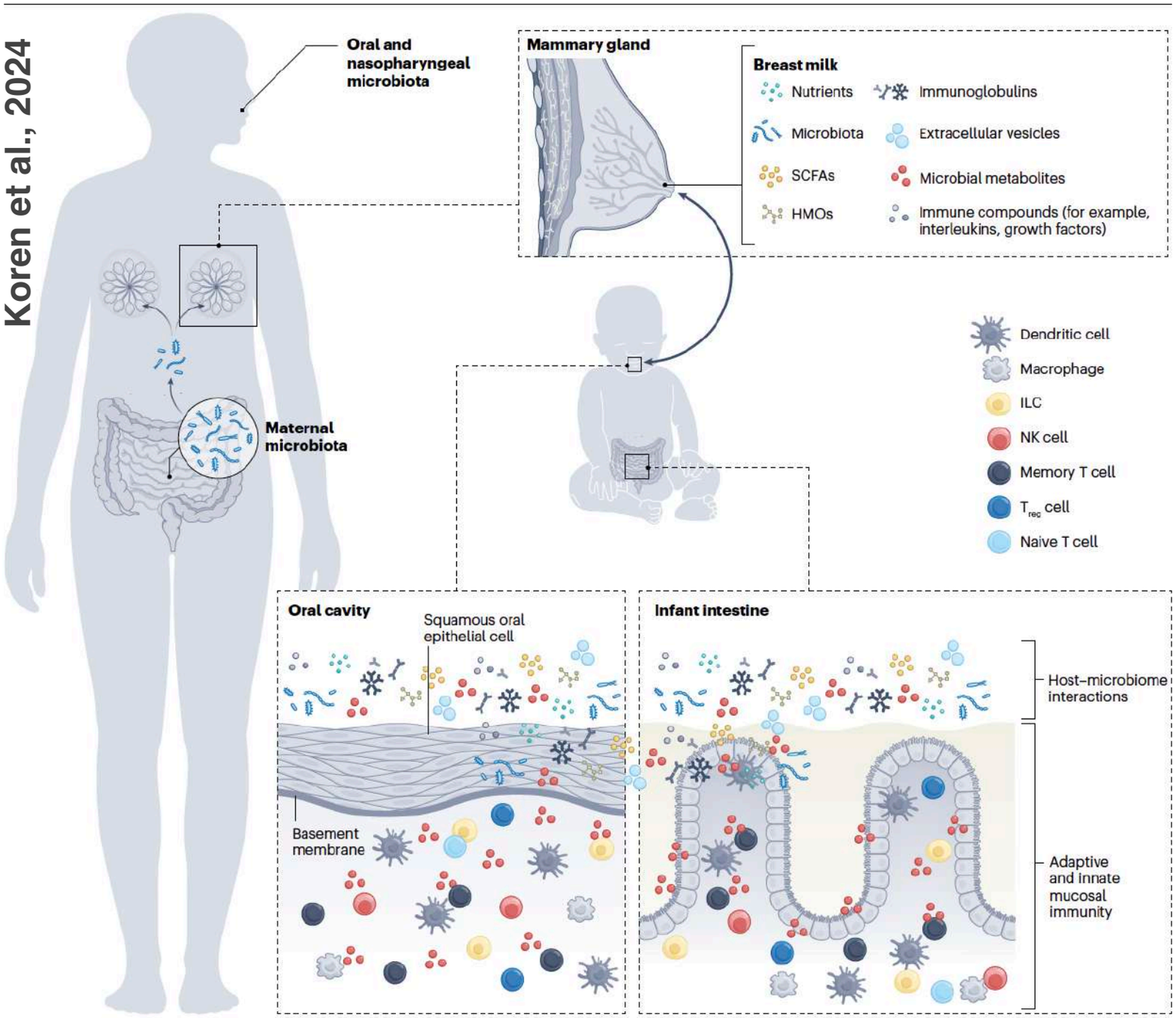
Koren et al., 2024

1) Maternal intestinal microbiota derived metabolites influence immune development in the placenta and fetal intestine in utero

2) The vaginal microbiome and microbial metabolites contribute to intestinal immune development at birth

5-AVAB, 5-aminovaleric acid betaine; AHR, aryl hydrocarbon receptor; HBC, Hoffbauer cell; ILC, innate lymphoid cell; NK, natural killer; Treg cell, regulatory

Human milk microorganisms and their metabolites support the gut microbiome and immune system in the offspring



Breast milk composition is complex and unique

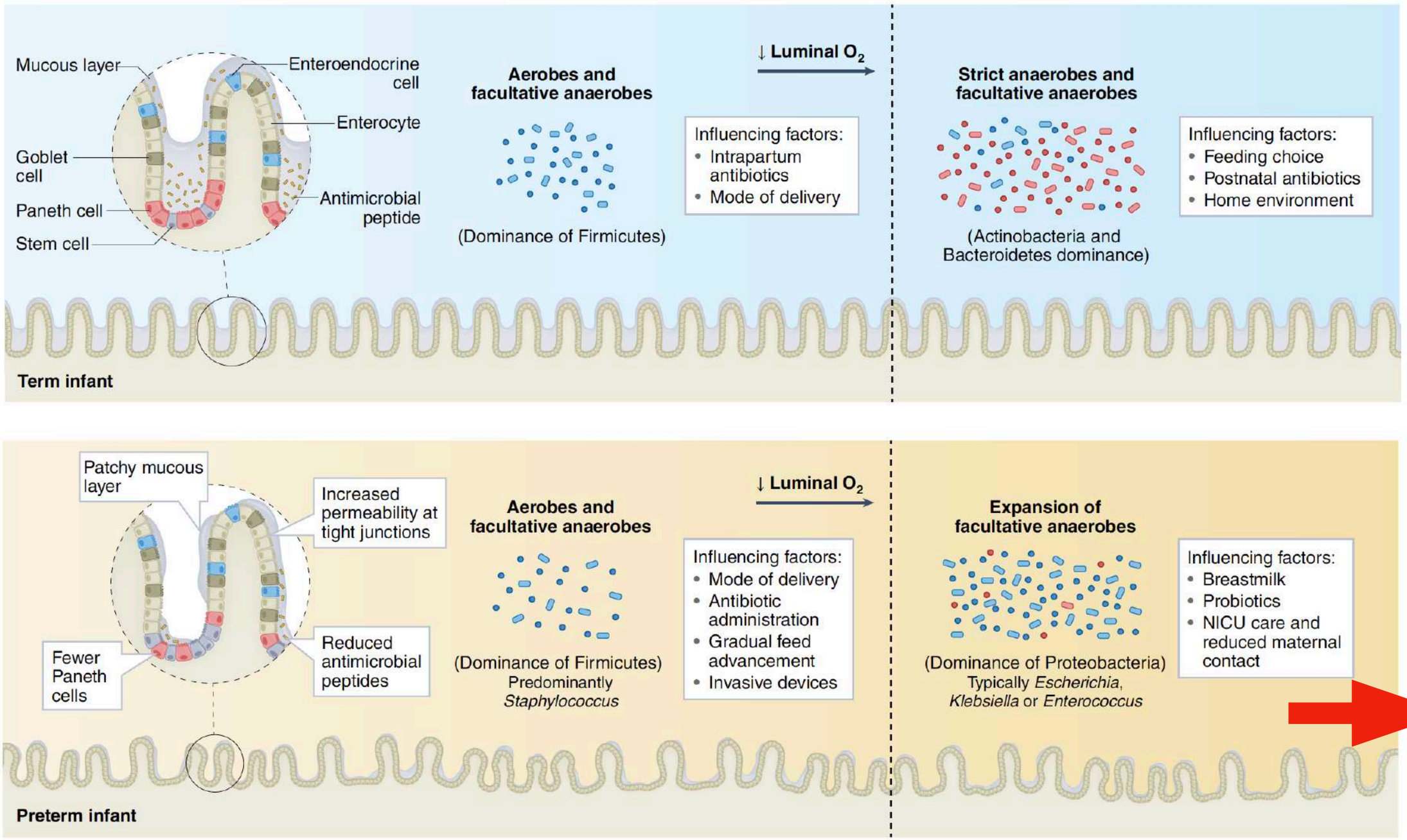
Milk contains nutrients and specific bioactive compounds:

- microbiota & metabolites (including SCFAs)
- microorganism-derived products (cell walls, membrane, DNA, specific secreted proteins, and other fragments or structures)
- human milk oligosaccharides (HMOs)
- immune-related compounds (secretory IgA, immunoglobulins, lactoferrin and lysozyme)
- CD14 T cells, cytokines, growth factors, defensins
- extracellular vesicles, which can cargo microRNAs, long non-coding RNAs, proteins and lipids, as well as maternal cells, including leukocytes and stem cells

This complexity is key to adaptive and innate mucosal immunity in the neonate and to support neonatal microbial assembly by interacting closely with intestinal epithelial cells and intestinal receptors signalling to the immune system (modulating the adaptive immune response via a T helper cell response and stimulating regulatory T (Treg) cells and regulatory B cells) and generating immune tolerance

ILC, innate lymphoid cell; NK, natural killer

Term and Preterm infant



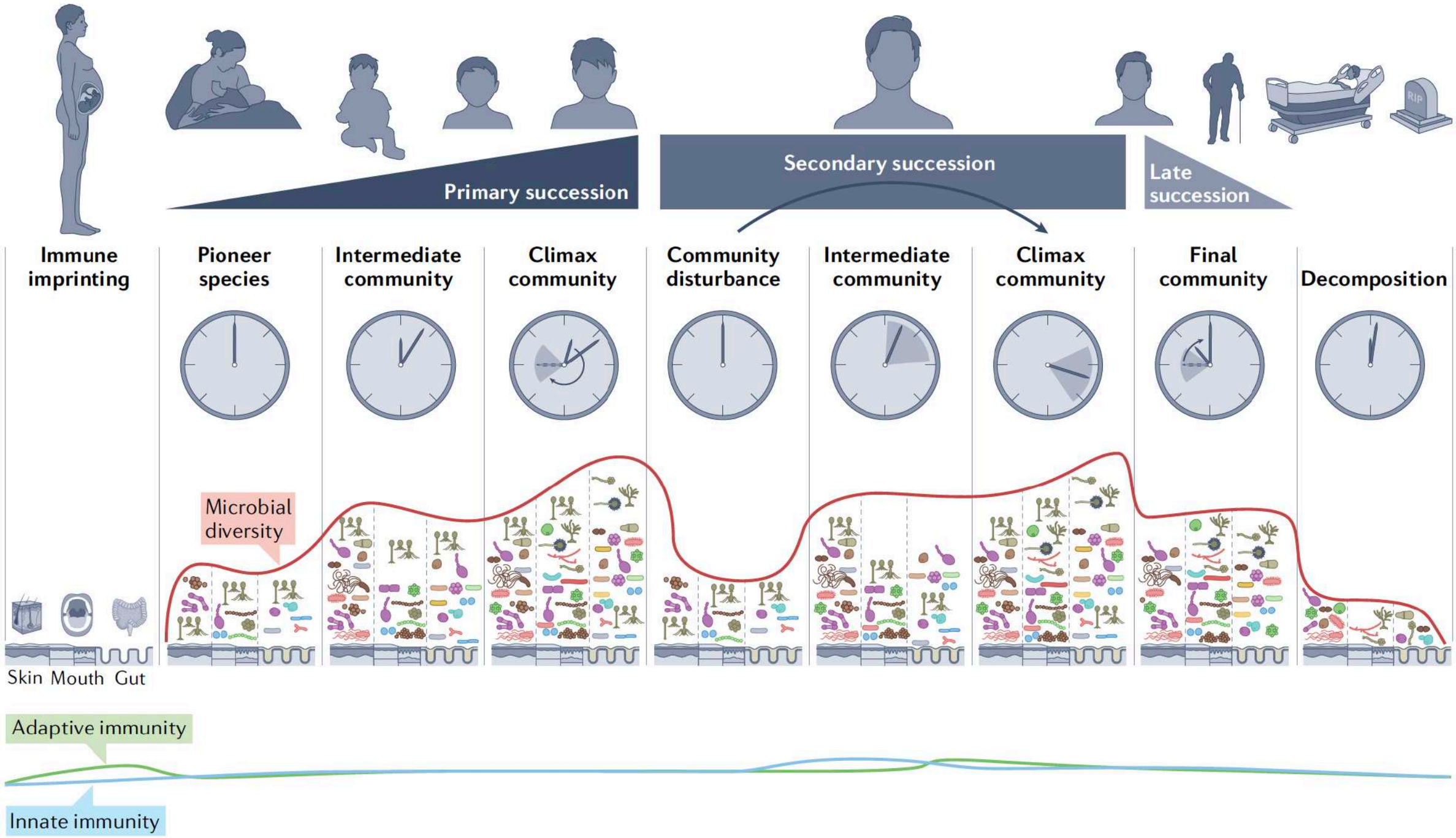
Healy et al., 2022

Anatomical differences, successional development of bacterial communities, and factors influencing microbiome establishment in term and preterm infants

The intestinal anatomy of the preterm infant is immature, with poor differentiation of epithelial cells leading to weakened gut-barrier defences

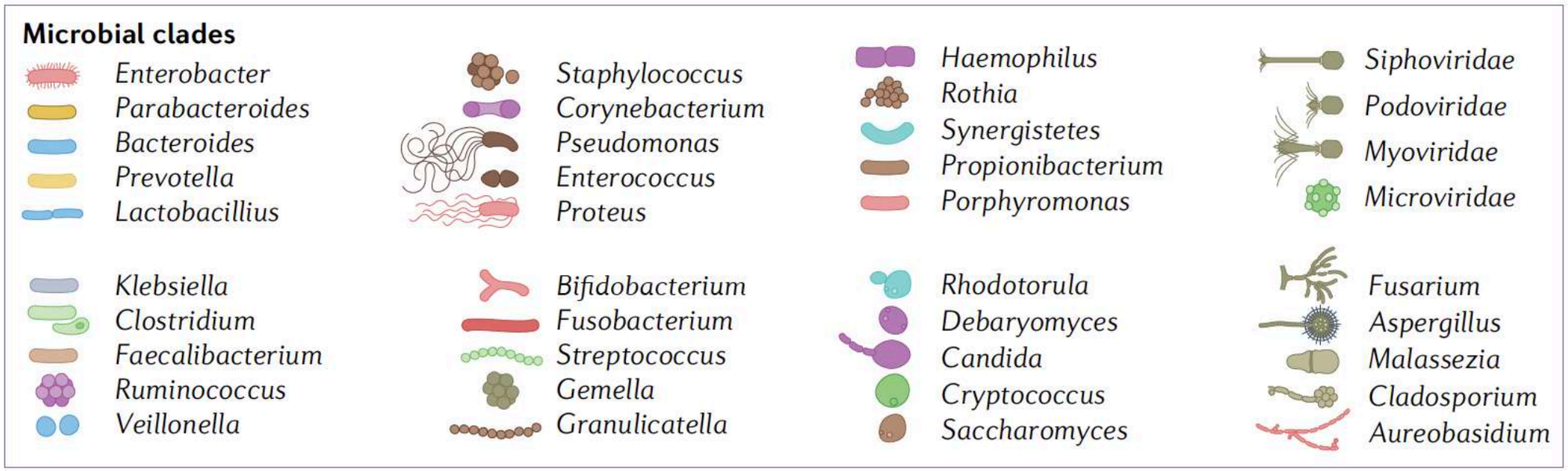
The initial colonizers of the gut are similar for term and preterm infants but, over time (hours to days) (represented by the vertical dashed line), various influencing factors and alterations in community dynamics lead to the establishment of considerably different populations of microbiota

The succession of the human microbiota from conception to death

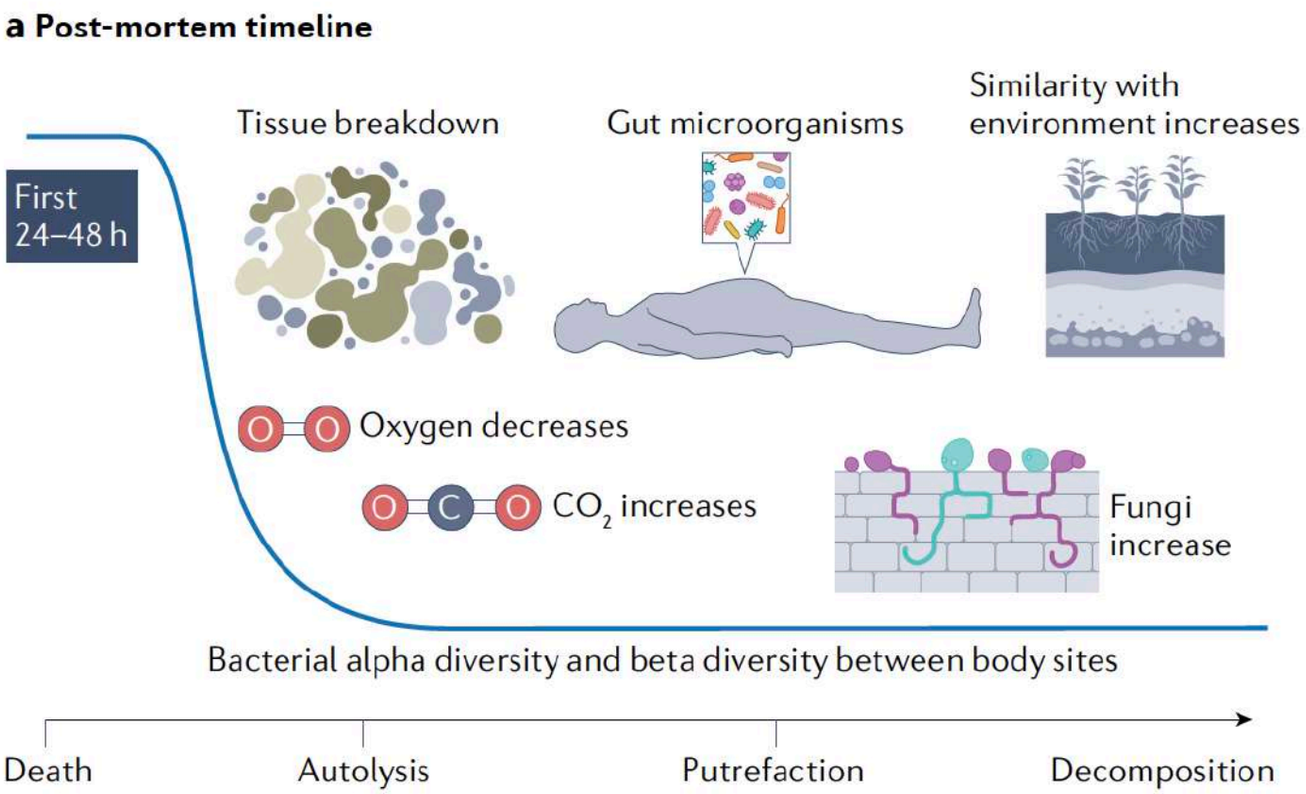


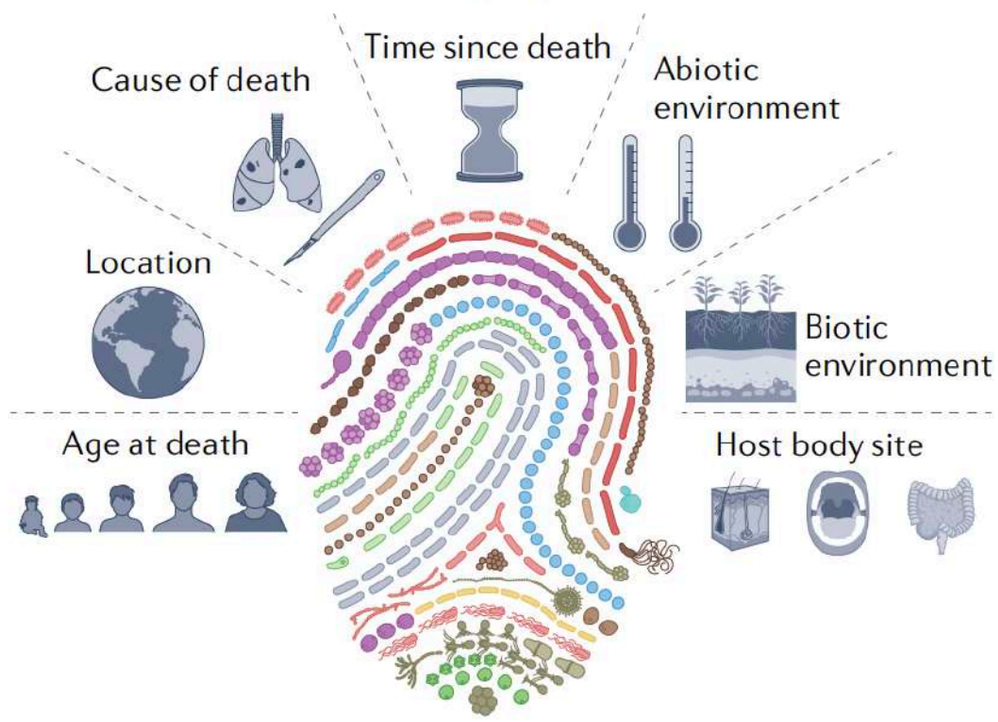
Martino et al., 2022

- Immune imprinting begins before birth through the mother's microbiota and its metabolites
- Initial colonization of pioneer species begins at birth, and body site- specific microbial communities emerge
- These communities increase in complexity until they reach a relatively stable community structure


Microbial clades
Enterobacter
Parabacteroides
Bacteroides
Prevotella
Lactobacillius
Staphylococcus
Corynebacterium
Pseudomonas
Enterococcus
Proteus
Haemophilus
Rothia
Synergistetes
Propionibacterium
Porphyromonas
Siphoviridae
Podoviridae
Myoviridae
Microviridae
Klebsiella
Clostridium
Faecalibacterium
Ruminococcus
Veillonella
Bifidobacterium
Fusobacterium
Streptococcus
Gemella
Granulicatella
Rhodotorula
Debaryomyces
Candida
Cryptococcus
Saccharomyces
Fusarium
Aspergillus
Malassezia
Cladosporium
Aureobasidium

The microbiota after death





Martino et al., 2022

- After death the microbiota is relatively stable in the first 24–48 h
- The tissue then begins to break down during autolysis, leading to bloom in the gastrointestinal microbiota and a decrease in alpha diversity and a decrease in beta diversity between body sites
- During putrefaction, the role of fungi increases, and the microbiota of the body becomes more similar to the microbiota of the surrounding environment
- The post- mortem microbiota is unique to each body and is distinct between bodies on the basis of the time since death, cause of death, environment, location and age at death, at the beginning, between body sites