

제12차 천식연구회 · COPD연구회 공동심포지엄

Microbiome and Asthma

한양대학교병원 호흡기알레르기내과

김 상 헌

Disclosure

내용

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Lung Microbiome

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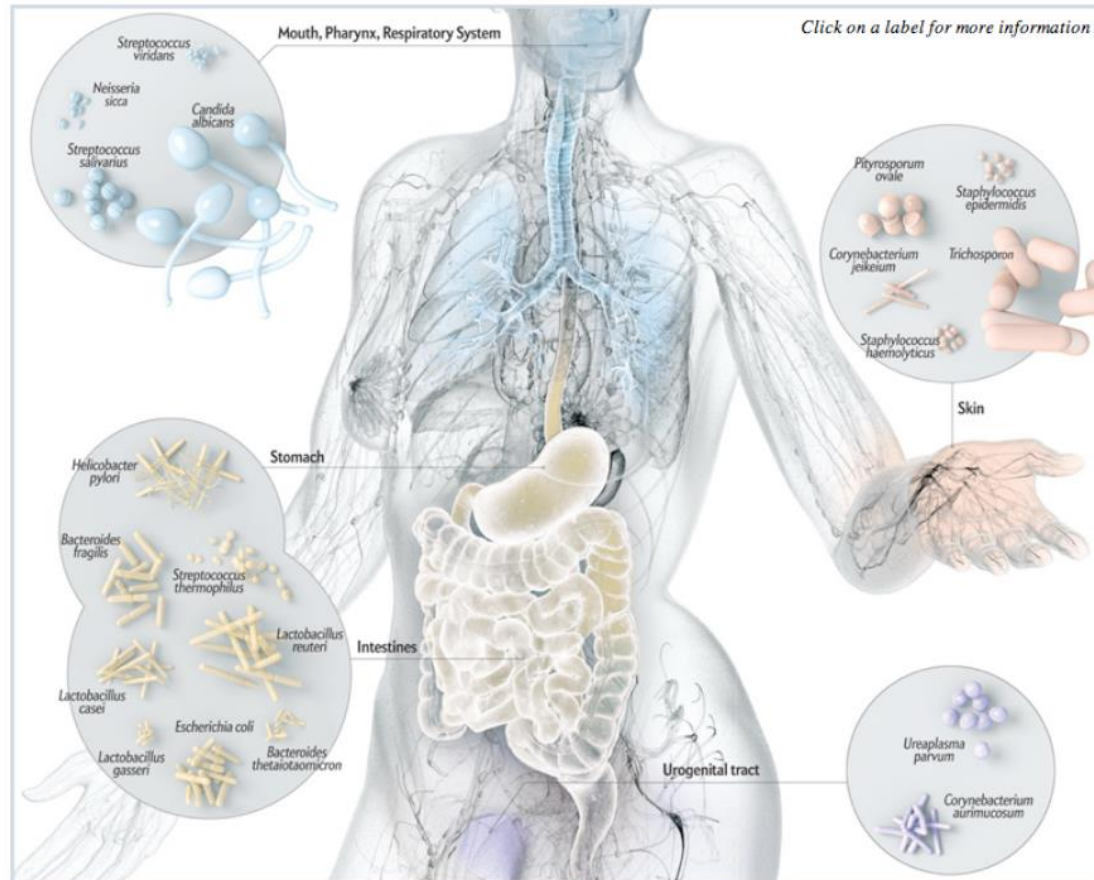
Lung Microbiome and Asthma

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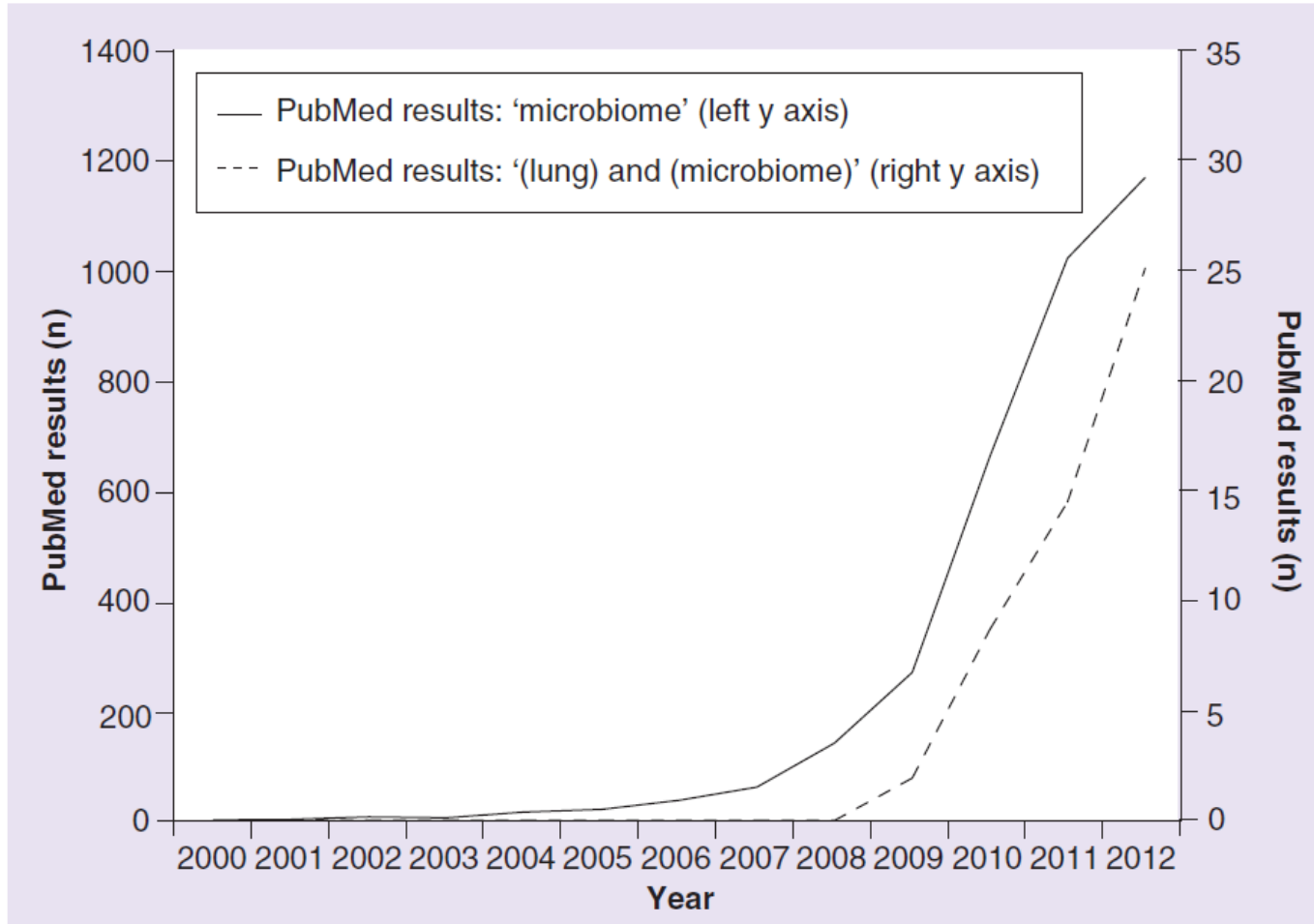
Gut Microbiome and Asthma

Microbiome and Microbiota

- **human microbiome** is the collection of all the microorganisms living in association with the human body



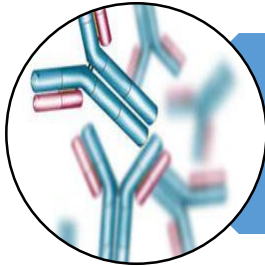
Microbiome: Publication



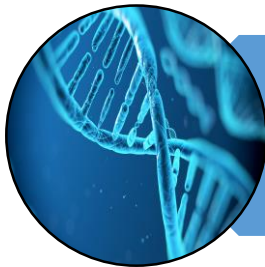
Microbiome: Proof of Presence so far



traditional culture (cultivation)

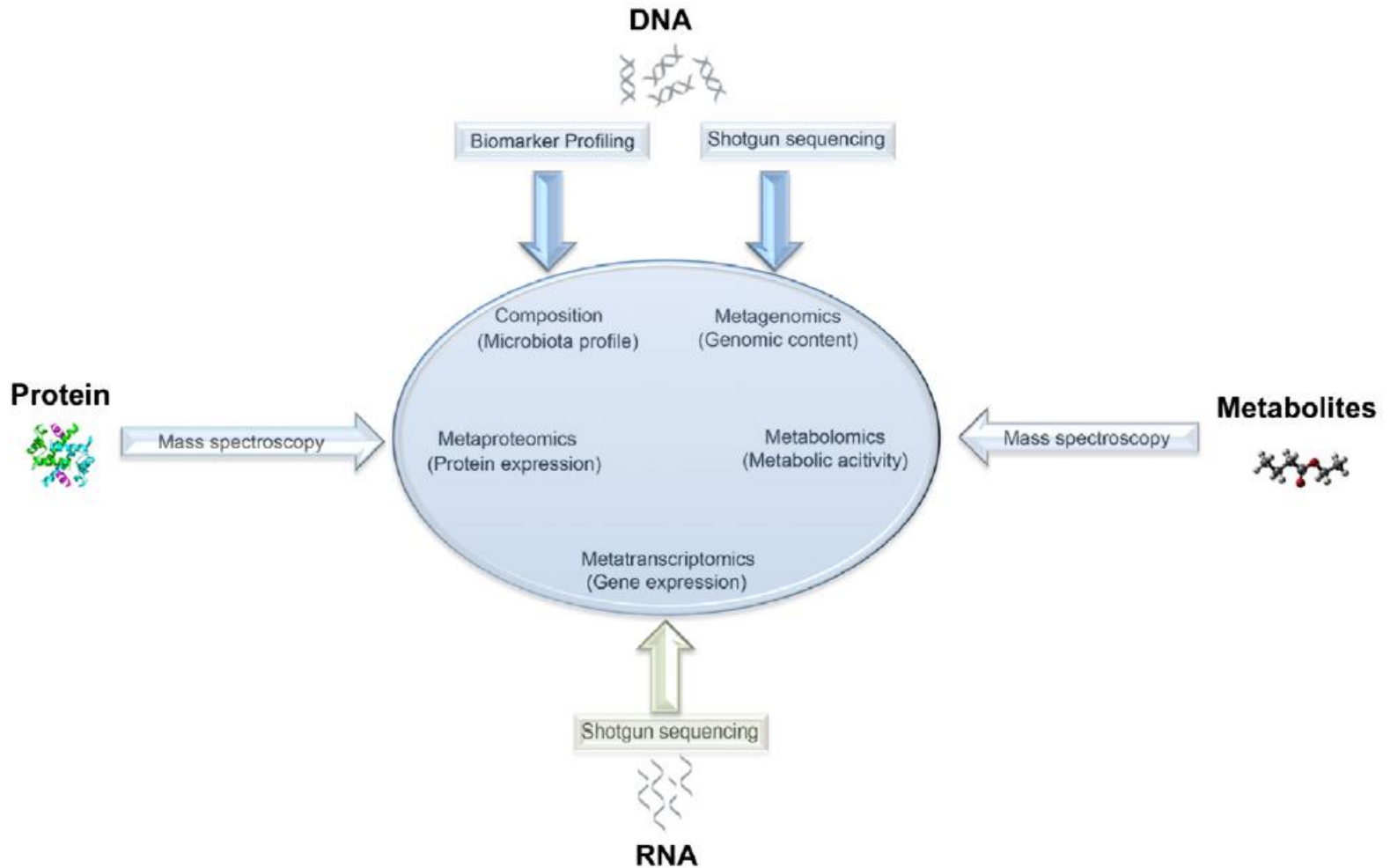


specific serological test



species-targeted PCR

Microbiome: Molecular Tools



Metagenome and Metagenomics

- **Metagenome**

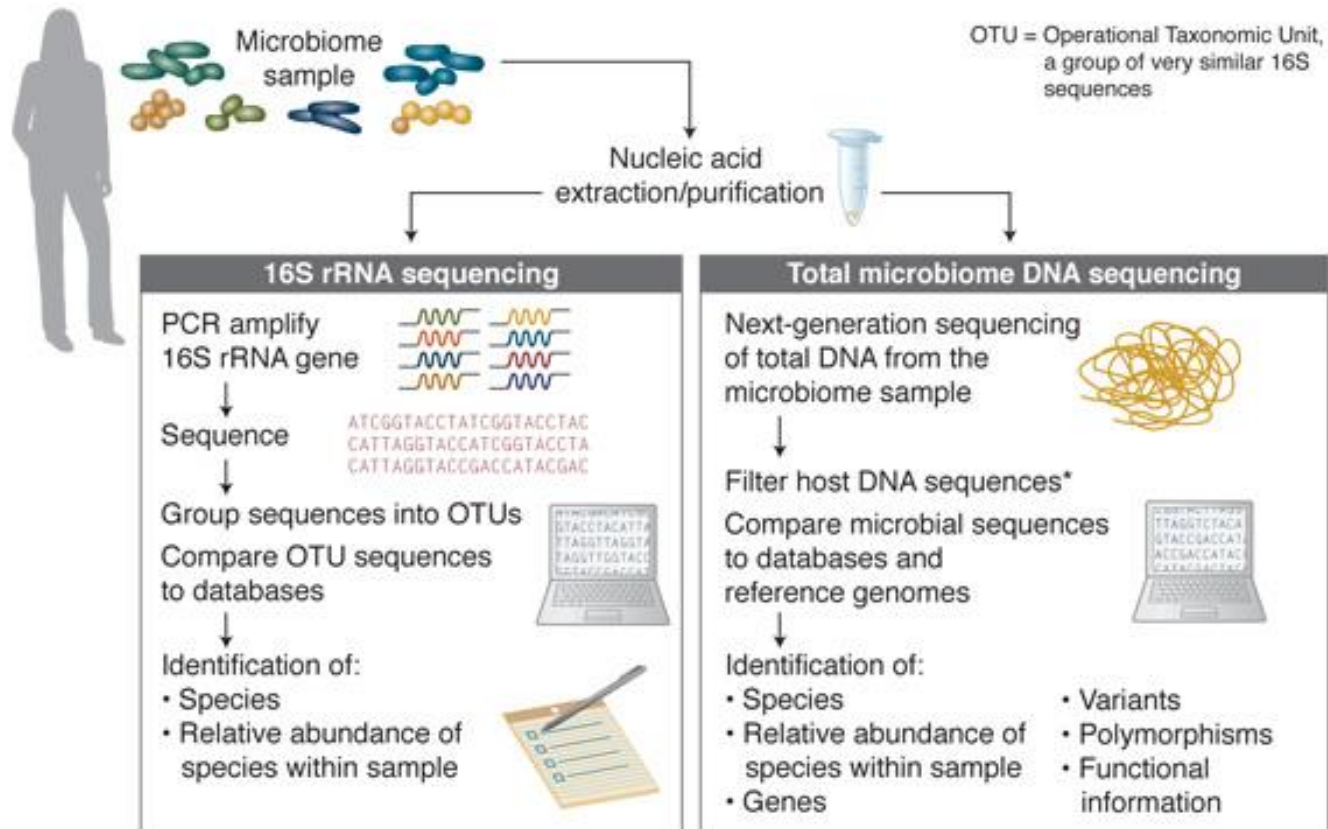
genetic material recovered directly from environmental samples

(Wikipedia)

- **Metagenomics**

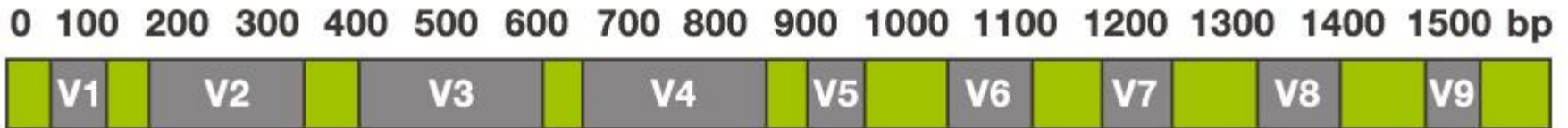
the study of metagenome

Marker Gene vs. Total (Shotgun) Analysis



16S ribosomal RNA

- Universal gene (1500 bp)
- Conserved and 9 variable regions
- Comparison of similarity for classification
- Operational Taxonomic Units (OTU) clustering and taxonomic profiling



CONSERVED REGIONS: unspecific applications

VARIABLE REGIONS: group or species-specific applications

Human Microbiome Project: 2008-2013

- 300 healthy individuals, across several different sites on the body : nasal, oral cavity, skin, GI tract, and urogenital tract

The screenshot displays the NIH Human Microbiome Project website. On the left is a sidebar with the HMP logo and navigation links for Current News, Publications, and Partner Resources. The main content area features a top navigation bar with categories like Overview, Reference Genomes, Microbiome Analysis, Health & Ethics, Resources, Outreach, and Data Browser. Below this is a welcome message and buttons for 'GET DATA' and 'GET TOOLS'. A featured section titled 'Areas of Interest' highlights 'Human Microbial Sampling' with a detailed description of the project's goals.

HMP
NIH HUMAN MICROBIOME PROJECT

Current News

- January 2015
Metagenome Analysis Workshop
March 3-6
- September 2014
IHMC 2015 from Mar. 31 to Apr. 2
- May 2014
Poster and Booth at ASM 2014

More News Items

Publications

- Microbial community assembly and metabolic function during mammalian c...
- HIV-induced immunosuppression is associated with colonization of the p...
- Comparative metabolomics in vegans and omnivores reveal constraints on...

More Publications

Partner Resources

- NIH Common Fund
- NCBI HMP Data Repository

OVERVIEW REFERENCE GENOMES MICROBIOME ANALYSIS HEALTH & ETHICS RESOURCES OUTREACH DATA BROWSER

Welcome to the Data Analysis and Coordination Center (DACC) for the National Institutes of Health (NIH) Common Fund supported Human Microbiome Project (HMP). This site is the central repository for all HMP data. The aim of the HMP is to characterize microbial communities found at multiple human body sites and to look for correlations between changes in the microbiome and human health. More information can be found in the menus above and on the NIH Common Fund site.

GET DATA

GET TOOLS

Areas of Interest

Human Microbial Sampling
16S RNA and whole metagenome sequencing of samples collected from 300 healthy human participants, to characterize complexity of microbial communities at individual body sites and to provide insights into functions performed by the human microbiome...

+ DACC Member Organizations

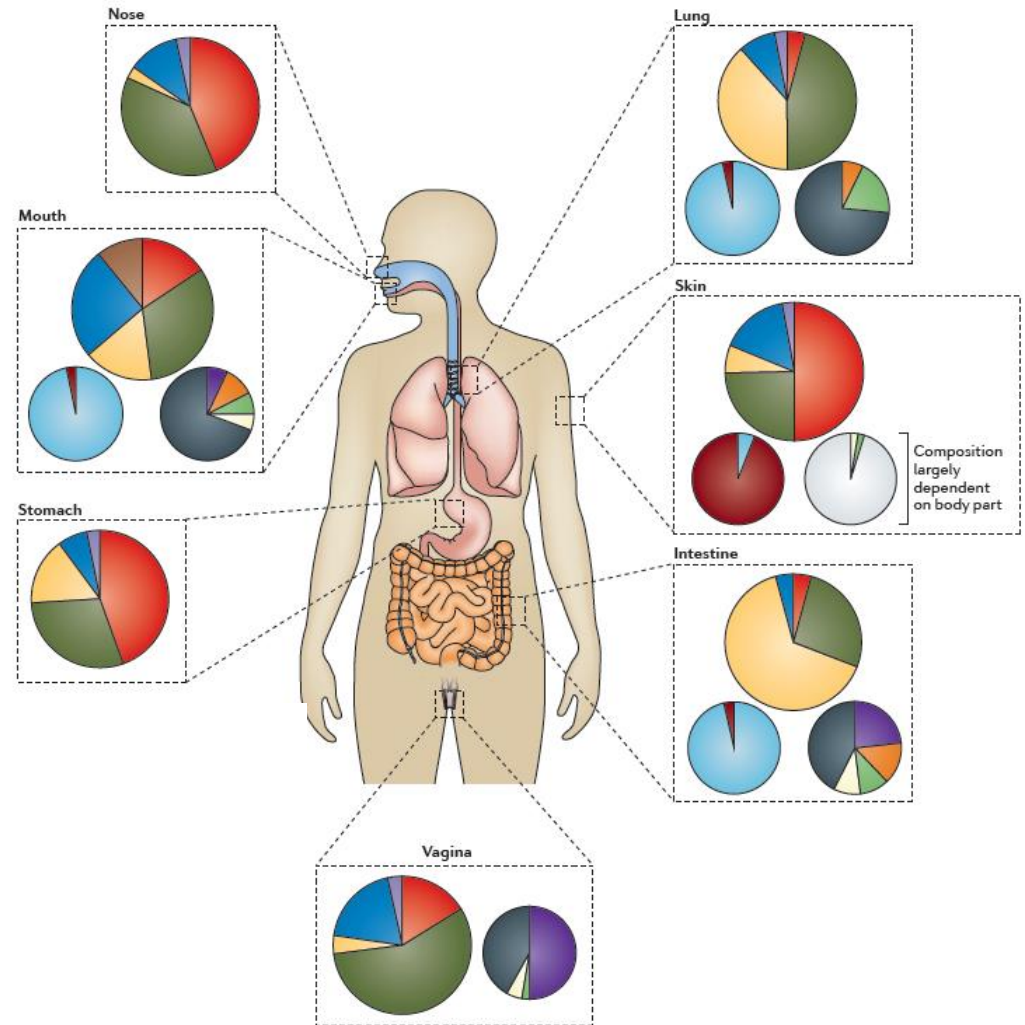
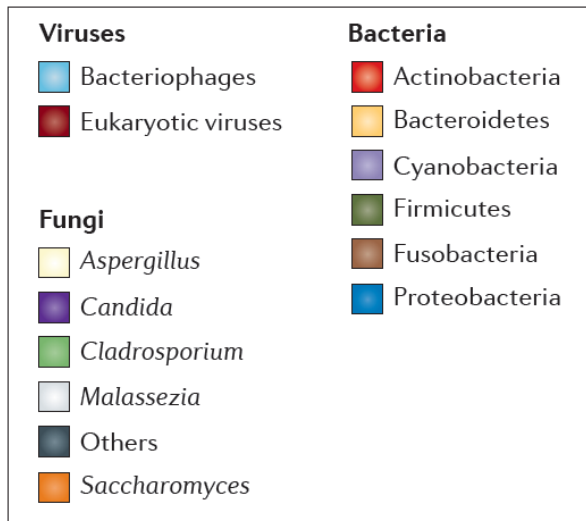
+ Related Sites

HMP Stage 2: from 2014-

correlations between changes in the microbiome and health

- Project 1: Pregnancy & Preterm Birth
- Project 2: Inflammatory Bowel Disease
- Project 3: Prediabetes

Microbiome Composition: Habitat dependent



Microbiome: Roles

- They do Nothing? or Something good or bad?
- Gut microbiome is involved in
 - absorption of nutrients
 - synthesis of vitamins
 - metabolism of xenobiotics
 - Immune modulation
- Site specific roles

Lung Microbiome

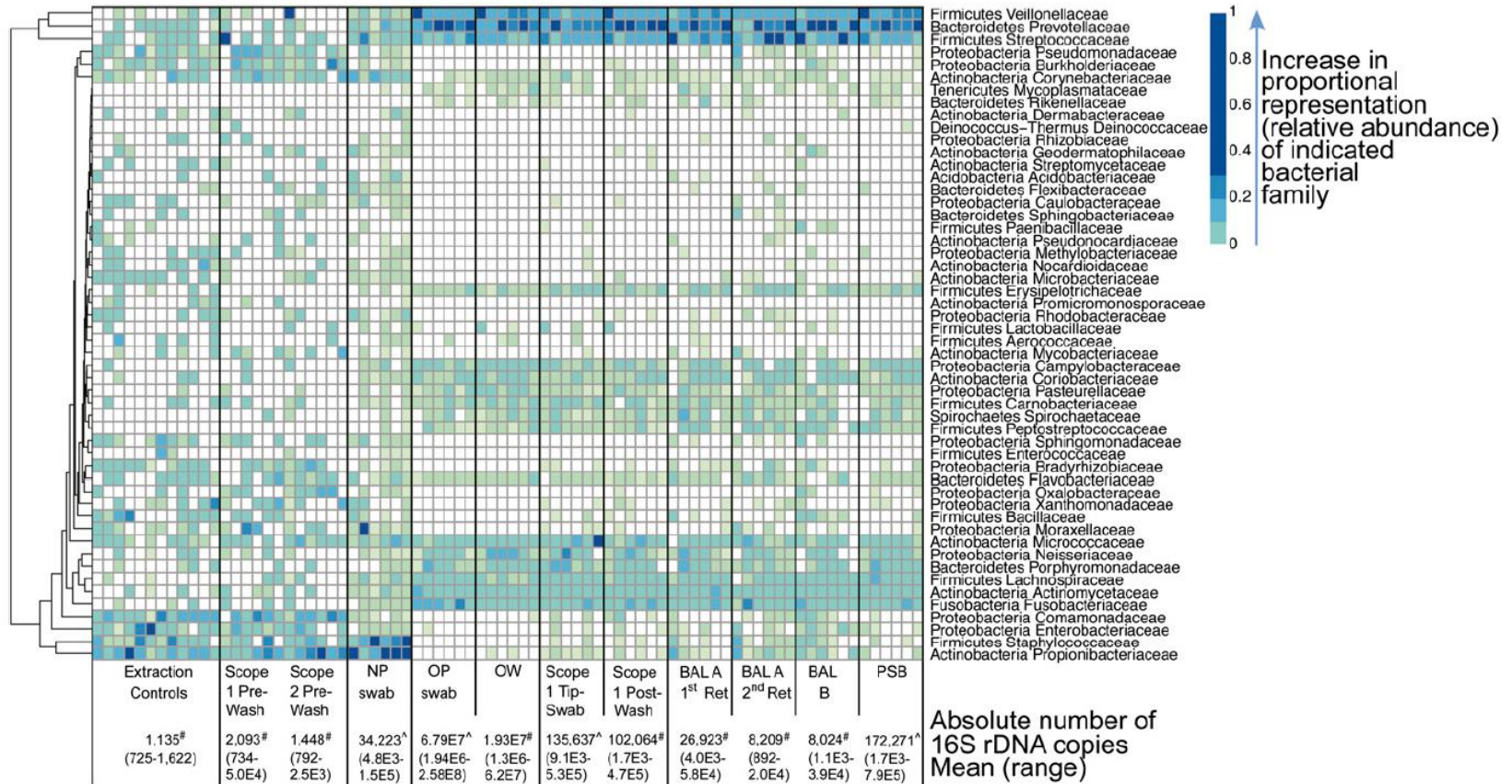
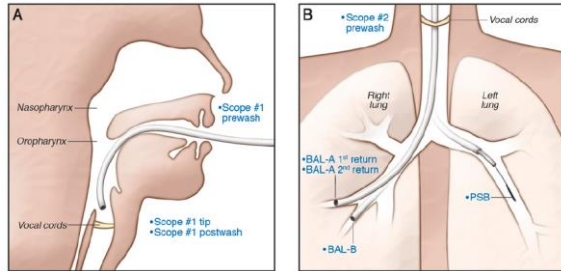
- What is there?
- What is the physiological role?
- Association with diseases? Then how?



Lung Microbiome: versus Gut

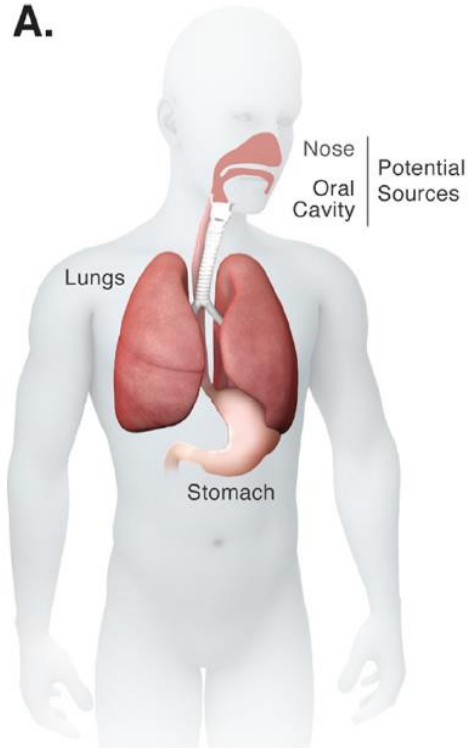
- Lower biomass
- Less diverse
- Risk of contamination from the upper airway during sampling

Lung Microbiome: in healthy subjects

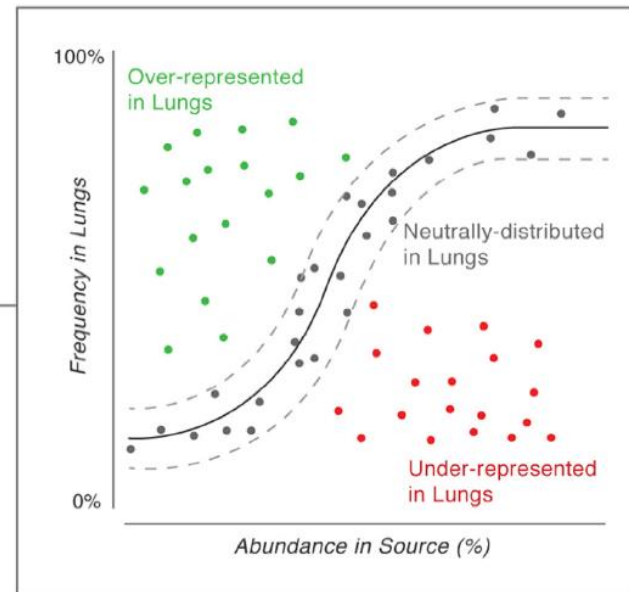
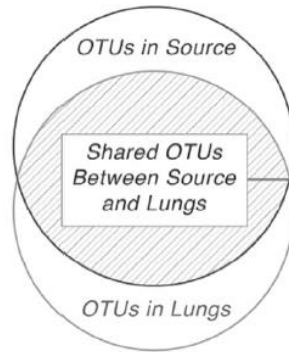


Lung Microbiome: Possible Origin

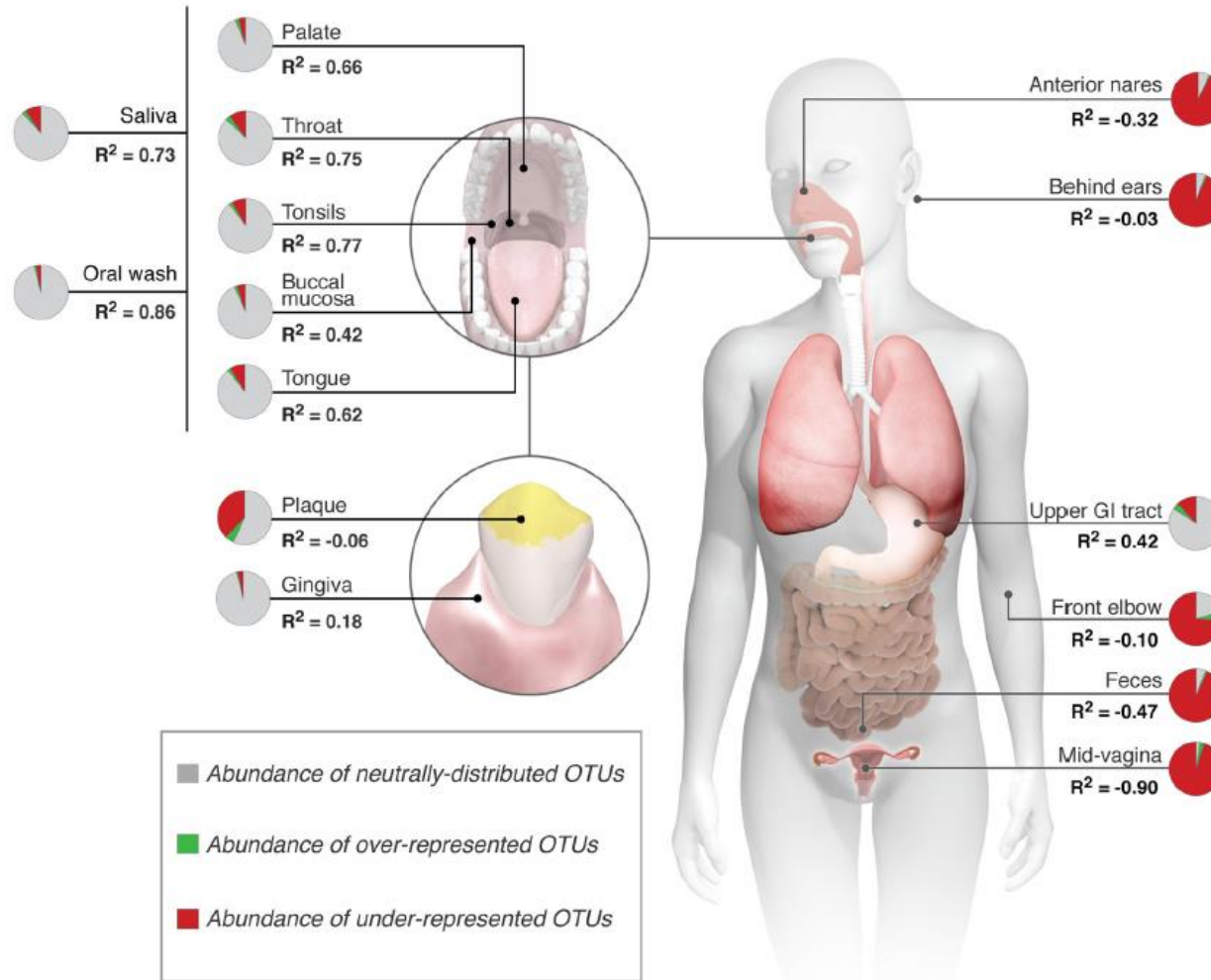
A.



B.



Lung Microbiome: Possible Origin



Lung Microbiome: In healthy subjects

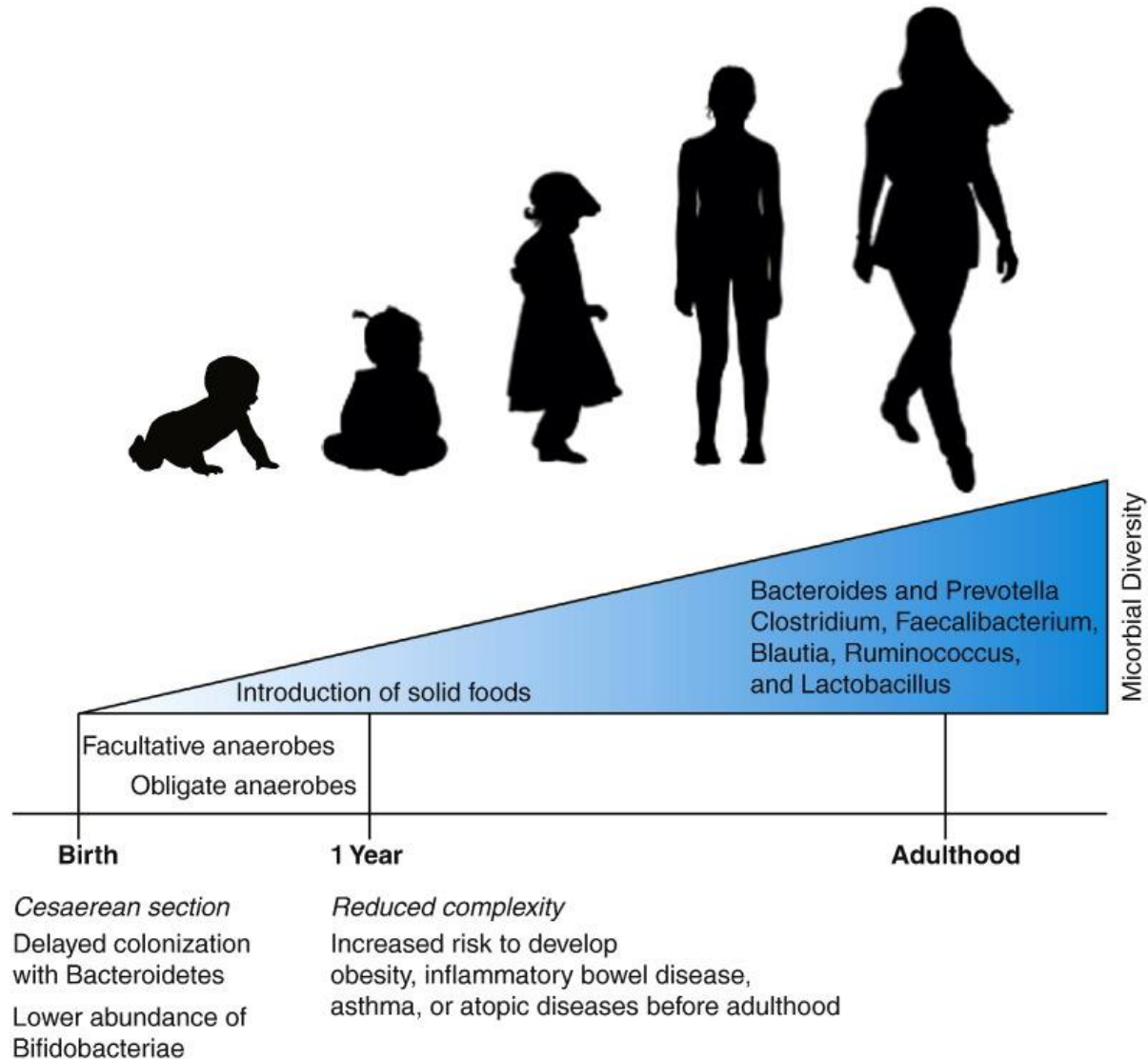
- Phylum level by abundance

Phylum (문)	Bacteroidetes	Firmicutes	Proteobacteria
Genus (속)	<ul style="list-style-type: none">• Prevotella• Bacteroides	<ul style="list-style-type: none">• Veillonella• Streptococcus• Staphylococcus	<ul style="list-style-type: none">• Pseudomonas• Haemophilus• Moraxella• Neisseria• Acinetobacter• Escherichia

Microbiome: possible affecting factors

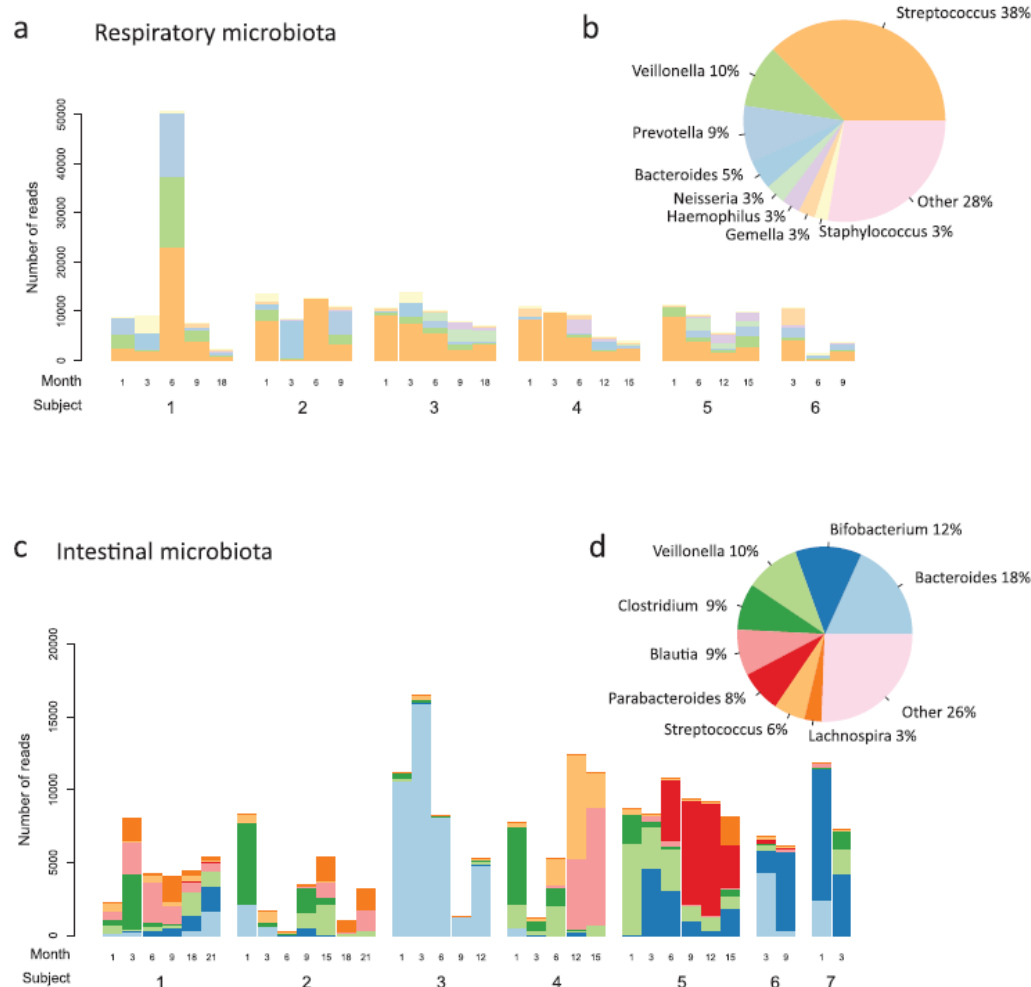
- Age
- Ethnicity
- Diet
- Smoking
- Mode of birth (delivery)
- Antibiotics and probiotics

Gut Microbiome: Changes & Diversity

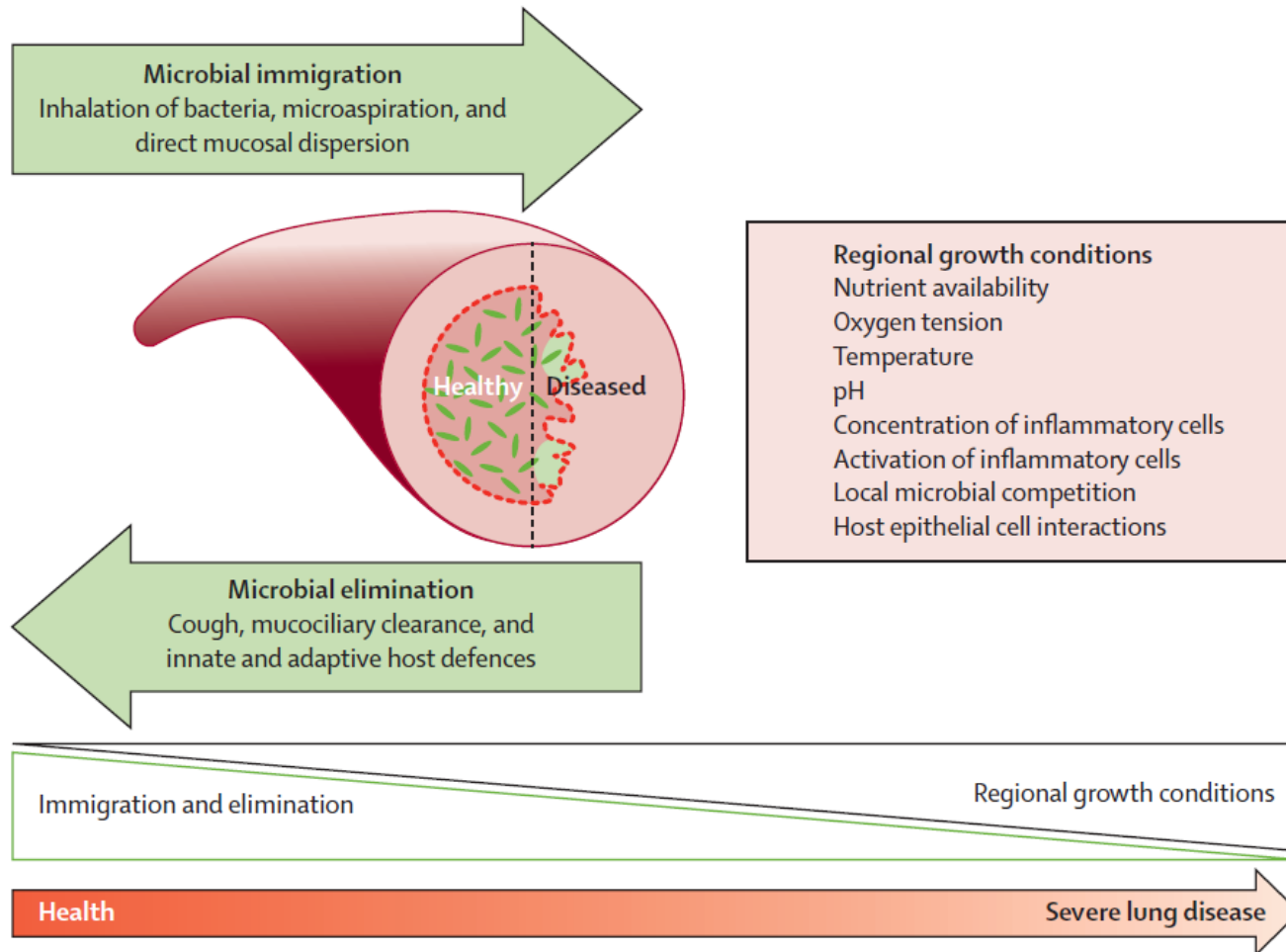


Microbiome: Stability over Time

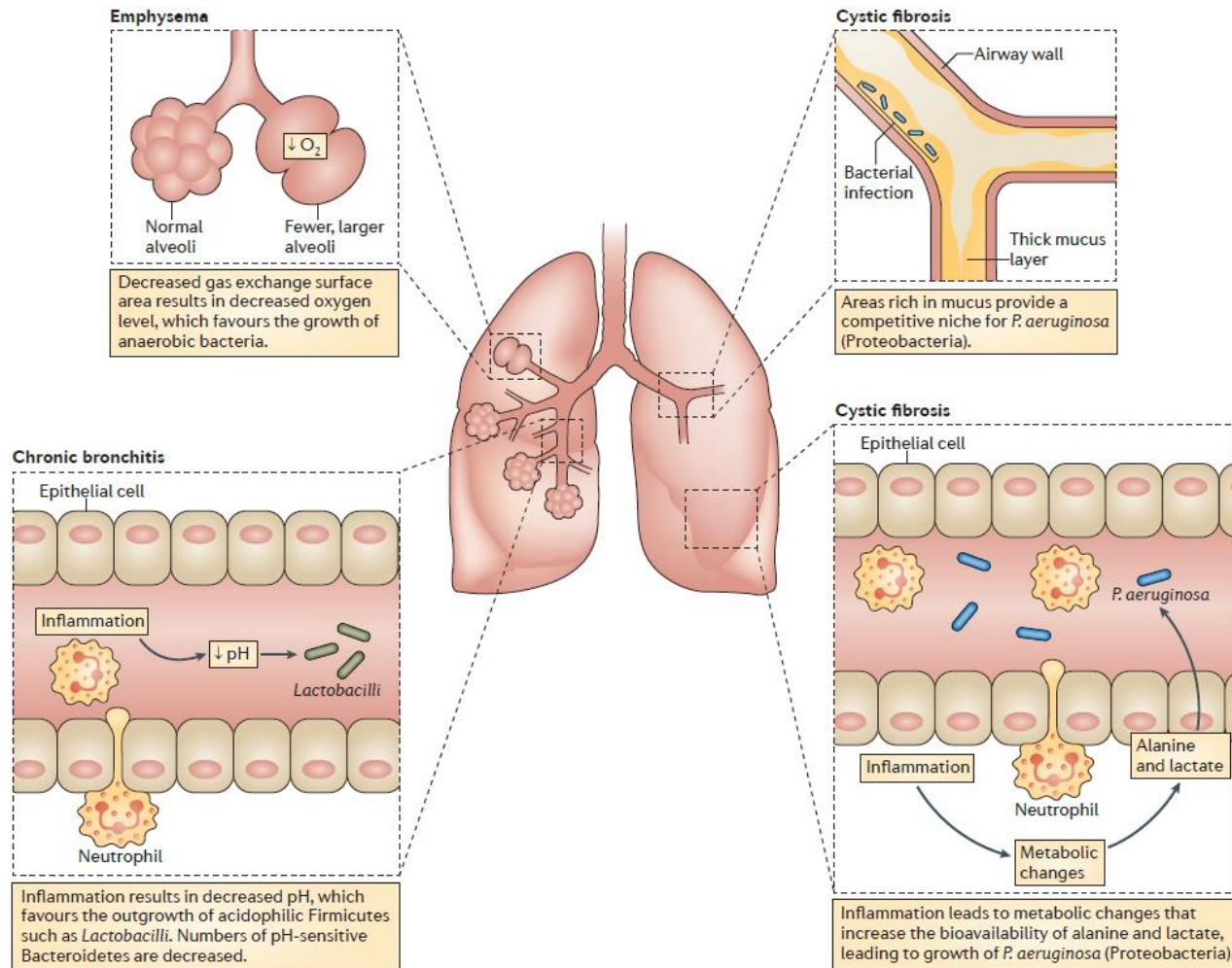
- Serial Analysis of the Gut and Respiratory Microbiome in Cystic Fibrosis in Infancy



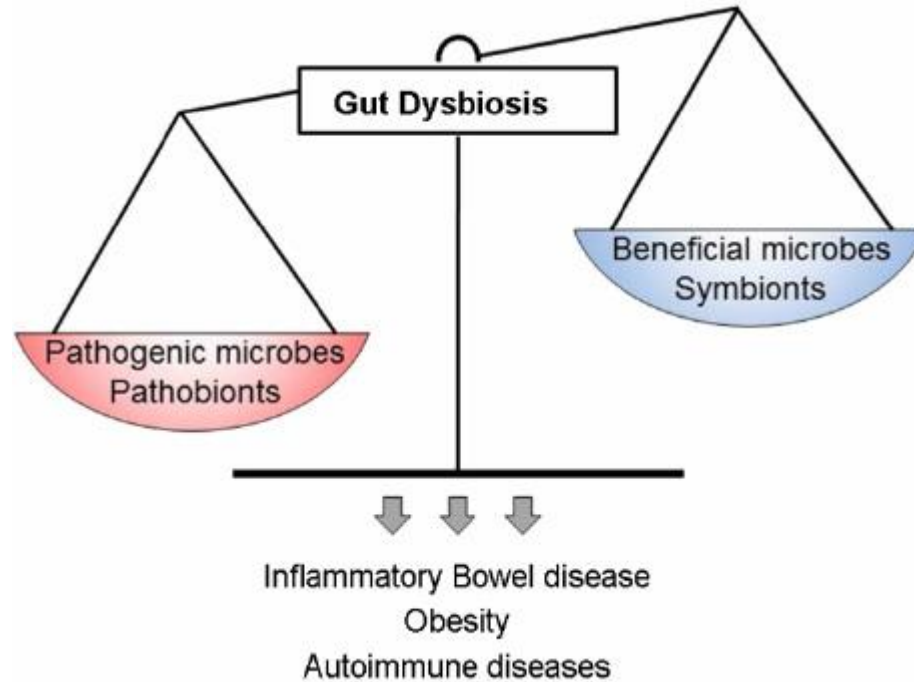
Lung Microbiome: 3 Major Determinants



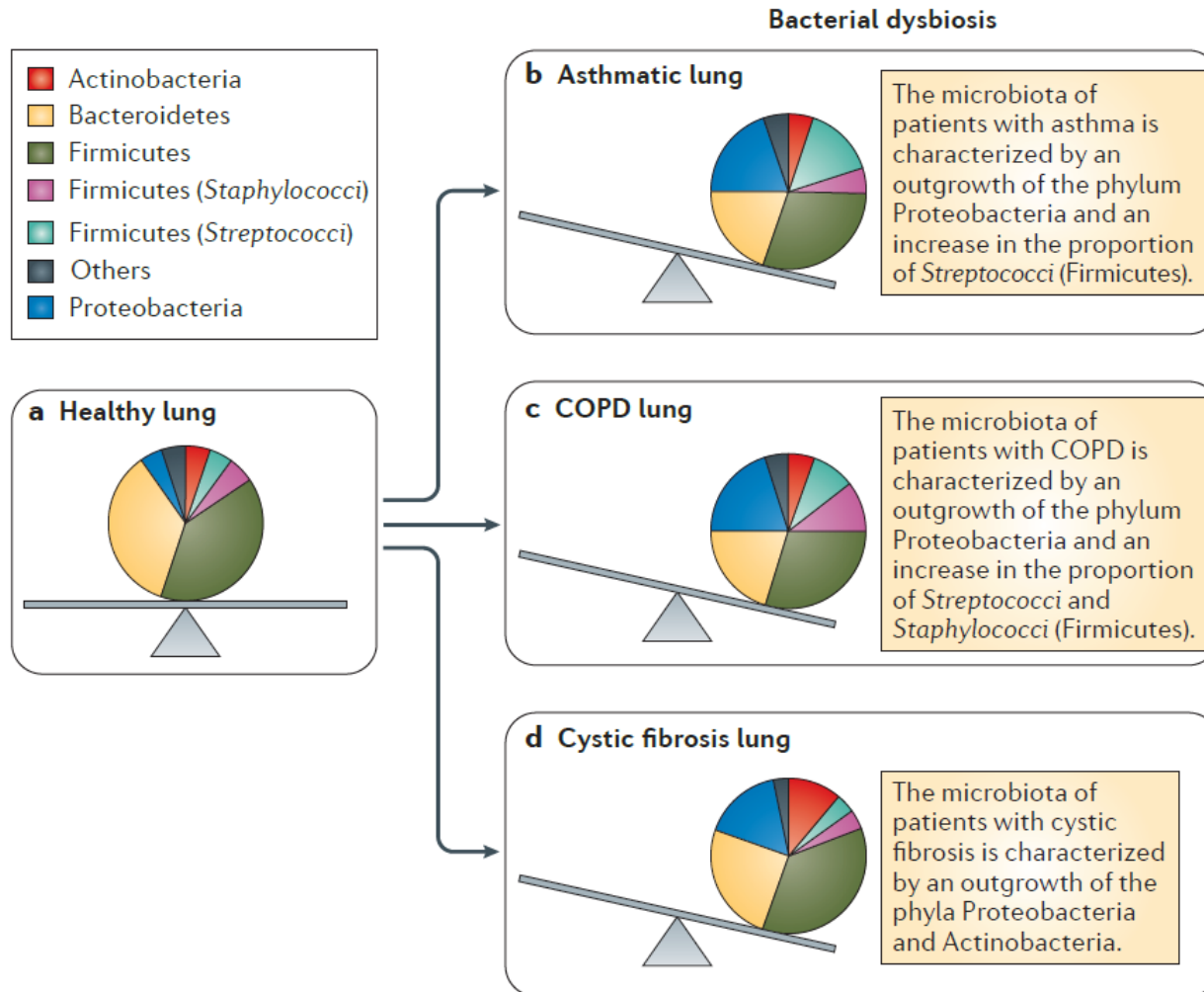
Lung Microbiome: affected by local sites



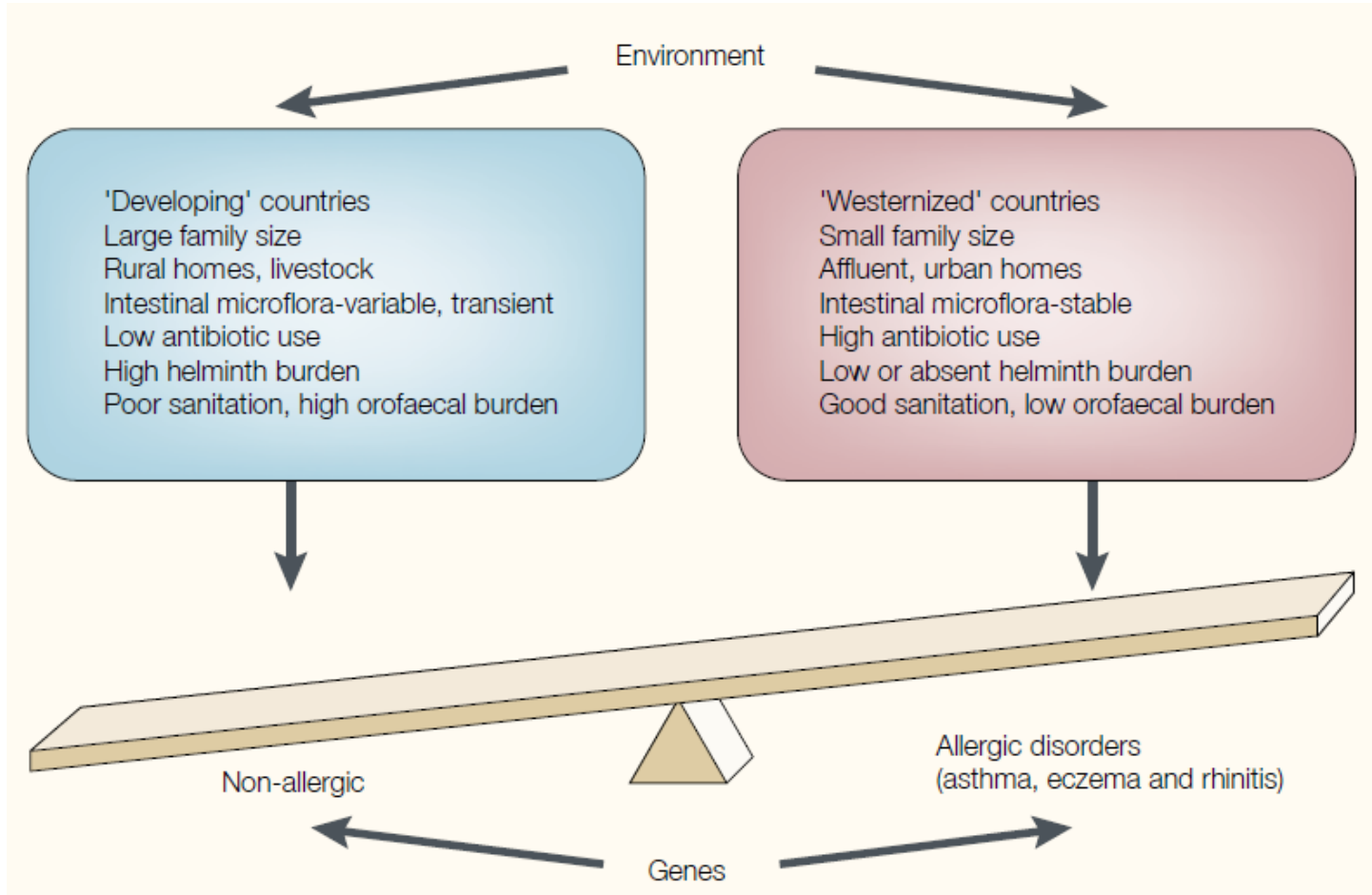
Gut Dysbiosis and Diseases



Lung Microbiome: dysbiosis and diseases

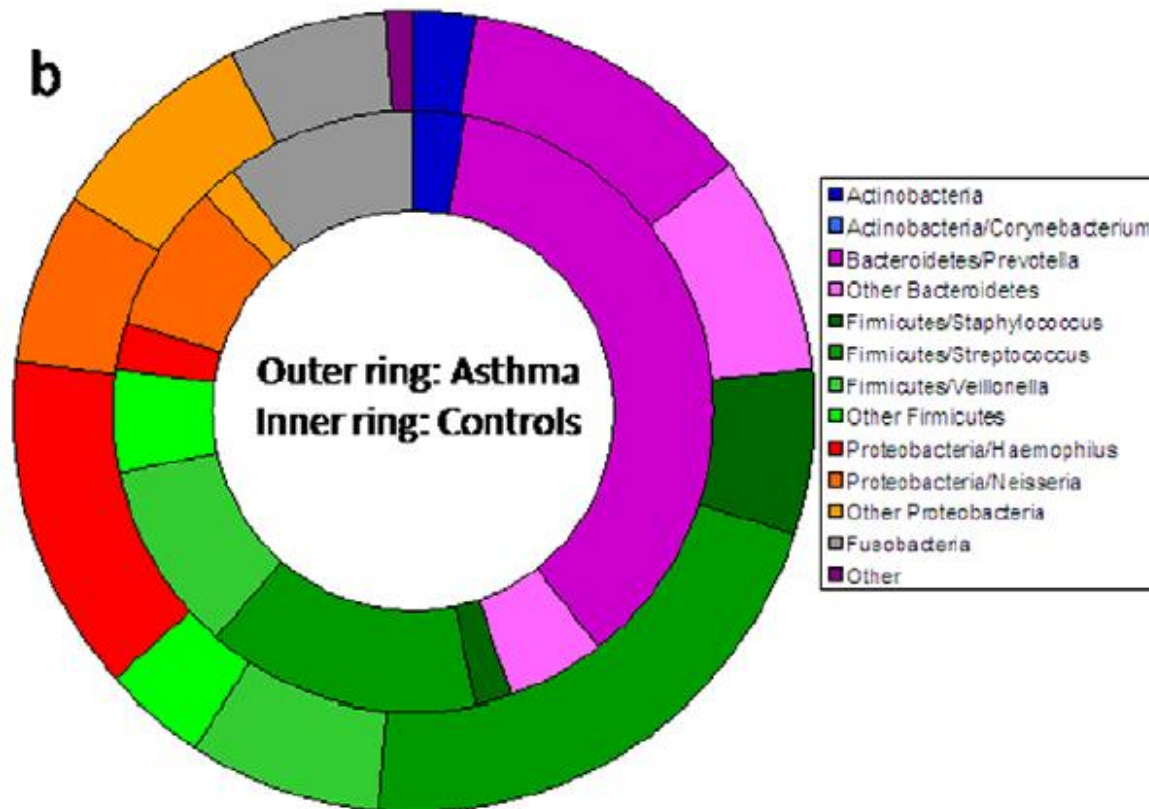


Microbiome may explain Hygiene Hypothesis



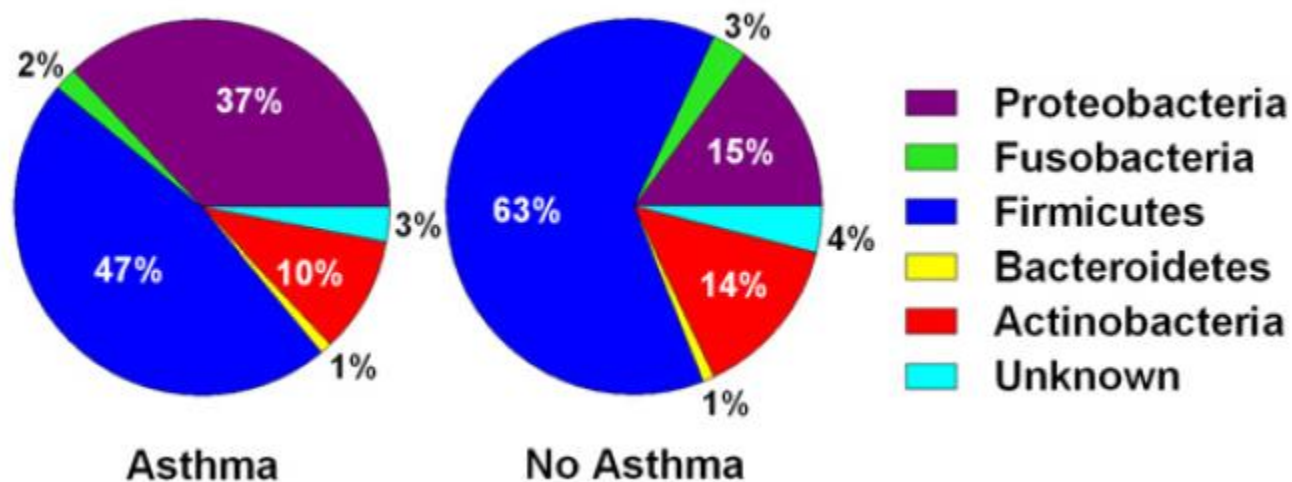
Asthma Microbiome: BAL from Children

- broncho-alveolar lavage (BAL) in children with difficult asthma and controls
- Proteobacteria, particularly *Haemophilus* spp., were much more frequent.



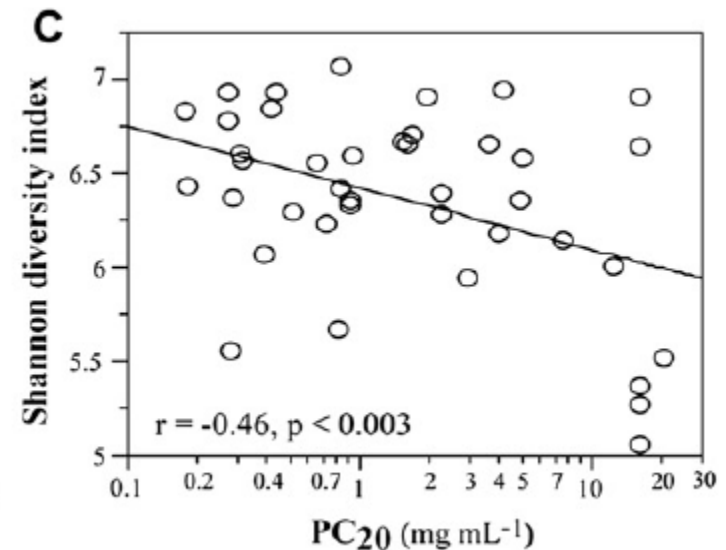
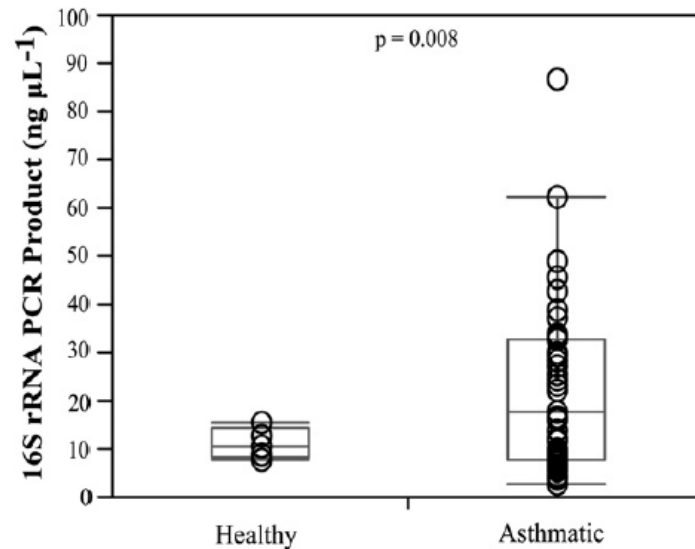
Asthma Microbiome: Sputum from adults

- Induced sputum from 10 adults with mild asthma (8/10, no ICS use) and 10 controls
- Confirmation of greater prevalence of Proteobacteria



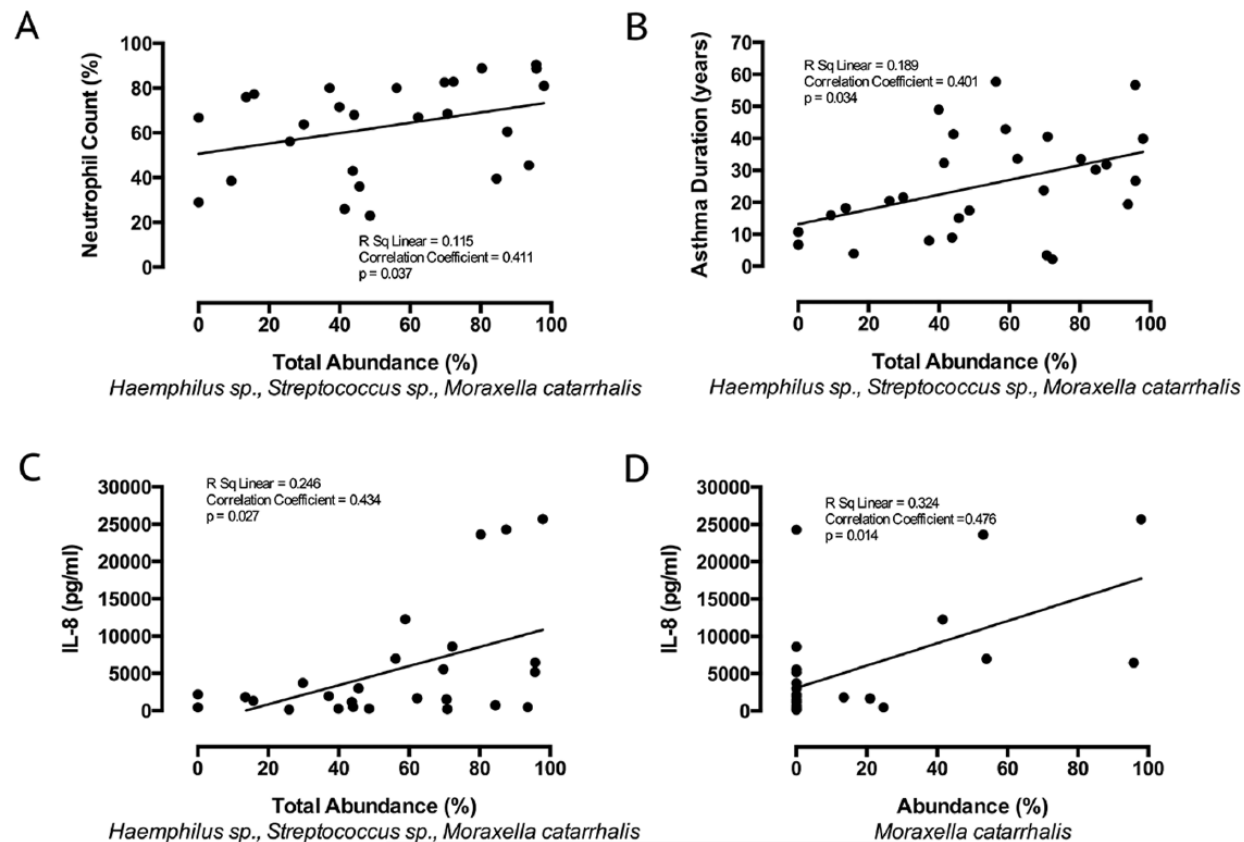
Asthma Microbiome: association with AHR

- 16S ribosomal RNA amplicon concentrations (a proxy for bacterial burden) higher in asthma
- bacterial diversity were significantly higher among asthmatic patients.



Asthma Microbiome: association with phenotypes

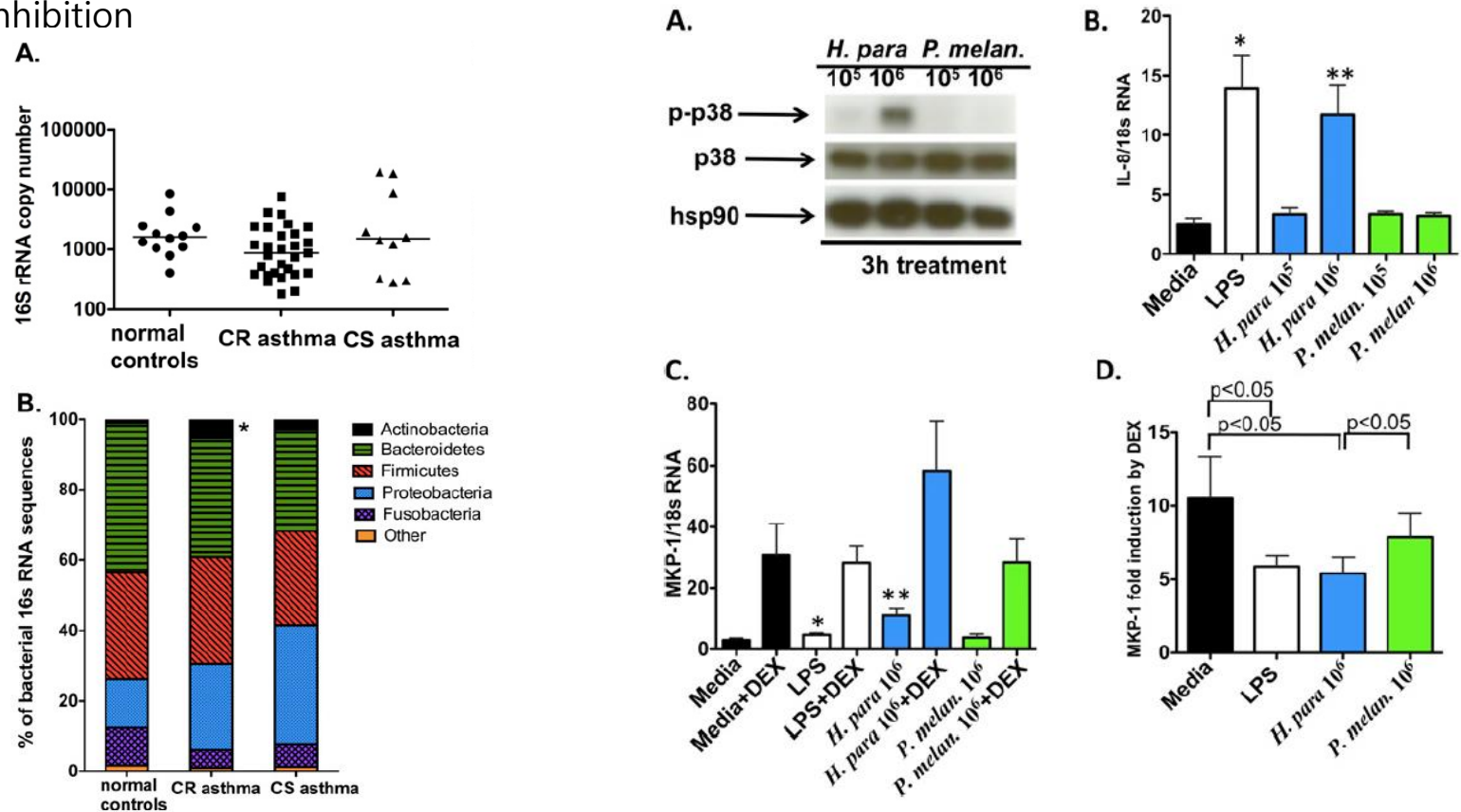
- Sputum from 28 adult patients with treatment-resistant asthma
- relative abundance of *M. catarrhalis*, *Haemophilus* or *Streptococcus* correlated with longer asthma duration, worse lung function and higher sputum neutrophil counts and IL-8 concentrations.



Asthma Microbiome

: association with oral steroid response

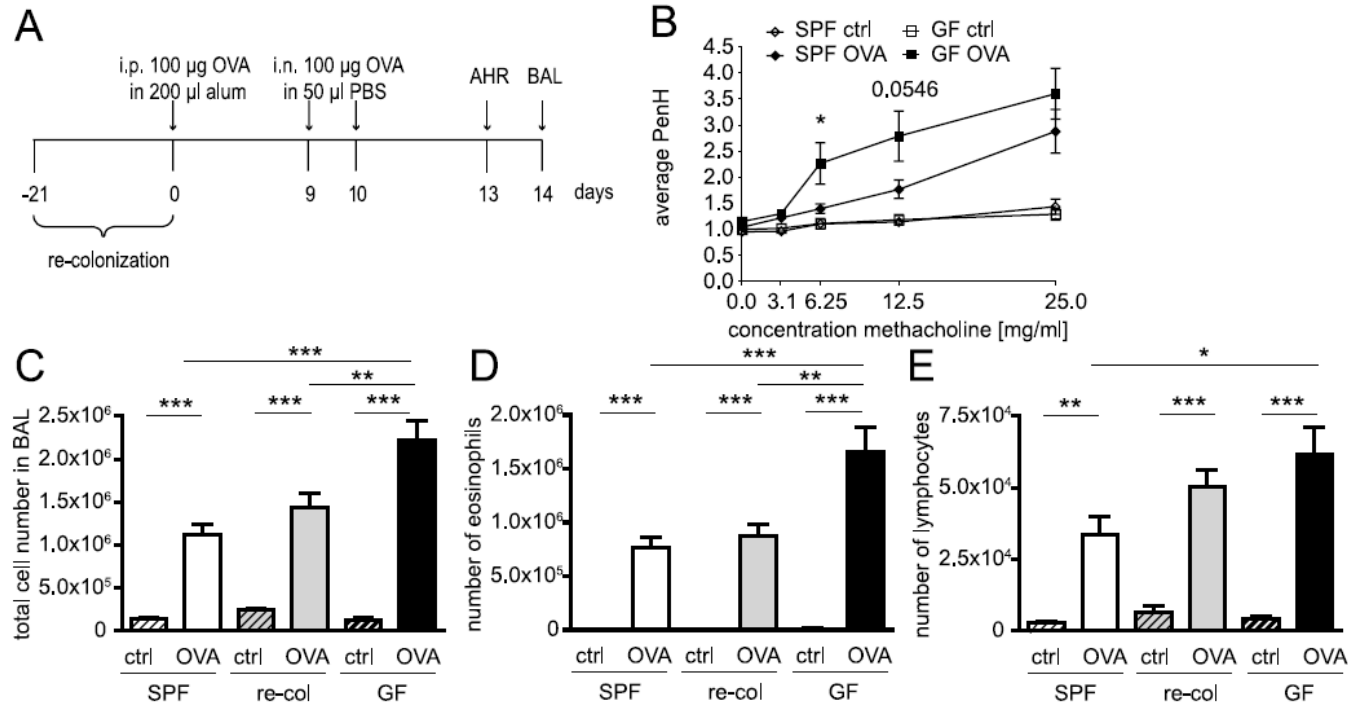
- BAL from 39 asthmatics and 12 controls
- No significant response in phylum level between CR and CS, while subset of patients with CR have an increased prevalence of *Haemophilus parainfluenzae*
- PBMC culture with *H. parainfluenzae* led to their activation and resistance to corticosteroid inhibition



Mice Experiments

: Allergic Airway Inflammation influenced by Microbial Colonization

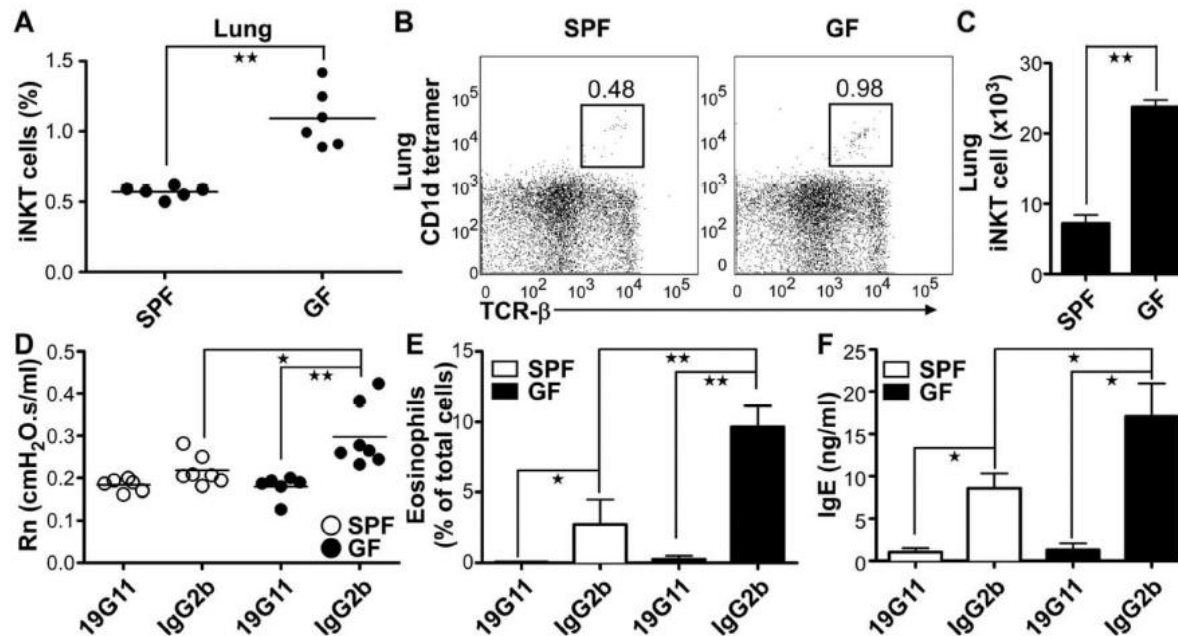
- lack of microbial colonization (Germ Free, GF) leads to increased allergic airway inflammation
- recolonization before allergen exposure is able to rescue the phenotype



Mice Experiments

: microbial exposure in early life has effects on iNKT cell function

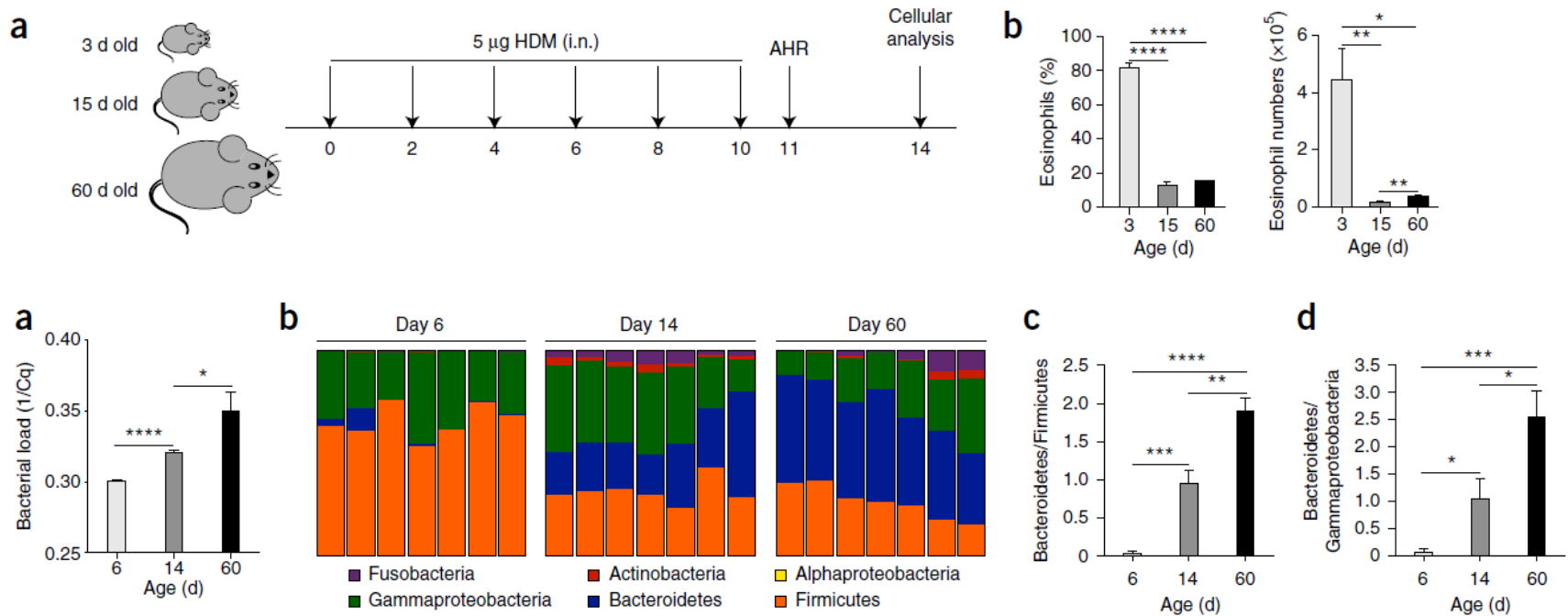
- Germ-free mice, which have exaggerated allergic responses, maintain a population of iNKT cells in the lungs that perpetuate the allergic responses.
- iNKT cell bias was only rectified if the mice were recolonized with a normal microbiota within the first 10 days after birth



Mice Experiments

: Lung microbiota promotes tolerance to allergens in neonate via PD-L1

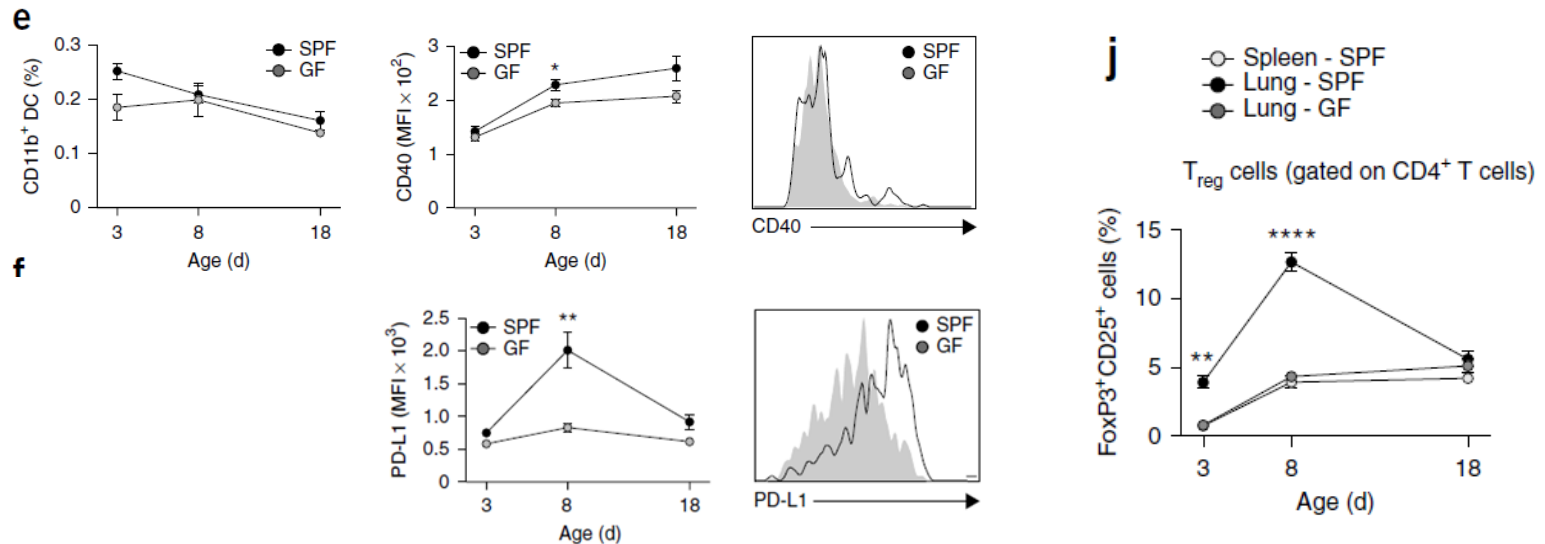
- development-related changes in lung bacterial load and community composition were associated with decreased airway responses to aeroallergen exposure



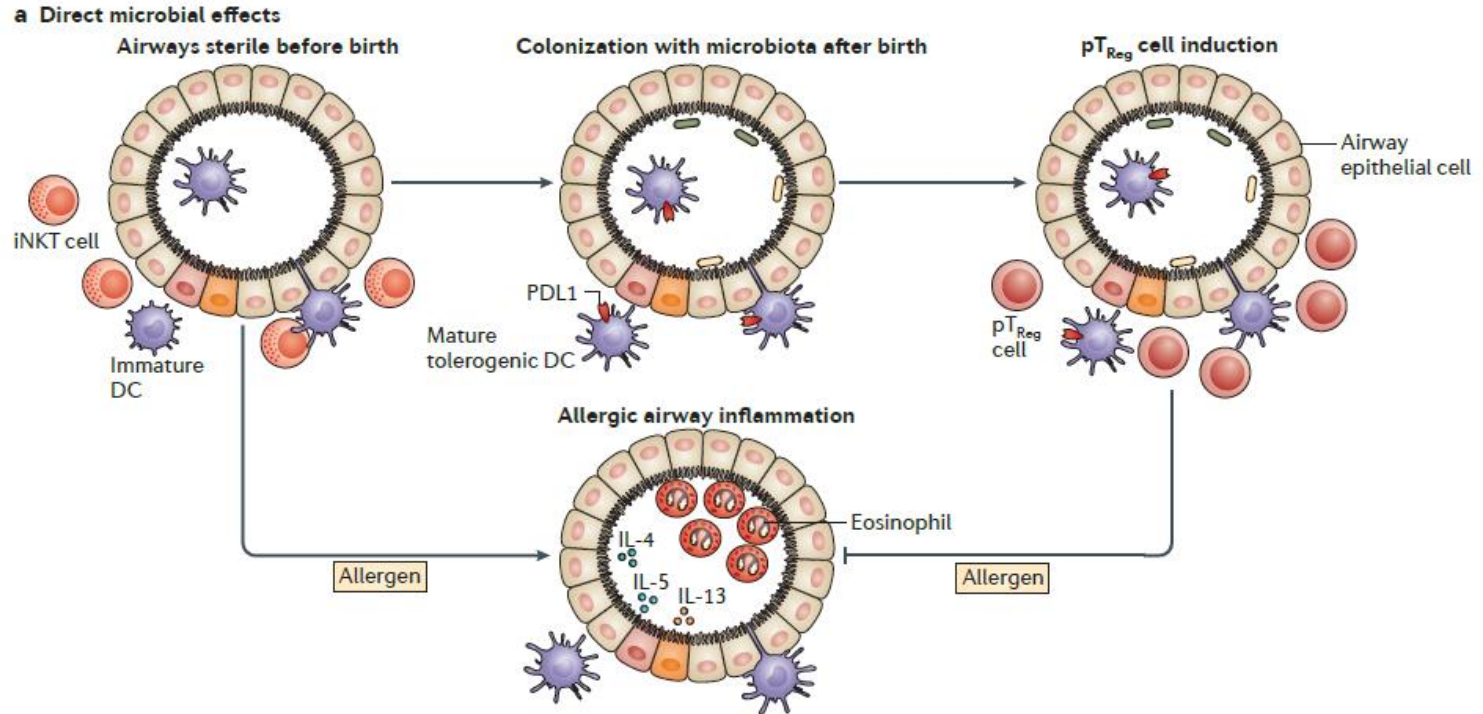
Mice Experiments

: Lung microbiota promotes tolerance to allergens in neonate via PD-L1

- tolerance was not associated with the existing presence of high numbers of regulatory T (Treg) cells in the lung at birth
- Tolerance induction with the development of a different Treg cell subset that seemed to require microbial presence during a critical early window after birth.



Lung Microbiome: Immune Modulating Effects

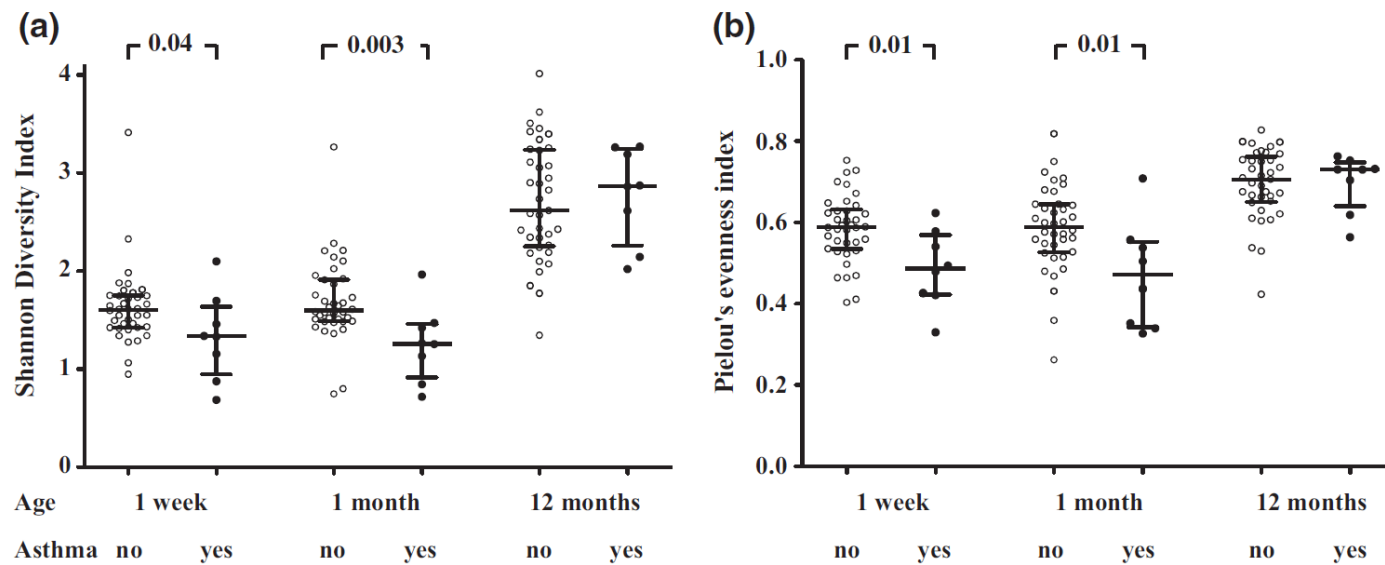


Gut Microbiome offers clues to Asthma



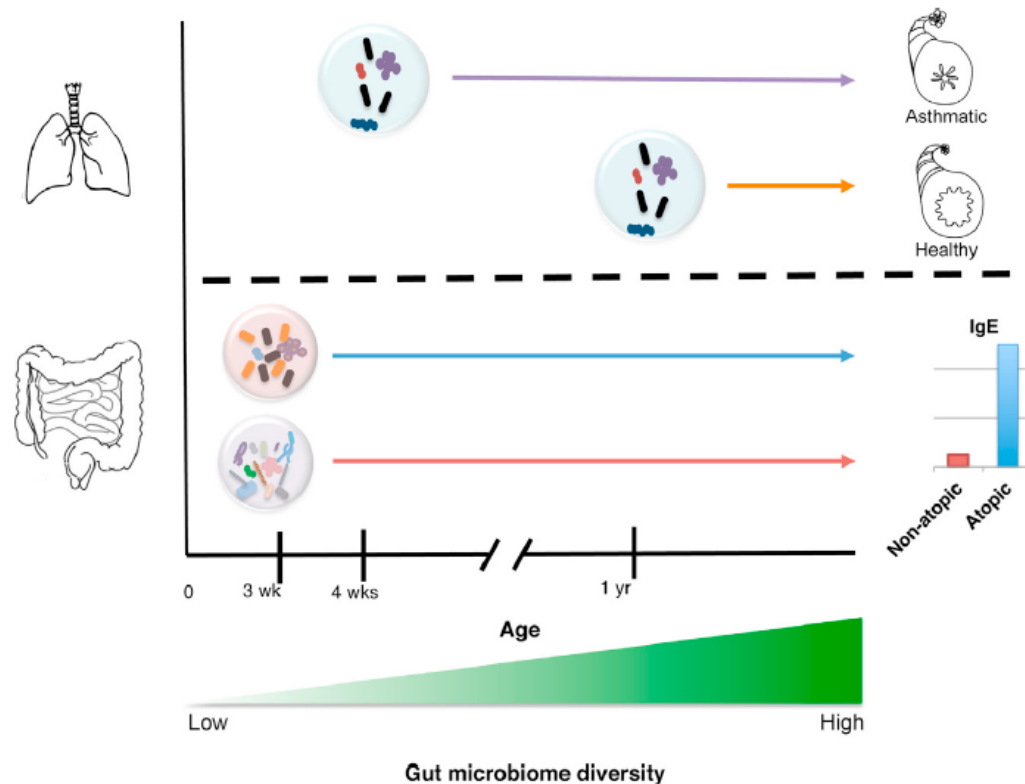
Asthma: decreased gut microbiome diversity

- children with asthma (at 7 years of age) have a lower intestinal bacterial diversity in the first month after birth



Very-Early-Life Exposures Influence Asthma and Allergy Development

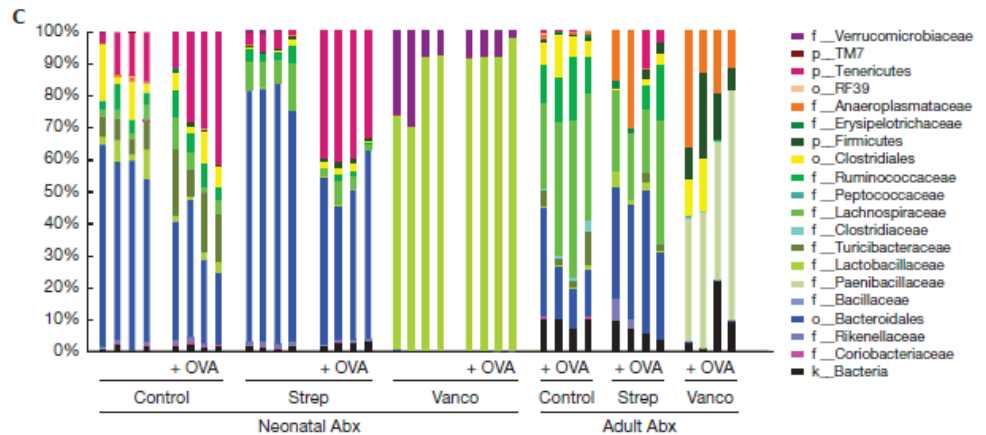
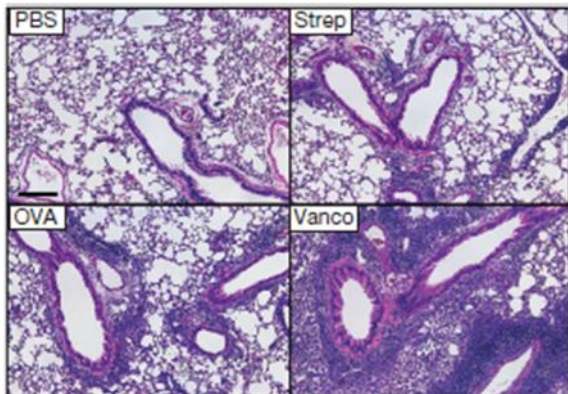
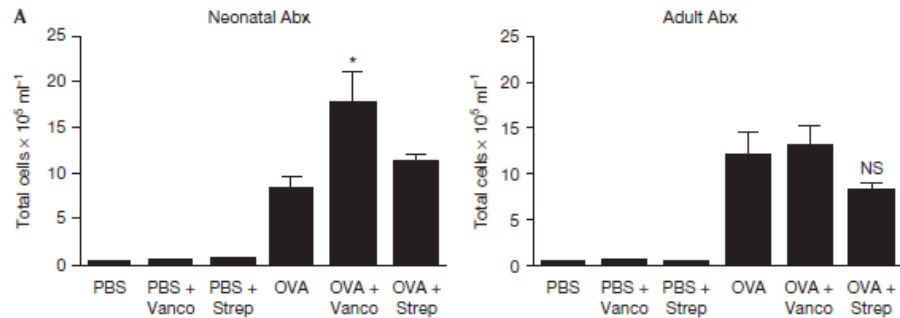
- Intestinal microbial diversity during early-life colonization shapes long-term IgE levels



Mice Experiments

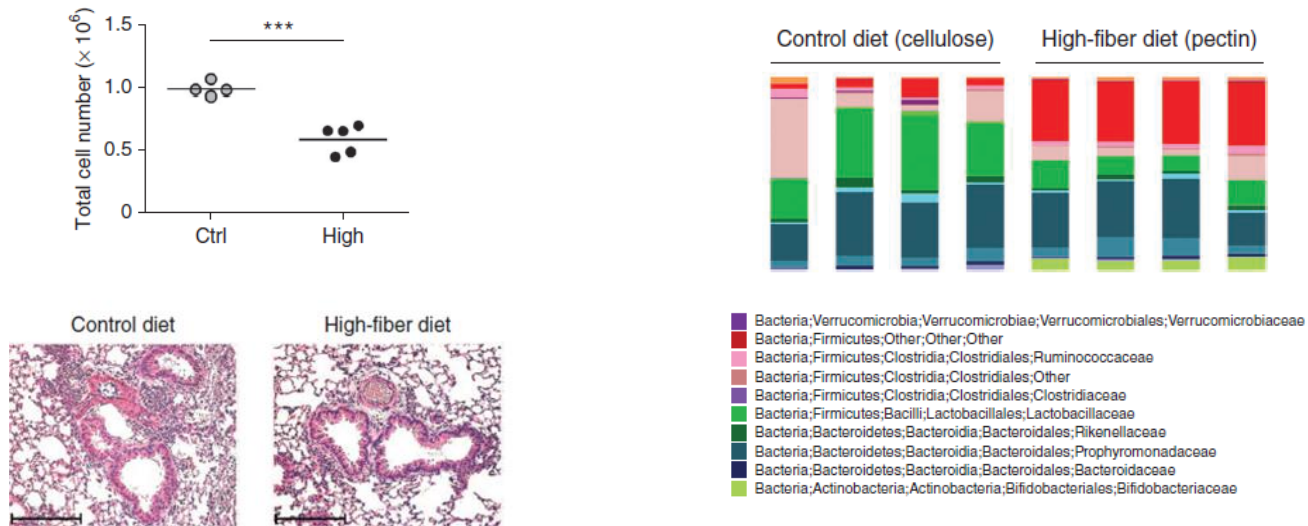
: Early life antibiotic-driven changes in microbiota affects asthma

- Vancomycin in neonates, not in adults, affected asthma susceptibility
- reduced microbial diversity, shifted the composition of the bacterial population

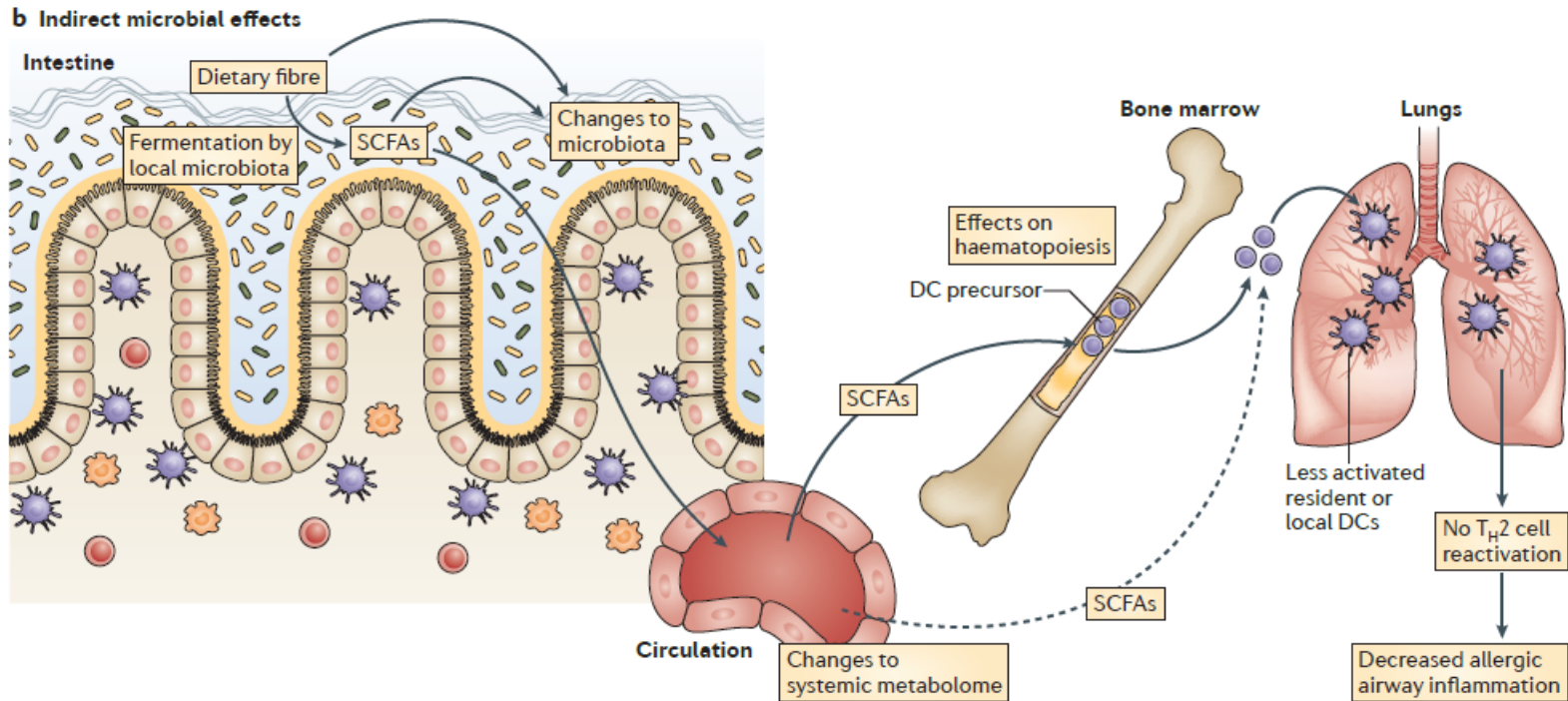


Diet affects Asthma by changing Gut Microbiome

- Mice with high fiber diet were protected against allergic lung inflammation with gut microbiota change and increased circulating levels of SCFAs



Gut Microbiome: Link between diet and asthma?



Microbiome and Asthma: Complex Interactions

