

BIODIVERSITÉ ET LE MICROBIOME HUMAIN

Caroline Roduit, Children's Hospital Zürich, Allergy Research Group
and CK-CARE

Bern, 15 Januar 2016

The incidence of allergic, autoimmune and inflammatory diseases

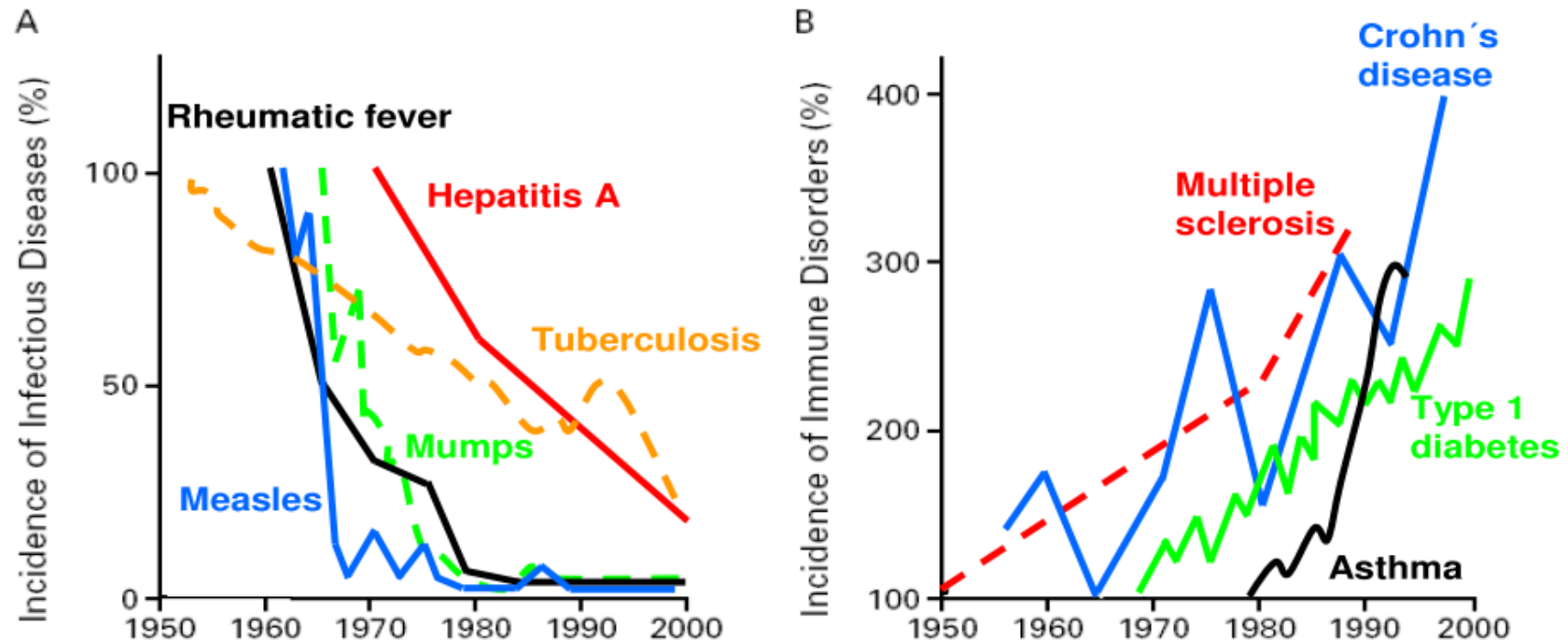
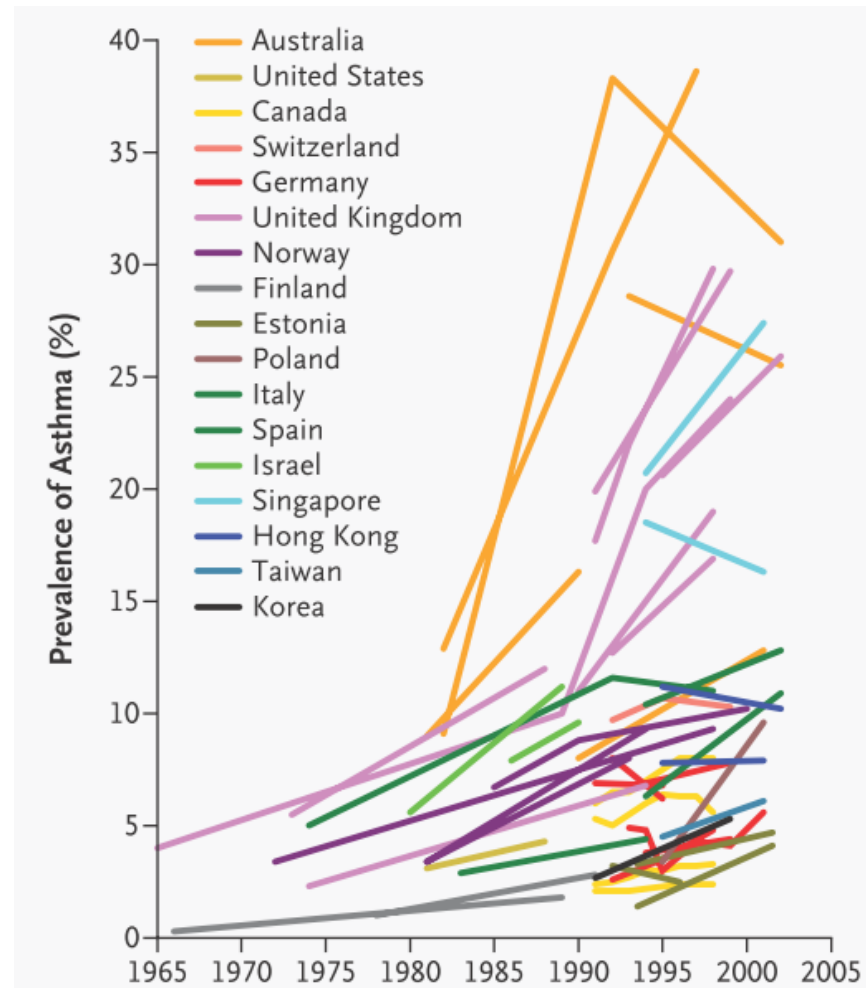


Figure 1. Inverse Relation between the Incidence of Prototypical Infectious Diseases (Panel A) and the Incidence of Immune Disorders (Panel B) from 1950 to 2000.

The incidence of asthma in childhood



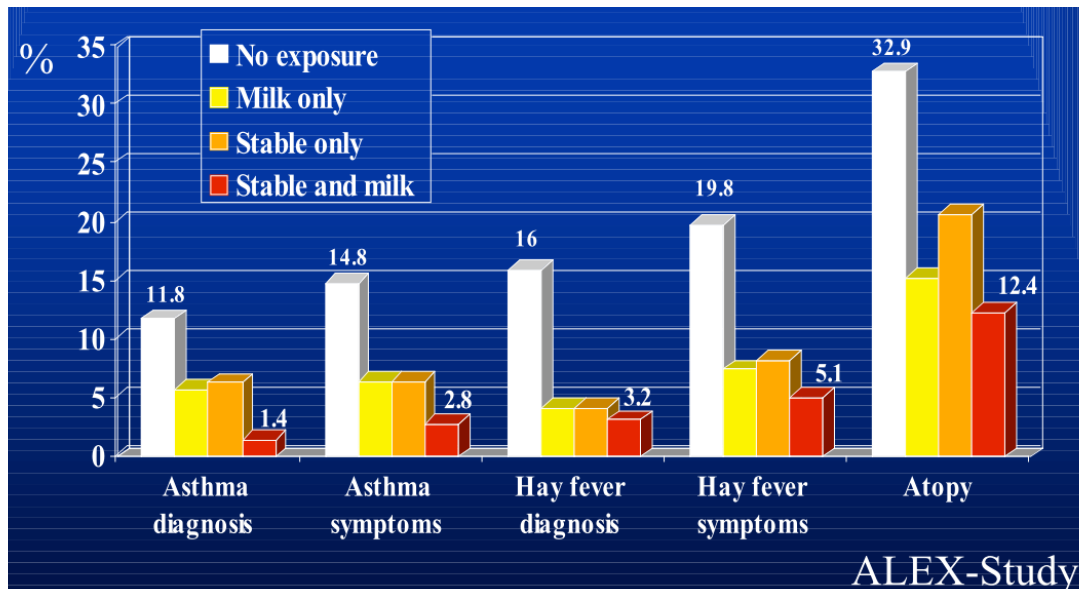
The hygiene hypothesis

Hay fever, hygiene, and household size

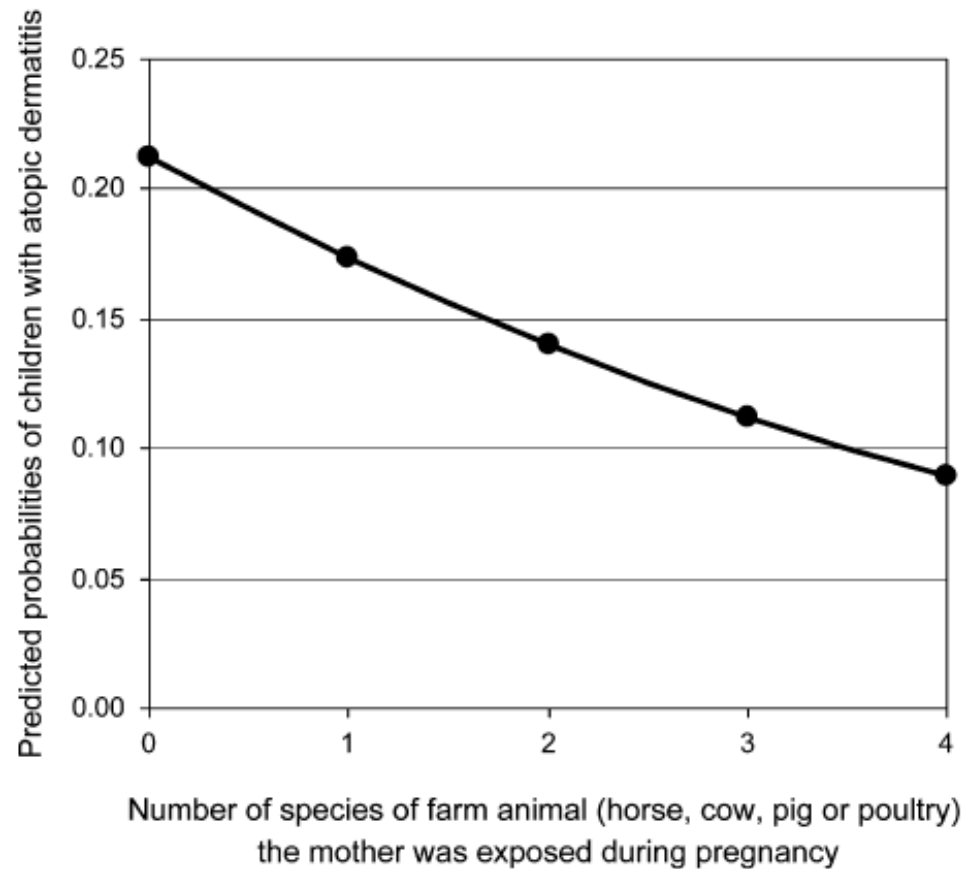
David P Strachan

- Less hay fever and atopic dermatitis among children with siblings, large families, having most likely more infections by contact as single children.
- Evidences from various studies suggested that “the hygiene hypothesis” plays a large role in the allergy epidemic.

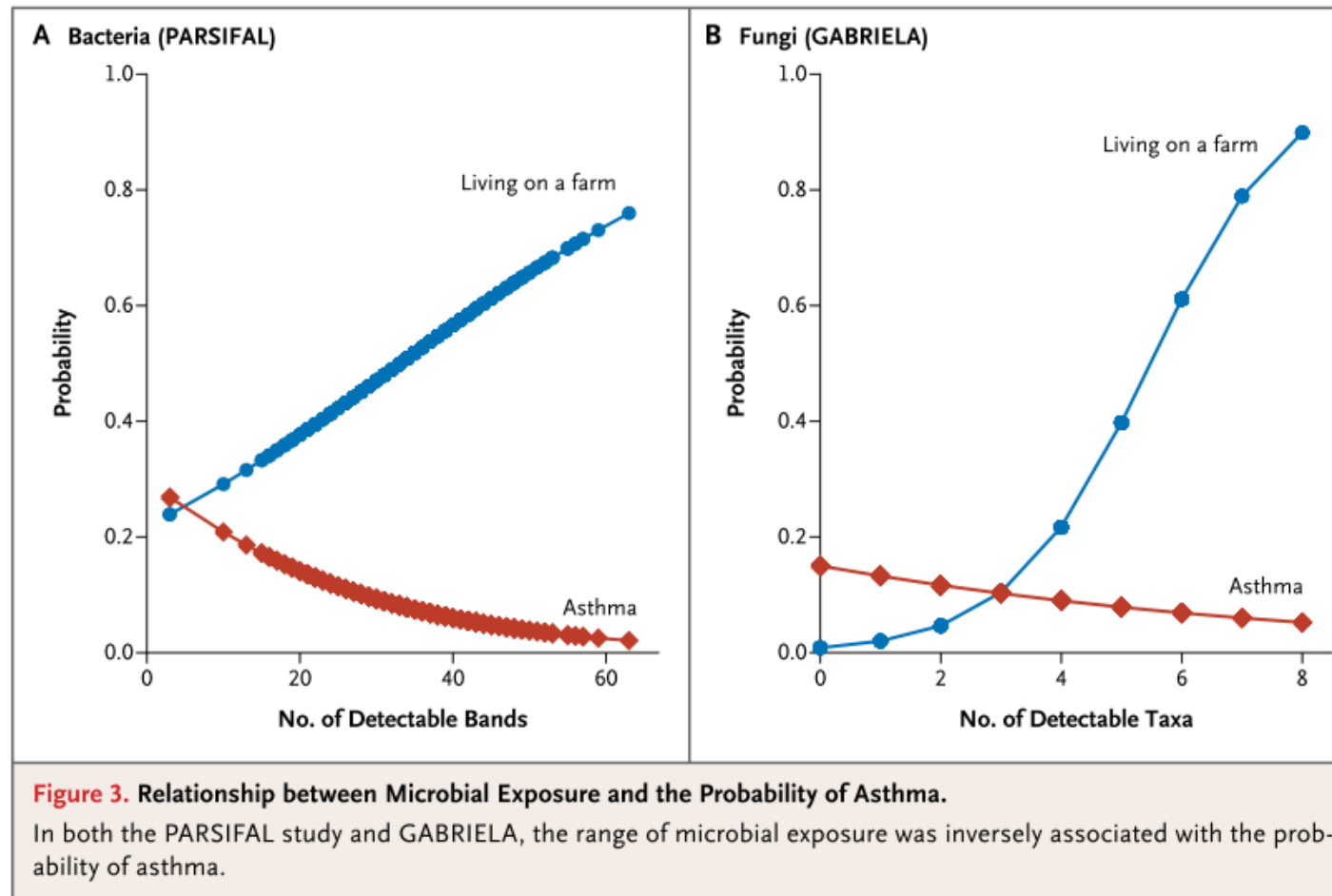
Farm environment protects against allergies



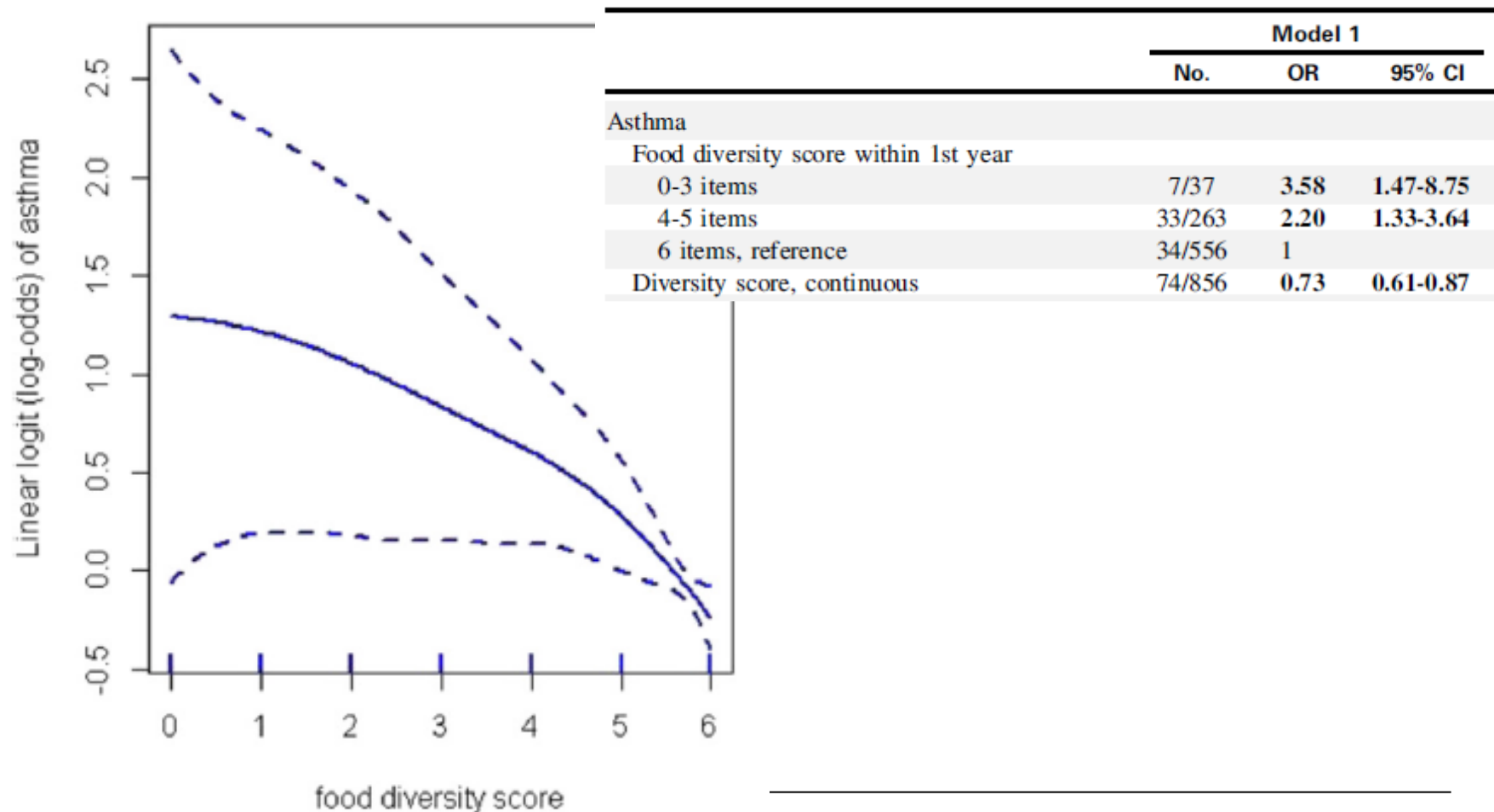
Prenatal exposure to an increasing number of farm animal species protects against atopic dermatitis



Exposure to a large diversity of microbes reduces the risk of asthma



Early postnatal environment: increased diversity of food introduced in the 1st year protects against asthma



Lifestyle changes in westernised countries:

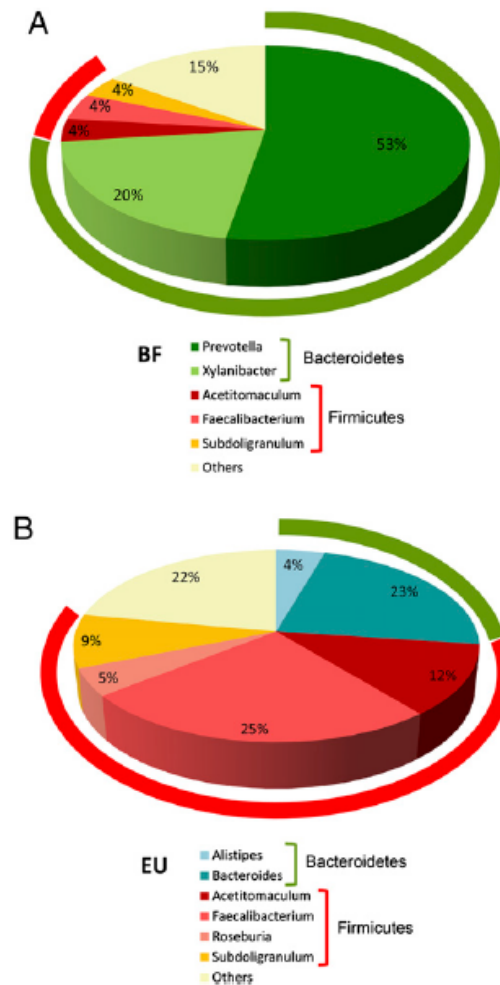
Reduction of consumption of fiber in industrialized countries compared to developing countries

- In **industrialized countries**:
average consumption of fibers: **20-25 g per day**
- While in **developing countries**:
100 g per day, (great consumption of vegetal products)



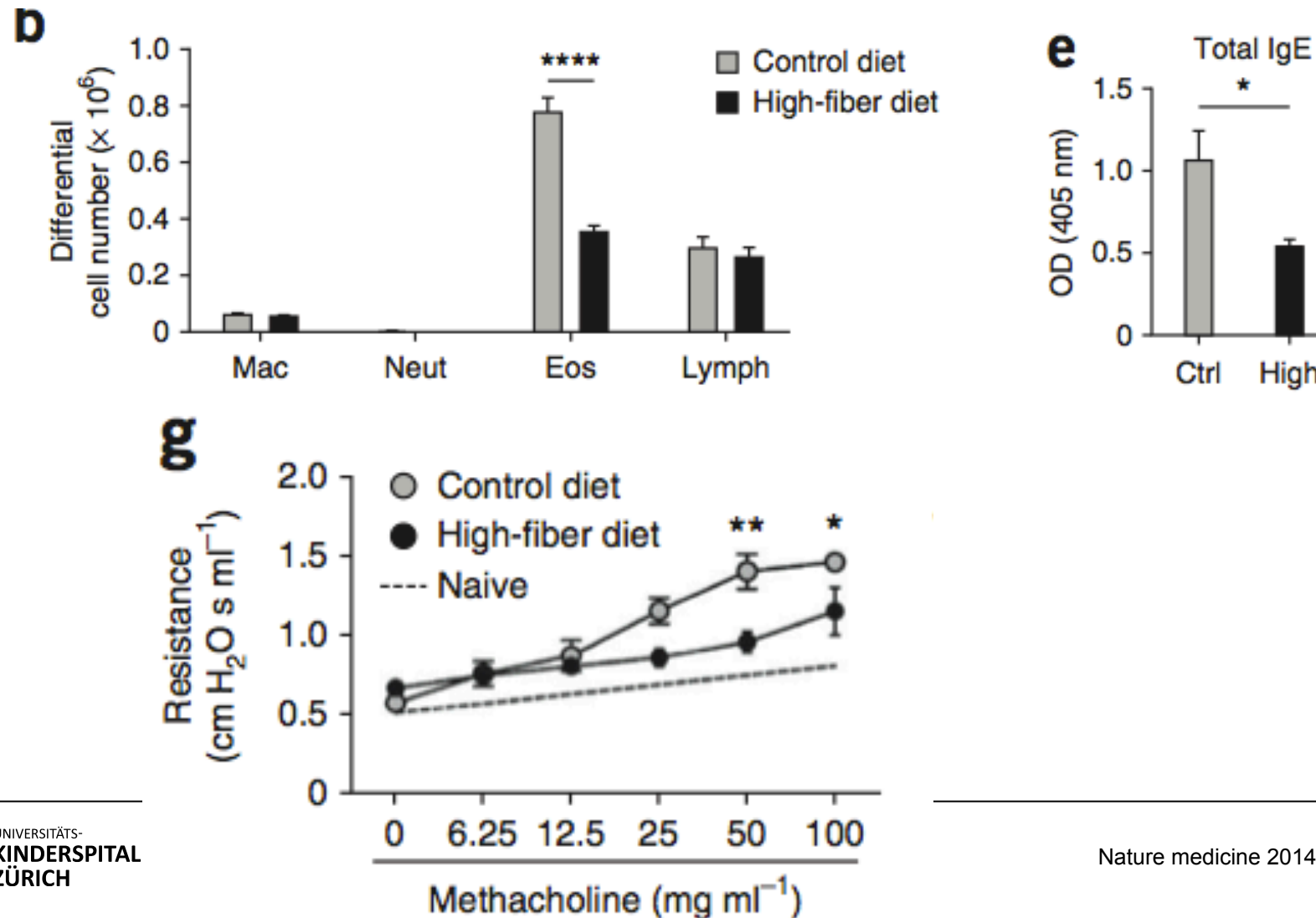
Impact of diet on gut microbiota

- Comparison of the fecal microbiota of European children (EU) and that of children from a rural African village of Burkina Faso (BF), where the diet is high in fiber content.
- Among children from Africa: a lower prevalence of allergic diseases was observed compared with the prevalence seen in children from western Europe



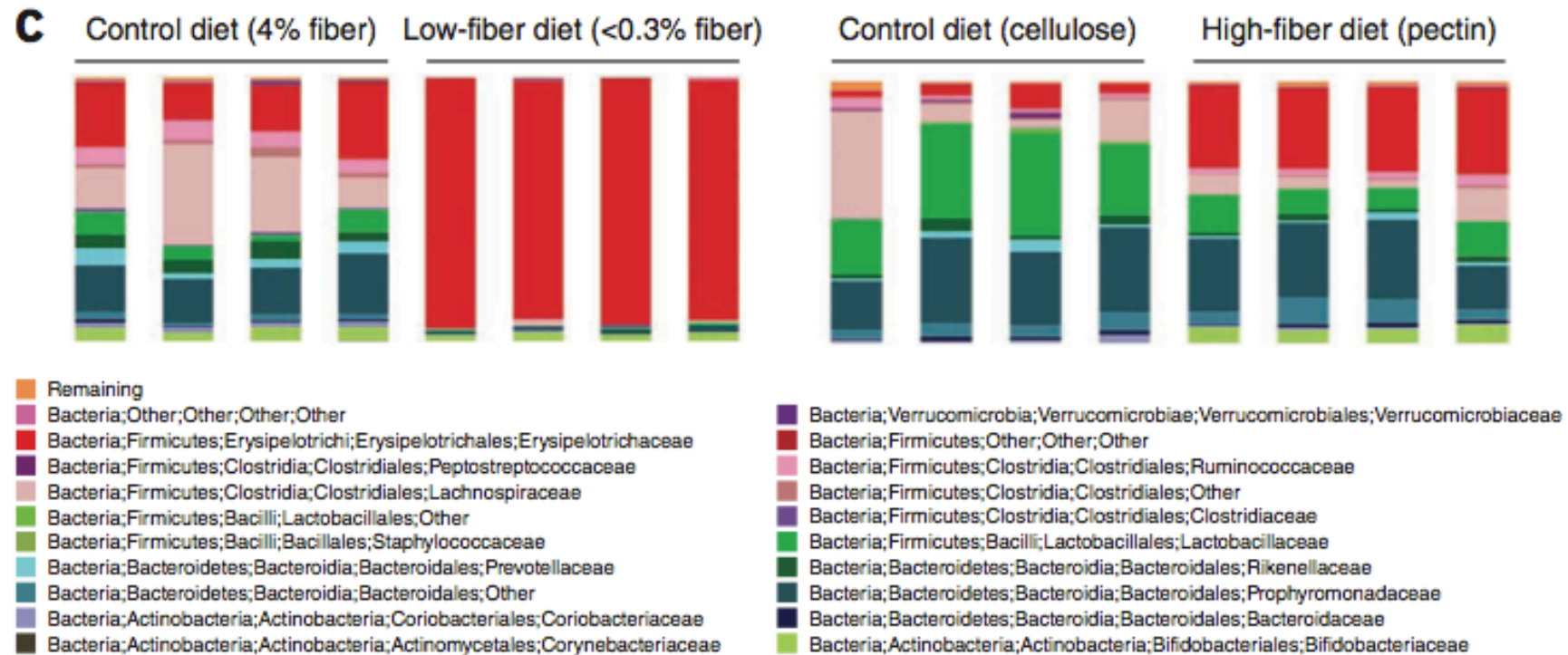
Gut microbiota metabolism of dietary fiber influences allergic airway disease and hematopoiesis

Aurélien Trompette¹, Eva S Gollwitzer¹, Koshika Yadava¹, Anke K Sichelstiel¹, Norbert Sprenger², Catherine Ngom-Bru², Carine Blanchard², Tobias Junt³, Laurent P Nicod¹, Nicola L Harris⁴ & Benjamin J Marsland¹



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Human microbiome

Cells:

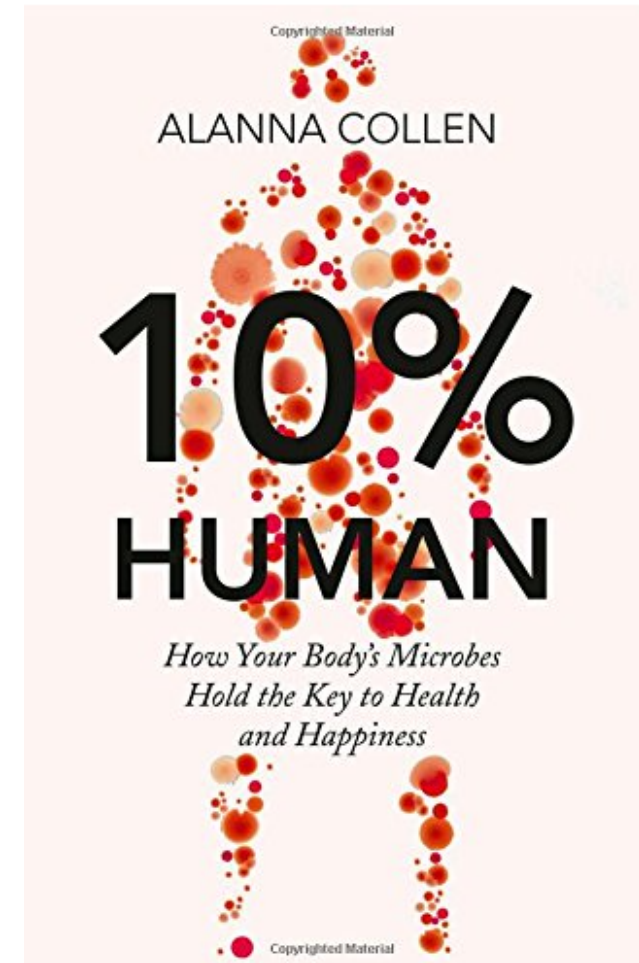
- 10% human
- 90% microbes

-> **Microbiota** = micro-organism within a given niche

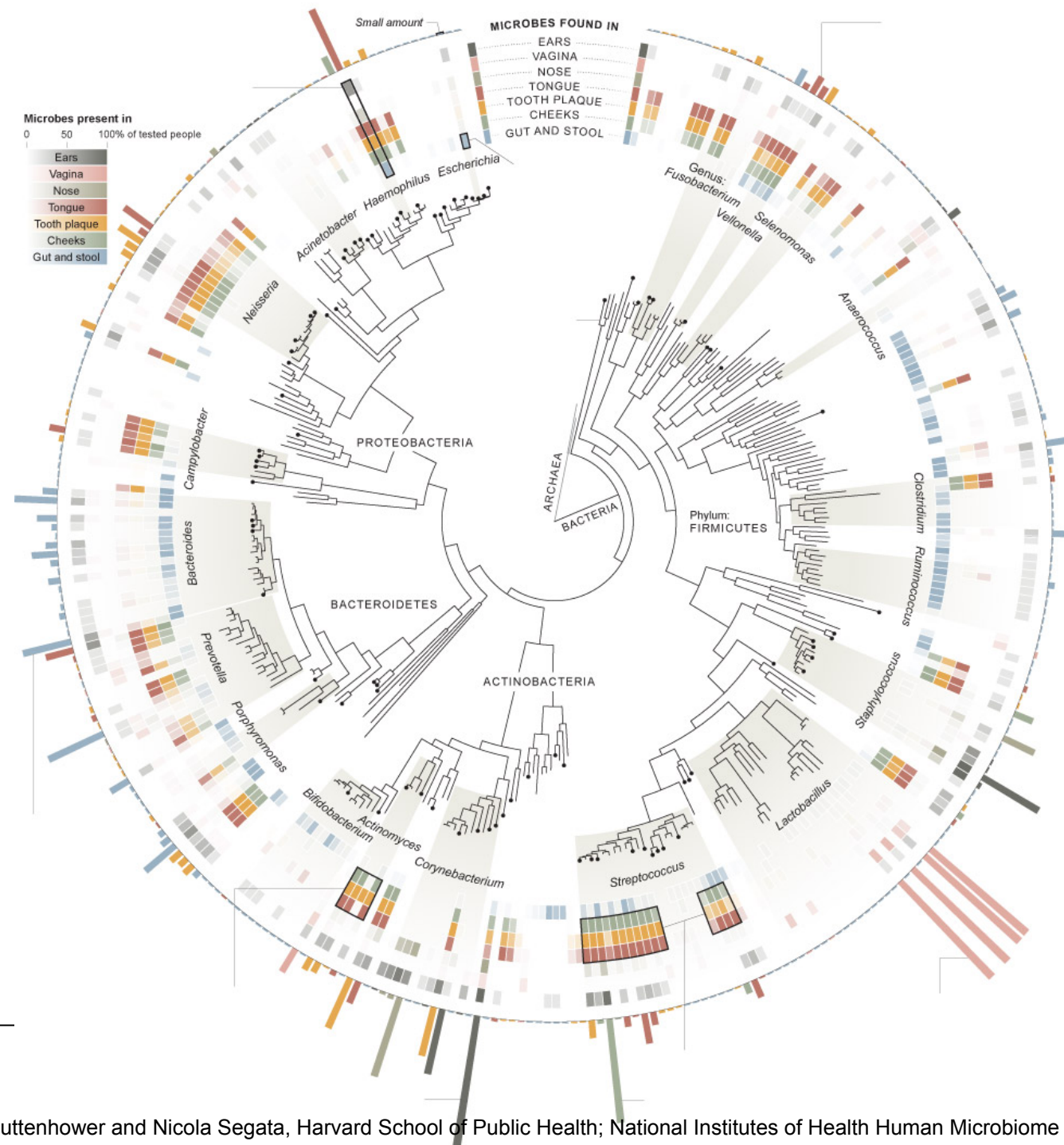
Genes:

- 1% human
- 99% microbes

-> **Microbiome** = all the genetic material of micro-organisms within a given niche



Human microbiome



Are we born with bacteria?

Review

Microbial Programming of Health and Disease Starts during Fetal Life

Petya T. Koleva*¹, Ji-Sun Kim², James A. Scott², and Anita L. Kozyrskyj^{1,3}

The pioneer microbiota of the neonatal gut are essential for gut maturation, and metabolic and immunologic programming. Recent research has shown that early bacterial colonization may impact the occurrence of disease later in life (microbial programming). Despite early conflicting evidence, it has long been considered that the womb is a sterile environment and human microbial colonization begins at birth. In the last few years, several findings have reiterated the presence of microbes in infant first stool (meconium) and pointed to the existence of in utero microbial colonization of the infant gut. The dominant bacterial taxa detected in meconium specimens belong to the *Enterobacteriaceae* family (*Escherichia* genus) and lactic acid bacteria (notably members of the genera *Leuconostoc*, *Enterococcus*, and *Lactococcus*). Maternal atopy promotes dominance of *Enterobacteriaceae* in

newborn meconium, which in turn may lead to respiratory problems in the infant. This microbial interaction with the host immune system may in fact, originate during fetal life. Our review evaluates the evidence for an intrauterine origin of meconium microbiota, their composition and influences, and potential clinical implications on infant health.

Birth Defects Research (Part C) 105:265–277, 2015.
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Key words: meconium; microbiota; fetal programming; infancy; childhood diseases

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Gut microbiota alterations are associated with diseases:

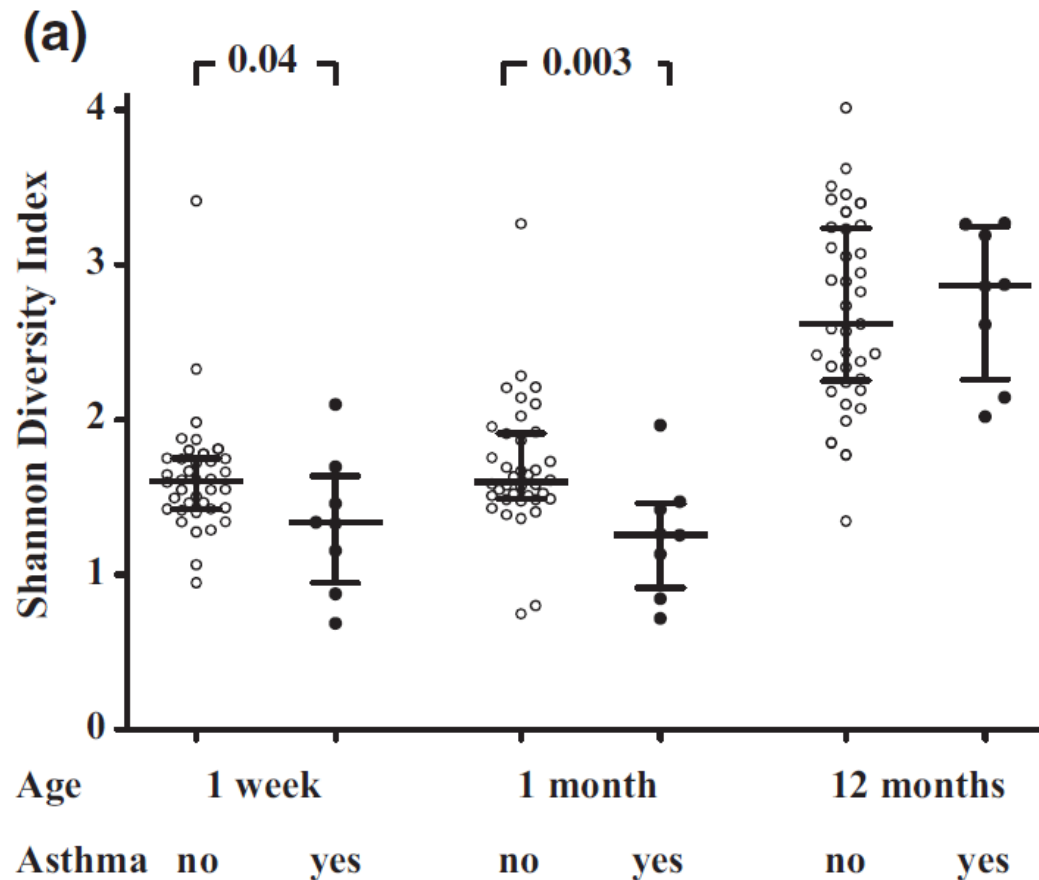
| | |
|--|---|
| - Crohn's disease | Diversity decrease – reduced <i>F. prausnitzii</i> |
| - Ulcerative colitis | Diversity decrease – reduced <i>A. muciniphila</i> |
| - Irritable bowel syndrome | Increased <i>Dorea</i> and <i>Ruminococcus</i> |
| - <i>Clostridium difficile</i> infection | Strong diversity decrease |
| - Obesity | Specific bacterial ratios (<i>Bacteroidetes/Firmicutes</i>) |
| - Colorectal cancer | Variation in <i>Bacteriodes</i> spp |
| - Celiac disease | Altered composition |
| - Allergy, asthma | Altered diversity |
| - Diabetes | |
| - Mental health disorders | |
| - Alzheimer | |

➡ **Low diversity of the microbiome appears to be less healthy**

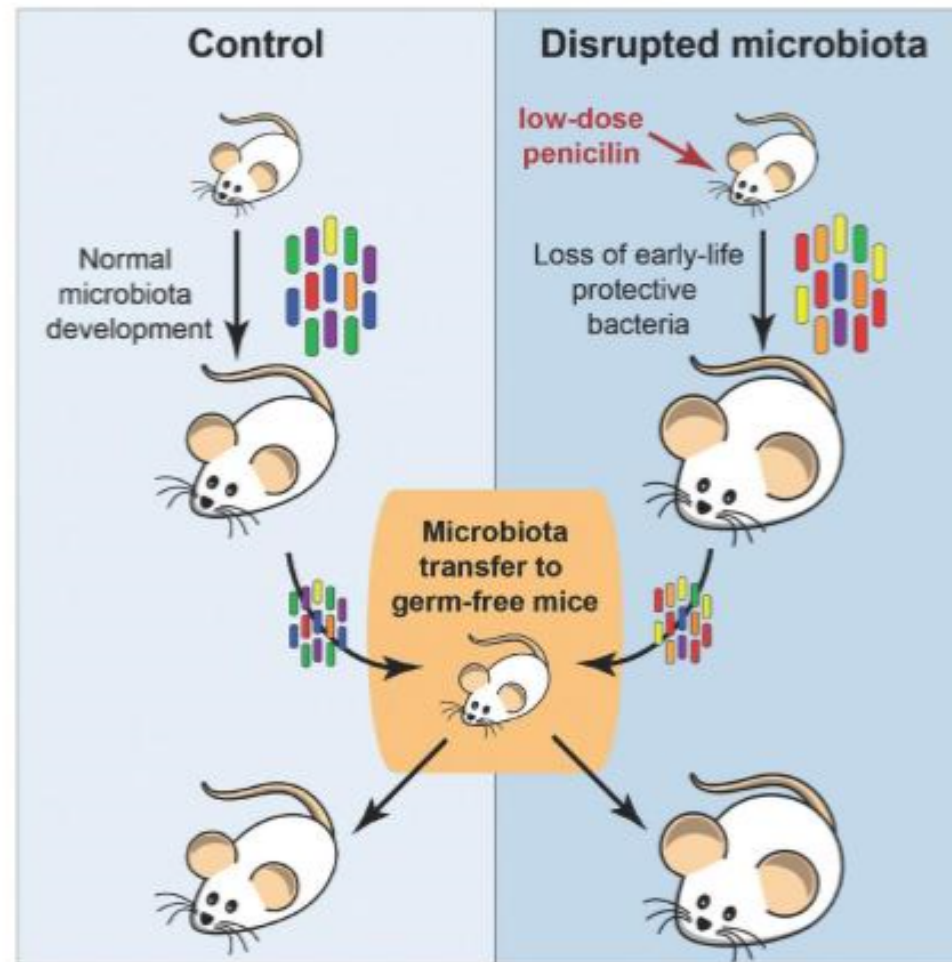
Low gut microbiota diversity in early infancy precedes asthma at school age

T. R. Abrahamsson¹, H. E. Jakobsson², A. F. Andersson³, B. Björkstén^{4,5}, L. Engstrand^{2,3} and M. C. Jenmalm^{1,6}

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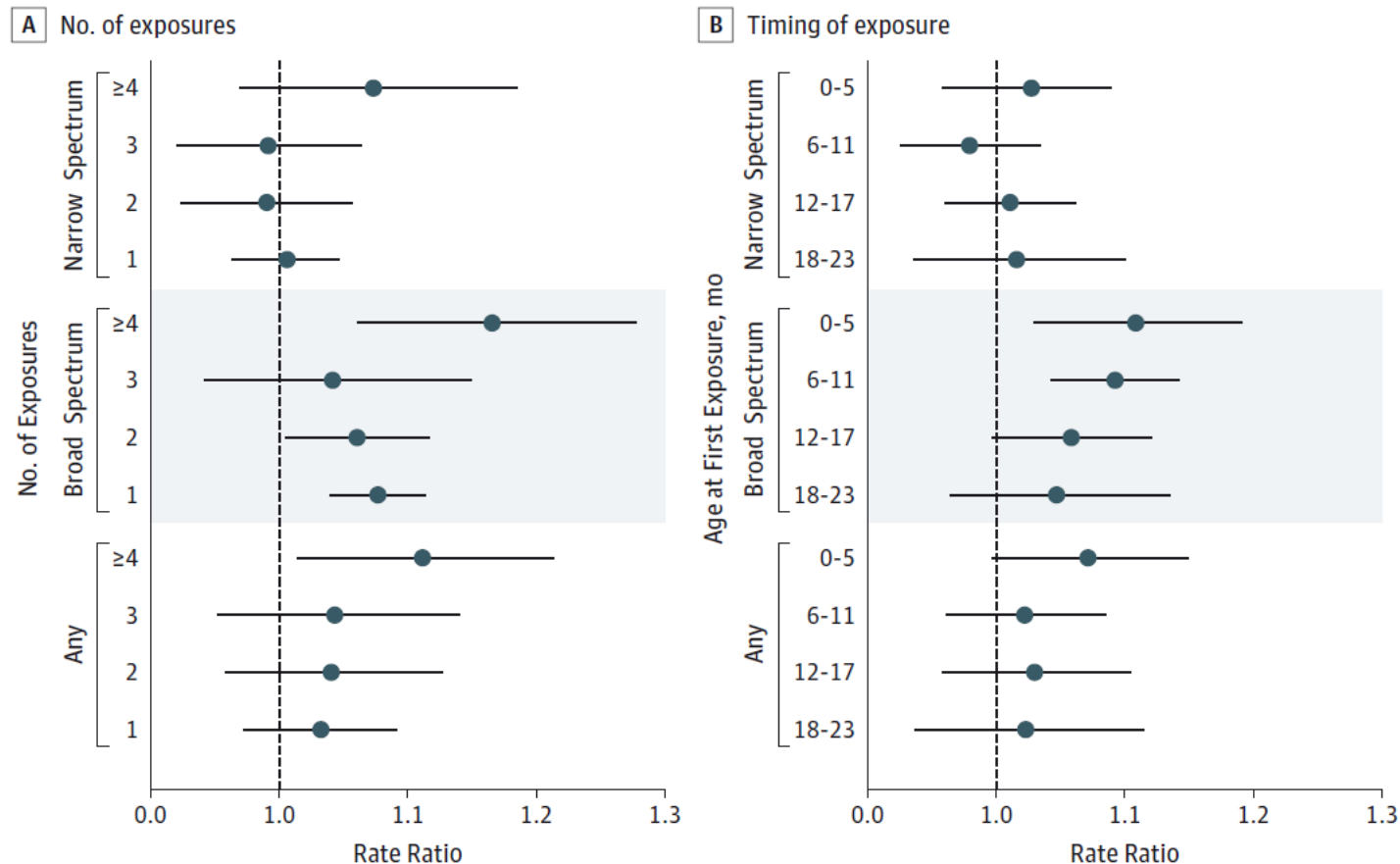


Gut microbiota and obesity



Transferring the gut microbes of mice treated with low dose of penicillin from early life into germ-free mice results in weight gain in the recipient mice

Antibiotic exposure during the first 24 months promotes obesity later in life





The gastrointestinal tract microbiome and potential link to Alzheimer's disease

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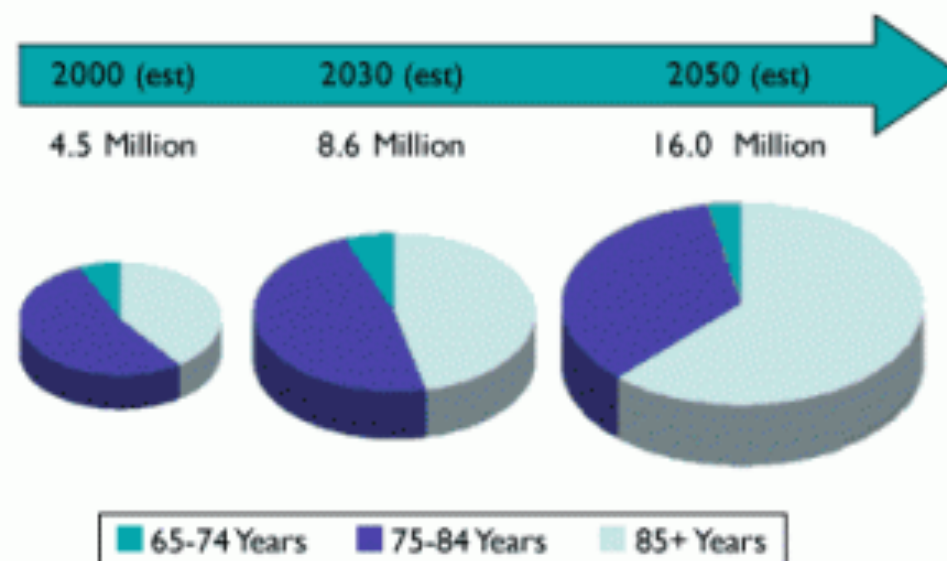
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Reviewed by:

Laurent Gautron, University of Texas Southwestern Medical Center, USA

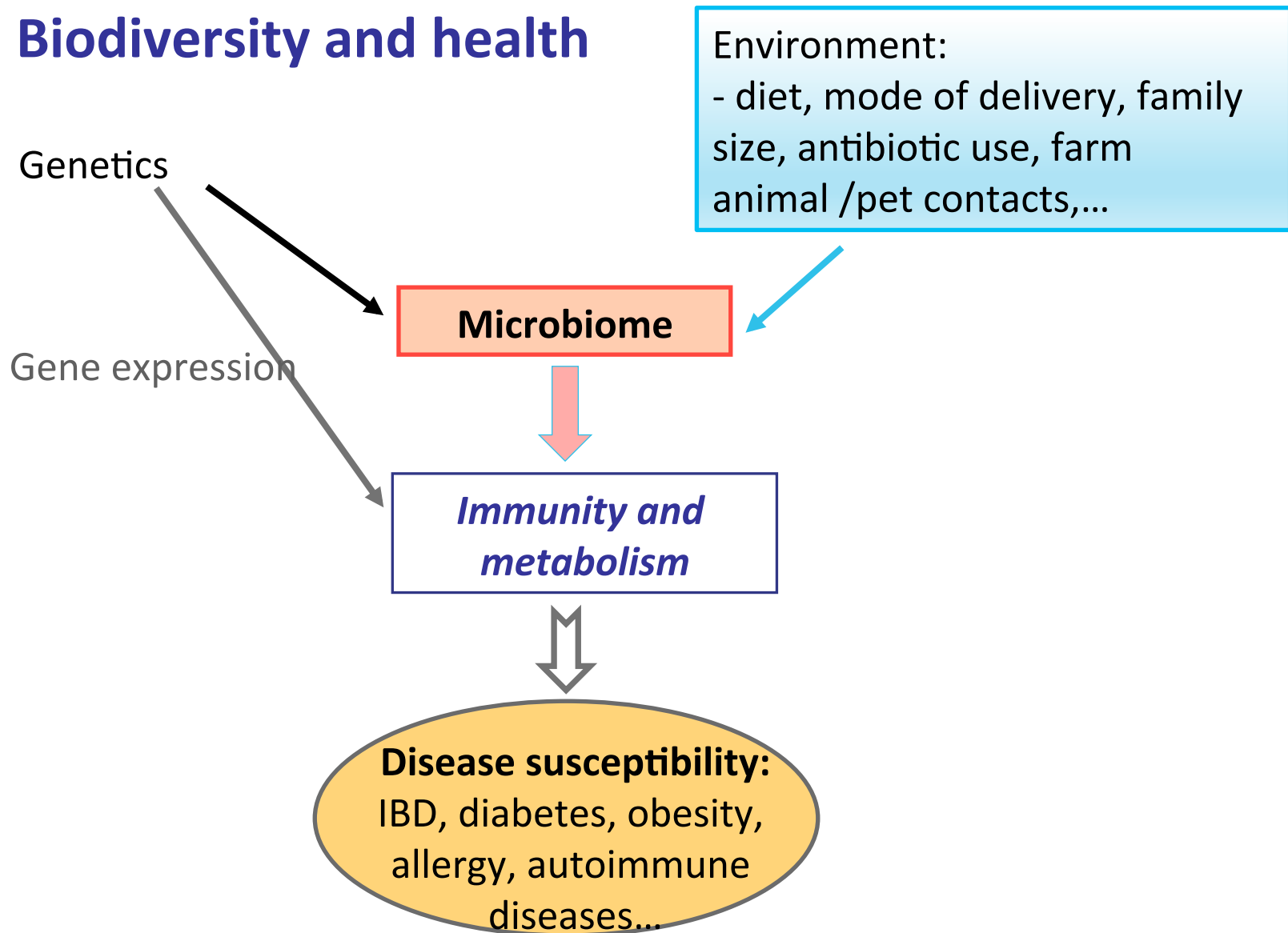
Keywords: Alzheimer's disease, microbiome, genetic complexity, evoluti

Forecast of Alzheimer's Disease Prevalence in the US



Source: Hebert LE et al. Arch Neurol.2003;60:1119-1122.

Biodiversity and health



The biodiversity hypothesis

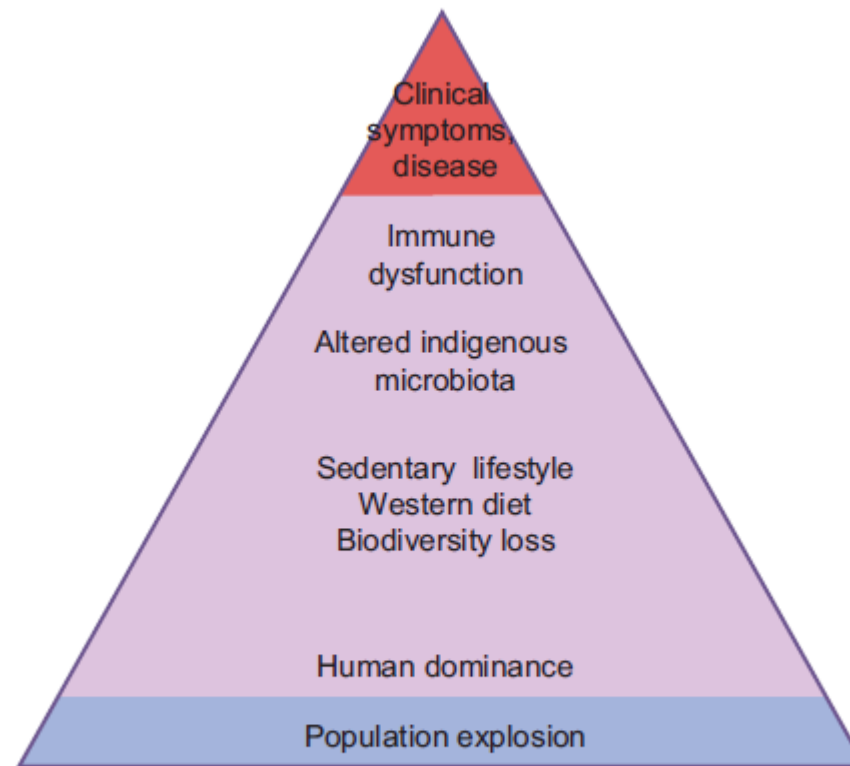


Figure 1. Biodiversity loss, together with sedentary lifestyle and unhealthy diet, may lead to immune dysregulation, poor tolerance, and ultimately to clinical disease. Modified from (116).

POSITION ARTICLE AND GUIDELINES

Open Access

The biodiversity hypothesis and allergic disease: world allergy organization position statement

Tari Haahtela^{1*}, Stephen Holgate², Ruby Pawankar³, Cezmi A Akdis⁴, Suwat Benjaponpitak⁵, Luis Caraballo⁶, Jeffrey Demain⁷, Jay Portnoy⁸, Leena von Hertzen¹, and WAO Special Committee on Climate Change and Biodiversity

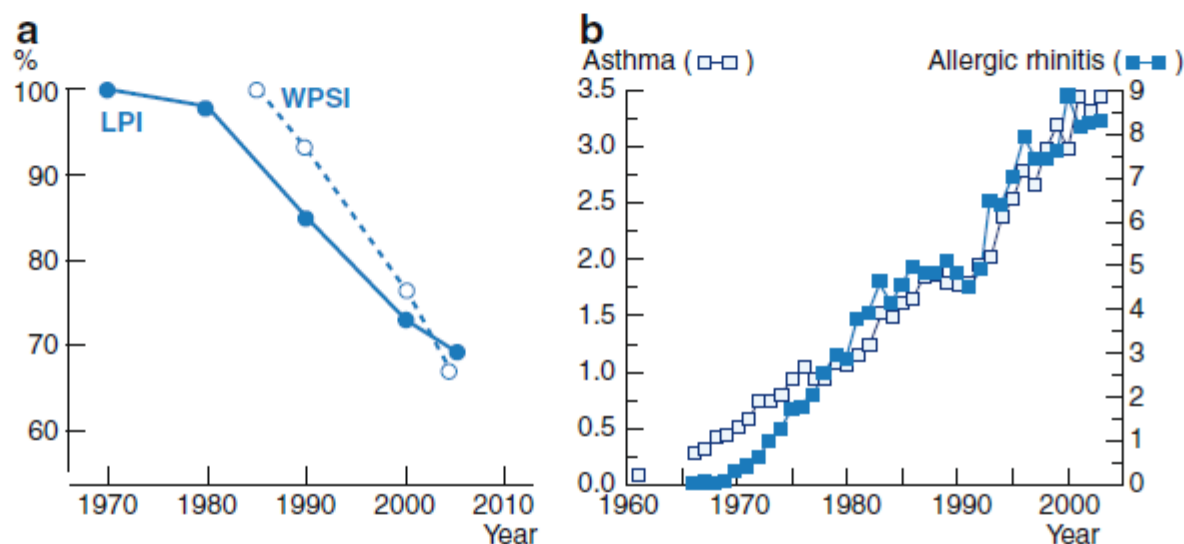
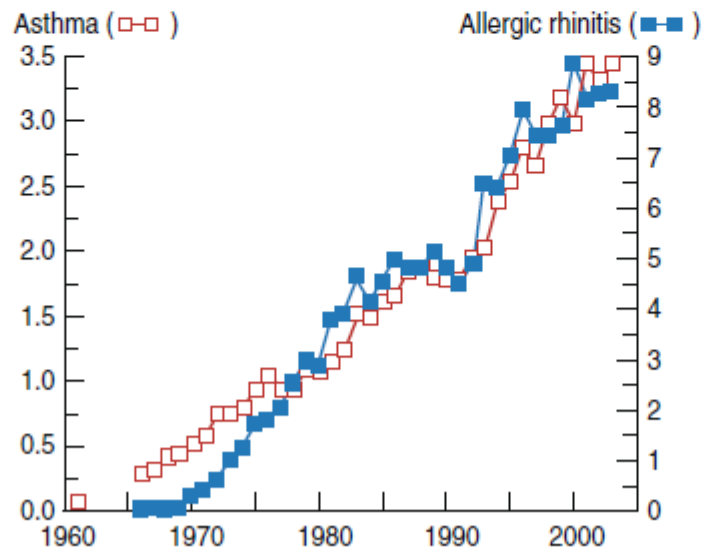


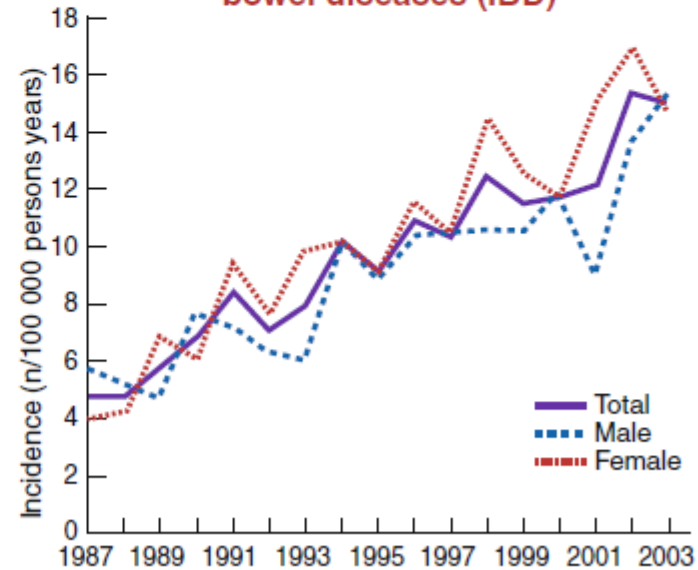
Figure 1 Two global megatrends in biodiversity and public health. (a) Declining biodiversity (percentage change) since 1970 as measured by two indices. WPSI=Waterbird Population Status Index; LPI=Living Planet Index [14]. (b) Increasing trends in the prevalence of inflammatory civilization diseases, asthma and allergic rhinitis among military conscripts in 1966-2003 [165] as an example (modified from ref. [14]).

a)



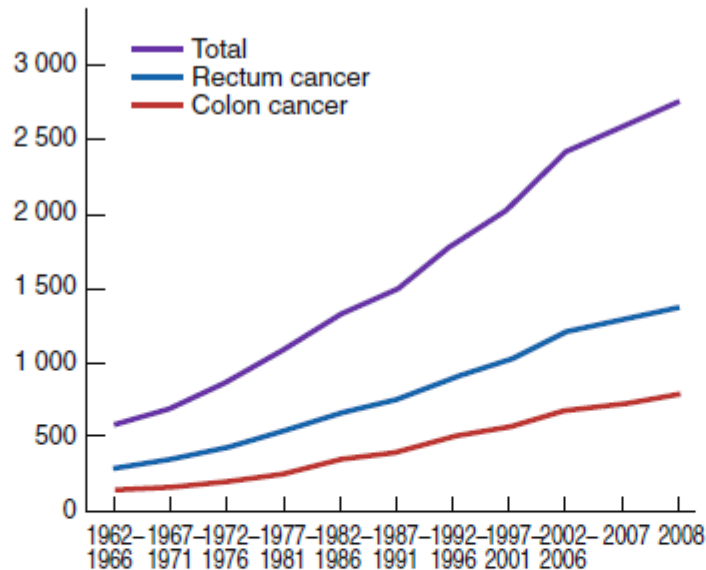
b)

Incidence of pediatric inflammatory bowel diseases (IBD)



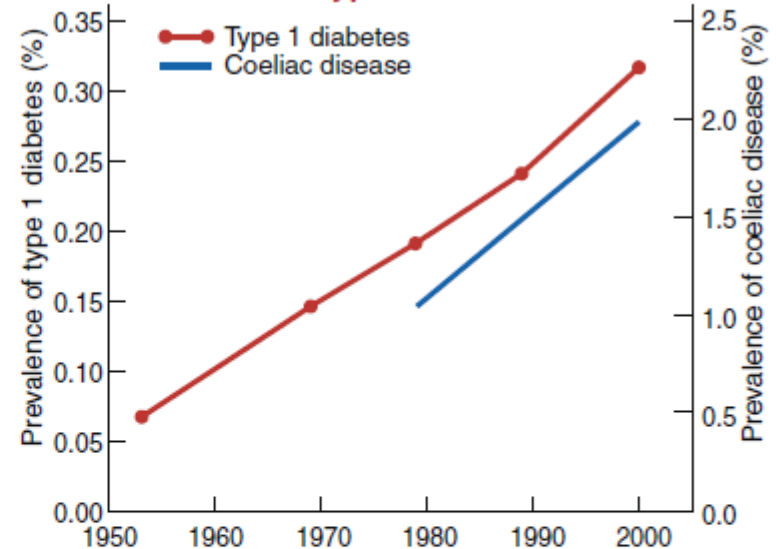
Lehtinen P, et al. Inflamm Bowel Dis 2010

c)



d)

Prevalences of coeliac disease and type 1 diabetes



Lohi S, et al. Aliment Pharmacol Ther 2007

Everything that we eat, drink, touch, and breathe is reflected in our microbiota

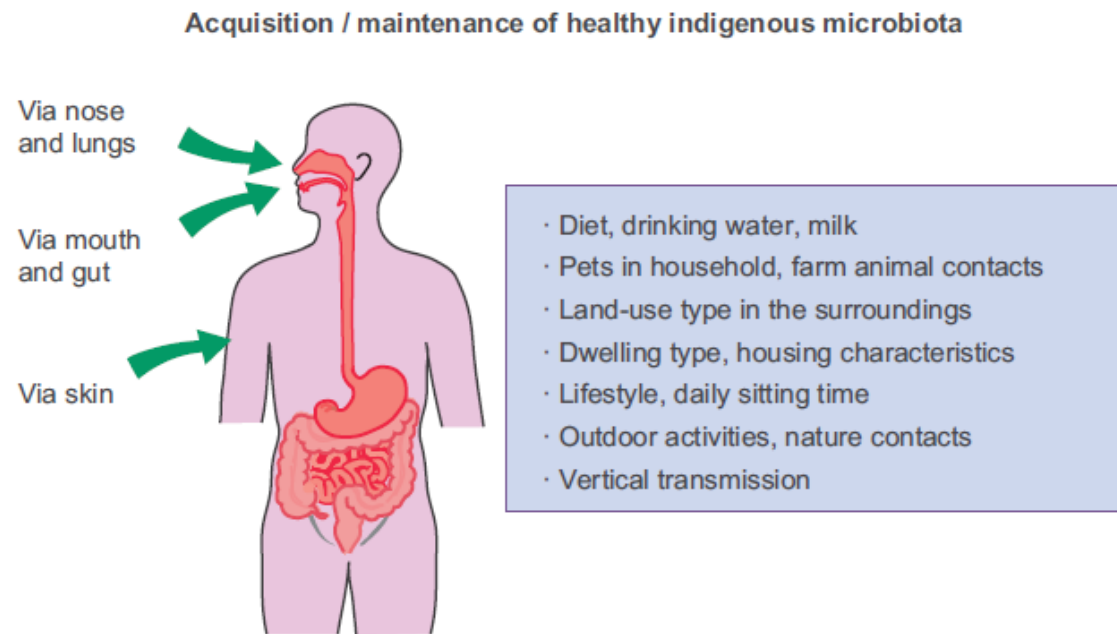
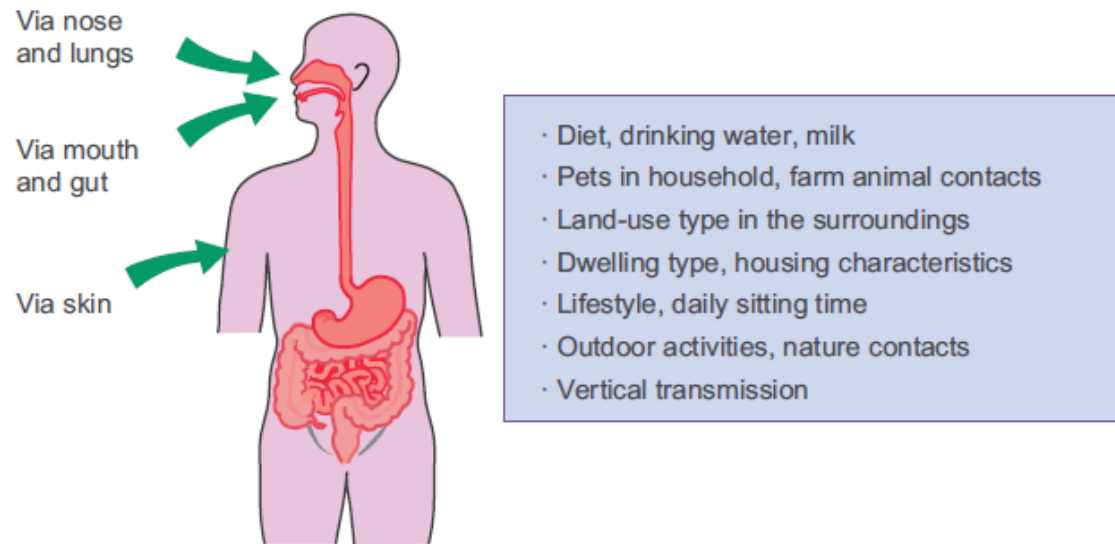


Figure 2. 'We are what we host, and we host what we eat, touch, and breathe'. Outdoor activities in biodiverse environments together with unprocessed food can provide us with microbial exposures necessary for the development and maintenance of healthy balanced microbiota and immunoregulatory circuits.

Everything that we eat, drink, touch, and breathe is reflected in our microbiota

Acquisition / maintenance of healthy indigenous microbiota



Outdoor activities in biodiverse environments together with unprocessed food can provide us with microbial exposures necessary for the development and maintenance of healthy balanced microbiota and immunoregulatory circuits.

Thank you for your attention

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