

Novità nella ricerca sul microbiota intestinale umano e la modulazione con i probiotici

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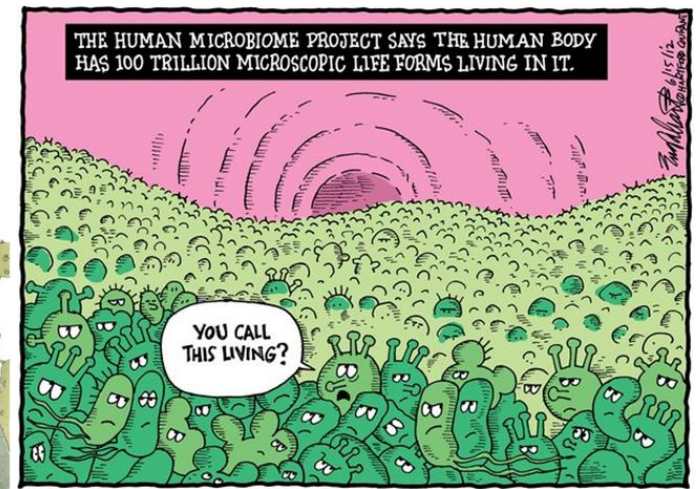
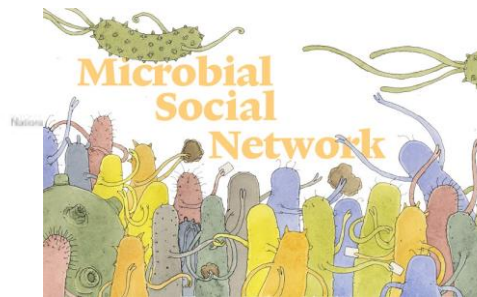
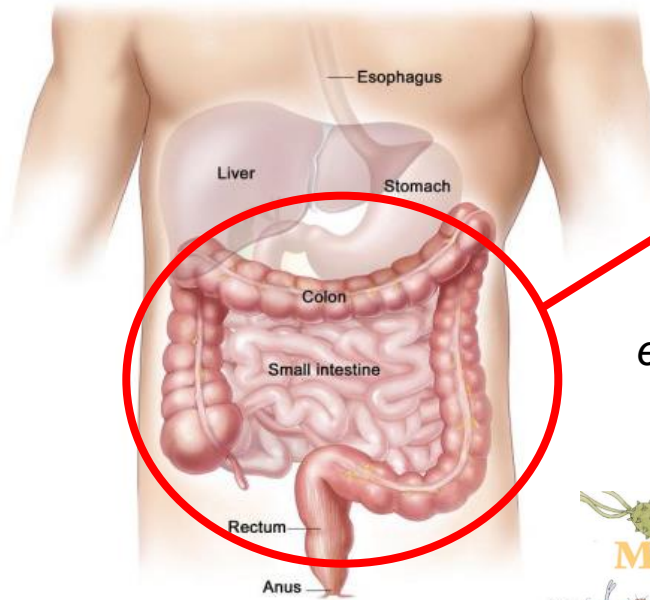
THE HUMAN INTESTINAL MICROBIOTA

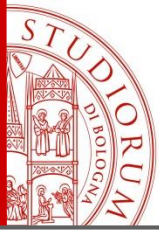
10^{13} – 10^{14} habits our body and the great majority of these microorganisms is hidden in the gastrointestinal tract

- 10^{12} CFU/g
- up to 1.5 kg

the most dense bacterial ecosystem on our planet

organized in a ecosystem of highly interconnected microbes





GIT MICROBIOTA: THE MOST COMPLEX ECOSYSTEM



Human organism contains

10^{13} cells = 10.000 billion

and harbors a microbial population of

10^{14} cells = 100.000 billion



1 human cell → 10 microbial cells



1 human gene → 150 microbial genes

we are 90% bacteria (10^{13} – 10^{14})

METAORGANISM

result of millennia of co-evolution

with an incredible number of symbiont microbial cells living in our body

HOW DO WE KNOW THIS?

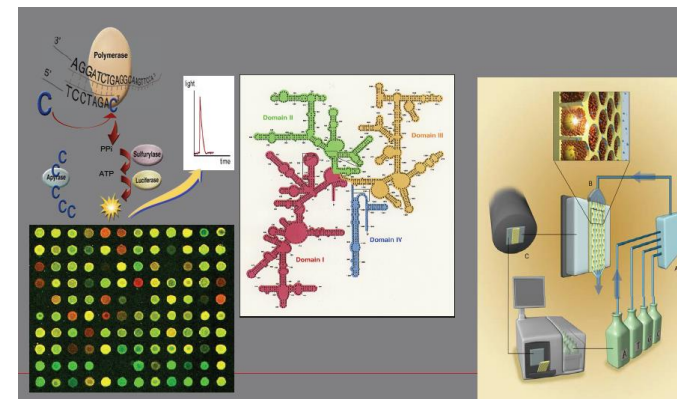
**Culture-based methods allow to recover
20-30% of total microscopic counts**

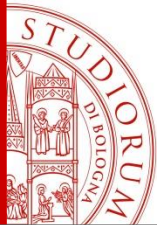


MOSTLY UNCULTURED!

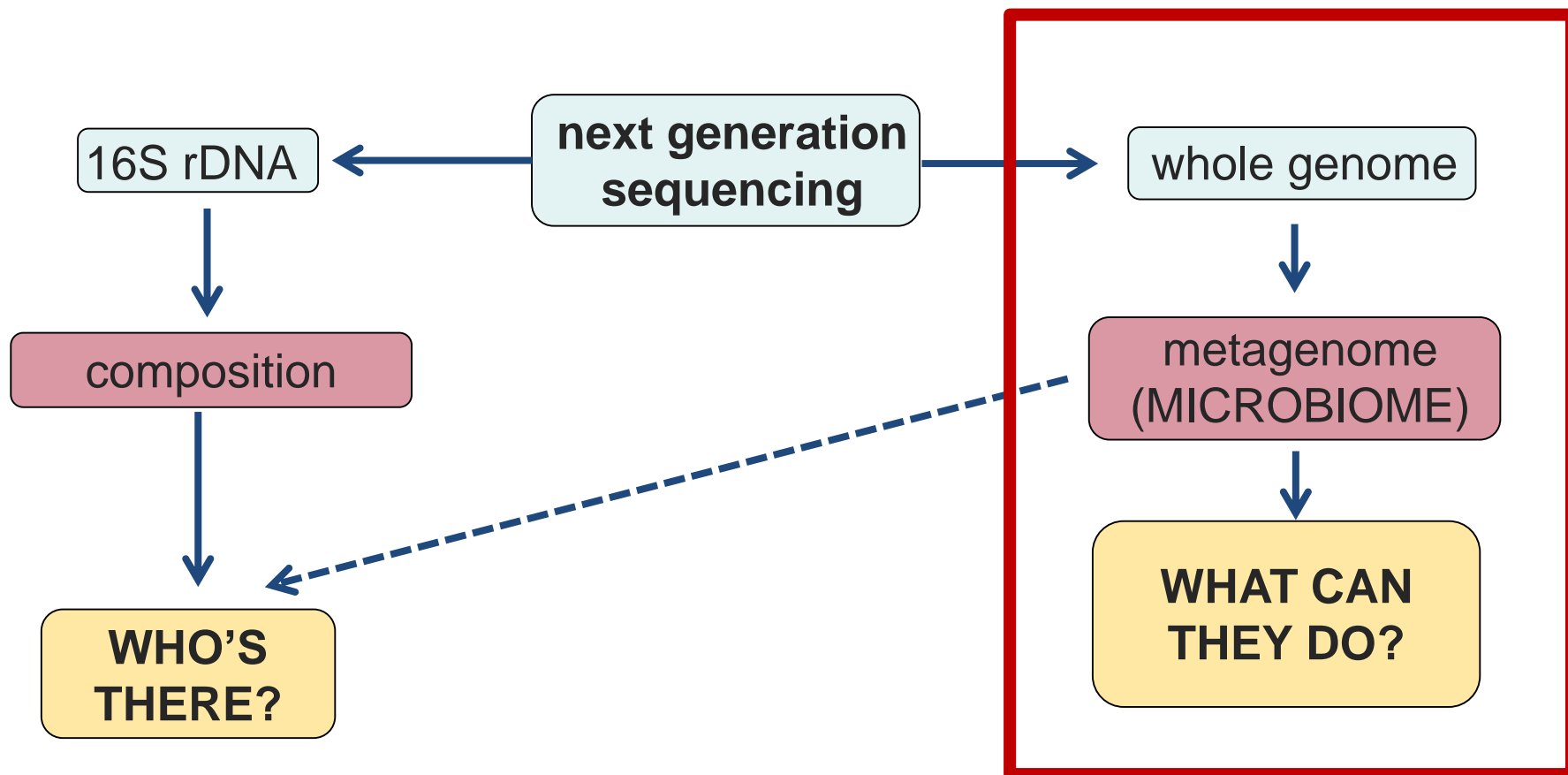
Culture-independent molecular survey:

- DNA extraction from gut samples
- 16S based molecular techniques

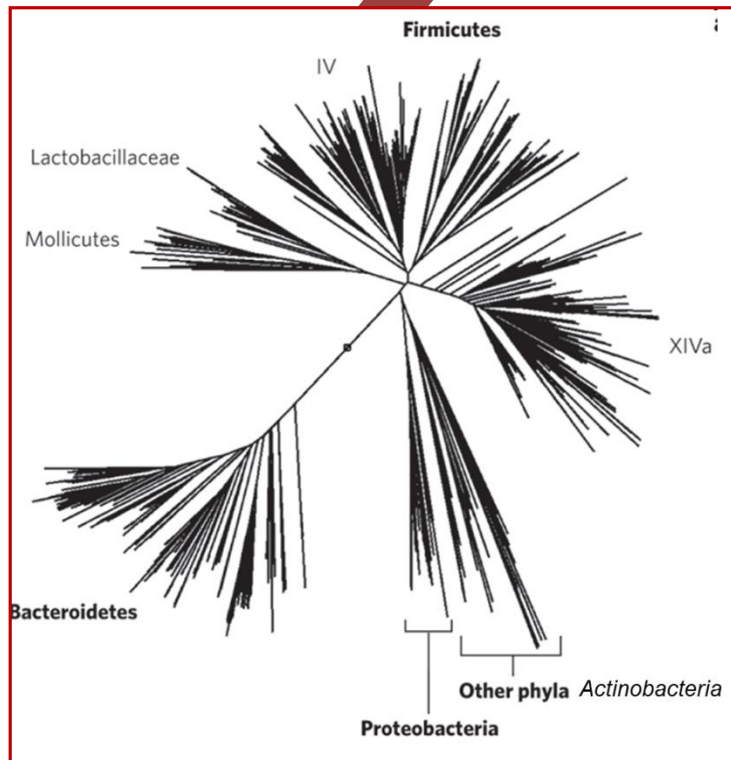




MICROBIOTA MOLECULAR ASSESSMENT



PHYLOGENETIC DIVERSITY

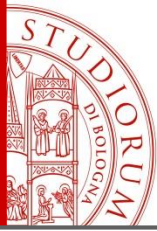


> 1000 species



6 (out of 100) bacterial phyla

- Firmicutes, Bacteroidetes : 90%
- Actinobacteria, Proteobacteria, Fusobacteria and Verrucomicrobia : 10%



FUNCTIONAL DIVERSITY

MICROBIOME

(collective genome of the
microbiota)



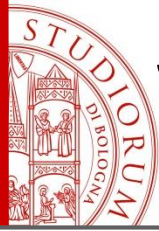
10⁶ GENES

58% KNOWN

- carbohydrate metabolism (CAZymes)
- energy metabolism
- amino acid metabolism
- biosynthesis of secondary metabolites
- metabolism of cofactors and vitamins

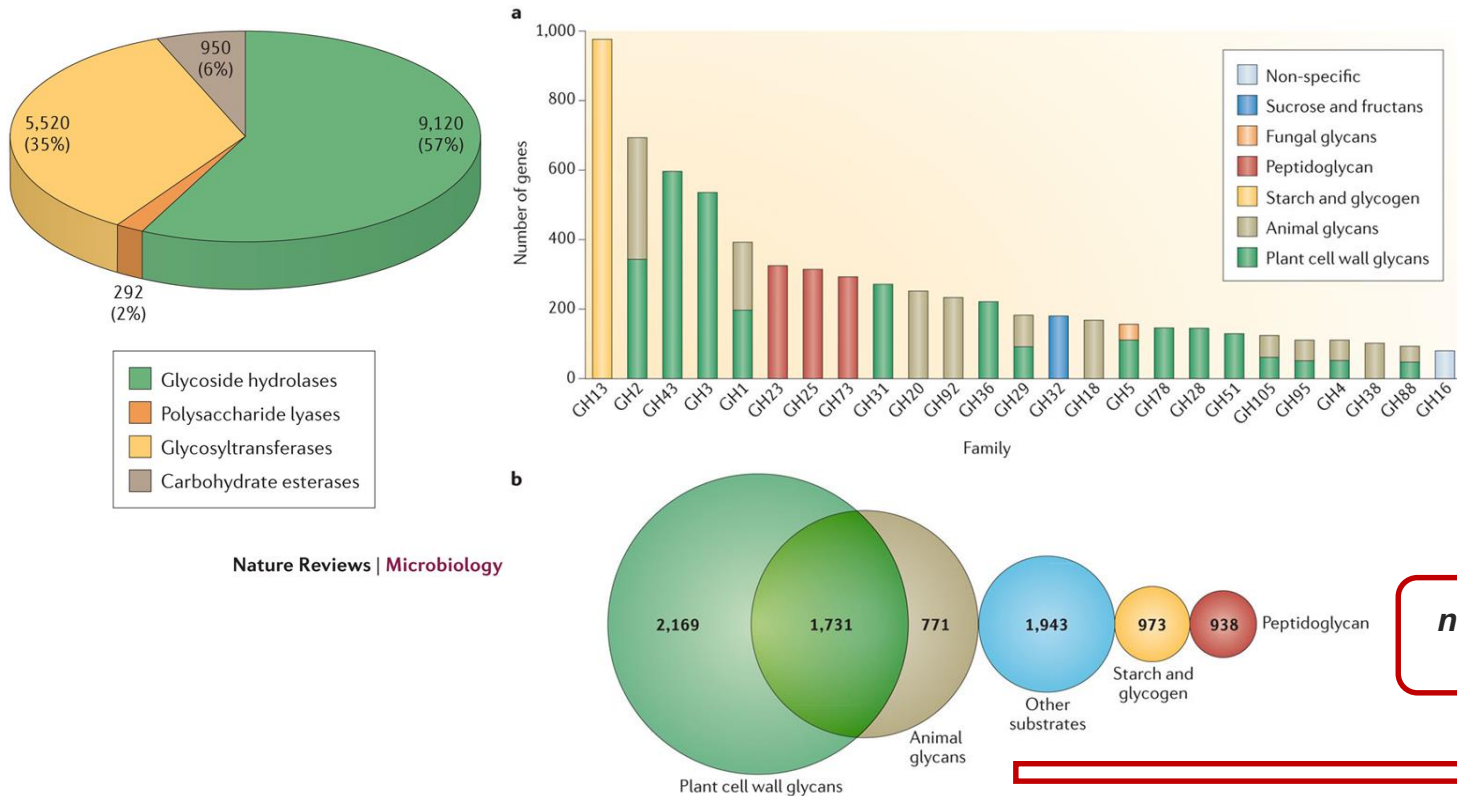
42% UNKNOWN

Schloissing et al, Nature 2013



SUBSTRATES OF THE GM CAZymes ARSENAL

thousands of enzymes while we possess only 17

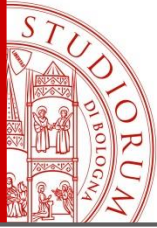


Nature Reviews | Microbiology

Nature Reviews | Microbiology

The GM possesses a broad glycobiome complexity, complementing the limited diversity of the human glycobiome and enhancing the superorganism capacity to metabolize complex polysaccharides

El Kaoutari *et al.*, Nat Rev Microbiol. 2013



IMPACT OF MICROBIOTA ON HOST HEALTH AND DISEASE

our bacterial counterpart provides essential features we have not evolved

- **enhancement of the digestive efficiency and modulation of energetic homeostasis**
- vitamin synthesis
- competitive barrier against colonization/invasion
- **development, education and function of the immune system**
- strengthening of the GIT epithelium impermeability
- detoxification of xenobiotics

And more recently:

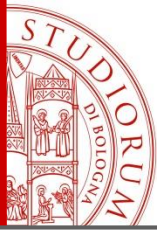
- *central nervous system modulation*
- *endocrine system modulation*

HOW DO WE KNOW THIS?

- Microbiome sequence analysis
- Observation of human gut microbiota in different physiological/pathological condition
- In vitro studies using complex bacterial communities

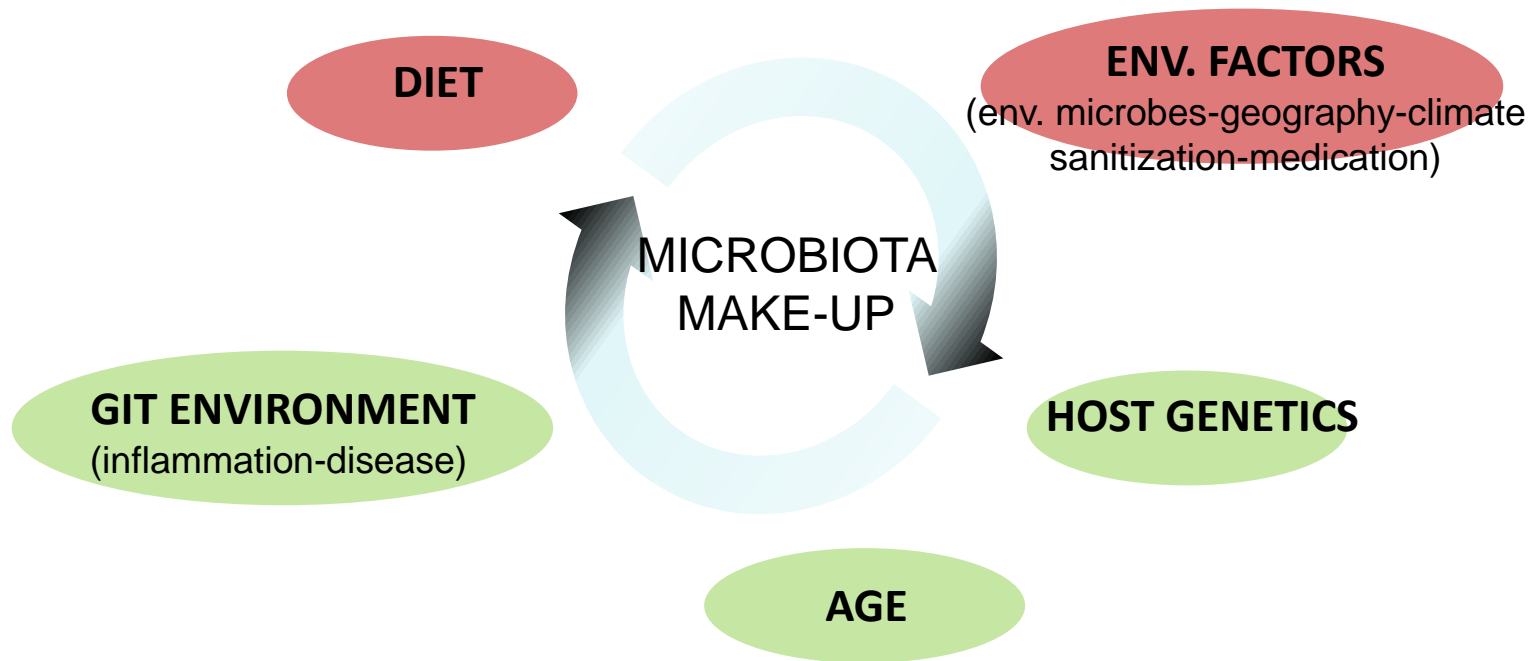


THE ADOPTION OF GERM-FREE
MICE ALLOWED TO MEASURE
THE IMPACT OF GUT
MICROBIOTA-HOST MUTUALISM
ON SEVERAL PHYSIOLOGICAL
PARAMETERS



MICROBIOTA PLASTICITY

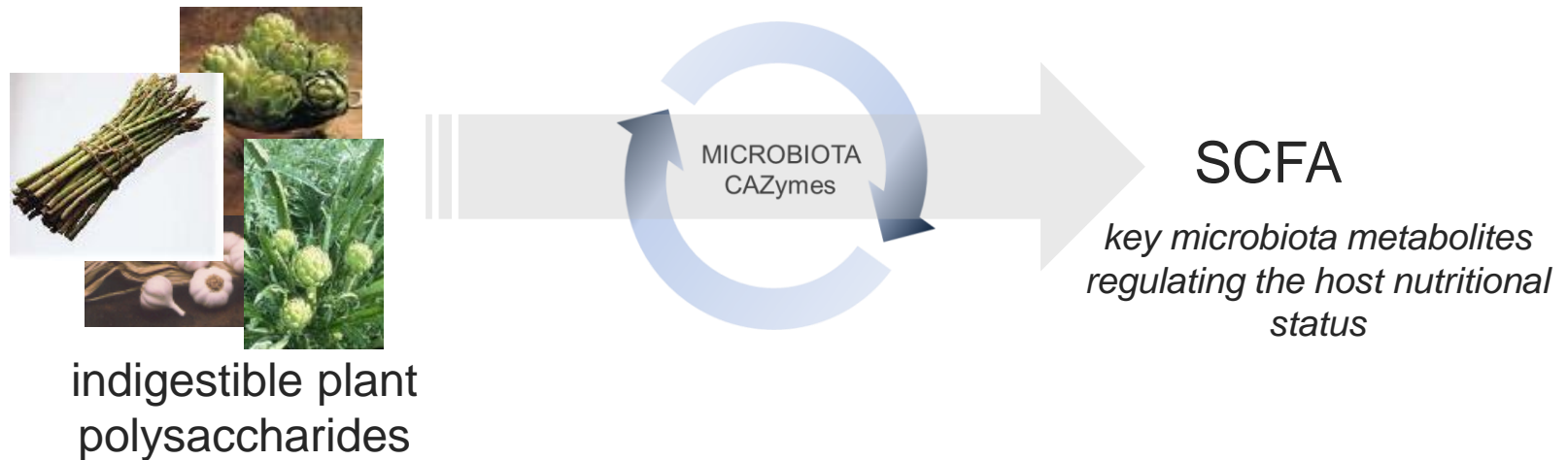
THE INDIVIDUAL MICROBIOTA COMPOSITION CONTINUOUSLY CHANGES IN RESPONSE TO **EXTRINSIC** AND **INTRINSIC** VARIABLES



IN A MUTUALISTIC CONTEXT, THE PLASTICITY OF THE HUMAN MICROBIOTA GUARANTEES A RAPID ADAPTATION OF THE SUPER-ORGANISM IN RESPONSE TO DIET CHANGES, AGE, ETC
there is a strong selection towards a readily changeable individual microbiome profile

IMPACT ON HOST NUTRITION

indigestible plant polysaccharides (xylan, pectin, arabinose containing-dietary carbohydrates as plant-derived pectin, cellulose, hemicellulose, resistant starches) reach unchanged the colon where they are metabolized by the intestinal microorganisms

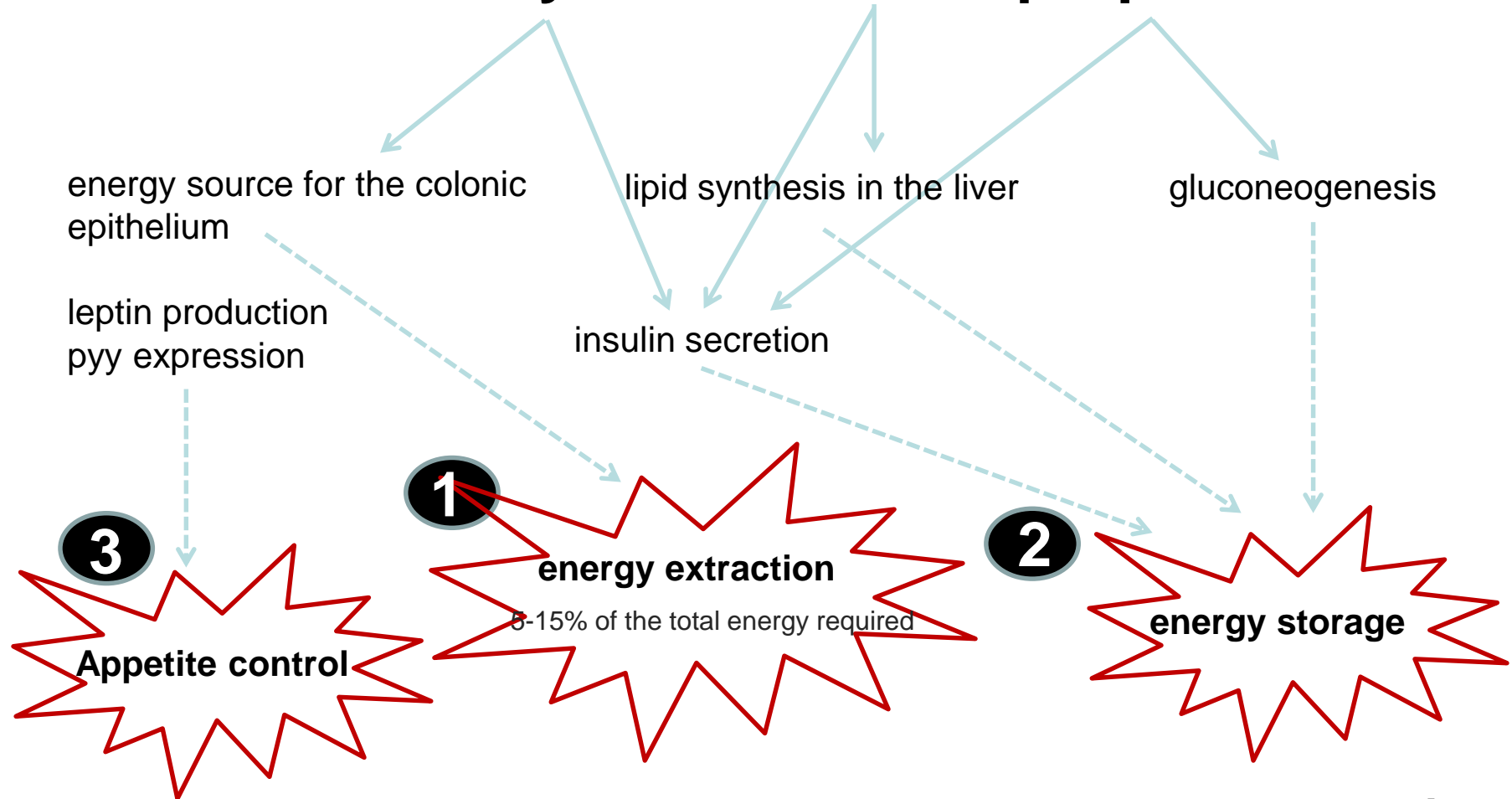


equipped with a real arsenal of CAZymes – absent in human genome – intestinal microorganisms degrade plant polysaccharides to SCFA



SCFA, MICROBIAL METABOLITES WITH A KEY MULTIFACTORIAL ROLE IN HOST NUTRITION

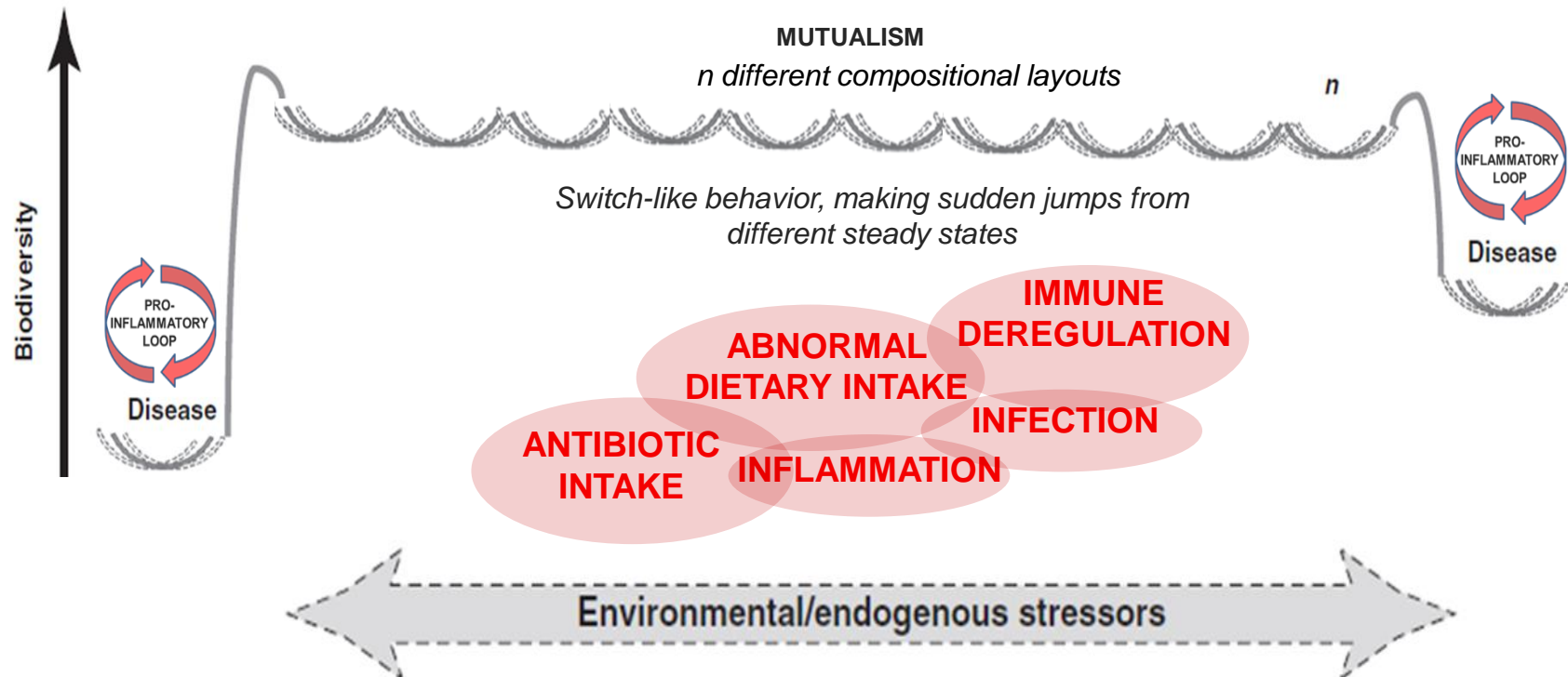
SCFA: butyrate - acetate - propionate



SCFA also possess immunomodulating and antimicrobial properties

MUTUALISM BREAKDOWN

the GM is a multistable system with a variable fraction at 40% of the total community

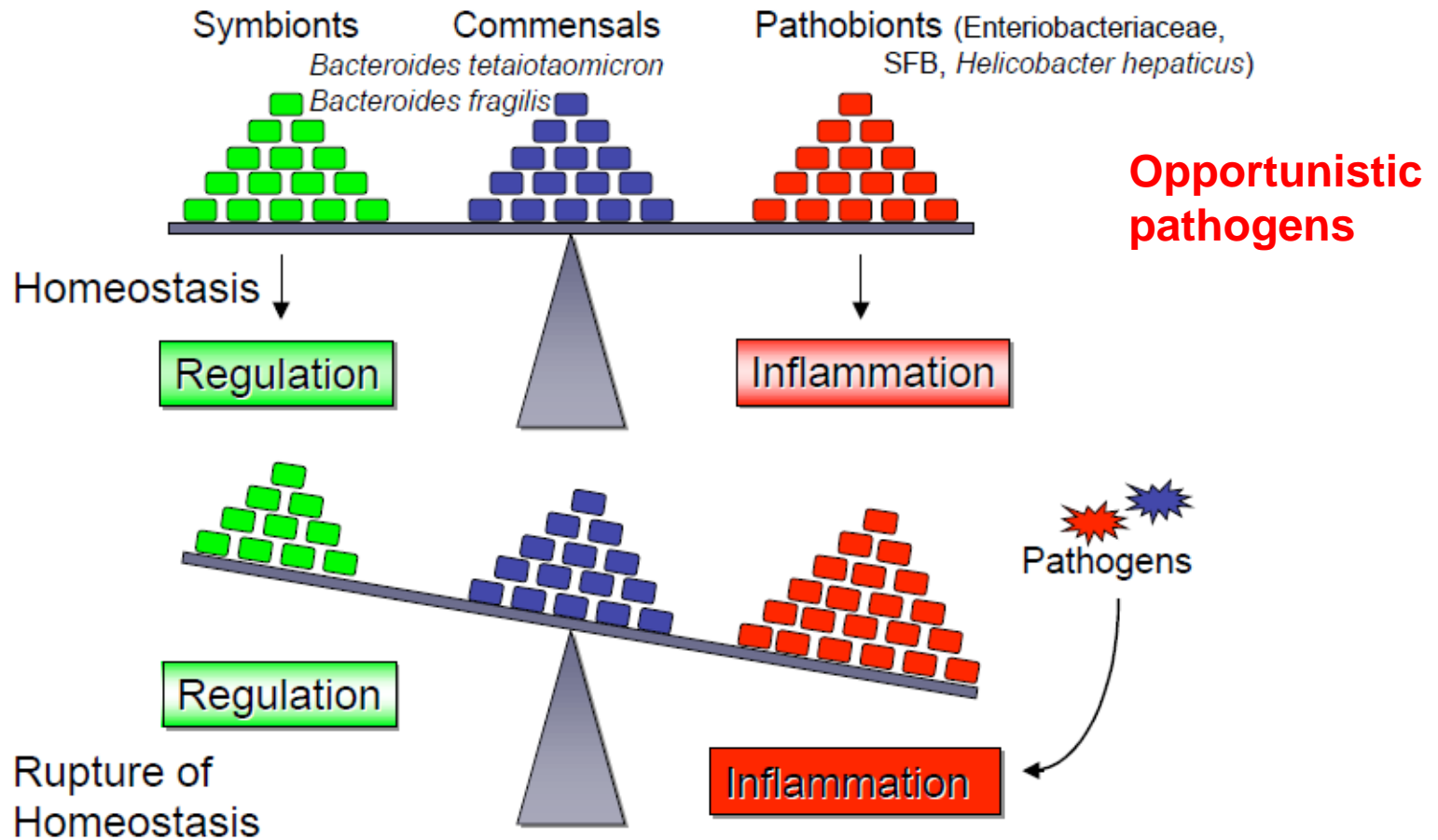


**RUPTURE OF THE GM-HOST MUTUALISTIC AGREEMENT AND
COMPROMISED HOST ENERGY BALANCE AND IMMUNE
HOMEOSTASIS**

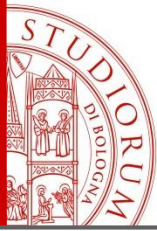


IMMUNOLOGICAL DISREGULATION ASSOCIATED WITH MICROBIOTA DYSBIOSIS

Immuno-
modulatory
bacteria
(butyrate
producers)

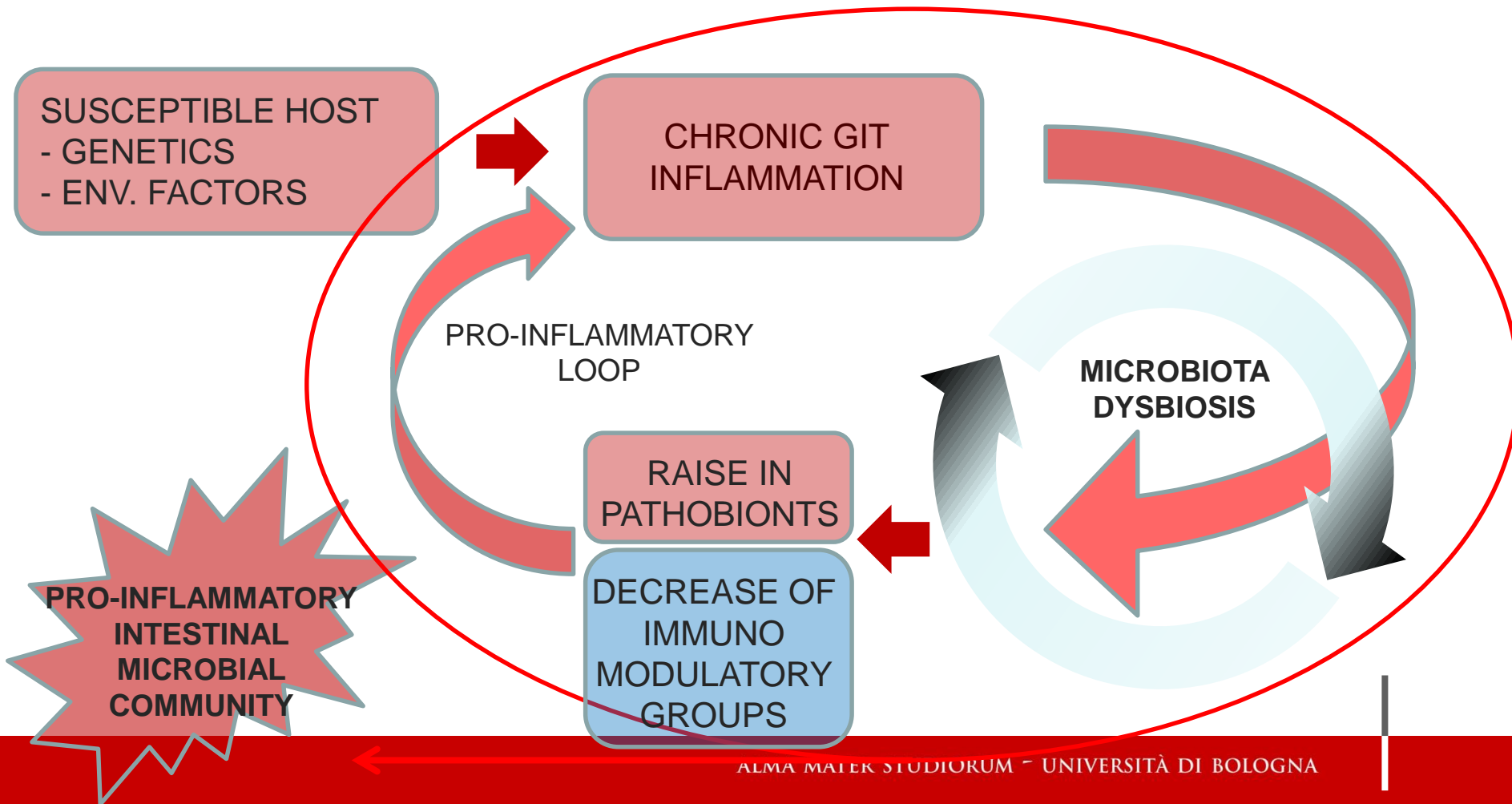


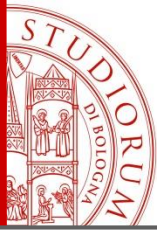
From Round JL & Mazmanian SK. 2009. Nat.Rev.Immunol.,9:313-323



INFLAMMATION AND MICROBIOTA

A non-controlled pro-inflammatory pathway can dramatically impact on the composition of the intestinal microbiota





GUT MICROBIOTA-ASSOCIATED DISORDERS

- **Inflammatory bowel diseases** Peterson et al. Cell Host and Microbe, 2008
- **Obesity** Turnbaugh PJ et al. Nature, 2006 (Increase in energy-harvesting bacterial populations)
- **Diabetes (type 1, 2)** Brugman S et al. Diabetologia, 2006, Amar et al. Am.J.Clin.Nutr., 2008 (Carbohydrate intake and glycemic control, insulin resistance)
- **Cardio-vascular diseases** (+ cholesterol dysregulation) Bäckhed F. Clin.Exp.Immunol., 2010
- **Atopy/allergy** Isolauri et al. Curr. Pharm. Des., 2008
- **Colorectal Cancer**: Wu et al. Nature Med., 2009 (chronic inflammation)
- **Gut Brain Axis** (IBS, depression, autism)

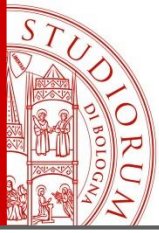


THE GUT MICROBIOTA DESCRIBES AN ADAPTIVE TRAJECTORY ALONG HUMAN AGING

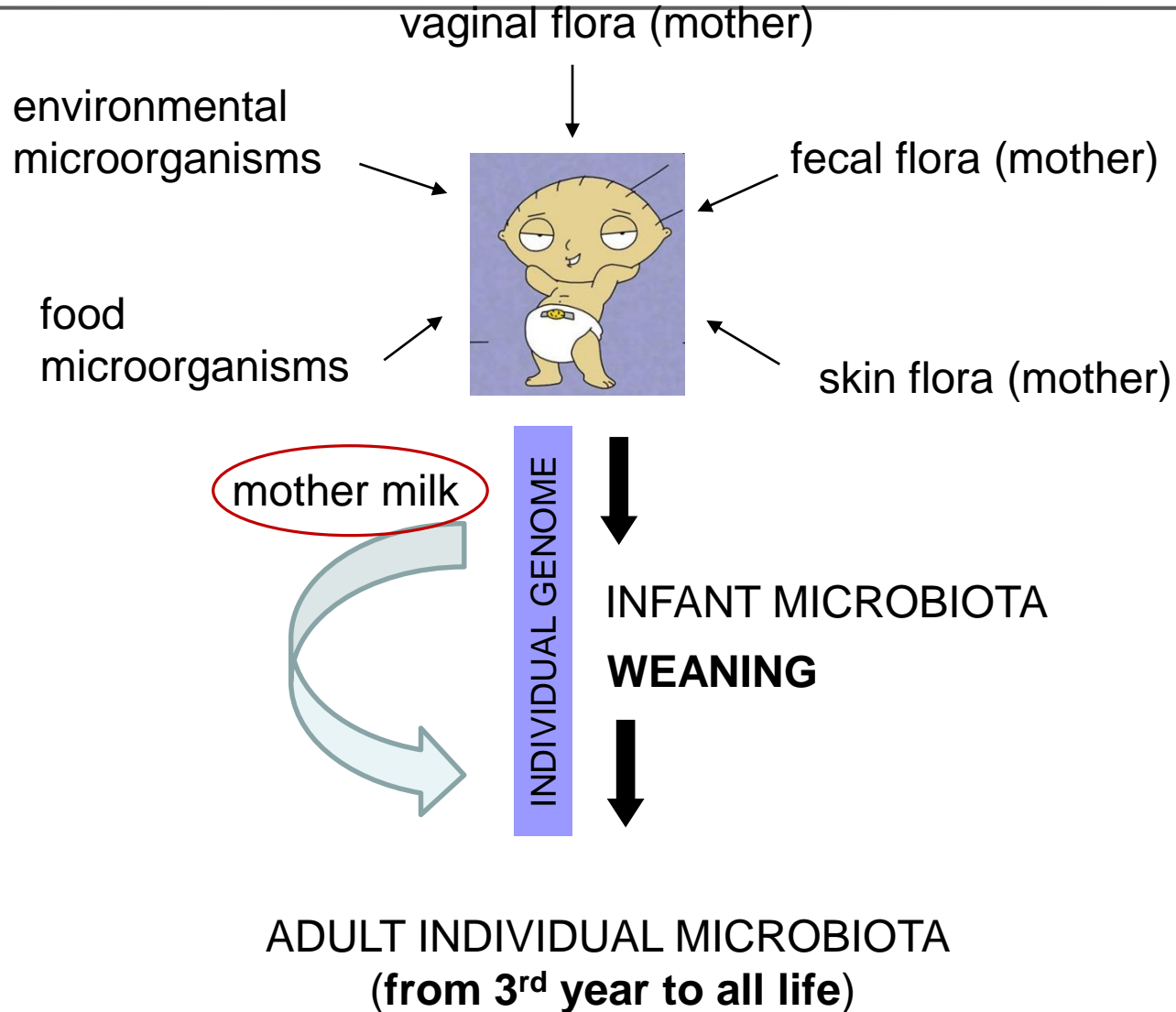


AGE RELATED CHANGES OF THE GUT MICROBIOTA PROVIDE THE HOST WITH **ECOLOGICAL SERVICES CALIBRATED FOR EACH STAGE OF LIFE**

Candela et al., Critical Rev Microbiol, 2013



WE ARE BORN STERILE IN A MICROBIAL WORLD



INFANT-TYPE MICROBIOTA: SIMPLE, READILY CHANGEABLE AND BIFIDOBACTERIUM-DOMINATED

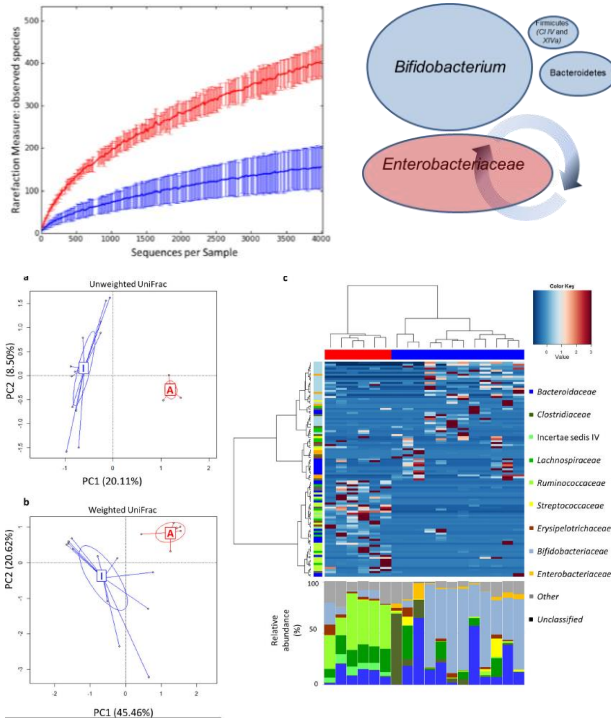


Table 3. TNF- α impact on the HT29 cell-associated microbiota fraction in breast-fed infants and adults.

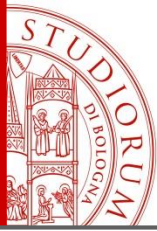
Microbial group	Breast-fed infants			Adults		
	- TNF- α	+ TNF- α	FRD	- TNF- α	+ TNF- α	FRD
<i>Bacteroides - Prevotella</i>	10.8	9.3	n.s.	23.5	15.4	0.008
<i>Clostridium</i> cluster IV	1.7	2.5	0.520	21.5	18.2	n.s.
<i>Clostridium</i> cluster IX	5.4	5.1	n.s.	5.2	3.4	n.s.
<i>Clostridium</i> cluster XIVa	5.0	4.8	n.s.	28.7	37.5	0.154
<i>Clostridium</i> cluster XI	0.5	0.6	n.s.	0.3	1.3	<0.001
<i>Clostridium</i> cluster I, II	1.4	1.3	n.s.	1.2	1.8	0.24
<i>Lactobacillaceae</i>	6.9	7.4	n.s.	1.9	2.1	n.s.
<i>Bifidobacteriaceae</i>	14.4	13.1	n.s.	4.0	5.8	n.s.
<i>Verrucomicrobiae</i>	0.8	1.0	n.s.	3.3	1.5	n.s.
<i>Bacillaceae</i>	5.5	6.3	n.s.	1.8	4.0	0.004
<i>Fusobacteriaceae</i>	0.6	0.8	0.570	1.1	1.7	0.132
<i>Enterococcales</i>	10.9	10.4	n.s.	1.6	2.5	0.430
<i>Enterobacteriaceae</i>	35.3	36.8	n.s.	5.5	3.8	0.360
<i>Campylobacteriaceae</i>	0.7	0.8	n.s.	0.3	1.1	<0.001

For each microbial group, mean relative abundance (%) and statistical significance

presence of
environmental
aerobes

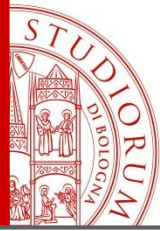
INFANT-TYPE MICROBIOTRA IS STRUCTURED TO COPE WITH INFLAMMATION, BEING CO-EVOLVED TO PRIME THE EARLY IMMUNE SYSTEM IN THE CONTEXT OF TRANSIENT INFLAMMATORY RESPONSES; MILK DIGESTION; FOLATE BIOSYNTHESIS

Centanni et al., PLoS ONE. 2013



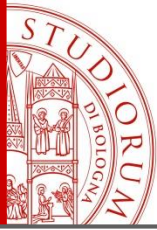
FECAL MICROBIOTA OF BREAST-FED INFANTS VS ADULTS

Phylum	Relative abundance (mean, %)		*P value
	Breast-fed infants	Adults	
<i>Actinobacteria</i>	46.0	7.6	0.024
<i>Firmicutes</i>	28.7	76.3	0.007
<i>Proteobacteria</i>	3.5	0.4	0.003
Genus			
<i>Bifidobacterium</i>	45.4	7.5	0.049
<i>Alistipes</i>	0	1.3	<0.001
<i>Streptococcus</i>	2.8	0.2	0.007
<i>Blautia</i>	0.04	6.6	<0.001
<i>Lachnospiraceae</i>	2.1	5.7	0.041
<i>Roseburia</i>	0.03	6.8	<0.001
<i>Faecalibacterium</i>	0.4	19.8	<0.001
<i>Oscillibacter</i>	0.01	1.5	<0.001
<i>Ruminococcaceae</i>	0.3	3.8	0.002
<i>Ruminococcus</i>	0.03	8.7	0.011
<i>Subdoligranulum</i>	0.1	3.0	0.001
<i>Veillonella</i>	1.7	0.01	0.006
<i>Erysipelotrichaceae</i>	0.3	2.8	0.004
<i>Escherichia/Shigella</i>	2.6	0.06	0.001



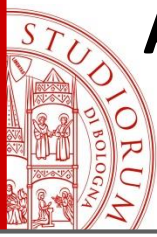
TNF-ALFA IMPACT ON THE HT29 CELL-ASSOCIATED MICROBIOTA FRACTION

Microbial group	Breast-fed infants		Adults	
	- TNF- α	+ TNF- α	- TNF- α	+ TNF- α
<i>Bacteroides - Prevotella</i>	10.8	9.3	23.5	15.4
<i>Clostridium</i> cluster IV	1.7	2.5	21.5	18.2
<i>Clostridium</i> cluster IX	5.4	5.1	5.2	3.4
<i>Clostridium</i> cluster XIVa	5.0	4.8	28.7	37.5
<i>Clostridium</i> cluster XI	0.5	0.6	0.3	1.3
<i>Clostridium</i> cluster I, II	1.4	1.3	1.2	1.8
<i>Lactobacillaceae</i>	6.9	7.4	1.9	2.1
<i>Bifidobacteriaceae</i>	14.4	13.1	4.0	5.8
<i>Verrucomicrobiae</i>	0.8	1.0	3.3	1.5
<i>Bacillaceae</i>	5.5	6.3	1.8	4.0
<i>Fusobacteriaceae</i>	0.6	0.8	1.1	1.7
<i>Enterococcales</i>	10.9	10.4	1.6	2.5
<i>Enterobacteriaceae</i>	35.3	36.8	5.5	3.8
<i>Campylobacteriaceae</i>	0.7	0.8	0.3	1.1



TAKE HOME MESSAGE

- The GM of breast-fed infants is selected for the establishment of a intense cross-talk with the host immune system
- Enriched in *Bifidobacterium* and *Enterobacteriaceae*, the infant-type microbiota is specifically structured to drive immune education in early infancy.
- *Enterobacteriaceae* provide genes associated with virulence functionality, which continuously boost the immunological response, whereas the bifidobacterial fraction - dominated by the species *B. breve* and *B. longum* - exert synergic immune modulatory and protective properties



ADULT-TYPE MICROBIOTA: COMPLEX AND ADAPTABLE ECOSYSTEM DOMINATED BY FIRMICUTES AND BACTEROIDETES

FUNCTIONALLY STRUCTURED TO PROVIDE THE HOST WITH SCFA FROM INDIGESTIBLE PLANT POLYSACCHARIDES

DIFFERENT DIETARY SUBSTRATES

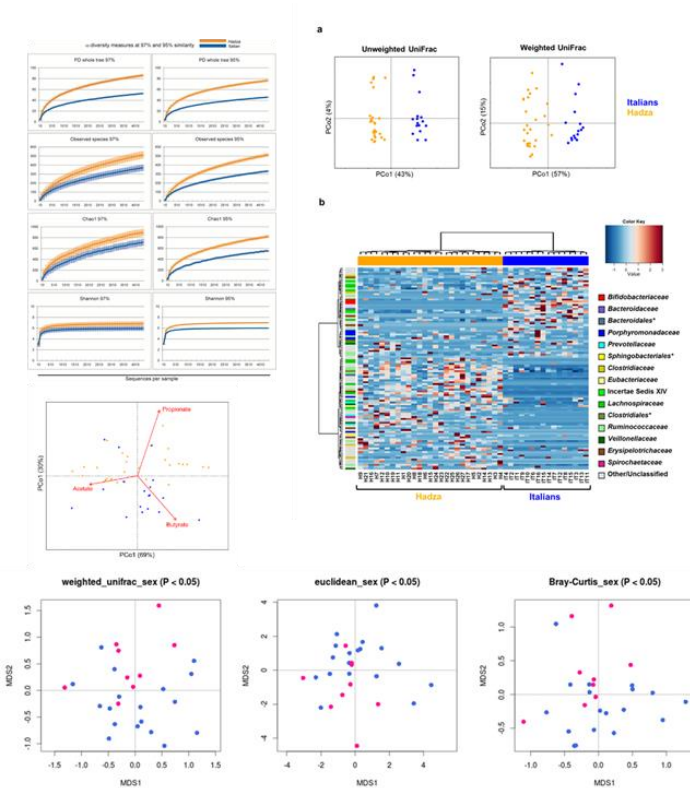


EXTRASOMATIC ADAPTATION TO DIFFERENT DIETARY HABITS AND LIFESTYLE FACTORS

IMPROVEMENT
OF ENERGY
EXTRACTION

CONTROL OF
ENERGETIC
HOMEOSTASIS

OPTIMIZATION OF
IMMUNOLOGICAL
PERFORMANCE



Schnorr et al., Nature Communication, 2014

CENTENARIAN GUT MICROBIOTA

Table 2. Genus-like bacterial groups that were found to differ significantly between centenarians (C), elderly (E) and young adults (Y).

Phylum/order	Genus-like phylogenetic group	Relative contribution (%) ^a			Ratio ^b		P value ^c	
		C	E	Y	C/E	C/Y	C vs E	C vs Y
Clostridium cluster XV	<i>Eubacterium limosum</i> et rel.	0.35	0.02	0.02	16	14.5	0.0009	0.01
Proteobacteria	<i>Klebsiella pneumoniae</i> et rel.	0.17	0.03	0.02	5.3	6.7	0.002	0.0009
	<i>Vibrio</i>	0.15	0.03	0.03	5.4	5.4	<0.0001	<0.0001
	<i>Enterobacter aerogenes</i> et rel.	0.05	0.03	0.02	1.9	2.1	0.03	0.04
Actinobacteria	<i>Eggerthella lenta</i> et rel.	0.11	0.06	0.04	1.8	2.7	0.02	0.0001
Bacilli	<i>Bacillus</i>	0.07	0.05	0.03	1.4	2.0	0.01	0.04
Clostridium cluster IV	<i>Clostridium leptum</i> et rel.	2.37	1.27	1.33	1.8	1.8	0.006	0.005
	<i>Sporobacter termitidis</i> et rel.	1.14	0.75	0.70	1.5	1.6	0.05	0.04
	<i>Anaerotruncus colihominis</i> et rel.	0.99	0.68	0.66	1.4	1.5	0.08	0.01
	<i>Clostridium orbicindens</i> et rel.	1.52	1.05	1.16	1.4	1.3	0.03	0.08
	<i>Faecalibacterium prausnitzii</i> et rel.	2.01	4.05	4.24	0.5	0.5	0.01	0.006
	<i>Papillibacter cinemacranus</i> et rel.	1.30	1.72	1.80	0.7	0.7	0.06	0.04
Clostridium cluster XIVa	<i>Clostridium calidum</i> et rel.	0.90	1.98	1.57	0.4	0.6	0.06	0.05
	<i>Clostridium sphenoides</i> et rel.	0.97	1.92	1.50	0.5	0.6	0.0002	0.003
	<i>Eubacterium hallii</i> et rel.	3.16	4.75	5.76	0.7	0.5	0.03	0.004
	<i>Eubacterium rectale</i> et rel.	1.68	3.61	3.02	0.5	0.5	0.001	0.004
	<i>Eubacterium ventriosum</i> et rel.	1.21	2.77	2.62	0.4	0.4	0.0005	0.0002
	<i>Lachnospirillum bovis</i> et rel.	1.15	1.98	1.46	0.6	0.8	0.007	0.03
Outgrouping Clostridium cluster XIVa		0.63	0.94	1.04	0.7	0.6	0.02	0.01
	<i>Roseburia intestinalis</i> et rel.	1.57	3.04	3.21	0.5	0.5	0.006	0.03
	<i>Ruminococcus lactaris</i> et rel.	0.65	1.07	0.87	0.6	0.7	0.002	0.01
	<i>Ruminococcus obeum</i> et rel.	1.73	2.79	2.65	0.6	0.6	0.003	0.01

^aRelative contributions of genus-like phylogenetic group to the fecal microbiota was calculated as percentage of signal intensities the total signal intensity.
^bRatio of the average relative abundance of each genus-like phylogenetic group calculated for subjects belonging to C and E groups, and to C and Y groups. Bacterial groups showing C/E and C/Y ratio <1 decreased in the subjects of group C.
^cIn italic, relevant groups with P values ranging from 0.05 to 0.08 (italics) are reported.
doi:10.1371/journal.pone.0010667.t002

• LOW DIVERSITY

• DECREASE IN BIFIDOBACTERIA

• INCREASE IN PATHOBIANTS

(*Fusobacteria*, *Bacillus*, *Staphylococcus*, *Enterobacteriaceae*)

• REARRANGEMENT OF BUTYRATE PRODUCERS

SUBDOMINANT FRACTION

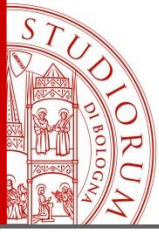
DOMINANT FRACTION

Ruminococcus obeum (CI XIVa)
Roseburia intestinalis (CI XIVa)
Eubacterium rectale (CI XIVa)
Faecalibacterium prausnitzii (CI IV)



Anaerotruncus colihominis (CI IV)
Eubacterium limosum (CI XV)

Biagi et al., PLoS ONE, 2010



CENTENARIAN GUT MICROBIOME

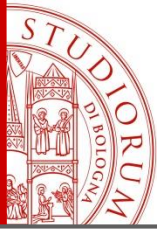
CENTENARIAN MICROBIOME IS ENRICHED IN GENES INVOLVED IN THE METABOLISM OF AROMATIC AMINO ACIDS (tryptophan and phenylalanine) AS WELL AS TYROSINE, VALINE AND LYSINE

**PROTEOLYTIC
METABOLISM**

ELDERLY AND **YOUNG ADULT** MICROBIOME IS ENRICHED IN GENES INVOLVED IN CARBOHYDRATE METABOLISM, PYRUVATE PRODUCTION AND AMINO ACID BIOSYNTHESIS

**SACCHAROLYTIC
METABOLISM**

Rampelli et al., Aging, 2013



WESTERN vs RURAL DIET

- HIGH FAT
- HIGH PROTEIN
- HIGH SUGAR
- FOOD PROCESSING
- FOOD STORING

WESTERN DIET

- LOW FAT
- STARCH AND PLANT POLYSACCHARIDE-RICH
- CONTAMINATED
- HOMEMADE
- PROMPTLY CONSUMED
- LOCALLY PRODUCED

RURAL AFRICAN DIET

MICROBIOTA MAKE-UP

+ *Firmicutes*
+ *Proteobacteria*

LOW FUNCTIONAL AND
PHYLOGENETIC
DIVERSITY

+ *Bacteroidetes*
+ *Actinobacteria*

HIGH FUNCTIONAL AND
PHYLOGENETIC
DIVERSITY

De Filippo et al., PNAS 2010





Current Biology

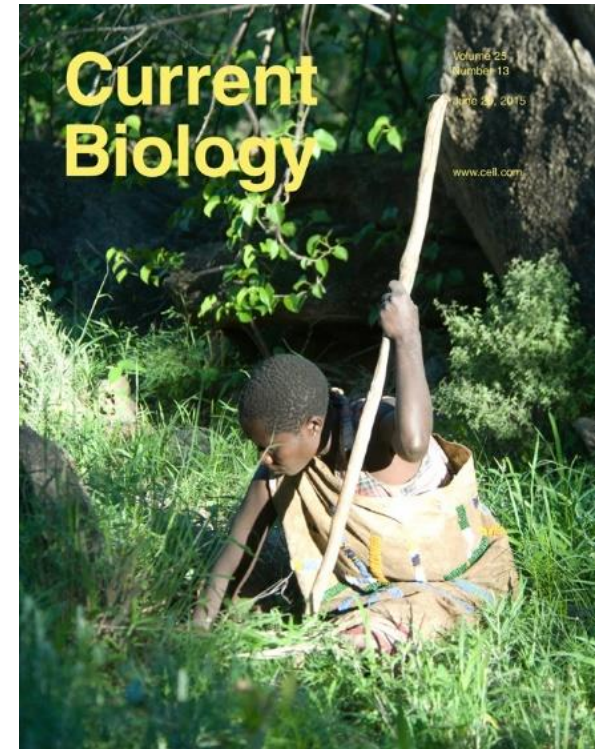
Volume 25, Issue 13, 29 June 2015, Pages 1682–1693



Article

Metagenome Sequencing of the Hadza Hunter-Gatherer Gut Microbiota

Simone Rampelli¹, Stephanie L. Schnorr²,  , Clarissa Consolandi³, Silvia Turrone¹, Marco Severgnini³, Clelia Peano³, Patrizia Brigidi¹, Alyssa N. Crittenden⁴, Amanda G. Henry², Marco Candela¹,  



Hazda lifestyle closely resembles that of paleolithic humans
(no cultivation or domestication of plants and animals)

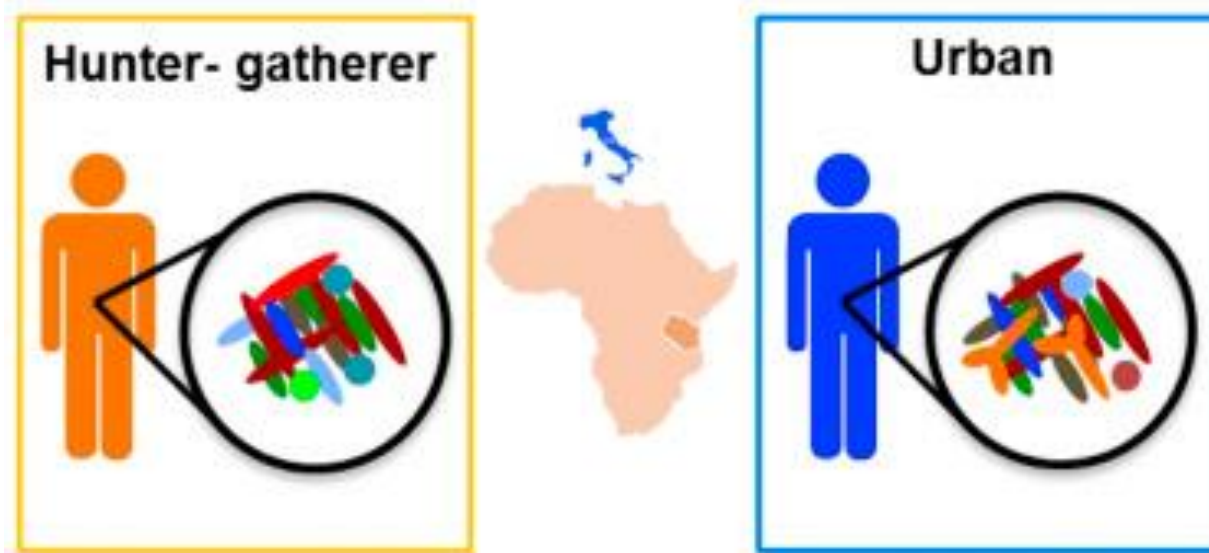
THE HADZA DIET



Wild foods consumed by Hazda:
meat, honey, baobab, berries
and tubers (no dairy foods)

Annual Hazda diet: 70% of kcal from plant foods; 30% from
bird and animal meat (dry season) ➔ diet rich in simple
sugars, starch and protein while lean in fat

SHOTGUN SEQUENCING OF TOTAL FAECAL DNA FROM 27 HADZA HUNTER-GATHERERS (AGE 8-70 Y) AND 16 ITALIANS (AGE 20-40 Y)



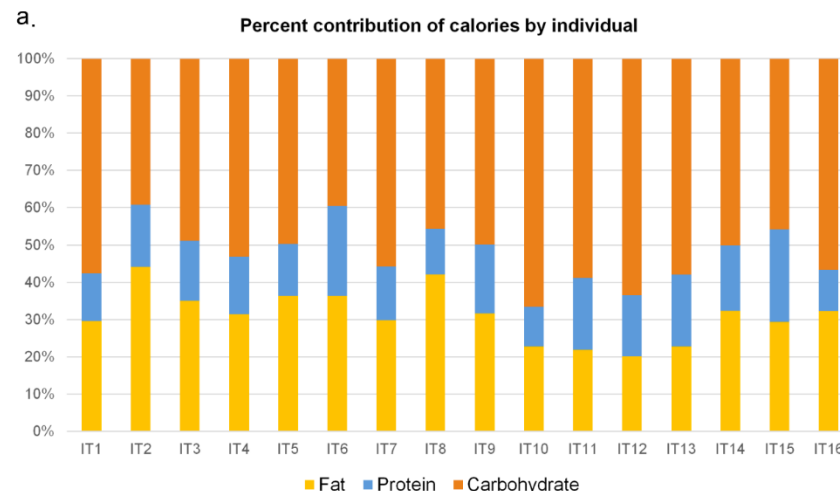
A total of 448.4 millions of 2x100 paired-end reads (11.8 millions \pm 1.7 per subject) were obtained

Schnorr et al., Nat Commun 2014

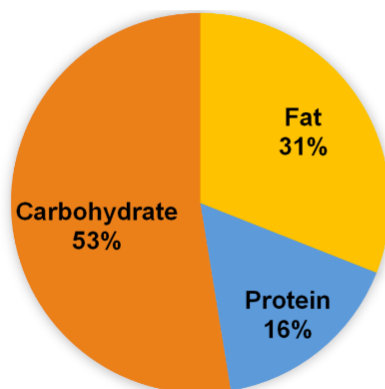
DIET OF THE ITALIAN COHORT

Mediterranean diet

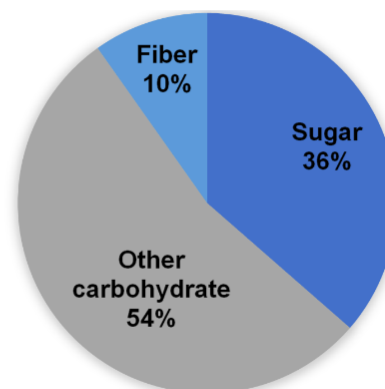
- abundant plant food, fresh fruit, pasta, bread and olive-oil;
- low to moderate amounts of dairy, poultry, fish and red meat



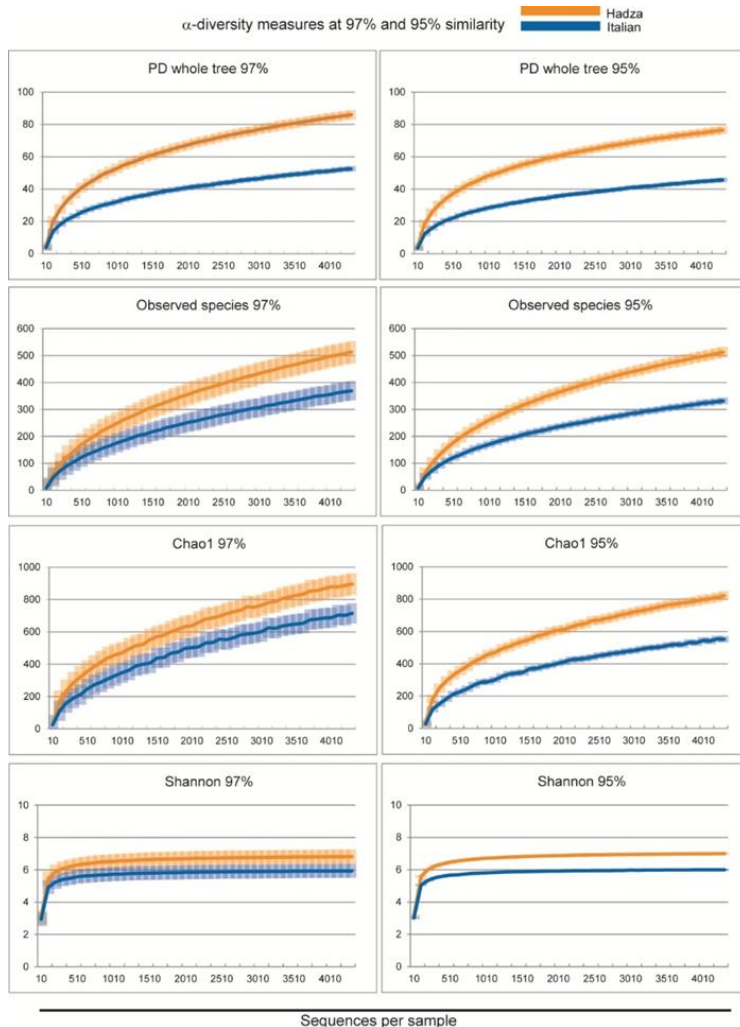
b. Macronutrient summary



Carbohydrate type summary



BIODIVERSITY OF THE HADZA MICROBIOTA



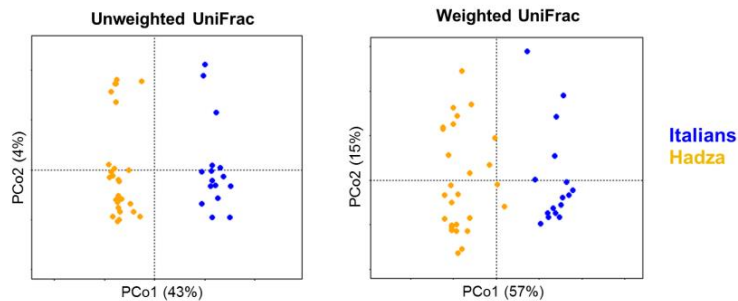
α- diversity at 97% and 95% similarity

Hadza have a more diverse gut microbe ecosystem compared to the Italian cohort.

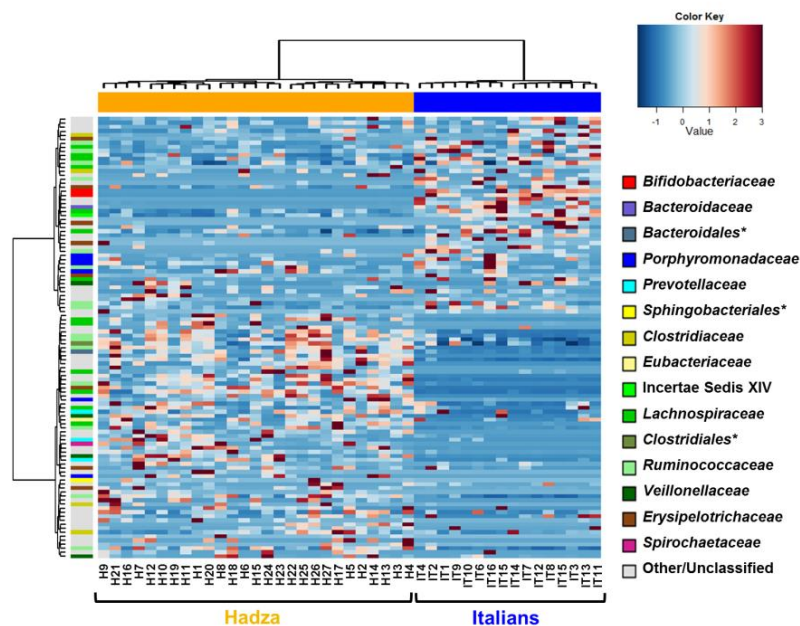
COMPARISON TO ITALIAN CONTROLS

Remarkable differences in subdominant phyla (< 10% relative abundance)

a

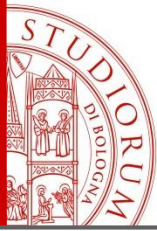


b



Hadza ↔ Italians

- depletion of butyrate producers of the *Clostridium* clusters IV and XIVa (*Faecalibacterium*, *Roseburia*, *Ruminococcus*)
- enriched in *Prevotella*, *unclassified Clostridiales* and *unclassified Ruminococcaceae*
- enriched in what are generally considered opportunistic microorganisms, such as members of *Proteobacteria*, *Succinivibrio*, and *Treponema* (cellulose and xylan hydrolizers)



ABSENCE OF *BIFIDOBACTERIUM* IN HAZDA

Never reported for any other human group (confirmed by qPCR)

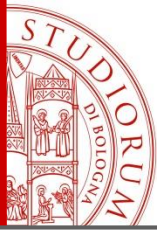
Hypothesis

- Absence of agro-pastoral-derived foods (consumption of dairy into adulthood could in most Western populations maintains a relatively large bifidobacteria presence in post weaning GM composition)
- Hadza neither domesticate nor have direct contact with livestock animals (swine, cattle and rabbit) → conditions for interspecies transfer and colonization of bifidobacteria do not occur

Absence of bifidobacteria combined with the enrichment in “opportunistic” bacteria (Proteobacteria and Spirochaetes)

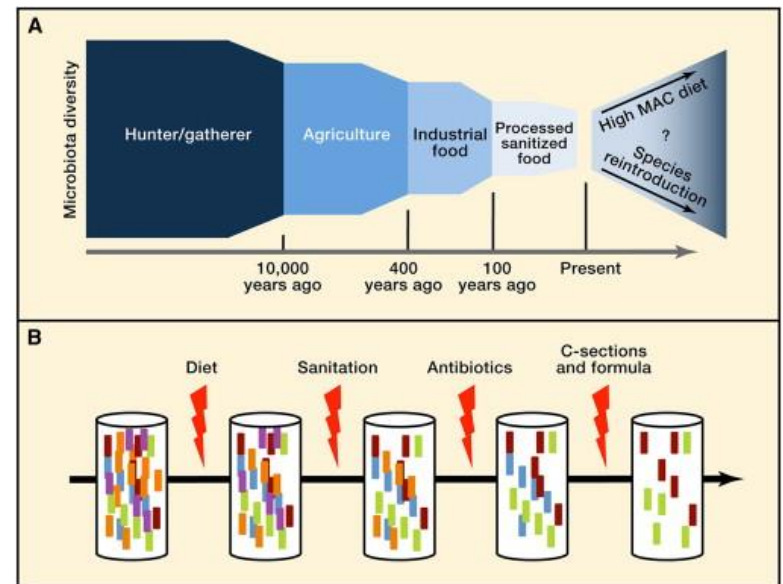
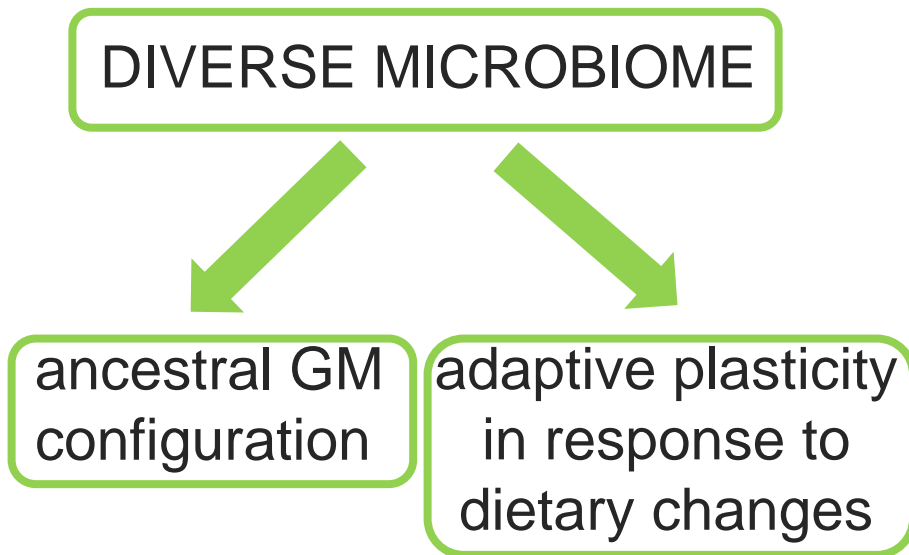


Hadza GM likely represents a new equilibrium that is beneficial and symbiotic to their living environment



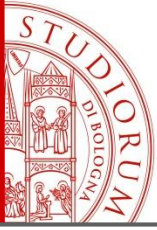
DIVERSITY, THE UNIVERSAL MARKER FOR A HEALTHY MICROBIOME

disease associated-GM dysbioses always involves a reduction of ecosystem diversity



Sonnenburg E, Sonnenburg J, *Cell Metabolism* 2014

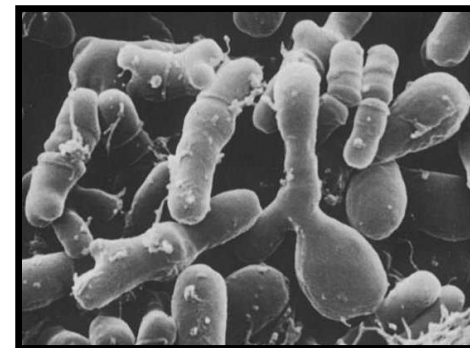
The transition from rural communities to modern urban societies involve the progressive loss of gut microbiome species



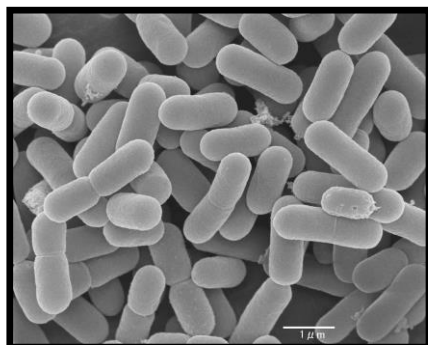
MANIPULATION OF THE HUMAN INTESTINAL MICROBIOTA

PROBIOTICS

A LIVE MICROBIAL FEED SUPPLEMENT
WHICH BENEFICIALLY AFFECTS THE HOST



PROBIOTICS SHOULD BE ABLE TO SURVIVE AND
MULTIPLY IN THE HOST GI TRACT BUT RAPIDLY
DISAPPEAR WHEN ORAL ADMINISTRATION IS STOPPED

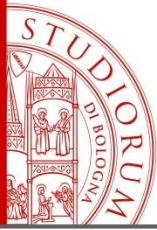


USE: FUNCTIONAL FOODS

(FERMENTED MILKS, INFANT FORMULA, FRUIT DRINKS)

PHARMACEUTICAL PREPARATION

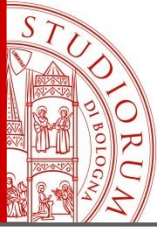
(DRIED SUPPLEMENTS)



PROBIOTICS SELECTION CRITERIA

For a microorganism to be characterized as *probiotic* a number of criteria have to be met:

- Non-pathogenic and non-toxic
- Beneficial effect on the consumer
- Survival in the gastrointestinal tract
- Preferably isolated from the same species as the intended use



MOST COMMONLY USED PROBIOTICS

LACTIC ACID BACTERIA

LACTOBACILLUS (*L. acidophilus*, *L. casei*, *L. delbrueckii*, *L. gasseri*, *L. rhamnonsus*, *L. cellobiosus*, *L. curvatus*, *L. fermentum*, *L. lactis*, *L. plantarum*, *L. reuteri*, *L. salivarius*, *L. brevis*)

BIFIDOBACTERIUM (*B. longum*, *B. bifidum*, *B. adolescentis*, *B. infantis*, *B. breve*, *B. animalis*, *B. lactis*)

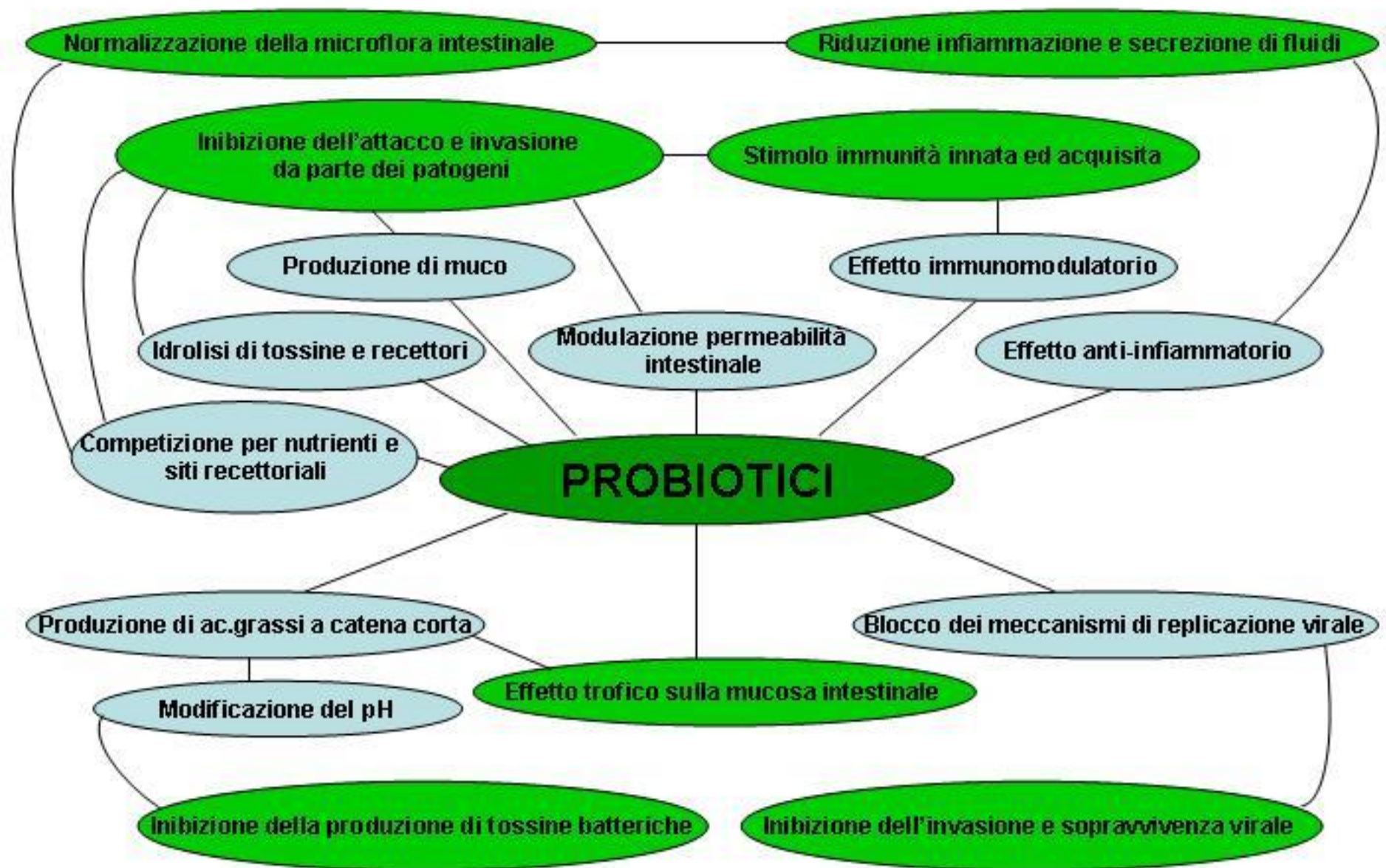
ENTEROCOCCUS (*E. faecalis*, *E. faecium*)

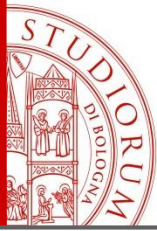
PROBIOTICS OTHER THAN LAB

BACILLUS SPORES (*B. cereus*, *B. clausii*, *B. subtilis*)

SACCHAROMYCES (*S. boulardii*, *S. cerevisiae*)

HEALTH PROMOTING EFFECTS OF PROBIOTICS





APPLICATION OF PROBIOTICS: DISEASE'S PREVENTION AND TREATMENT

Cardiovascular disease

Colon cancer

Diarrhea (acute diarrhea, antibiotic-associated diarrhea, radiation-induced diarrhea)

Allergy

Hepatic encephalopathy

Immune response

Inflammatory bowel disease (IBD, Pouchitis, Ulcerative colitis, Crohn's disease)

Irritable bowel syndrome (IBS)

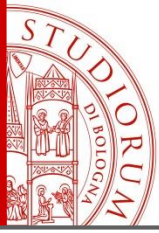
Lactose malabsorption

Necrotizing enterocolitis

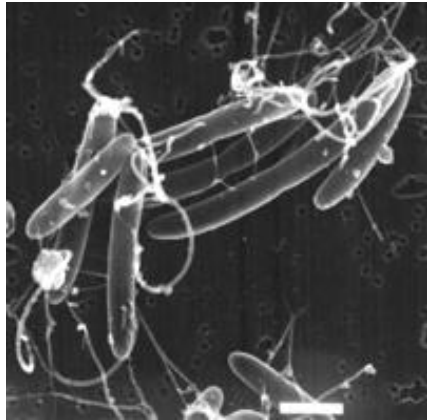
Nonalcoholic fatty liver disease

Prevention of systemic infections

NEXT GENERATION PROBIOTICS

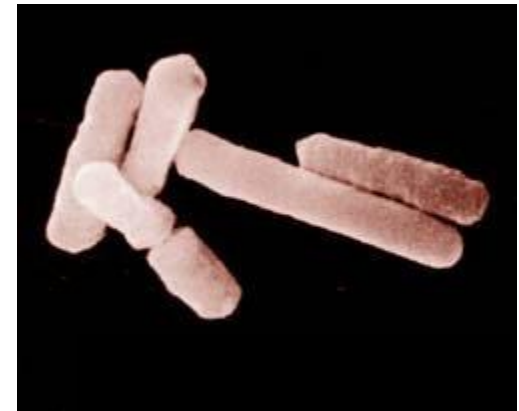


Faecalibacterium prausnitzii



Roseburia

Bacteroides





40 mamme

Campionamento del latte



Isolamento bifidi
(nuovi probiotici??)



NGS

40 neonati

Swab della bocca e feci

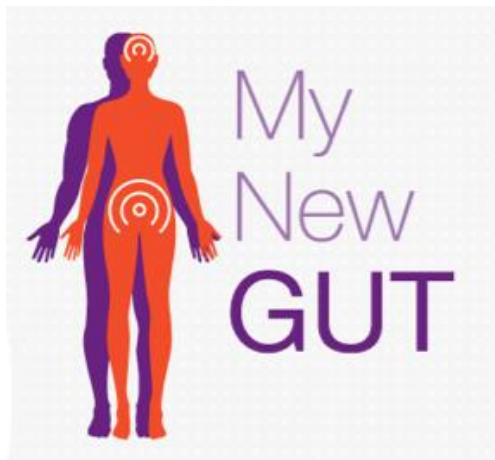


NGS

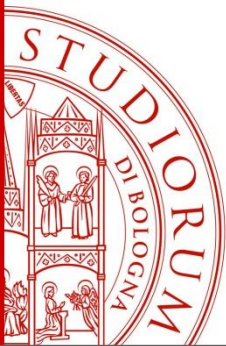
ONGOING STUDIES: FP7 KBBE PROJECTS



New dietary strategies addressing the specific needs of the elderly population for healthy ageing in Europe



Microbiome influence on energy balance and brain development/function put into action to tackle diet-related diseases and behaviour



THANKS FOR YOUR ATTENTION

