

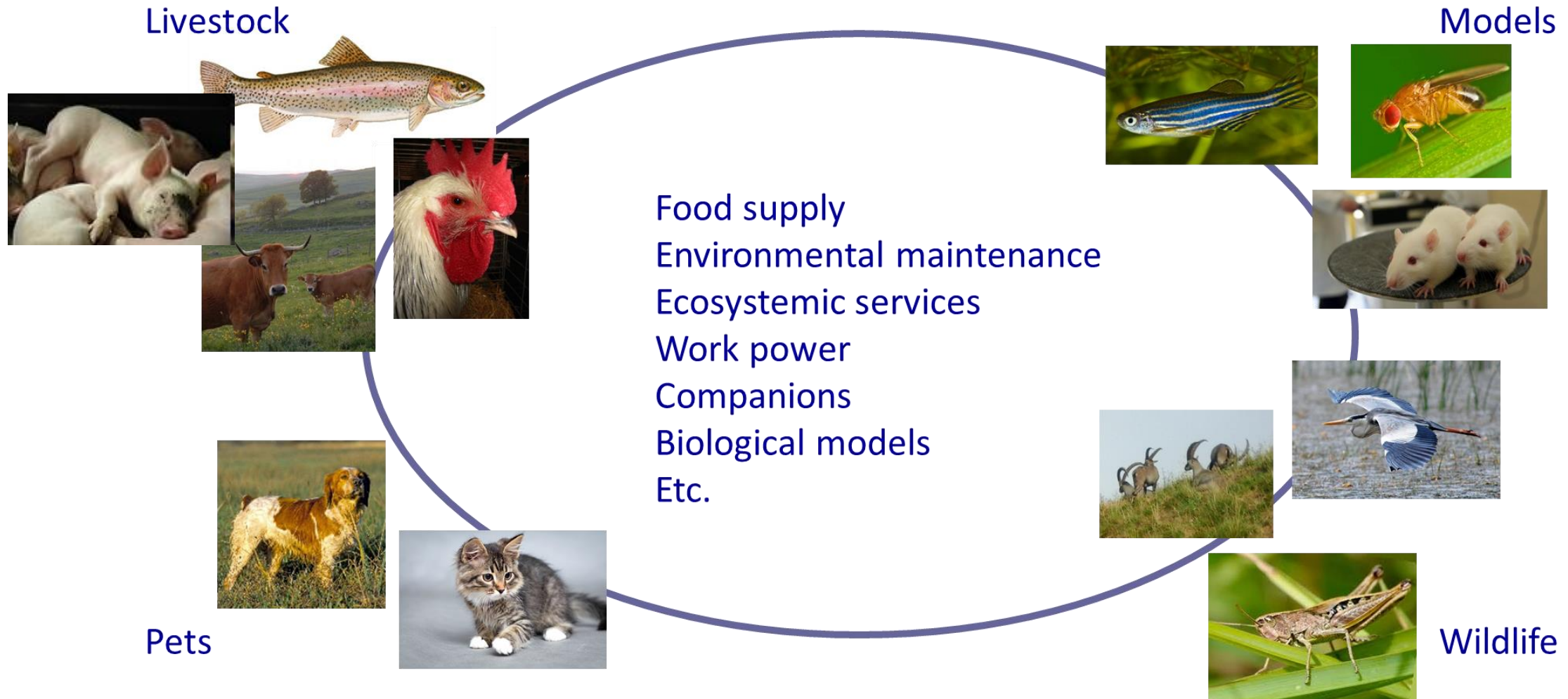
➤ HIGHLIGHTS ON ANIMAL MICROBIOMES

Claire Rogel-Gaillard

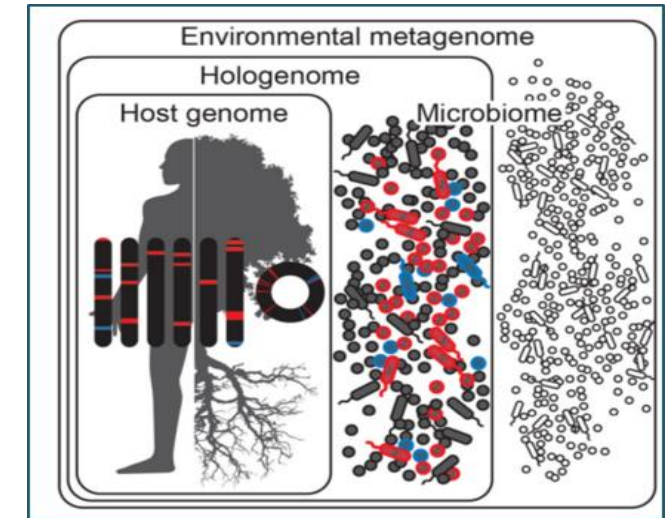
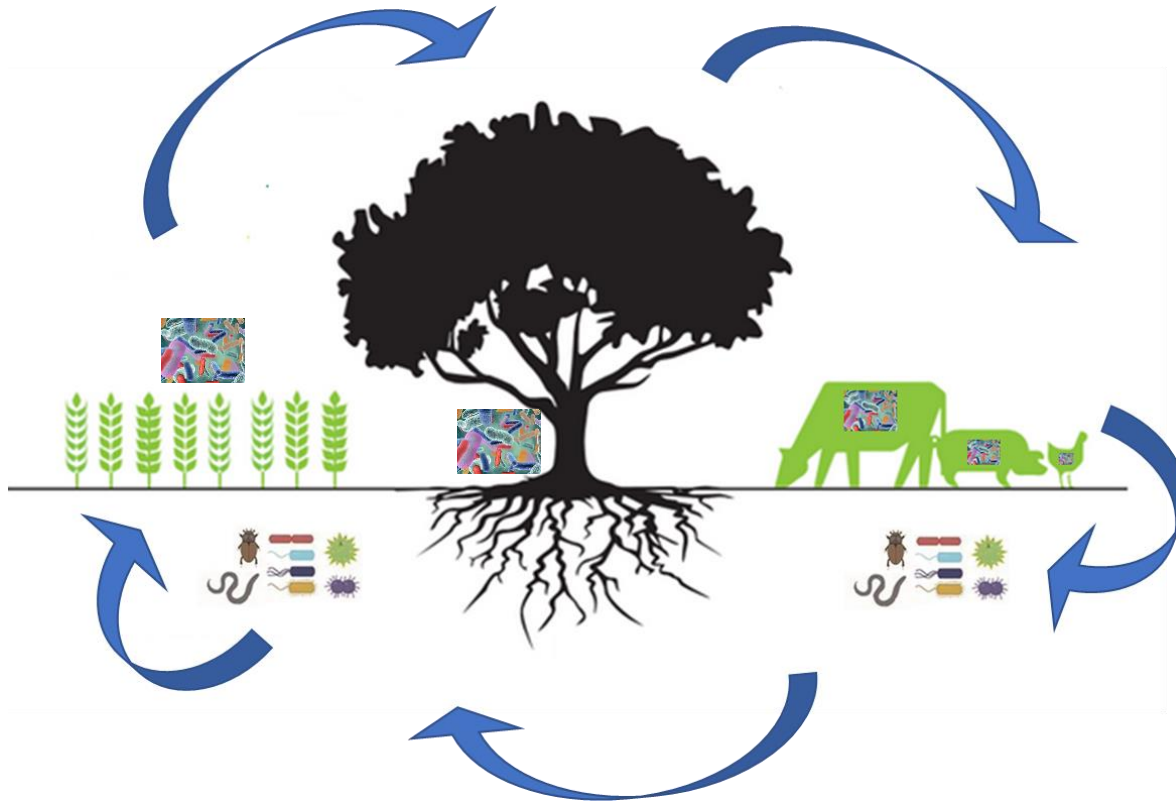
Email: claire.rogel-gaillard@inrae.fr



➤ ANIMALS SERVE A WIDE RANGE OF FUNCTIONS TO HUMAN SOCIETIES AND TO THE ENVIRONMENT: FOCUS ON LIVESTOCK



➤ LIVING ORGANISMS ARE INTERACTING HOLOBIONTS IN A SHARED ENVIRONMENT - DYNAMIC MICROBIAL FLUXES



Theis et al., mSystems, 2016



Source: European Commission

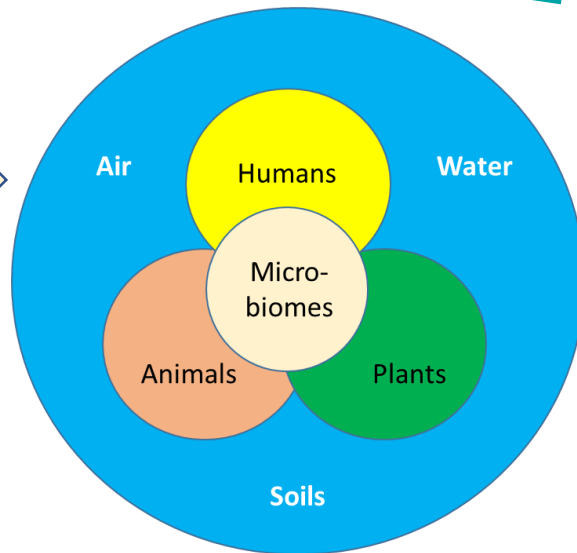
➤ THE AGROECOLOGICAL TRANSITION OF LIVESTOCK SYSTEMS

Multi-performance: environmental, societal, economical

- Yields
 - Growth
- ➔
- Product quality
 - Reproduction capacity
 - Resistance to diseases
- ➔

- Environmental footprint
- Climate change mitigation
- Adaptation to changing environments
- Resistance to disease
- Immune capacity
- Robustness
- Welfare, longevity

Genomes
X
Microbiomes
X
Environment
X
Practices
X
Socioeconomics



One World - One Health



Main concerns

- Reducing the use of antibiotics and antimicrobials
- Feed efficiency, greenhouse gas emissions
- Promoting health and welfare
- Combining sustainability and competitiveness

➤ FOR ANIMALS, THE GUT MICROBIOME OCCUPIES A STRATEGIC POSITION

Trophic and metabolic functions

- Energy expenditure
- Nutrient accessibility
- Short chain fatty acids
- Adiposity
- Vitamins

Intestine functions

- Tissue regeneration
- Gut motility
- Permeability

Intestinal vessel formation

Feed efficiency
Methane

Connectivity along the axis gut microbiota-brain

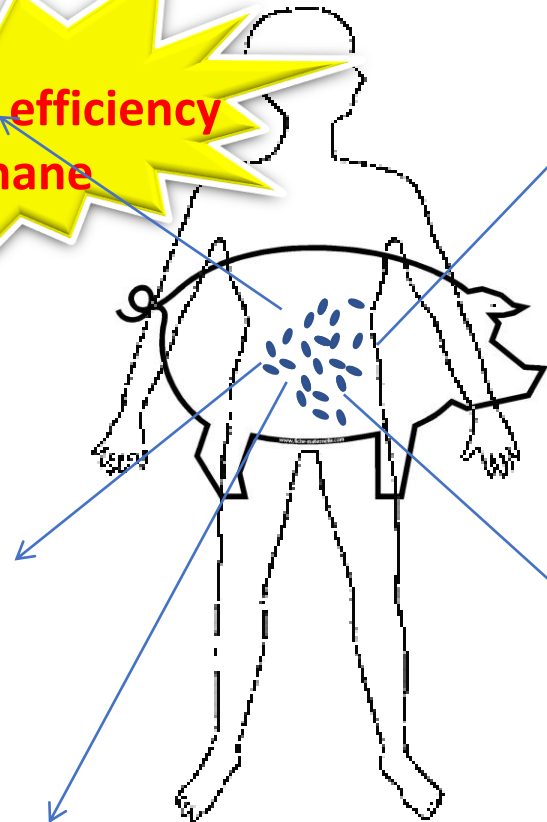
- Anxiety
- Pain perception
- Behavior

Animal welfare

Immunity functions and protection against pathogens

- Maturation of gut-associated lymphoid tissues (GALT)
- Local and systemic immunity

Immune capacity
resistance to diseases

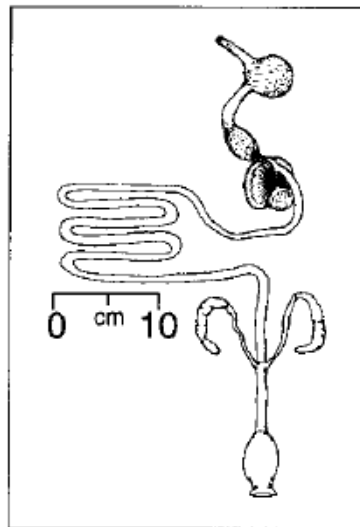


➤ THE DIGESTIVE TRACT: SPECIES-SPECIFIC EVOLUTION STRATEGIES



Chicken

(*Gallus domesticus*)
Body length: 46 cm

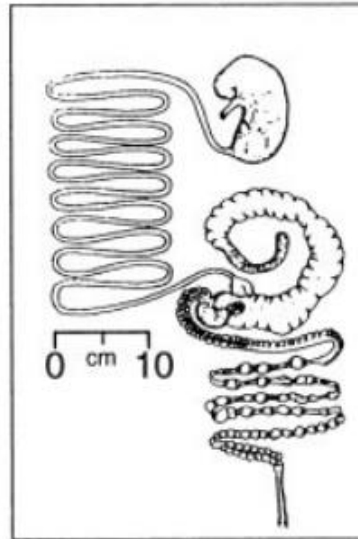


Caecum



Rabbit

(*Oryctolagus cuniculus*)
Body length: 48 cm

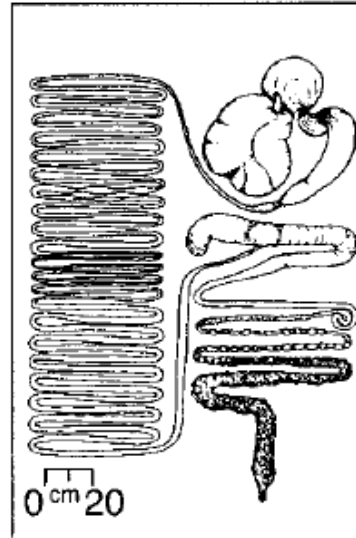


Caecum



Sheep

(*Ovis aries*)
Body length: 110 cm

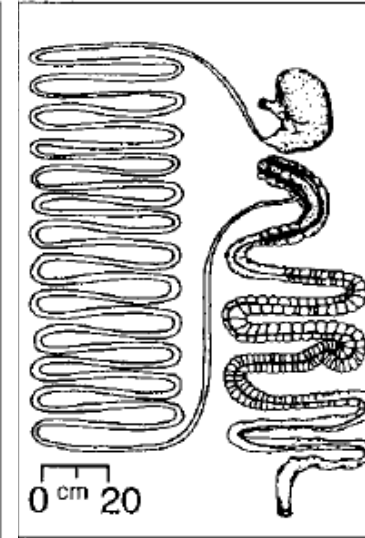


Rumen



Pig

(*Sus scrofa*)
Body length: 125 cm



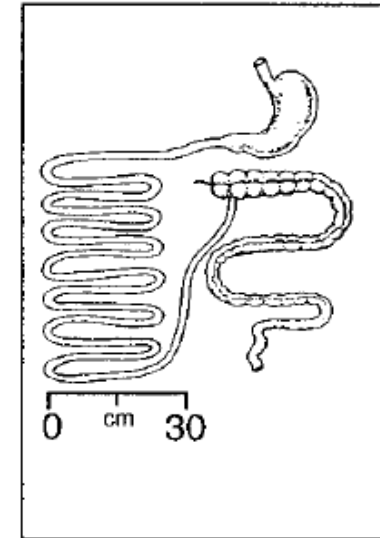
Gut

(surrogate samples: stools)



Adult Human

(*Homo sapiens*)
Body length: 180 cm



Gut

➤ COMPLEMENTARY QUESTIONS AND APPROACHES

Composition and variability ?

- 16S, 18S, 23S
- Shotgun metagenomics
- Reduced sequencing



Gene catalogs

Factors influencing microbiomes ?

- Host genetics
- Feed and feed additives
- Environment
- Age, sex
- Farm practices
- Medication



Host genetics

Links with traits of interest ?

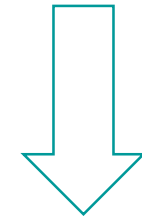
- Feed efficiency
- Methane emission
- Behavior and welfare
- Sensitivity to pathogens
- Immune capacity



Weaning

Prediction and diagnostics ?

- Microbiability
- Biomarkers



Vaccine response

➤ CONSTRUCTION OF GENE CATALOGS

2016

nature
microbiology

LETTERS

PUBLISHED: 19 SEPTEMBER 2016 | ARTICLE NUMBER: 16161 | DOI: 10.1038/NMICROBIOL.2016.161

A reference gene catalogue of the pig gut microbiome



2021

nature
COMMUNICATIONS


ARTICLE

 Check for updates

<https://doi.org/10.1038/s41467-021-21295-0>

OPEN

Expanded catalog of microbial genes and metagenome-assembled genomes from the pig gut microbiome

Congying Chen^{1,2,3}✉, Yunyan Zhou^{1,2}, Hao Fu¹, Xinwei Xiong¹, Shaoming Fang¹, Hui Jiang¹, Jinyuan Wu¹, Hui Yang¹, Jun Gao¹ & Lusheng Huang^{1,3} ✉

2018

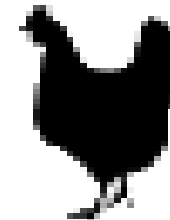
Huang *et al. Microbiome* (2018) 6:211
<https://doi.org/10.1186/s40168-018-0590-5>

Microbiome

RESEARCH

Open Access

The chicken gut metagenome and the modulatory effects of plant-derived benzyloquinoline alkaloids



> CONSTRUCTION OF GENE CATALOGS



2020

GigaScience, 9, 2020, 1–15

doi: [10.1093/gigascience/giaa057](https://doi.org/10.1093/gigascience/giaa057)

Research

RESEARCH

A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment

2021

Xie et al. *Microbiome* (2021) 9:137
<https://doi.org/10.1186/s40168-021-01078-x>

Microbiome

RESEARCH

Open Access

An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants

2020

SCIENTIFIC REPORTS

nature research

Co-abundance analysis reveals hidden players associated with high methane yield phenotype in sheep rumen microbiome

Leila Ghanbari Maman^{1,3}, Fahimeh Palizban^{1,3}, Fereshteh Fallah Atanaki¹, Naser Elmi Ghiasi¹, Shohreh Ariaeenejad², Mohammad Reza Ghaffari², Ghasem Hosseini Salekdeh^{1,2*} & Kaveh Kavousi^{1*}

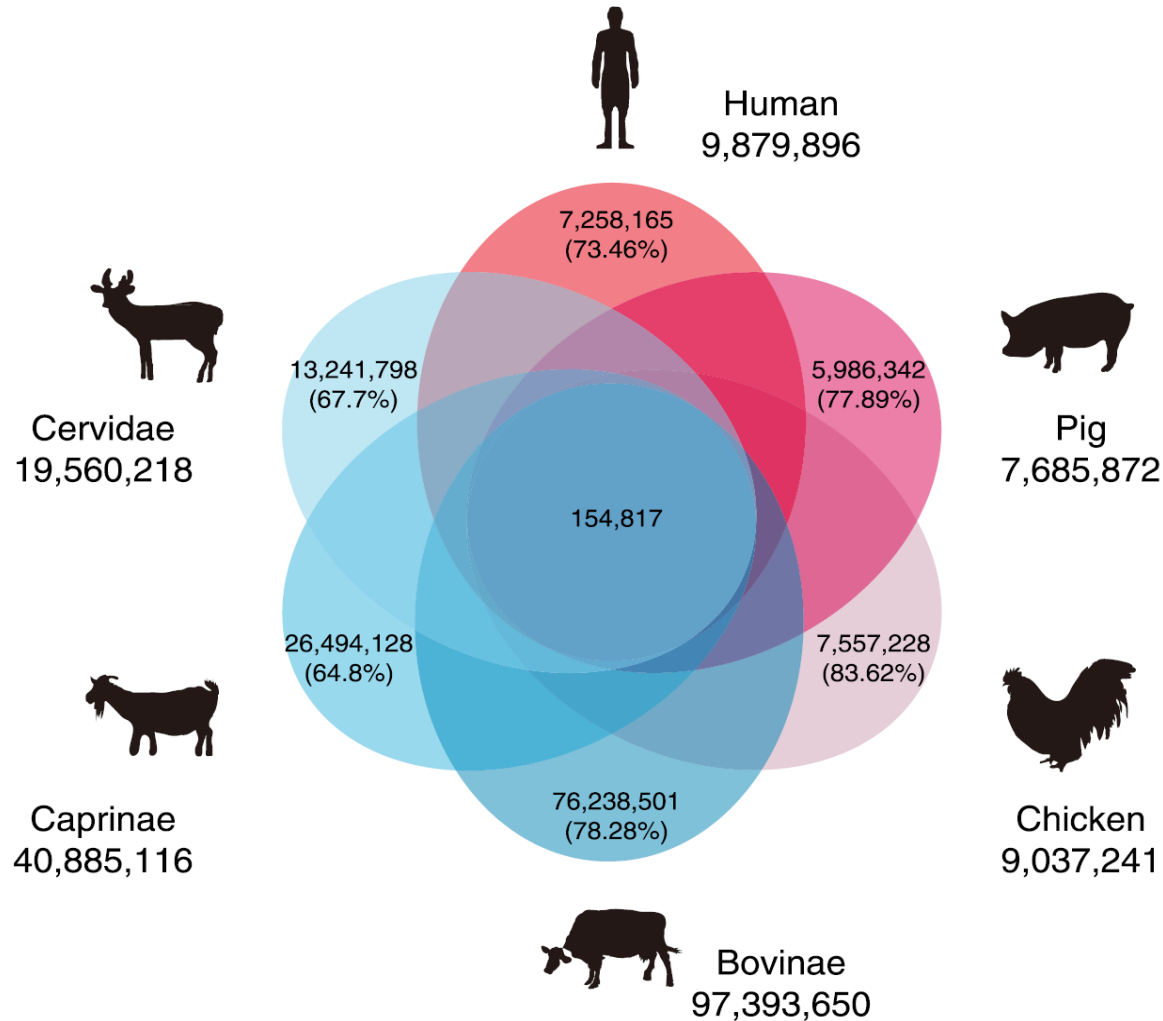
7 ruminant species:

- Dairy cattle
- Water buffalo
- Yak
- Goat
- Sheep
- Roe deer
- Water deer

10 GIT regions:

- Stomach: rumen, reticulum, omasum, abomasum
- Small intestine: duodenum, jejunum, ileum
- Large intestine: cecum, colon, rectum

➤ GENE CATALOGS OF MICROBIOMES TELL STORIES ON THEIR HOST SPECIES



Reference resources for functional metagenomics





Bioinformatics, 37(18), 2021, 2848–2857
doi: 10.1093/bioinformatics/btab216
Advance Access Publication Date: 1 April 2021
Original Paper

OXFORD

Sequence analysis

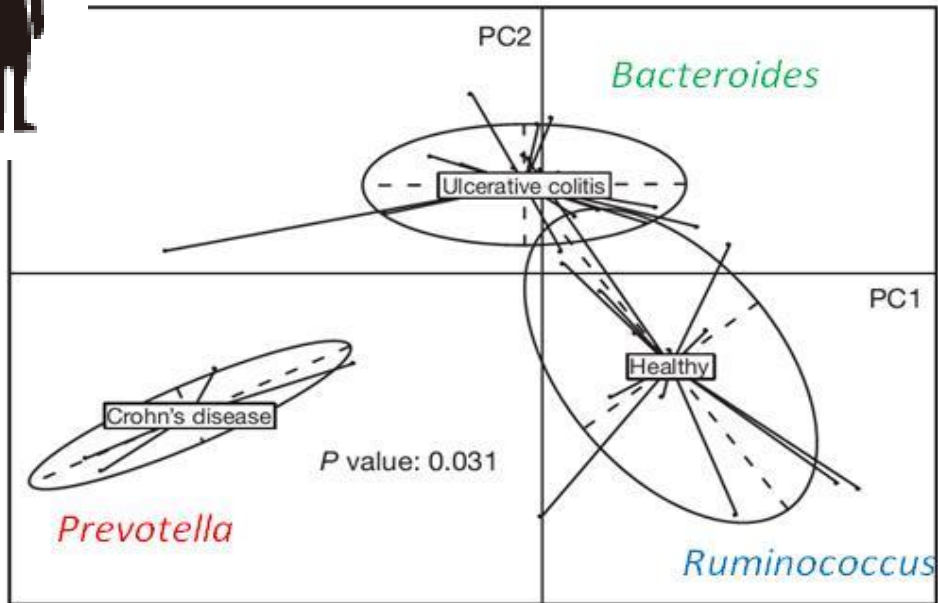
A critical assessment of gene catalogs for metagenomic analysis

Seth Commichaux^{1,2,3,†}, Nidhi Shah ^{1,4,†}, Jay Ghurye^{1,4}, Alexander Stoppel¹, Jessica A. Goodheart⁵, Guillermo G. Luque⁶, Michael P. Cummings¹ and Mihai Pop ^{1,4,*}

➤ EXISTENCE OF ENTEROTYPES



In humans



Qin et al, Nature, 2010

Stereotypes About Enterotype: the Old and New Ideas

Mingyue Cheng^a, Kang Ning^{*,b}

Genomics Proteomics Bioinformatics, 2019

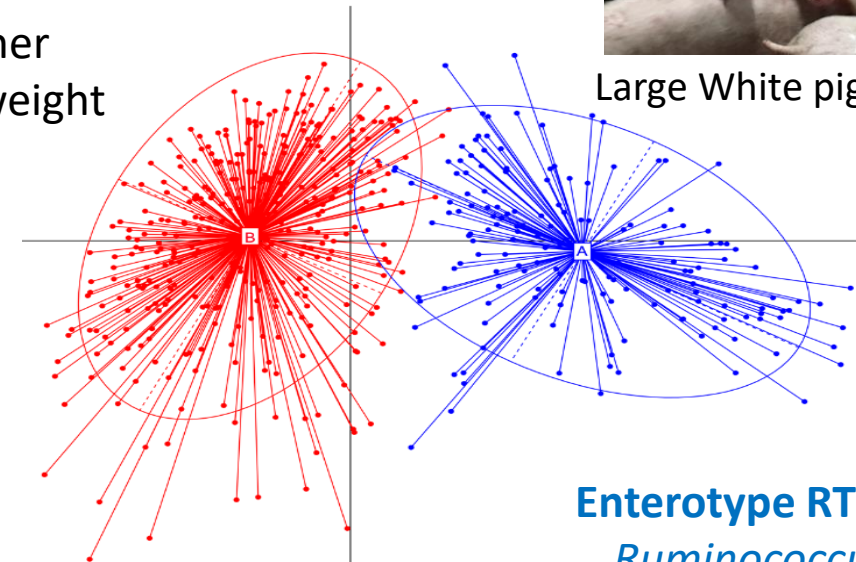
In pigs



Large White pigs (60d)

Higher
body weight

Enterotype PM
Prevotella
Mitsuokella



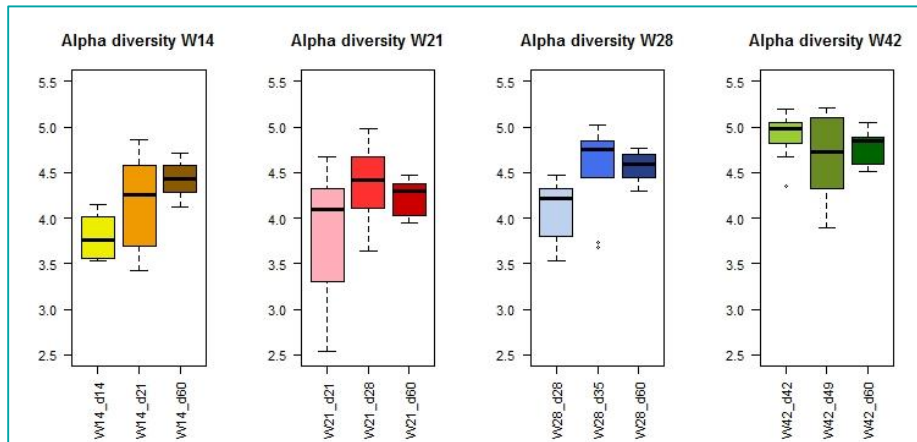
Enterotype RT
Ruminococcus
Treponema

Ramayo-Caldas et al., ISME J 2016

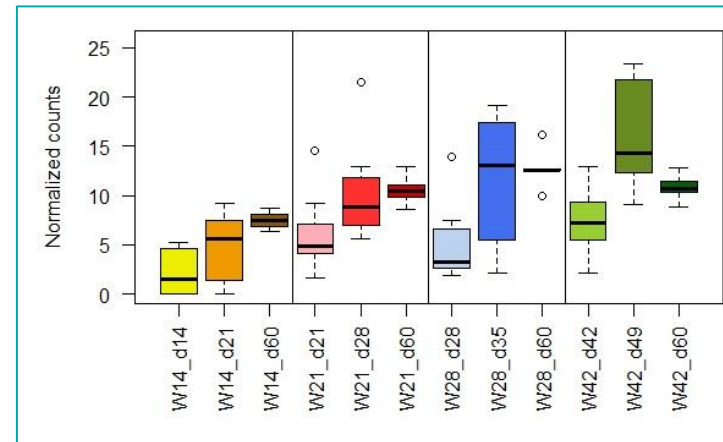
➤ GUT MICROBIOME AND VULNERABILITY AT WEANING: INFLUENCE OF THE AGE AT WEANING IN PIGS



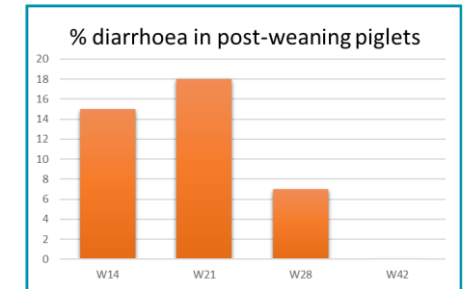
Increased microbial diversity with age at weaning



F. prausnitzii: increased relative abundance with age at weaning



Weaning at 42d: no record of diarrhoea



Massacci et al. *Animal Microbiome* (2020) 2:2
<https://doi.org/10.1186/s42523-020-0020-4>

Animal Microbiome

RESEARCH ARTICLE

Open Access

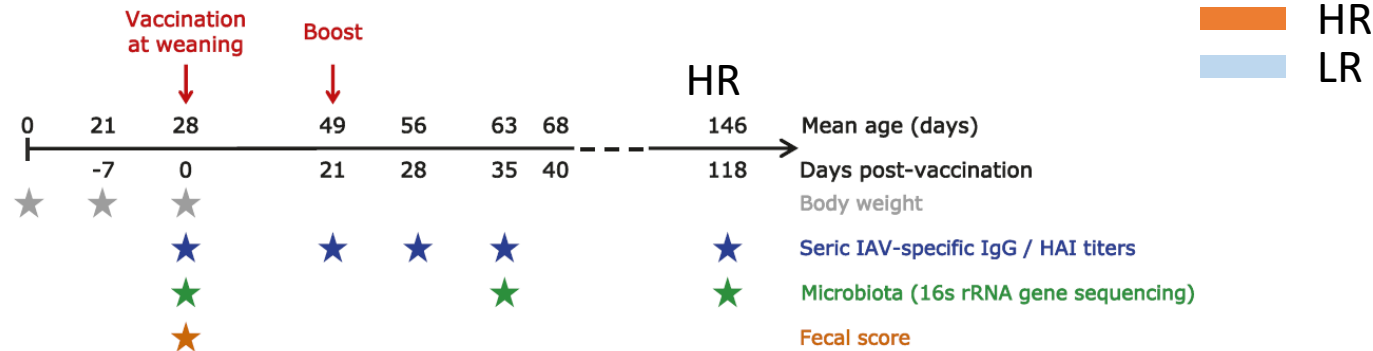
Late weaning is associated with increased microbial diversity and *Faecalibacterium prausnitzii* abundance in the fecal microbiota of piglets

Francesca Romana Massacci^{1,2,3*}, Mustapha Berni⁴, Gaetan Lemonnier¹, Elodie Guettier⁵, Fany Blanc¹, Deborah Jarret¹, Marie Noelle Rossignol¹, Marie-José Mercat⁶, Joël Doré^{7,8}, Patricia Lepage⁷, Claire Rogel-Gaillard¹ and Jordi Estelle^{1*}

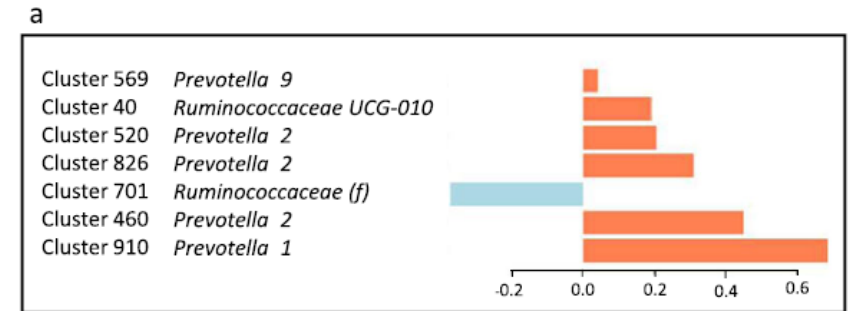
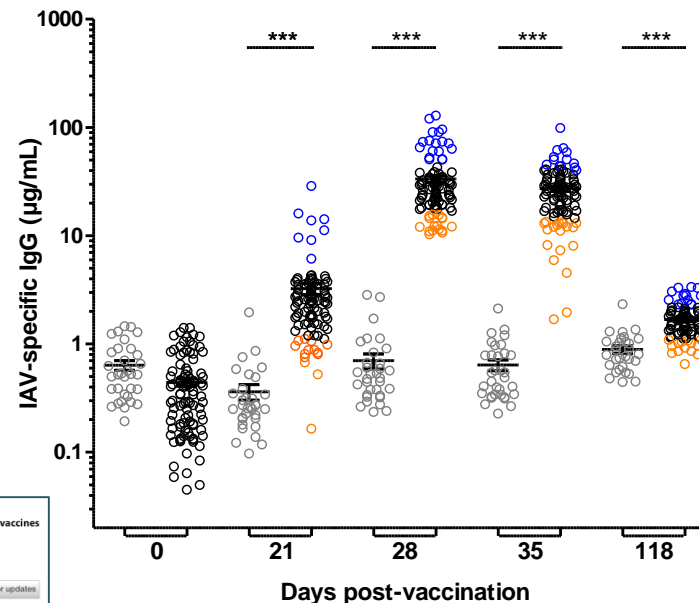
N = 12 / age ; 16S sequencing

Protective effect of *Faecalibacterium prausnitzii* ?
 Candidate probiotics?

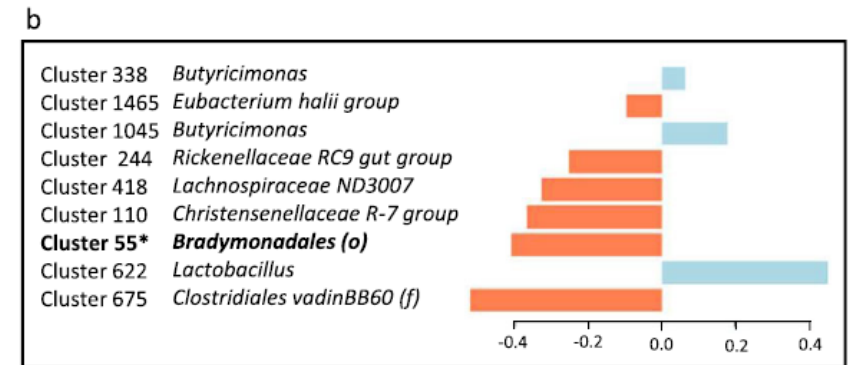
➤ THERE ARE PREDICTORS OF VACCINE RESPONSE LEVELS IN THE GUT MICROBIOTA BEFORE VACCINATION (IAV)



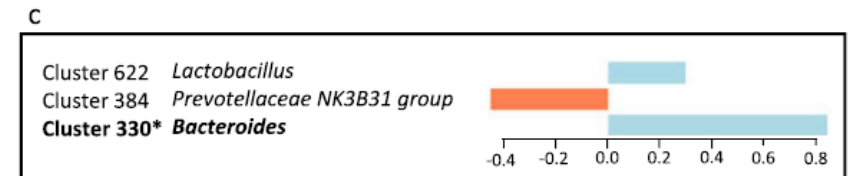
- non-vaccinated
- vaccinated
- low responders (LR)
- high responders (HR)



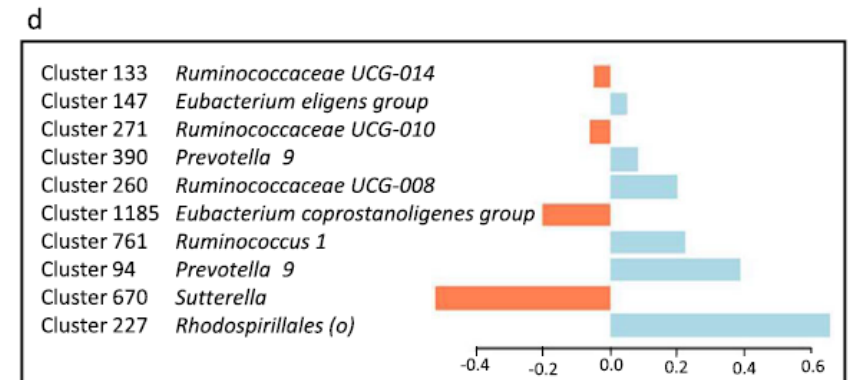
21 dpv



28 dpv



35 dpv



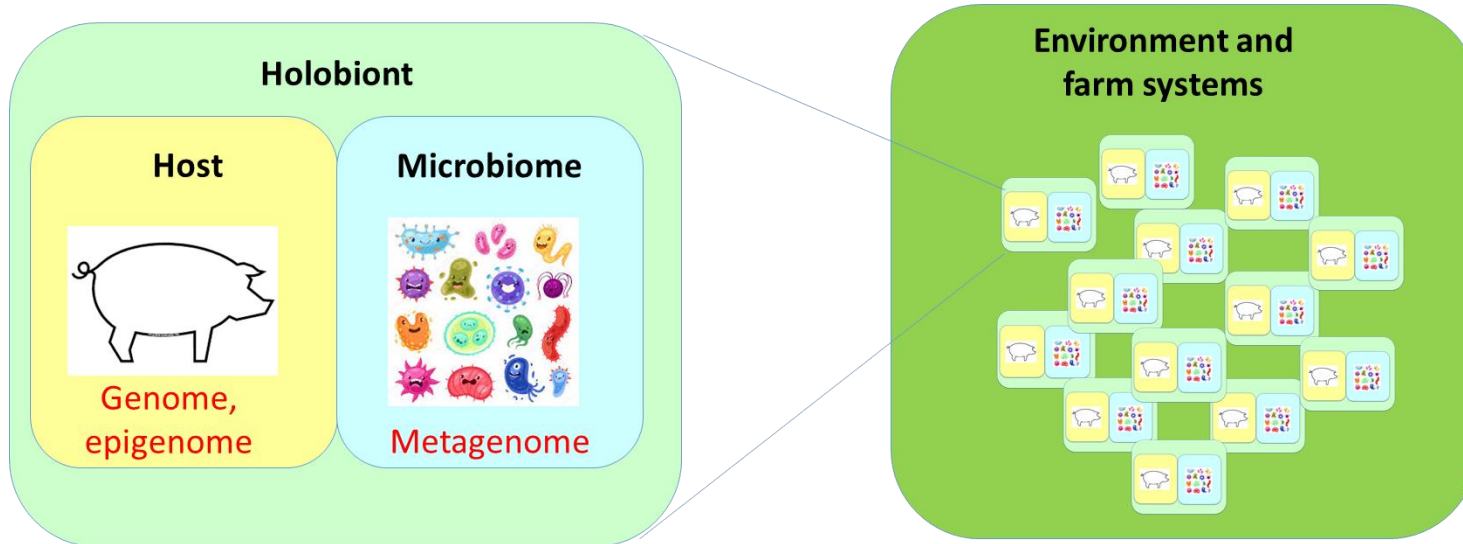
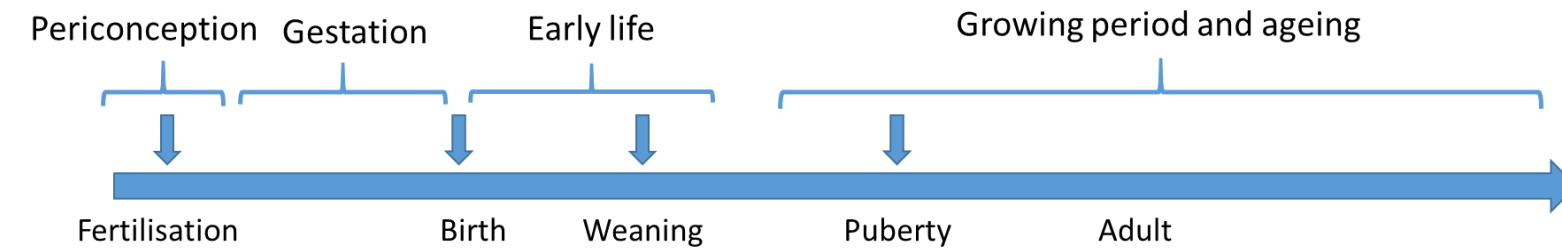
118 dpv

p. 13

➤ FEW CONCERNS

- Standardized methods to collect microbiomes on farms, to store and process samples for further analyses; large-scale ring tests would be useful as in humans for comparing protocols.
- Cost of shotgun metagenomics on large animal populations
- Analysis of microbiomes at all body sites (lung, skin, vagina, etc.)
- Availability of effective methods to assess a microbiome diagnosis on farms at individual and population levels
- Data interpretation for optimizing farm practices

> TAKE-HOME MESSAGES



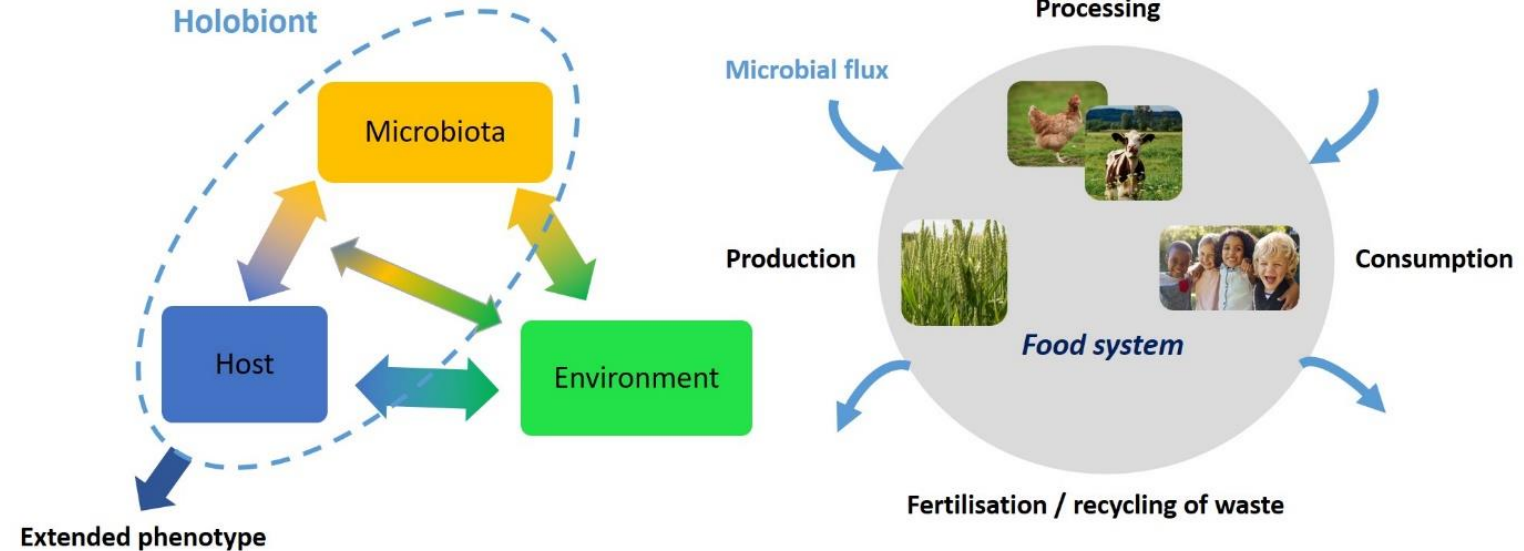
- Importance of the intervention time windows to efficiently modulate the microbiomes
- Microbiomes are genetic resources that contribute to sustainability and need to be preserved
- Holobiont: a new paradigm to study animal phenotype construction and plasticity (phenotype-genotype links)
- Implementation of hologenomics approaches : G+E+M

➤ HOLOFLUX: HOLOBIONTS AND MICROBIAL FLUX WITHIN AGRIFOOD SYSTEMS

HOLOFLUX : AN INTERDISCIPLINARY METAPROGRAMME AT INRAE

To understand, predict and control the functioning of holobionts and microbiomes as well as their interactions with the environment, in various agronomic contexts, taking into account the issues of sustainable food and health preservation.

https://www6.inrae.fr/holoflux_eng/



SCIENTIFIC AREAS

- Mechanisms underlying assembly and interactions within holobionts
- Microbial flux and dynamics within an agrifood system
- Control and management of microbial fluxes

The banner features a blue background with a DNA double helix on the left. The center contains text about the ISAG 2023 conference. On the right, a collage of hexagonal images shows various animals: a leopard, a chicken, an elephant, a horse, a monkey, an owl, a deer, a cow, and a pig. The background also includes a view of Table Mountain and the Cape Town harbor.

ISAG 2023

39th International Society
for Animal Genetics
CONFERENCE

2 – 7 July 2023
CAPE TOWN, SOUTH AFRICA
www.isag.us/2023



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39TH INTERNATIONAL SOCIETY FOR ANIMAL GENETICS CONFERENCE 2023

2 - 7 JULY
CAPE TOWN, SOUTH AFRICA

Visit our website for further information
WWW.ISAG.US/2023/

There is an ISAG standing committee on Animal Microbiomes
An exciting session in preparation !



Thank you for your attention