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INFLAMMAGING

Patologie Mieloidi in Geriatria,
Bologna 6 Maggio 2016

The arcades of the oldest university in the Western world
(founded in 1080)



ELSEVIER

Experimental Gerontology 35 (2000) 879–896

Experimental
Gerontology

www.elsevier.nl/locate/expgero

The network and the remodeling theories of aging: historical background and new perspectives

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THE “REMODELLING” THEORY OF AGING

(Franceschi et al., 1995; 2000)

The phenotype of old people is the result of the capability of the body to respond / adapt to:

1. the damaging stimuli we are exposed lifelong;
2. the unrepaired molecular and cellular damages continuously occurring in all tissues and organs, which have a signaling capacity



REMODELLING

(accumulation of damages/mutations +
local and systemic adaptive responses +
activation of the innate immune system)

An example of adaptation/remodelling: the Inflammatory Theory of Aging

Inflamm-aging

An Evolutionary Perspective on Immunosenescence

CLAUDIO FRANCESCHI,^{a,b,e} MASSIMILIANO BONAFÈ,^a SILVANA VALENSIN,^a
FABIOLA OLIVIERI,^b MARIA DE LUCA,^d ENZO OTTAVIANI,^c AND
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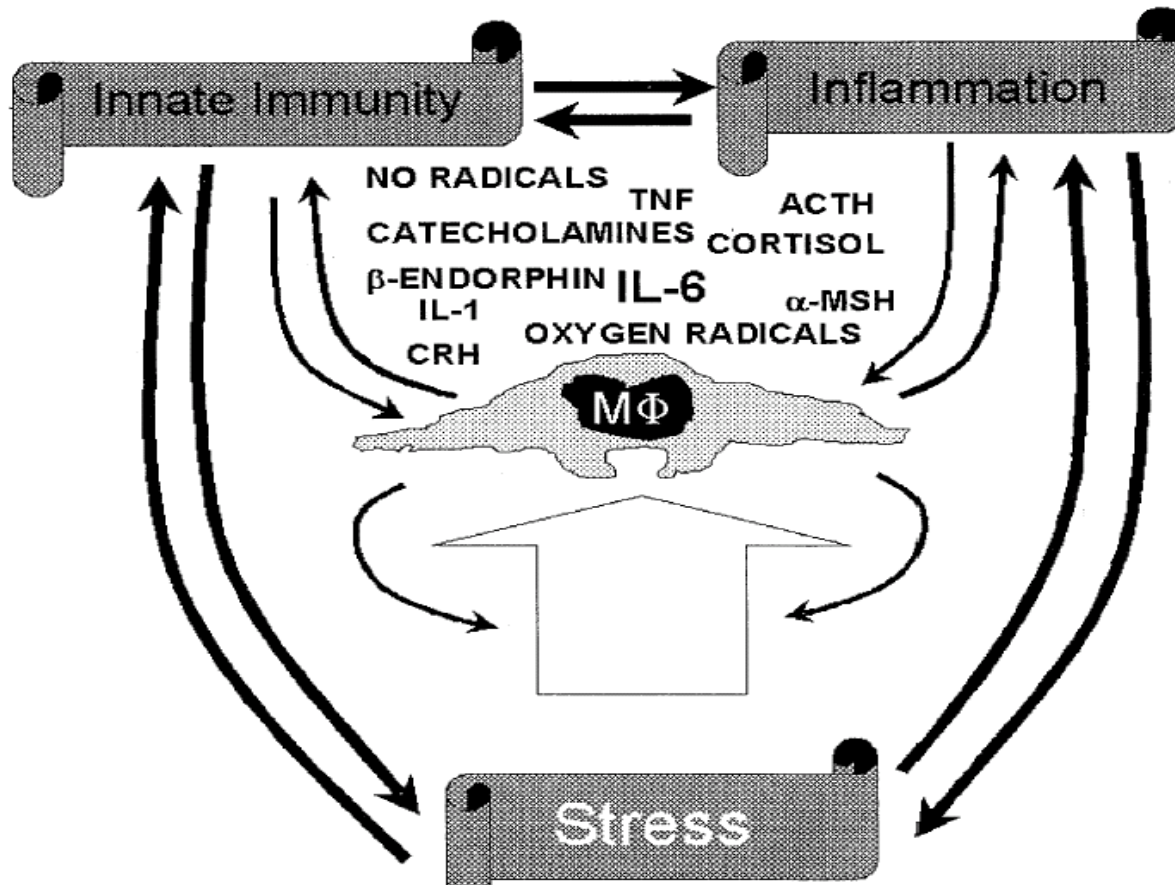
^d*Department of Cell Biology, University of Calabria, Calabria, Italy*

“chronic”, “low grade”, “sterile”

Ann. N.Y. Acad. Sci., 908, 244-254, 2000

Inflammaging is based on studies on the evolution of immune response and stress from invertebrates to mammals

innate immunity, response to stressors & inflammation
are evolutionary conserved from invertebrates to mammals,
highly interconnected & macrophage-centered



Franceschi et al., 2000

The Inflammaging Theory of Aging

**Metabolic syndrome
Type 2 Diabetes**

Cancer

**Cardiovascular
diseases**

AGING

INFLAMMAGING

**Alzheimer
PD**

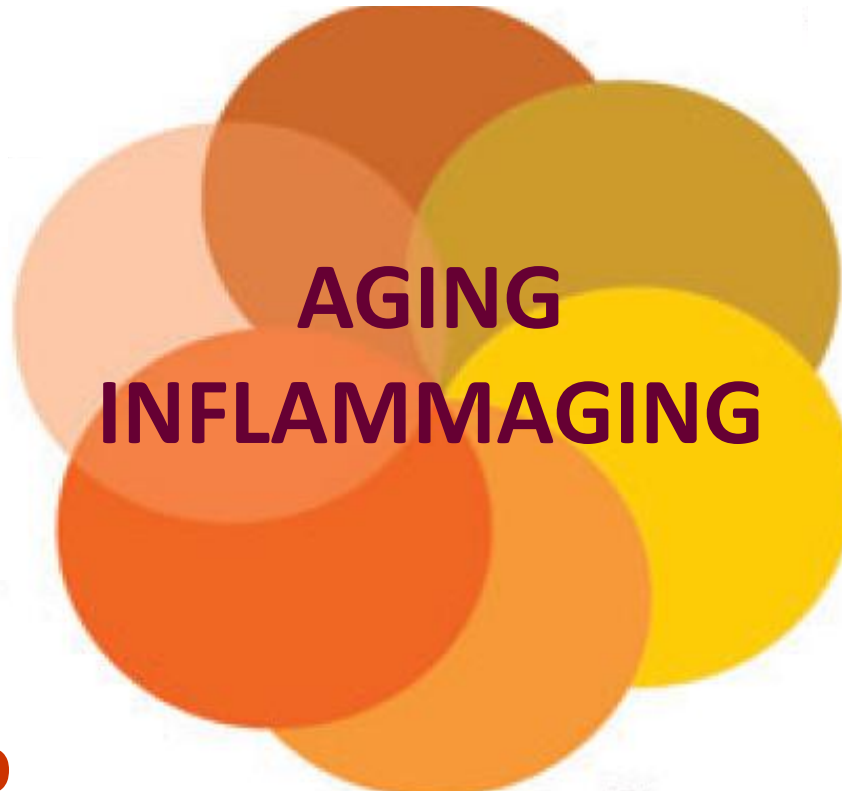
**Sarcopenia
Frailty**

PO Delirium

COPD

OA

Depression



The phenotype of CENTENARIANS
is an inextricable and dynamic mix of
accumulating damages/functional decline
and adaptive mechanisms



Inflammaging
+
+
+

The phenotype of CENTENARIANS
is an inextricable and dynamic mix of
accumulating damages/functional decline
and adaptive mechanisms

Anti-inflammaging

+
+
+



+
+
+

Inflammaging

Inflammaging and anti-inflammaging: A systemic perspective on aging and longevity emerged from studies in humans

Claudio Franceschi^{a,b,c,e,*}, Miriam Capri^a, Daniela Monti^d, Sergio Giunta^e, Fabiola Olivieri^e,
Federica Sevini^b, Maria Panagiota Panourgia^b, Laura Invidia^a, Laura Celani^b,
Maria Scurti^b, Elisa Cevenini^b, Gastone C. Castellani^{b,f}, Stefano Salvioli^{a,b,c}

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Mechanisms of Ageing and Development 128 (2007) 92–105

increasing levels of **pro-inflammatory** markers with
age stimulate a corresponding augmentation in
anti-inflammatory markers

pro-inflammatory agents **anti-inflammatory agents**



- RISK ALLELES
- circulating mtDNA
- inflamma-miR
- agalact N-glycans
- some eicosanoids
- gut microbiome

- PROTECTIVE LIFESTYLE
- PROTECTIVE ALLELES
- some eicosanoids
- some bacteria of gut microbiome

high resistance to infectious diseases
early life survival
↓
inflammaging
↓
inflammatory diseases
unsuccessful aging

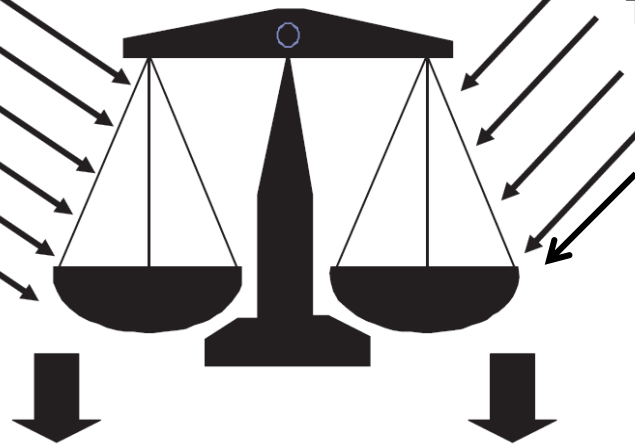
susceptibility to infectious diseases
↓
anti-inflammaging
↓
longevity
late life survival

pro-inflammatory agents

anti-inflammatory agents

- coagulation factors
- PG, LT
- HSP70
- TNF- α
- CRP
- IL-6

- cortisol
- TGF- β
- IL-10
- LPX



INFLAMMAGING
as an
Antagonistic Pleiotropy
trait

- RISK ALLELES
- circulating mtDNA
- inflamma-miR
- agalact N-glycans
- some eicosanoids
- gut microbiome

- PROTECTIVE LIFESTYLE
- PROTECTIVE ALLELES
- some eicosanoids
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high resistance to infectious diseases
early life survival
↓
inflammaging
↓
inflammatory diseases
unsuccessful aging

susceptibility to infectious diseases
↓
anti-inflammaging
↓
longevity
late life survival

**Fulvia, 109 anni,
Sarzana (Italy)**

Centenarians are
characterized by high
levels of circulating

**pro- & anti-
inflammatory**

molecules:

**TGF β , Cortisol, IL-1RA,
Adiponectin**



It is time to put Inflammaging within the «New Geroscience»

Leading Edge

Commentary

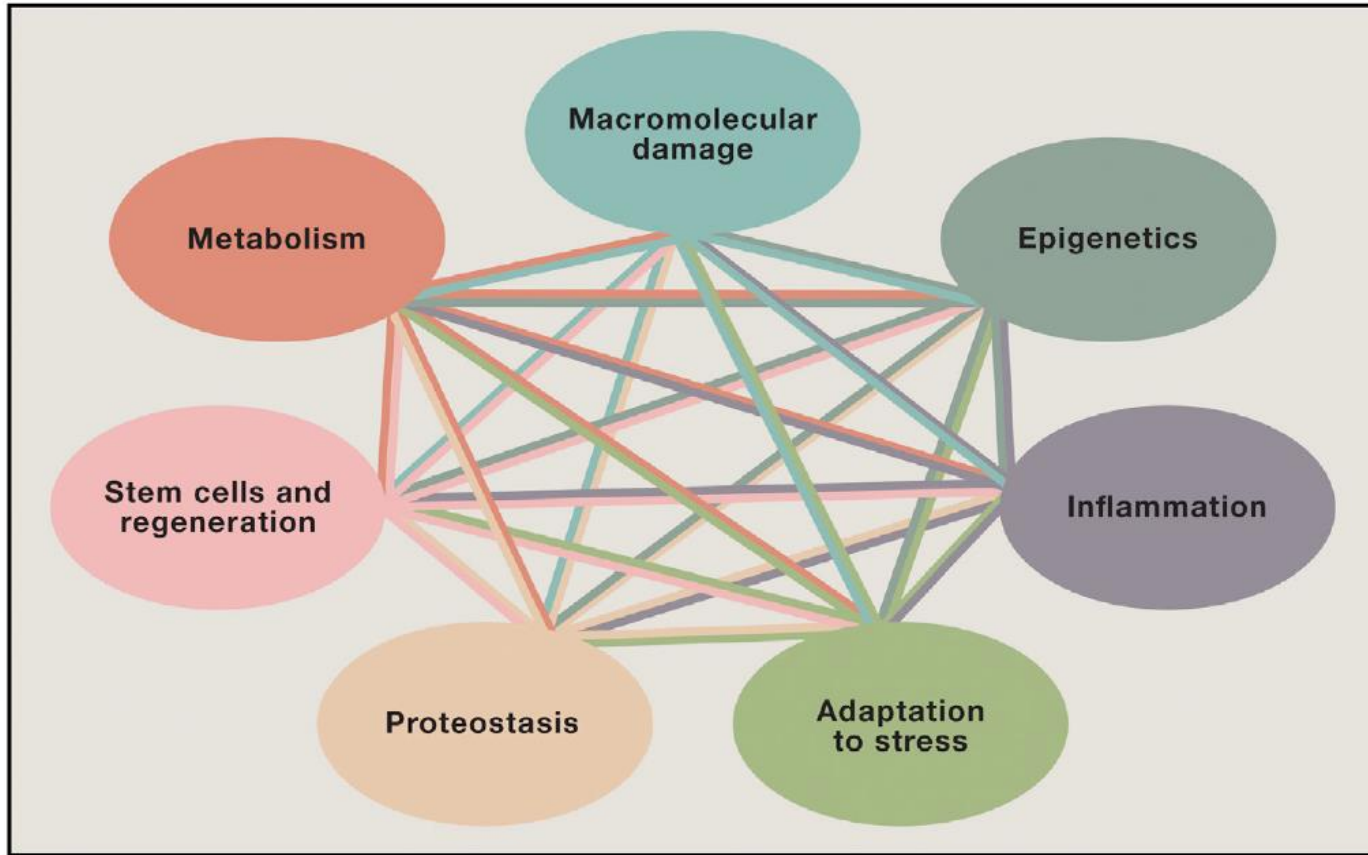
Cell

Geroscience: Linking Aging to Chronic Disease

Brian K. Kennedy,^{1,*} Shelley L. Berger,^{2,3} Anne Brunet,^{4,5} Judith Campisi,^{1,6} Ana Maria Cuervo,^{7,8} Elissa S. Epel,⁹ Claudio Franceschi,^{10,11,12} Gordon J. Lithgow,¹ Richard I. Morimoto,¹³ Jeffrey E. Pessin,¹⁴ Thomas A. Rando,^{5,15,16} Arlan Richardson,^{17,18} Eric E. Schadt,¹⁹ Tony Wyss-Coray,^{15,16} and Felipe Sierra²⁰

Cell 159, November 6, 2014

Inflammaging within a larger, systems biology, networking perspective (striking connectedness)



THE SEVEN HIGHLY INTERTWINED PILLARS OF AGING

Kennedy et al., 2014

Advances in Geroscience: Impact on Healthspan and Chronic Disease Perspective

Chronic Inflammation (Inflammaging) and Its Potential Contribution to Age-Associated Diseases

Claudio Franceschi^{1,2} and Judith Campisi^{3,4}

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²IRCCS Institute of Neurological Sciences, and CNR-ISOF, Bologna, Italy.

³Buck Institute for Research on Aging, Novato, California.

⁴Life Sciences Division, Lawrence Berkeley National Laboratory, California.

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J Gerontol A Biol Sci Med Sci 2014 June;69(S1):S4–S9

“GARBAGING” and INFLAMMAGING

- **INFLAMMAGING** is triggered by **DAMAGE/GARBAGE**, i.e. by a variety of "**danger signals**" which can be:
- **1. EXOGENOUS** or **PAMPs**, i.e. **viruses** such as CMV or HIV, **bacteria** including the **gut/oral-nasal/respiratory- & genito/urinary-tract MICROBIOTA** and its products, **parasites** (“exogenous exposome”)
- **2. ENDOGENOUS/SELF** or **DAMPs**, i.e. damaged and **SENESCENT CELLS, CELL DEBRIS**, altered/modified proteins & lipids, heme, **ROS, extracellular mtDNA, cardiolipin**, AGE, **agalactosylated N-glycans**, extracellular ATP, uric acid, ceramides, HMGB1, resulting from **organelle/cell 3D: Damage/Death/Debris** (“endogenous exposome”)

- Eukaryotic cells contain a plethora of **INTRACELLULAR MOLECULES** that are normally secured within the confines of organelles and the plasma membrane.

When cells are stressed/damaged or die as a result of exposure to pathogens and pathogen-products, nutrient excess, heat, radiation, sterile cellular injury after trauma, ischemia, or toxin-induced cell rupture these molecules, here collectively indicated as **GARBAGE, can be actively liberated/secreted or passively released in two compartments:**

1. Within the cell

2. In the extracellular milieu

In both cases they act as Alarmins or

Danger-Associated Molecular Patterns (DAMPs)

**THIS TYPE OF GARBAGING
AND INFLAMMAGING
IS **PHYSIOLOGICAL**
AND PRODUCED ALSO
BY YOUNG BODIES**

GARBAGE, DANGER SIGNALS & INFLAMMAGING

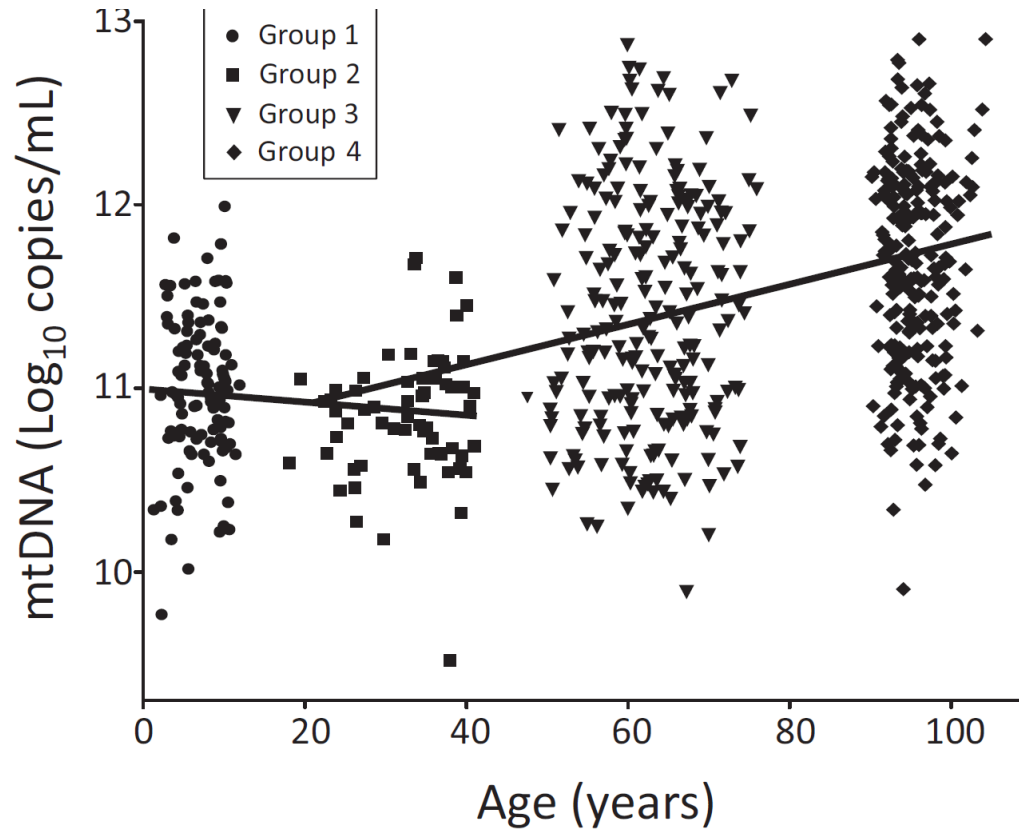
- With increasing age INFLAMMAGING is fostered by:
 - INCREASED EXPOSURE to **exogenous** PAMPs and "danger" signals (*e.g.* altered **MICROBIOTA**, persistent **CMV**) related to immunosenescence
 - INCREASED GENERATION of **endogenous/self** DAMPs and "danger" signals (*e.g.* increased number/amount of **SENESCENT CELLS, CELL DEBRIS, DYSFUNCTIONAL MITOCHONDRIA**)
 - DECREASED EFFICIENCY OF GARBAGE DISPOSAL, *i.e.* **UPS/PROTEASOMES, AUTO- and MITO-PHAGY**
 - INCREASED ACTIVATION of **NF- κ B & INFLAMMASOMES**

Circulating mitochondrial DNA increases with age and is a familiar trait: Implications for “inflamm-aging”

*Marcello Pinti*¹, Elisa Cevenini*^{2,3}, Milena Nasi⁴, Sara De Biasi⁴,
Stefano Salvioli^{2,3}, Daniela Monti⁵, Stefania Benatti¹, Lara Gibellini⁴,
Rodolfo Cotichini^{6,7}, Maria Antonietta Stazi⁶, Tommaso Trenti⁸,
Claudio Franceschi^{2,3} and Andrea Cossarizza⁴*

- **Circulating mtDNA increases with age and is a powerful inflammatory stimulus** contributing to inflammaging.
- The number of copies of circulating mtDNA is significantly correlated between siblings, suggesting that **it is a familial/genetic trait.**

Age-related increase of circulating mtDNA plasma level in the different age groups. Data are generated from 831 samples, and are expressed as \log_{10} mtDNA copies/mL of plasma.



Linear Regression for log 10 mt DNA by age

Groups	Number of obs.	R-squared	Beta Co eff.	Age p	95% CI
Group 1 and 2	171	0.0215	-0.0045	0.055	-0.0091 0.0001
Group 2, 3 and 4	516	0.1590	0.0115	<0.001	0.0092 0.0138

SELF GARBAGE

misplaced cell components – cell debris

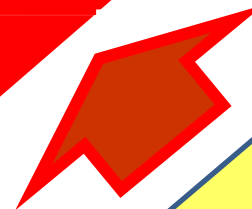


INFLAMMAGING

**NUTRIENTS
(EXCESS)**
MIETABOLITES



**MICROBIOMES
VIROMES**

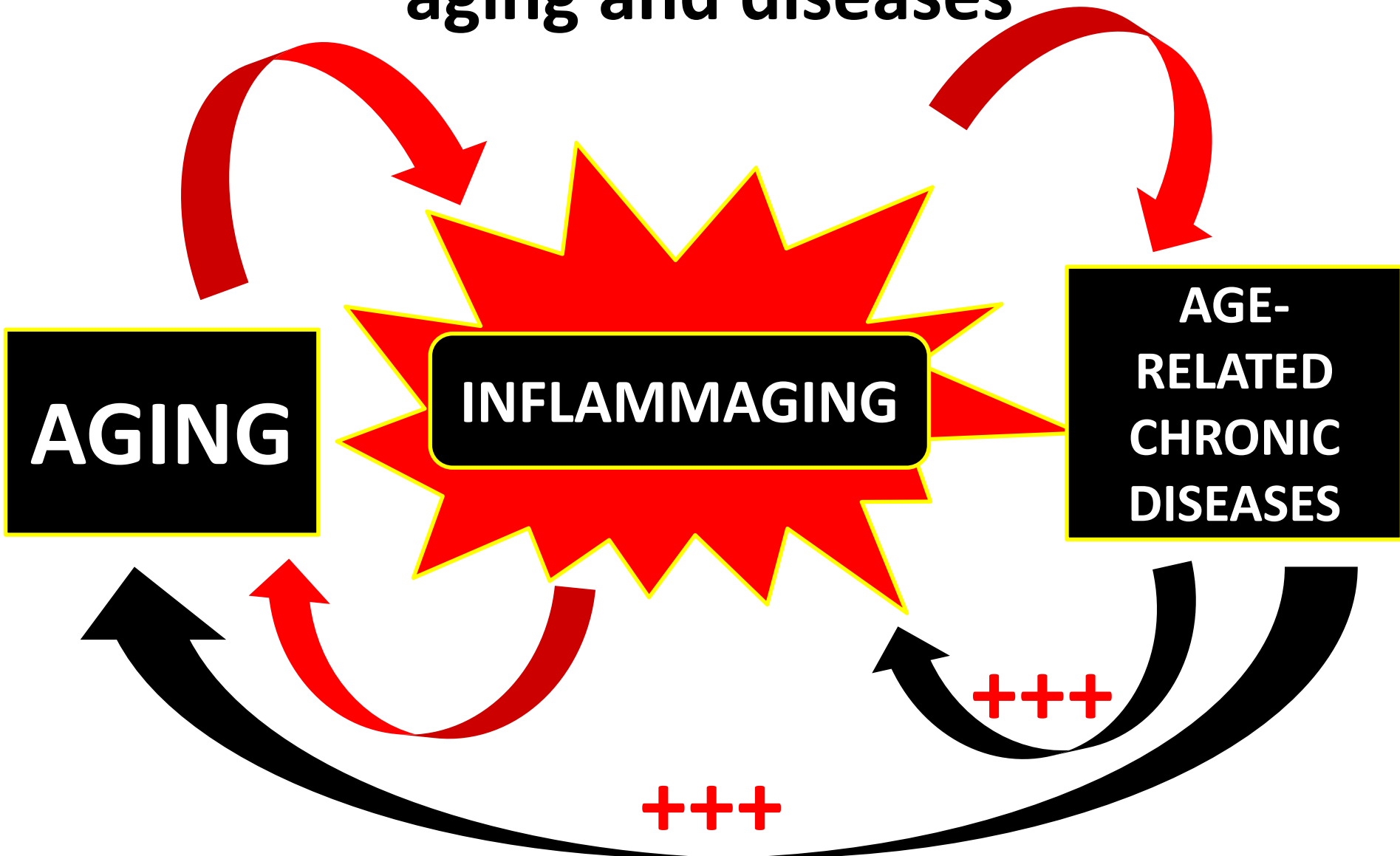


**This perspective assumes that there is
a CONTINUUM between:**

- young and old bodies**
- aging physiology and pathology**

**Inflammaging would represent
the progressive impairment with age
of the physiological garbage disposal.**

The complex relationship between aging and diseases



INFLAMMAGING & age-related diseases

HYPOTHESIS:

All/most age-associated diseases can be conceptualized as “segmental” accelerated aging syndromes, involving/affecting (for genetic and/or lifestyle reasons) specific organs/pathways (more than others), where the aging process and inflammaging propagated faster

Aging and the blurring of the distinction between self and not self

INFLAMMAGING and AGE-RELATED DISEASES can largely be conceptualized as the result of a low grade, progressive/slow, systemic, **lifelong** **AUTO-INFLAMMATORY PROCESS**

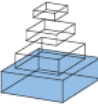
- **driven** by a peculiar type of chronic stimulation,
- **triggered** by external and internal EXPOSOMES
- **favored** by the functional decline of immune responses, *i.e.* by what Roy Walford called ***“immunosenescence”***.

“IMMUNOBIOGRAPHY” & the “Liquid Immunological Self”

frontiers in
IMMUNOLOGY

HYPOTHESIS AND THEORY ARTICLE

published: 09 April 2014
doi: 10.3389/fimmu.2014.00153



Towards a liquid self: how time, geography, and life experiences reshape the biological identity

**Andrea Grignolio^{1*}†, Michele Mishto^{2,3†}, Ana Maria Caetano Faria⁴, Paolo Garagnani⁵,
Claudio Franceschi^{1,5,6,7} and Paolo Tieri^{8*}**

¹ Interdepartmental Center “Luigi Galvani” for Bioinformatics, Biophysics and Biocomplexity, University of Bologna, Bologna, Italy

² Centro Interdipartimentale di Ricerca sul Cancro “G. Prodi”, University of Bologna, Bologna, Italy

³ Institut für Biochemie, Charité – Universitätsmedizin Berlin, Berlin, Germany

⁴ Departamento de Bioquímica e Imunologia, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil

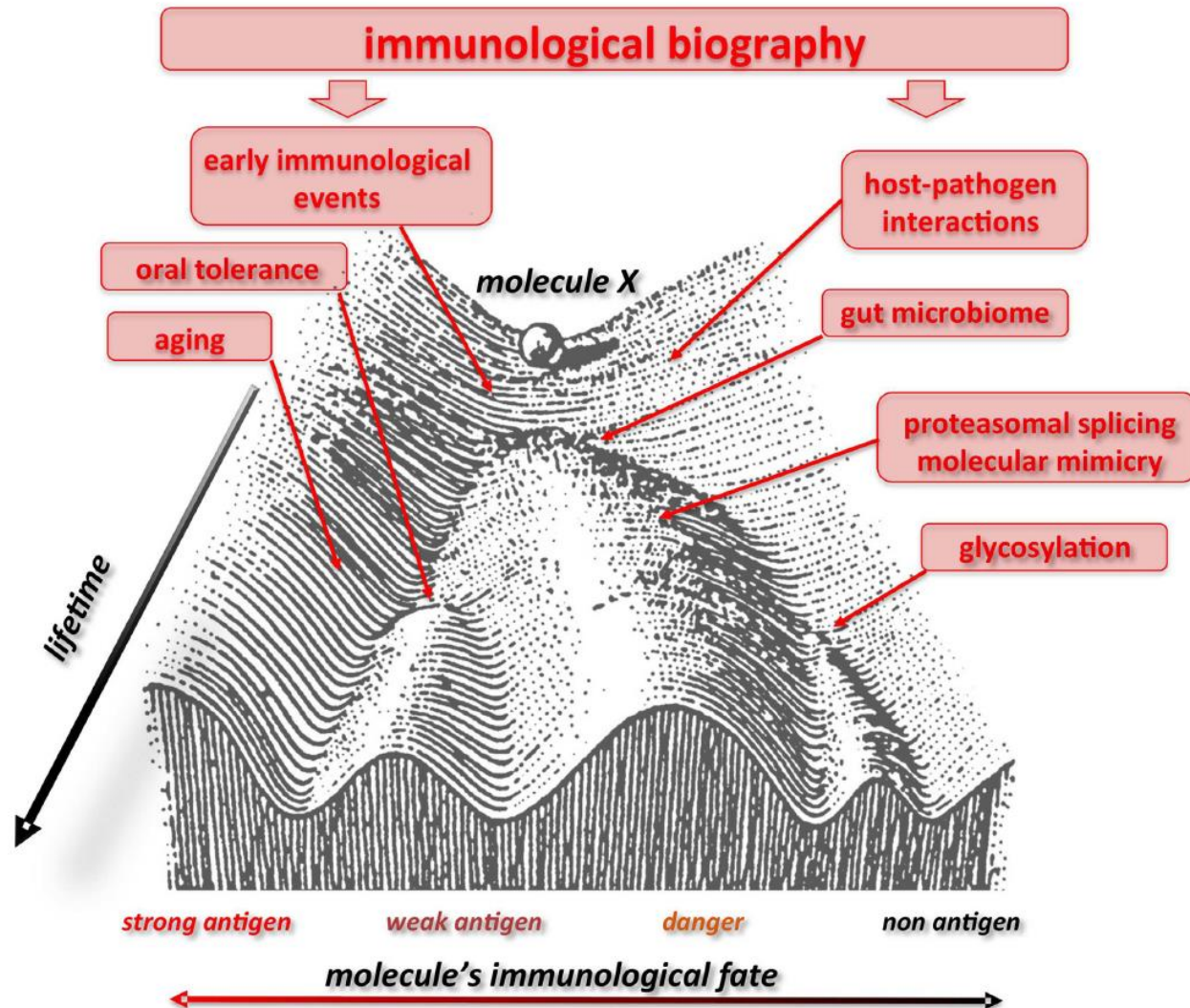
⁵ Department of Experimental, Diagnostic and Specialty Medicine, University of Bologna, Bologna, Italy

⁶ IRCCS of Neurological Science, Bologna, Italy

⁷ Institute of Organic Synthesis and Photoreactivity, National Research Council, Bologna, Italy

**Aging and the blurring of self/non-self
discrimination**

Waddington landscape of the “liquid immunological self”



“inflammaging is a fire”

There is evidence that:

- The aging phenotype is **maintained** by the aged micro/macro-environment.
- Inflammaging can **propagate** from cells to cells (and from organs to organs ?)

Circulating inflammation-miR

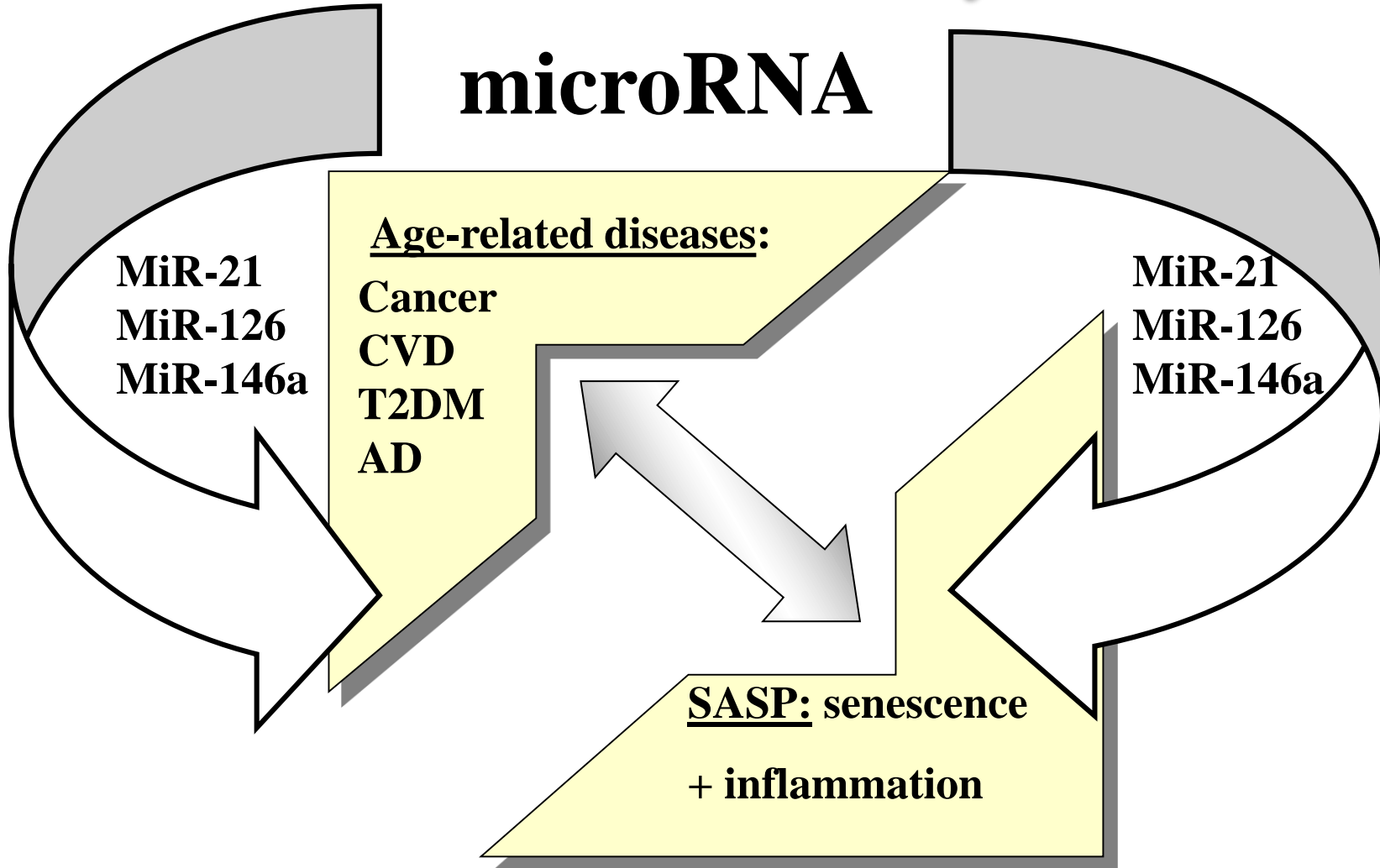
**MicroRNAs linking inflammaging,
cellular senescence and cancer**

**Olivieri F, Rippo MR, Monsurro V,
Salvioli S, Capri M, Procopio AD and
Franceschi C**

Aging Research Reviews, 2013

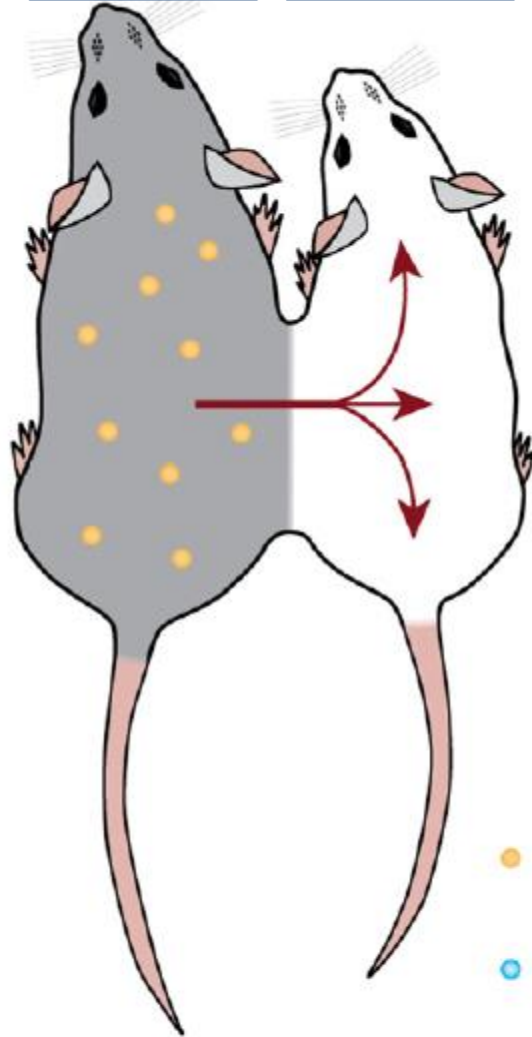
Pro-inflammatory

microRNA



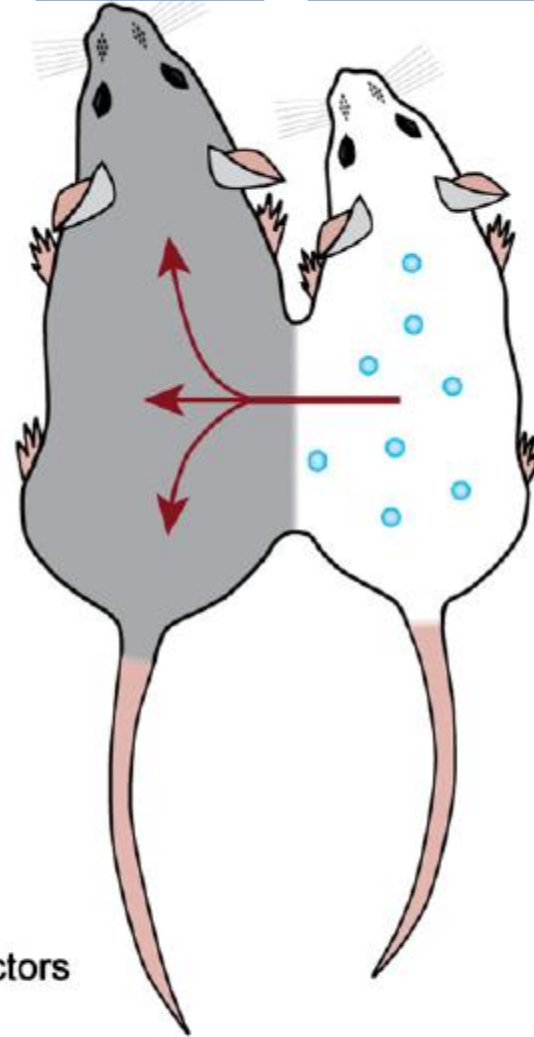
Circulating Inflammation-miRs

A OLD YOUNG



Aging

B OLD YOUNG



Rejuvenation

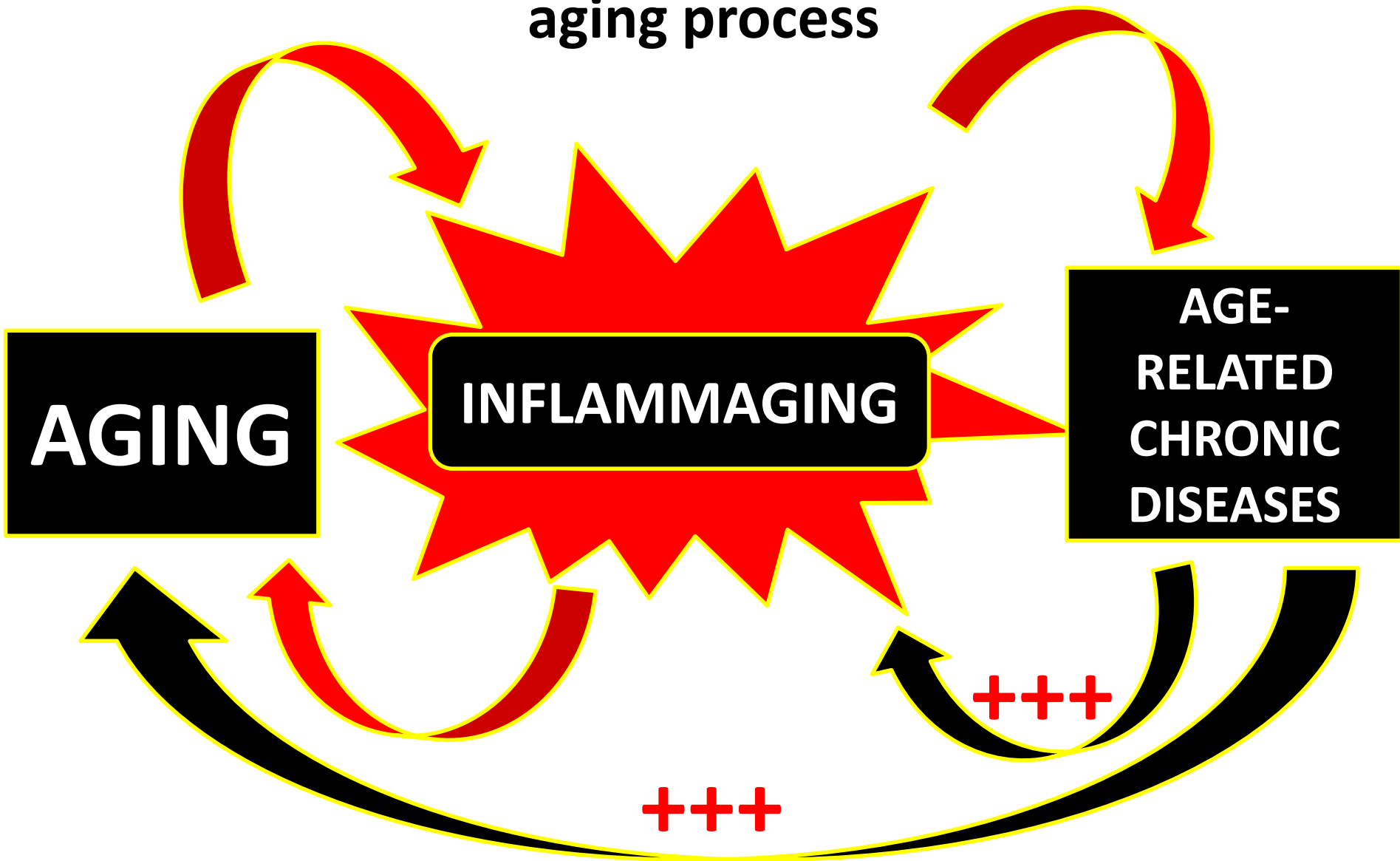
- Aging and immune factors
- Rejuvenating factors

The model of heterochronic parabiosis

A **PROPAGATING** VIEW OF AGING & INFLAMMAGING

- **UNIBO-studied** candidate stimuli present in the blood (**circulating**) which could **maintain and propagate aging and inflammaging**:
- circulating mtDNA
- agalattosylated N-glycans
- inflamma-miR
- gut microbiota products and metabolites
- lipid metabolites

The «communicome» of an age-related disease likely contribute to propagate and accelerate the aging process

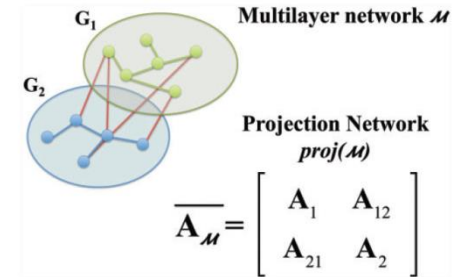
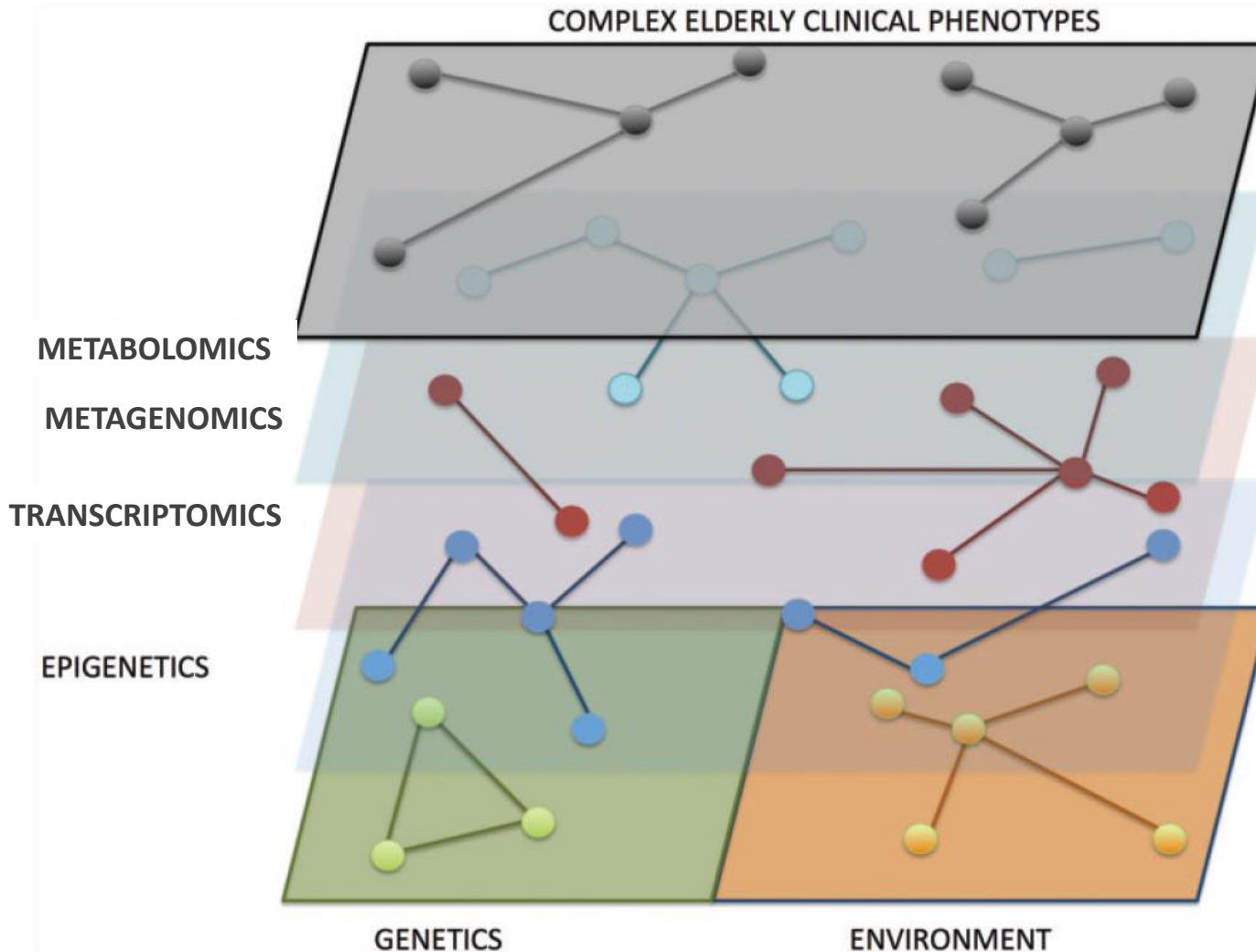


Systems medicine of inflammaging

Gastone C. Castellani*, Giulia Menichetti*, Paolo Garagnani, Maria Giulia Bacalini, Chiara Pirazzini, Claudio Franceschi, Sebastiano Collino, Claudia Sala, Daniel Remondini, Enrico Giampieri, Ettore Mosca, Matteo Bersanelli, Silvia Vitali, Italo Faria do Valle, Pietro Liò and Luciano Milanesi

“INFLAMMAGING is a unifying Biomedical Hypothesis particularly attractive for Systems Medicine as it is multi-scale, multi-organs and propagating among multiple spatial and temporal scales. INFLAMMAGING can be mapped onto a **MULTILAYER NETWORK capable to model and quantify the endogenous and exogenous interactions”**

A SYSTEMIC APPROACH TO AGING/INFLAMMAGING



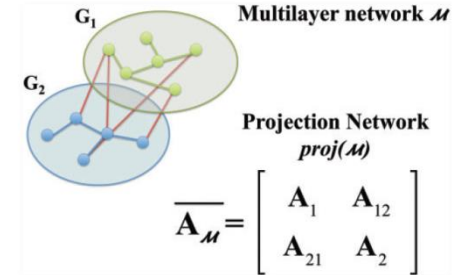
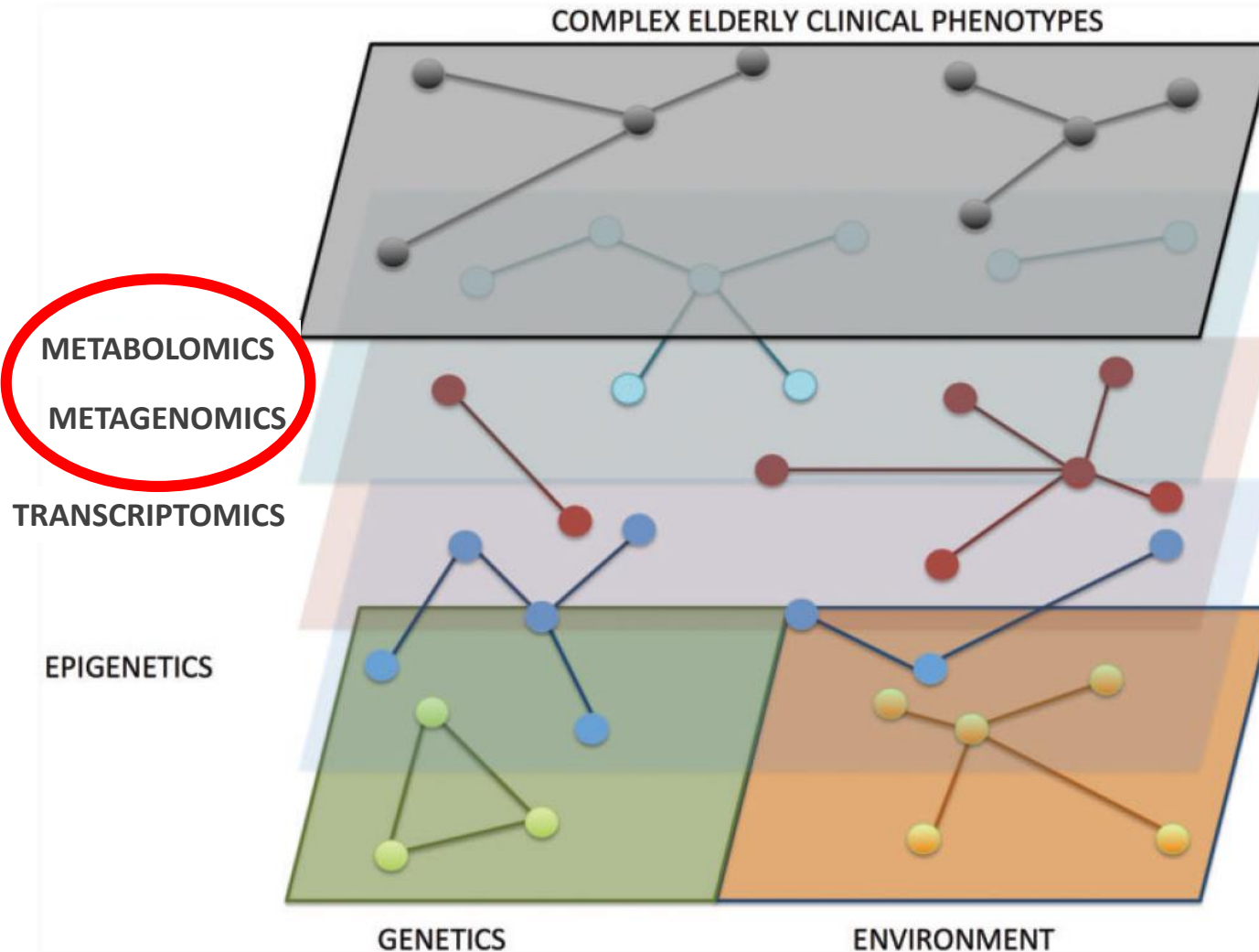
A MULTIPLEX is a set of networks or layers with common nodes.

Each layer corresponds to a given OMIC.

*Intra and inter-layers links are treated with the new concept of **MULTI-LINKS** are (correlation and causal relationships).*

*The basal layer is divided into **GENETICS** and **ENVIRONMENT** to quantify their relative role in a given phenotypical trait*

A SYSTEMIC APPROACH TO AGING/INFLAMMAGING

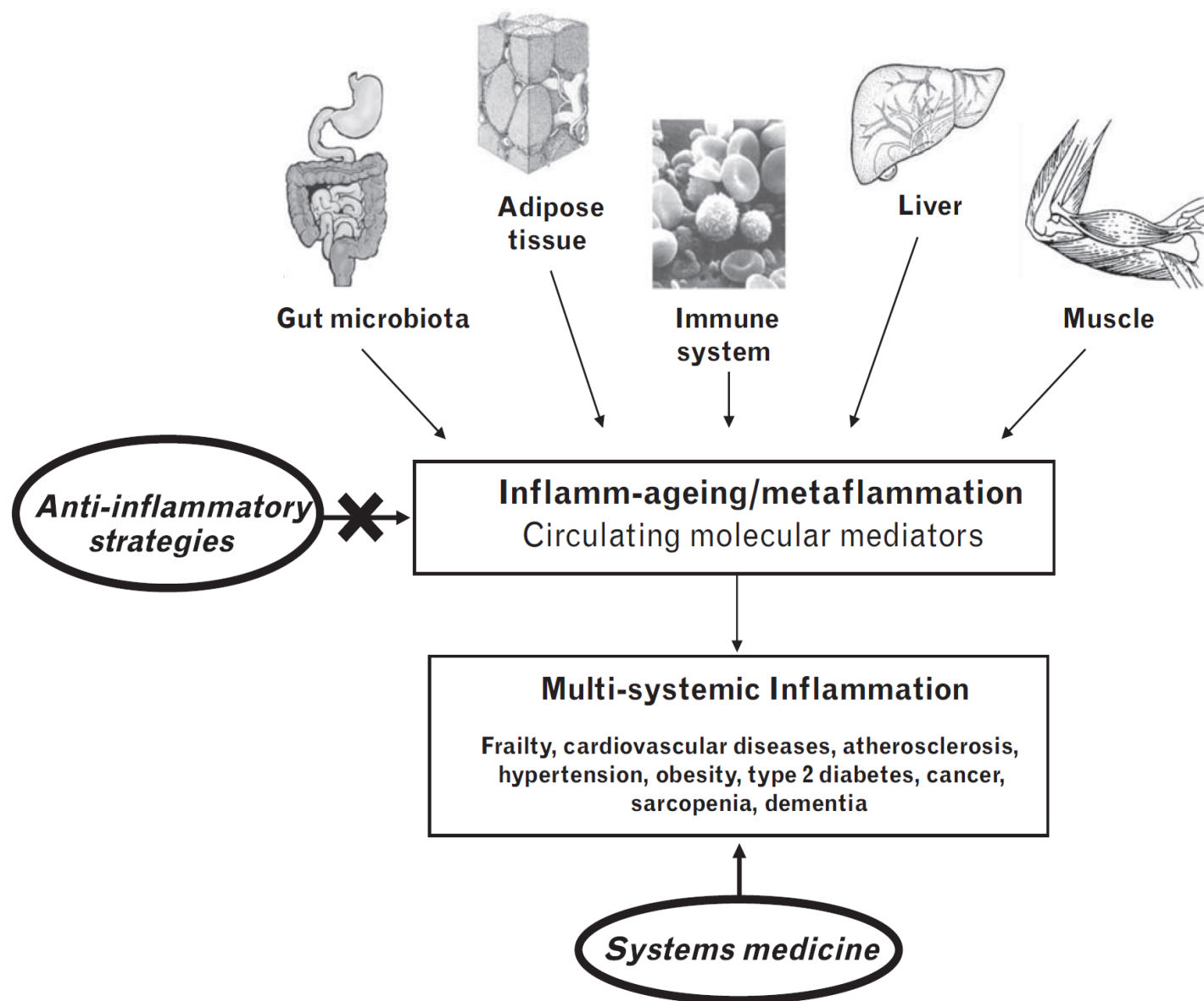


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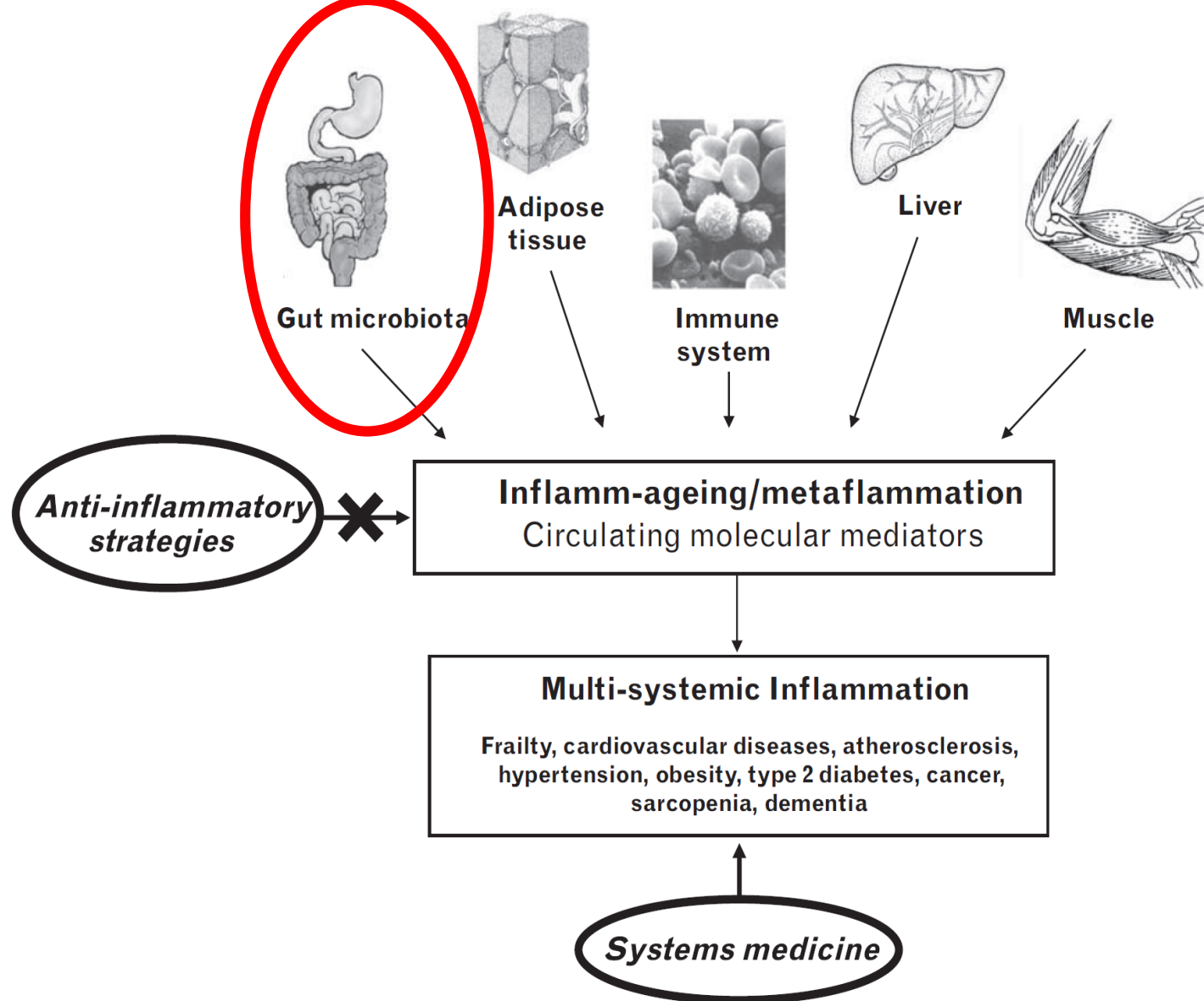
Intra and inter-layers links are treated with the new concept of **MULTI-LINKS** are (correlation and causal relationships).

The basal layer is divided into **GENETICS** and **ENVIRONMENT** to quantify their relative role in a given phenotypical trait



The complex, **systemic** nature of INFLAMMAGING

Cevenini et al., Curr Opin Clin Nutr Metab Care 2012

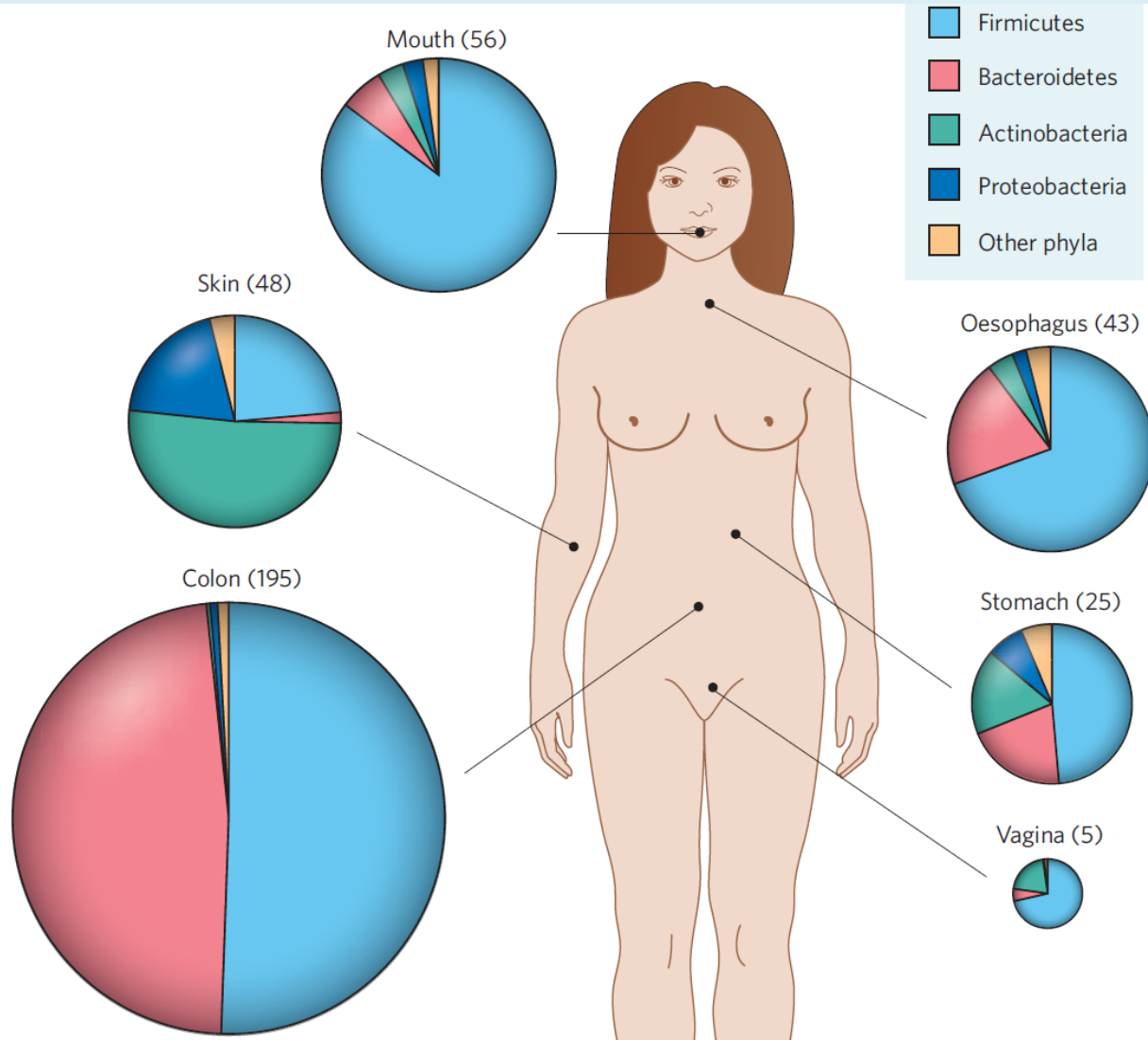


The complex, systemic nature of INFLAMMAGING

Cevenini et al., Curr Opin Clin Nutr Metab Care 2012

Invisible Partners

bacteria in the different body sites



Invisible Partners

bacteria in the different body sites

- **90% of bacteria reside within the gastrointestinal tract** which harbors more than 500 different bacterial species, and about **10^{11} bacteria per gram of luminal content.**
- The human gut microbiome is functional and exerts both **local and long-distance effects** involving hormonal intermediates, metabolites, and immunologic messengers .
- Host-microbe interactions thus have the potential to influence **carcinogenesis** and to promote the onset of others age-related diseases through mechanisms such as **chronic inflammation, induction of genotoxic responses, alteration of the microenvironment, and metabolism**

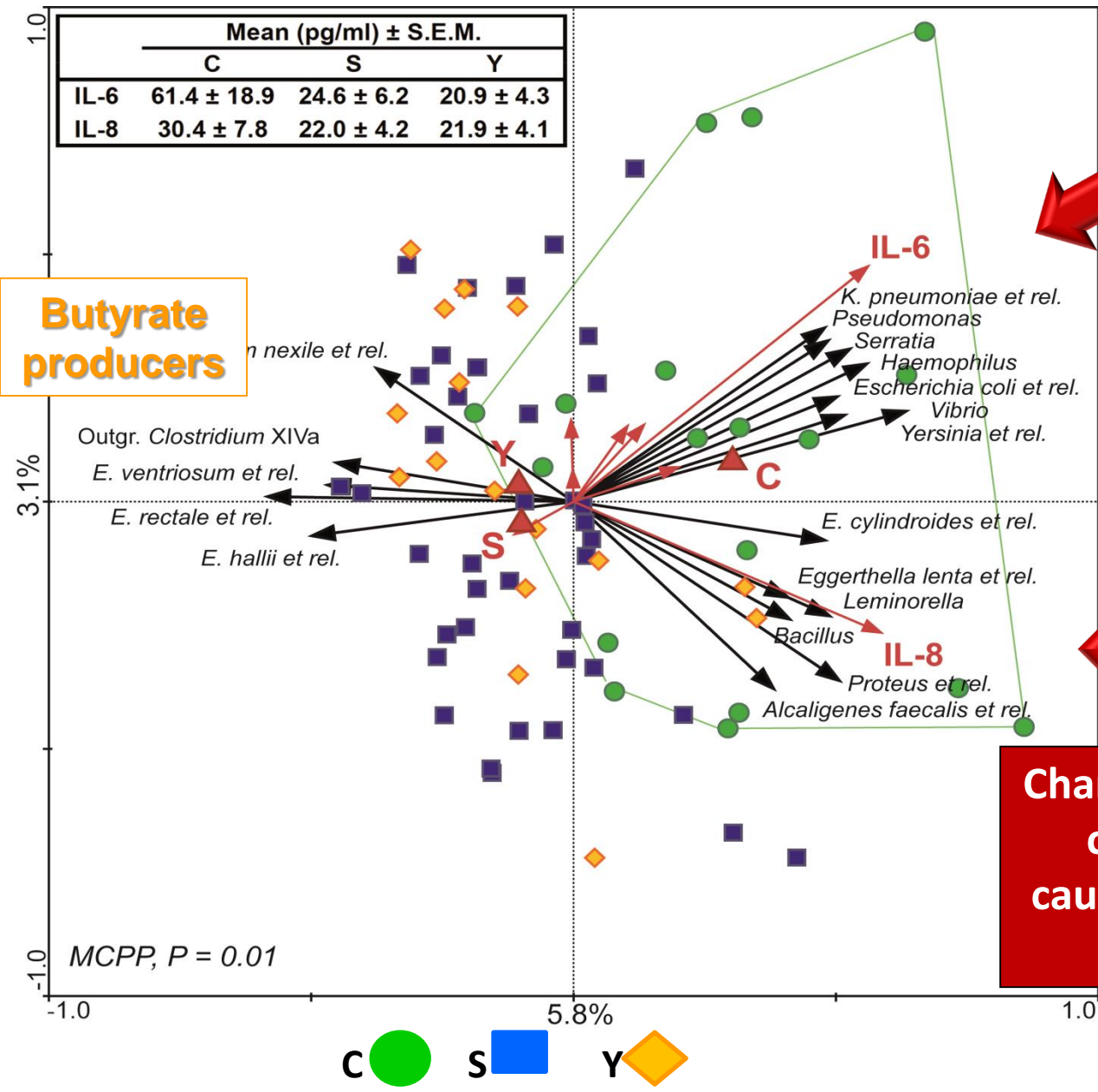
Through Ageing, and Beyond: Gut Microbiota and Inflammatory Status in Seniors and Centenarians

Elena Biagi^{1*}, Lotta Nylund^{2,3}, Marco Candela¹, Rita Ostan⁴, Laura Bucci⁴, Elisa Pini⁴, Janne Nikkila³, Daniela Monti⁵, Reetta Satokari², Claudio Franceschi⁴, Patrizia Brigidi¹, Willem De Vos^{3,6}

1 Department of Pharmaceutical Sciences, University of Bologna, Bologna, Italy, **2** Functional Foods Forum, University of Turku, Turku, Finland, **3** Division of Microbiology and Epidemiology, Department of Basic Veterinary Medicine, University of Helsinki, Helsinki, Finland, **4** Department of Experimental Pathology and CIG-Interdepartmental Center L. Galvani, University of Bologna, Bologna, Italy, **5** Department of Experimental Pathology and Oncology, University of Florence, Florence, Italy, **6** Laboratory of Microbiology, Wageningen University, Wageningen, The Netherlands

PLoS One 2010

CENTENARIAN MICROBIOTA AND INFLAMMATION



8.9% of the total variability of the GM is correlated with the pattern of pro-inflammatory cytokines

Pathobionts

Changes in the microbiota composition can be caused by and contribute inflammaging

Functional metagenomic profiling of intestinal microbiome in extreme ageing

Simone Rampelli ¹, Marco Candela ¹, Silvia Turrone ¹, Elena Biagi ¹, Sebastiano Collino ², Claudio Franceschi ³, Paul W O'Toole ⁴, and Patrizia Brigidi ¹

By **Illumina shotgun sequencing** of the fecal microbial DNA from the centenarians, elderly and young people, we generated **a total of 214.6 million paired-end reads**, with **an average of 23.8 million reads per subject**.

Metagenome function analysis

- We found an age-related **reduction of the pathways involved in Short Chain Fatty Acids (SCFA) production** via proteolytic fermentation.
- Genes involved in SCFA production, showed an inverse association with aging.

Rampelli *et al.*, AGING 2013

SCFA contribute to intestinal homeostasis

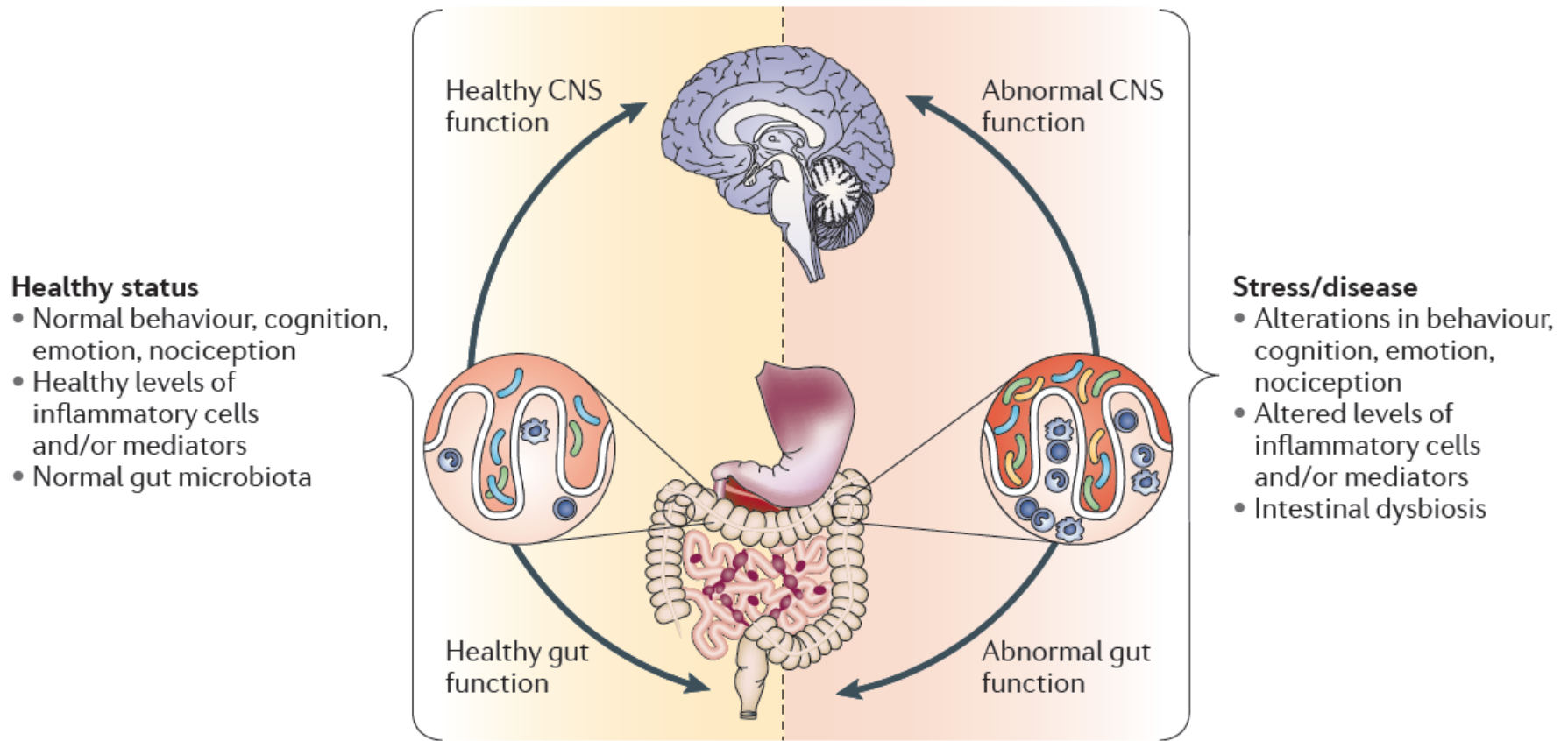
- SCFA such as **acetate, n-propionate, and n-butyrate**:
- are end products of bacterial anaerobic fermentation of **dietary fibers**;
 - are **secreted in high amounts by commensals bacteria** (*e.g.* clusters IV and XIV of Clostridia);
 - can be found at **high concentrations in the large intestine** (*e.g.* 20mM n-butyrate in colonic lumen);
 - are **an important energy source**
 - have **strong anti-inflammatory properties**

Butyrate is mainly produced by clusters IV and XIV of Clostridia and contributes to the maintenance of intestinal homeostasis:

- Acts as an **energy source** for normal colonic epithelial cells (throphic effect)
- **Upregulates histone H3 acetylation** at regulatory regions of Foxp3 gene facilitating the **differentiation of CD4+ T cells into Treg cells**
- Induces **TGF-beta secretion** by epithelial cells
- Triggers the production of cytoprotective cytokine IL-18 and stimulate **IL-10 and retinoic acid production** by dendritic cells and macrophages
- Suppresses the proliferation of cancerous epithelial cells

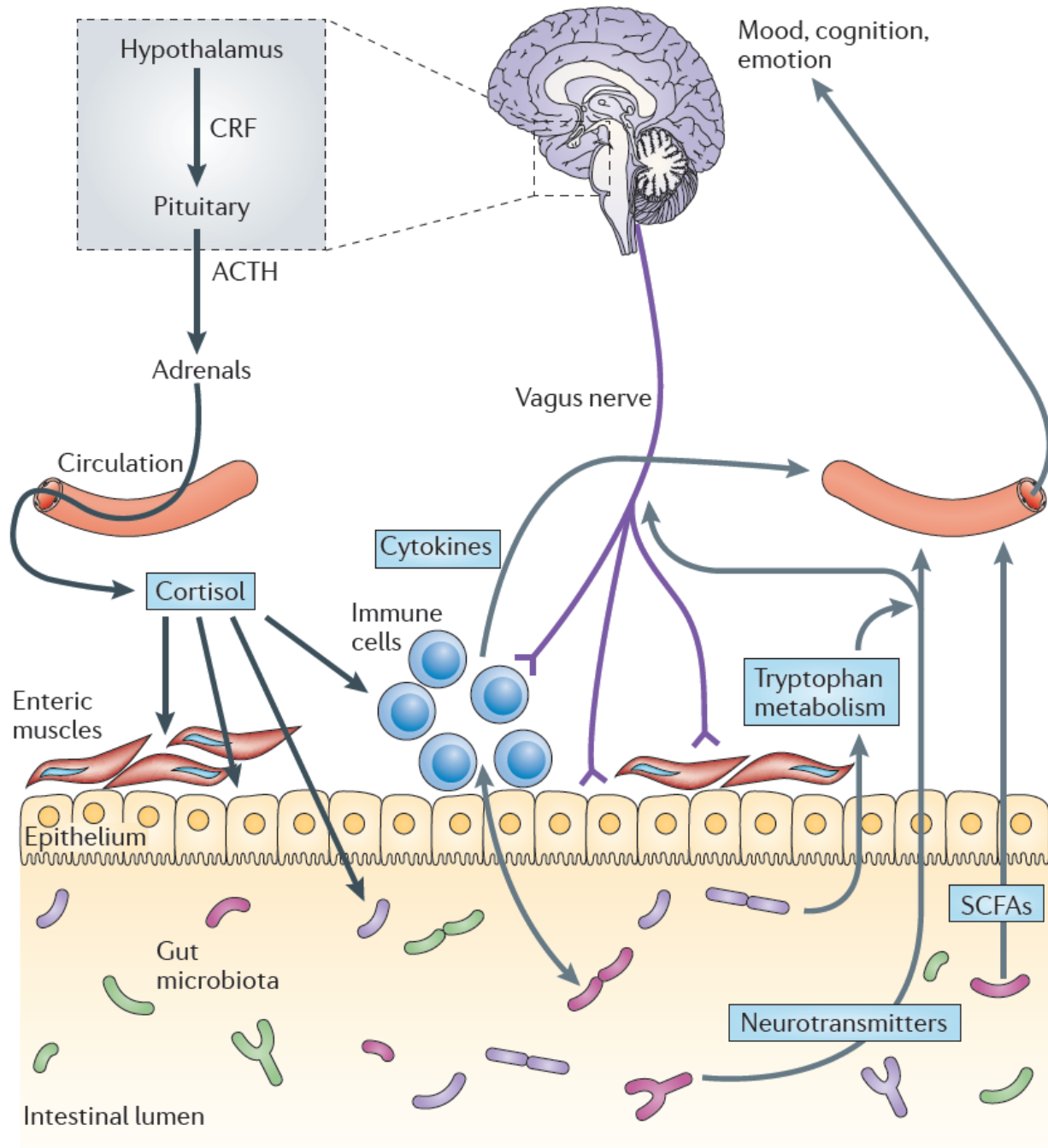
Aging Microbiome, Inflammaging and tryptophan metabolism

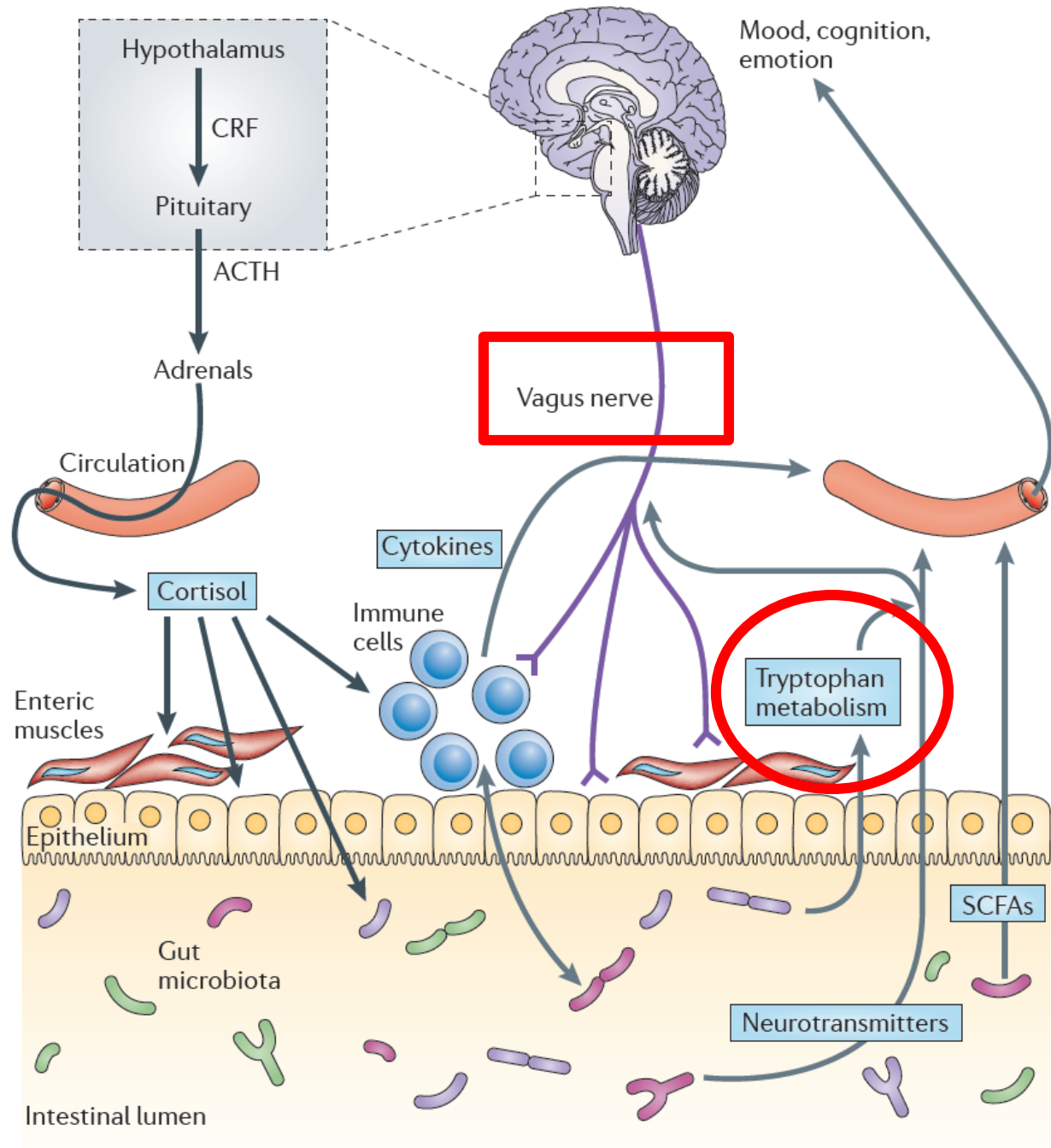
- We observed an age-related **increase of genes involved in the tryptophan metabolism pathway**
- This observation is in agreement with the **reduction of tryptophan in the plasma** of 100+
- Reduced plasma tryptophan levels are related to increase of **immune activation**.
- **The increased consumption of tryptophan by the gut microbiota**, affects its bioavailability within the host, and **can contribute to inflammaging**.



The gut-brain axis

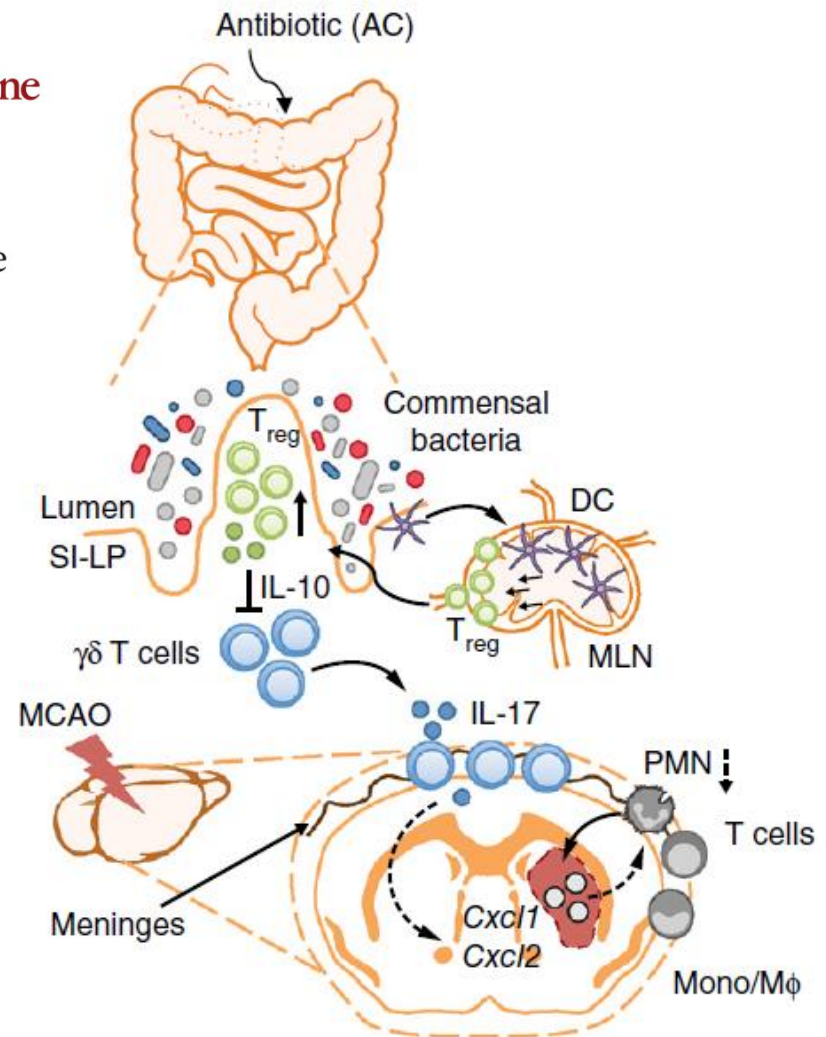
Cryan and Dinan, 2012





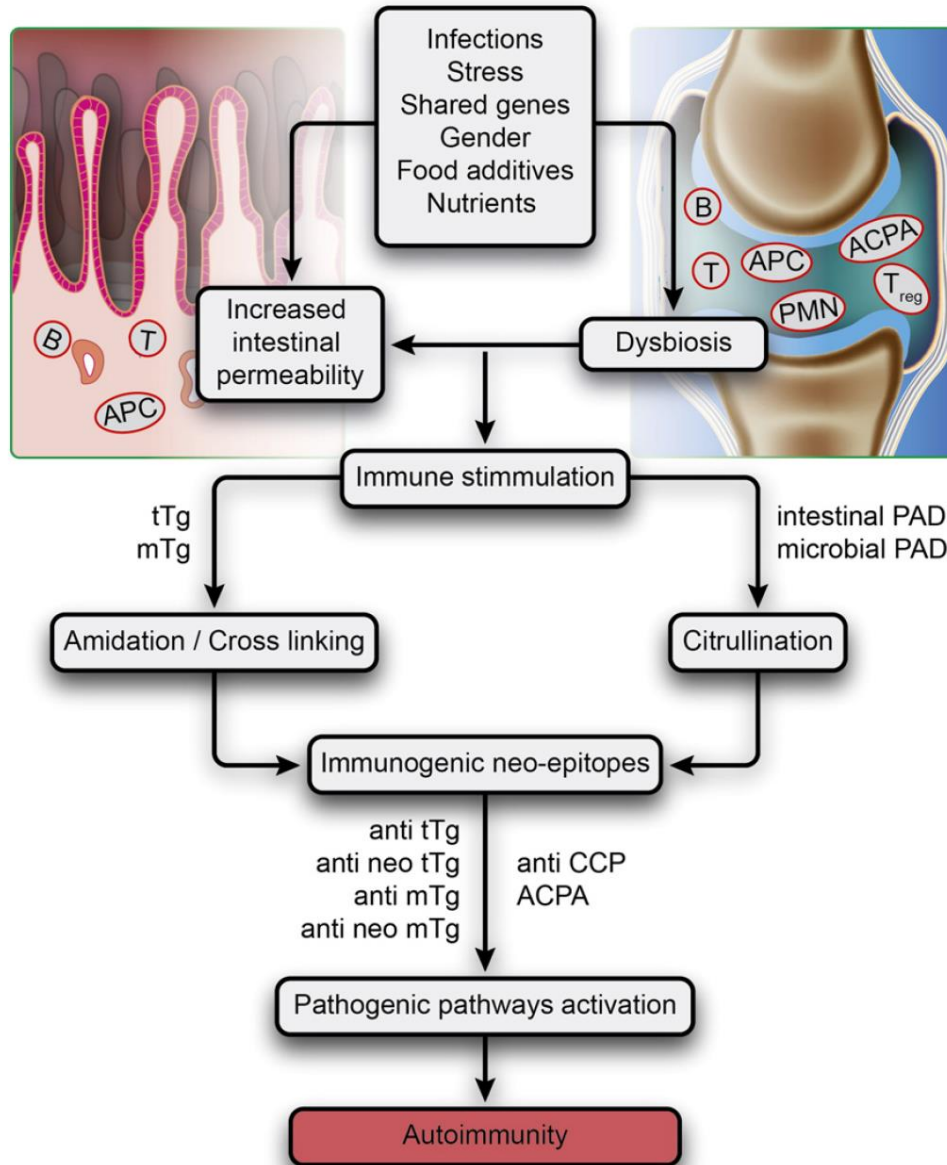
Commensal microbiota affects ischemic stroke outcome by regulating intestinal $\gamma\delta$ T cells

Corinne Benakis^{1,5}, David Brea^{1,5}, Silvia Caballero^{2,3}, Giuseppe Faraco¹, Jamie Moore¹, Michelle Murphy¹, Giulia Sita¹, Gianfranco Racchumi¹, Lilan Ling⁴, Eric G Pamer²⁻⁴, Costantino Iadecola¹ & Josef Anrather¹



Commensal gut bacteria impact the host immune system and can influence disease processes in several organs, including the brain. However, it remains unclear whether the microbiota has an impact on the outcome of acute brain injury. Here we show that antibiotic-induced alterations in the intestinal flora reduce ischemic brain injury in mice, an effect transmissible by fecal transplants. Intestinal dysbiosis alters immune homeostasis in the small intestine, leading to an increase in regulatory T cells and a reduction in interleukin (IL)-17–positive $\gamma\delta$ T cells through altered dendritic cell activity. Dysbiosis suppresses trafficking of effector T cells from the gut to the leptomeninges after stroke. Additionally, IL-10 and IL-17 are required for the neuroprotection afforded by intestinal dysbiosis. The findings reveal a previously unrecognized gut-brain axis and an impact of the intestinal flora and meningeal IL-17⁺ $\gamma\delta$ T cells on ischemic injury.

The gut-joint axis



Gut microbiota and extreme longevity

Biagi Elena^{1,*}, Franceschi Claudio^{2,3,4}, Rampelli Simone¹, Severgnini Marco⁵, Ostan Rita^{2,3}, Turroni Silvia¹, Consolandi Clarissa⁵, Quercia Sara¹, Scurti Maria^{2,3}, Monti Daniela⁶, Capri Miriam^{2,3}, Brigidi Patrizia¹, Candela Marco^{1,*}.

Biagi et al., *Curr Biol* in press

- We highlighted the presence of **a core microbiota** of highly occurring, symbiotic bacterial groups (mostly belonging to the Ruminococcaceae, Lachnospiraceae and Bacteroidaceae families), that represented the majority of the intestinal ecosystem in terms of relative abundance in all samples, but **with a cumulative percentage decreasing along with age.**
- The ageing microbiota is characterized by **an increasing contribution of subdominant species**, as well as a rearrangement in their co-occurrence network.

Table 1. Age-related trajectory of bacterial groups contributing to the sample separation.

Bacterial group	Average relative abundance (%)				Trajectory
	Group Y	Group E	Group C	Group S	
<i>Coprococcus</i>	8.4	5.4	4.9	3.3	↘
<i>Roseburia</i>	7.9	4.6	2.3	2.4	↘
<i>Faecalibacterium</i>	8.6	7.6	4.5	2.6	↘
Uncl. <i>Lachnospiraceae</i>	6.1	5.9	4.9	4.6	↘
<i>Oscillospira</i>	0.9	2.1	3.2	3.6	↗
<i>Odoribacter</i>	0.08	0.2	0.5	0.3	↗
<i>Butyricimonas</i>	0.03	0.07	0.2	0.1	↗
<i>Eggerthella</i>	0.07	0.1	0.1	0.3	↗
<i>Akkermansia</i>	1.1	2.3	2.6	4.0	↗
<i>Anaerotruncus</i>	0.01	0.03	0.05	0.1	↗
<i>Bilophila</i>	0.05	0.08	0.1	0.1	↗
<i>Christensenellaceae</i>	0.5	1.1	2.7	3.3	↗
<i>Synergistaceae</i>	0	0.2	0.6	0.9	↗

AGEING

EXTREME LONGEVITY

22-48y

65-75y

99-104y

105-109y

core
microbiota

subdominant
variable fraction

LONGEVITY:

- CORE MICROBIOTA SHRINKAGE
- ACQUISITION OF A LONGEVITY-ADAPTED SUBDOMINANT FRACTION

**Another
example of
age-related
re-modelling**

Metabolic Signatures of Extreme Longevity in Northern Italian Centenarians Reveal a Complex Remodeling of Lipids, Amino Acids, and Gut Microbiota Metabolism

Sebastiano Collino^{1*}, Ivan Montoliu², François-Pierre J. Martin¹, Max Scherer¹, Daniela Mari^{3,4}, Stefano Salvioli^{5,6}, Laura Bucci^{5,6}, Rita Ostan^{5,6}, Daniela Monti⁷, Elena Biagi⁸, Patrizia Brigidi⁸, Claudio Franceschi^{5,6}, Serge Rezzi¹

1 Proteomics and Metabonomics, Nestlé Institute of Health Sciences SA, Campus EPFL, Quartier de l'innovation, Lausanne, Switzerland, **2** Applied Mathematics, NESTEC SA, Nestlé Research Center, Lausanne, Switzerland, **3** Department of Medical Sciences, University of Milan, Milan, Italy, **4** Geriatric Unit Ca' Grande Foundation Maggiore Policlinico Hospital, Milan, Italy, **5** Department of Experimental Pathology, University of Bologna, Bologna, Italy, **6** Interdepartmental Centre L. Galvani, University of Bologna, Bologna, Italy, **7** Department of Experimental Pathology and Oncology, University of Florence, Florence, Italy, **8** Department of Pharmaceutical Sciences, University of Bologna, Bologna, Italy

PLOS ONE March 2013 | Volume 8 | Issue 3 | e56564

A total of 457 individuals:

N= 143 centenarians

N= 220 offspring of centenarians

N= 73 offspring of non long-lived parents

N= 21 young subjects

Serum profiling of healthy aging identifies phospho- and sphingolipid species as markers of human longevity

Ivan Montoliu¹, Max Scherer², Fiona Beguelin², Laeticia DaSilva², Daniela Mari^{3,4}, Stefano Salvioli^{5,6}, François-Pierre J. Martin², Miriam Capri^{5,6}, Laura Bucci^{5,6}, Rita Ostan^{5,6}, Paolo Garagnani^{5,6}, Daniela Monti⁷, Elena Biagi⁸, Patrizia Brigidi⁸, Martin Kussmann^{2,9,10}, Serge Rezzi², Claudio Franceschi^{5,6}, and Sebastiano Collino²

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¹⁰Faculty of Science, Interdisciplinary NanoScience Center (iNANO), Aarhus University, Aarhus, Denmark;

DNA methylation profile of 105+

Semi-supercentenarians (105+), their Offspring and age- and sex-matched Controls

illumina *Infinium* HumanMethylation450 BeadChip

	Milano **	Bologna *	Calabria ***	TOTAL	Mean Age (± std)	Male (N)	Female (N)
105+	29	33	20	82	105.5 ± 1.7	18	64
Offspring	28	22	13	63	69.8 ± 7.2	22	25
Controls	17	16	14	47	71.6 ± 8.0	26	37
TOTAL	74	71	47	192			

* PI: Prof. Claudio Franceschi, DIMES, UNIBO

** PI: Prof. Daniela Mari, DIP. DI SCIENZE CLINICHE E DI COMUNITA', UNIVERSITÀ DI MILANO

***PI: Prof. Giuseppe Passarino, DIP. DI BIOLOGIA, ECOLOGIA E SCIENZE DELLA TERRA,
UNIVERSITÀ DELLA CALABRIA

DATA ANALYSIS:

Paolo Garagnani, Chiara Pirazzini, Steve Horvath

Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring

Steve Horvath^{1,2*}, Chiara Pirazzini^{3,4*}, Maria Giulia Bacalini^{3,4,5}, Davide Gentilini⁶, Anna Maria Di Blasio⁶, Massimo Delledonne^{5,7}, Daniela Mari^{8,9}, Beatrice Arosio^{8,9}, Daniela Monti¹⁰, Giuseppe Passarino¹¹, Francesco De Rango¹¹, Patrizia D'Aquila¹¹, Cristina Giuliani¹², Elena Marasco^{3,4}, Sebastiano Collino¹³, Patrick Descombes¹⁴, Paolo Garagnani^{3,4,15,§}, and Claudio Franceschi^{3,4,16,17,§}

THE EPIGENETIC CLOCK

Using data of more than 8000 samples present in 82 databases on DNA methylation data obtained by Illumina platforms (**Infinium 450K and 27K**) Steve Horvath (UCLA) identified in the whole genome **353 CpGs** whose methylation level is a

MULTI-TISSUES PREDICTOR OF AGE

which allows to estimate

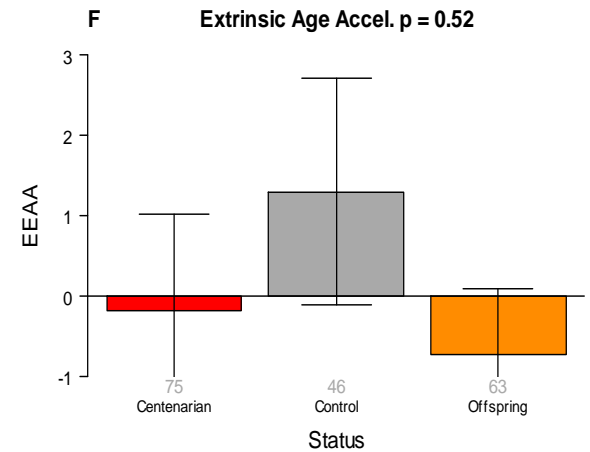
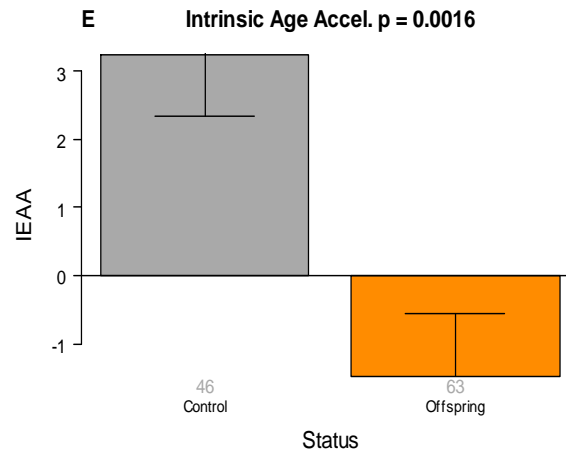
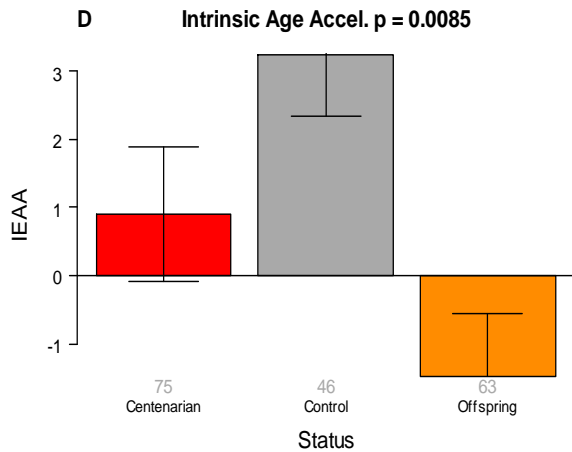
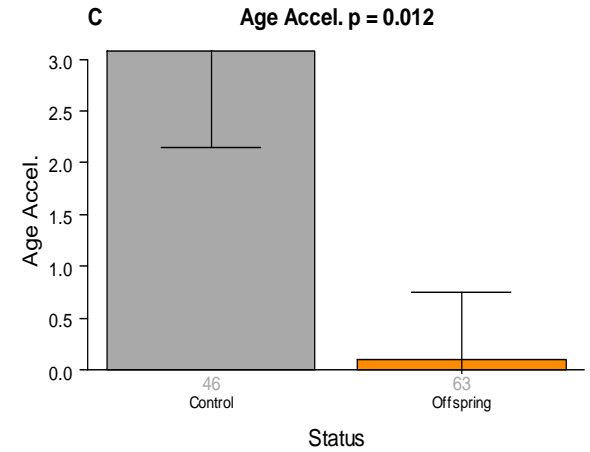
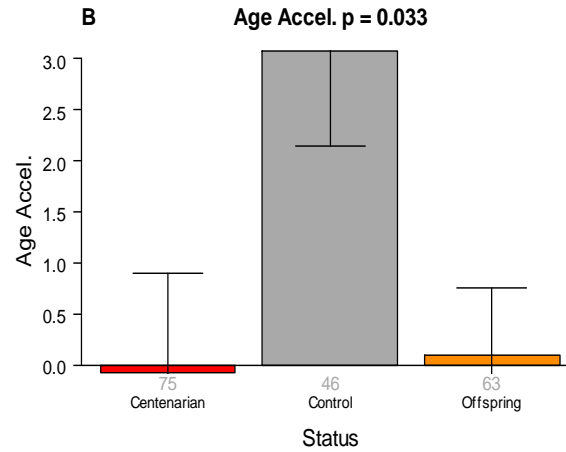
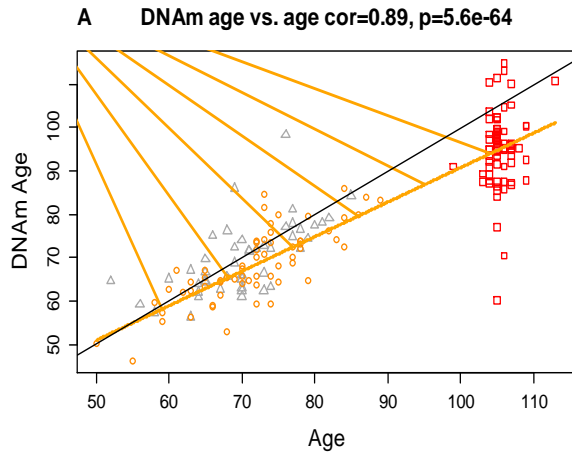
EPIGENETIC AGE VERSUS CHRONOLOGICAL AGE

***i.e.* the DNA METHYLATION AGE (DNAm Age)**

Steve Horvath
DNA methylation age
of human tissues and cell types
Genome Biology 2013, 14:R115

Correlation between
DNAm age and
chronological age = 0.97,
error = 2.9 years

Measures of epigenetic age acceleration/deceleration



**105+ and their offspring age
more slowly than expected
based on their chronological age**

According to this model,
semi-supercentenarians are on average
8.7 years younger than expected based on
chronological age, and **offspring of 105+**
are **5.2 years younger** ($p=0.00051$) than
age- matched controls even after adjusting
for sex and blood cell counts.



**Thanks
for
your
attention**

**BOLOGNA/UNIBO: the arcades of the oldest university in the
Western world (founded in 1080)**