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La genetica degli animali e l'interazione con il microbiota per la sostenibilità delle produzioni zootecniche

Luca Fontanesi

Animal and Food Genomics Group

Department of Agricultural and Food Sciences

University of Bologna

Alcuni scenari globali per le produzioni zootecniche

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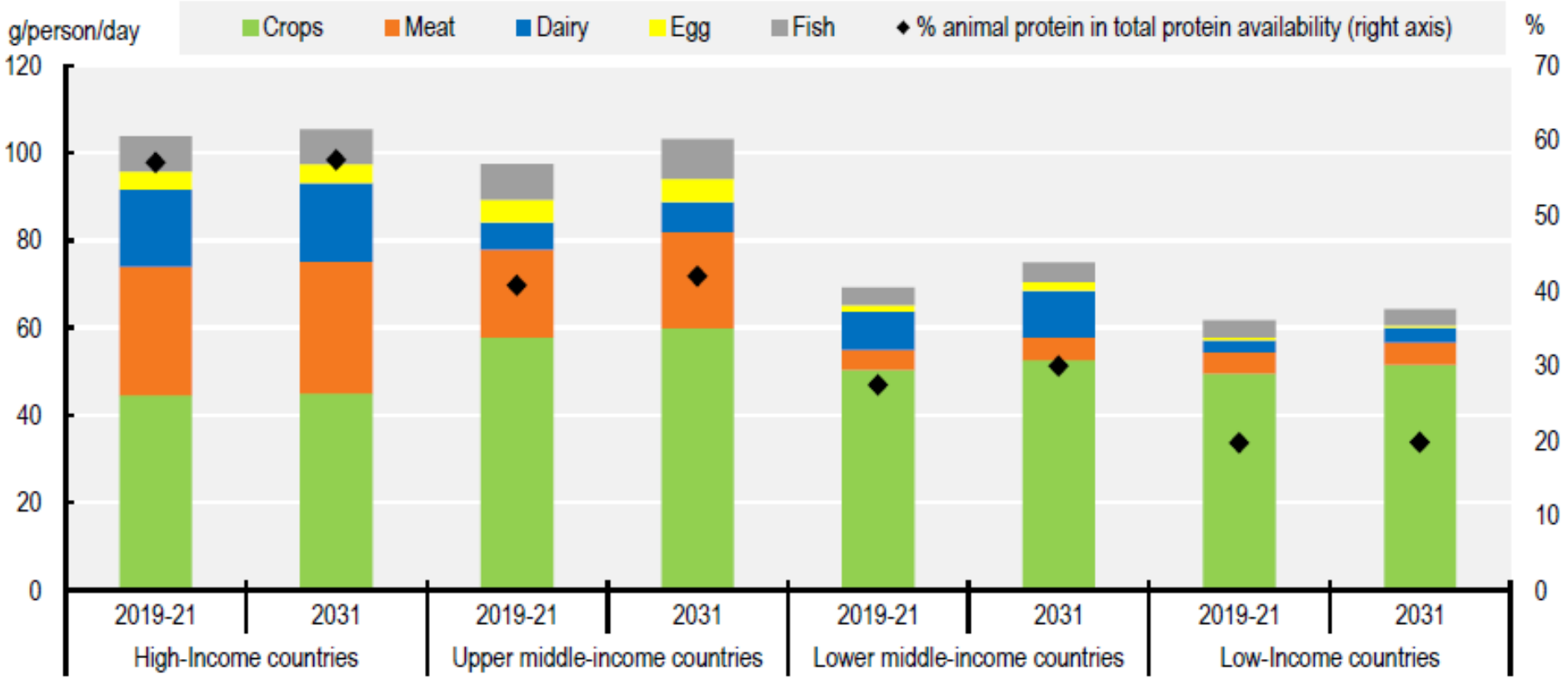
Disponibilità pro-capite di proteine per origine (e per tipologia di paese)



Source: FAO-OECD (2022)

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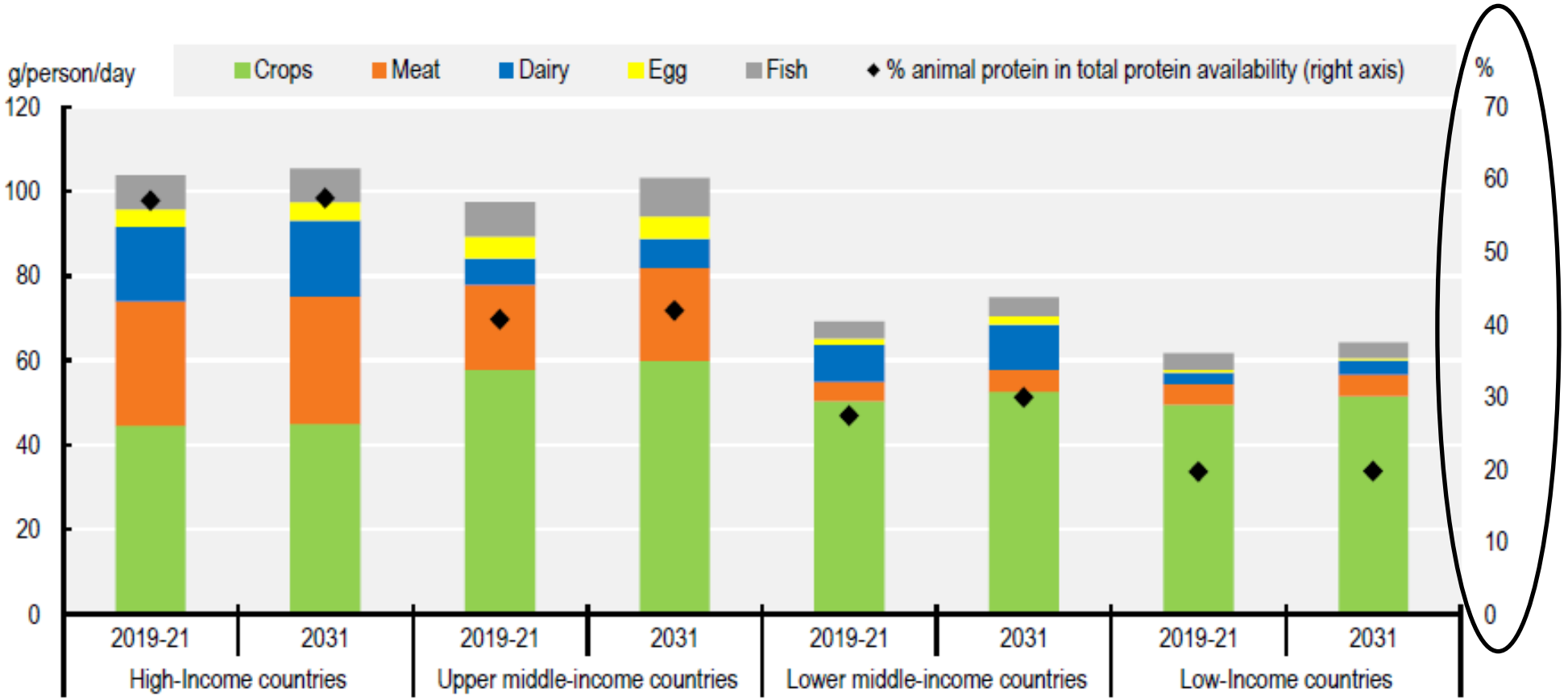

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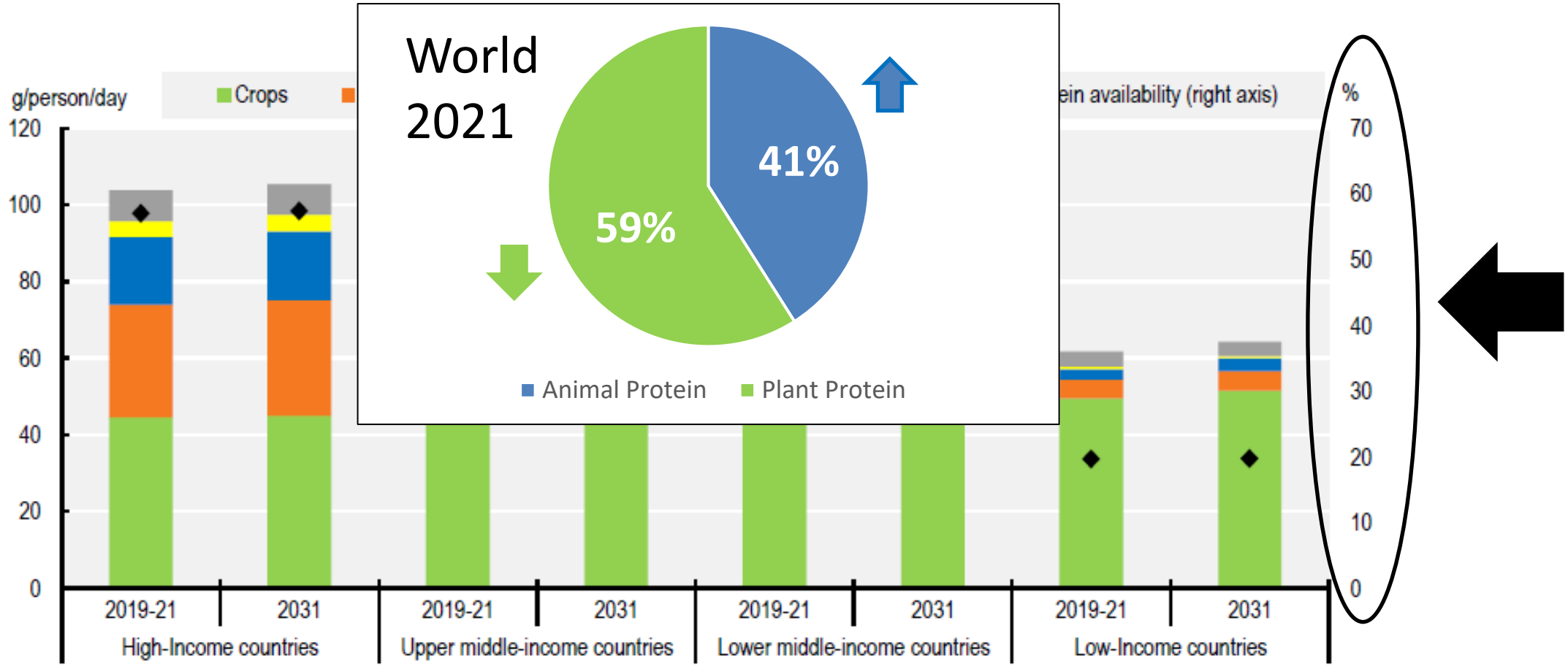

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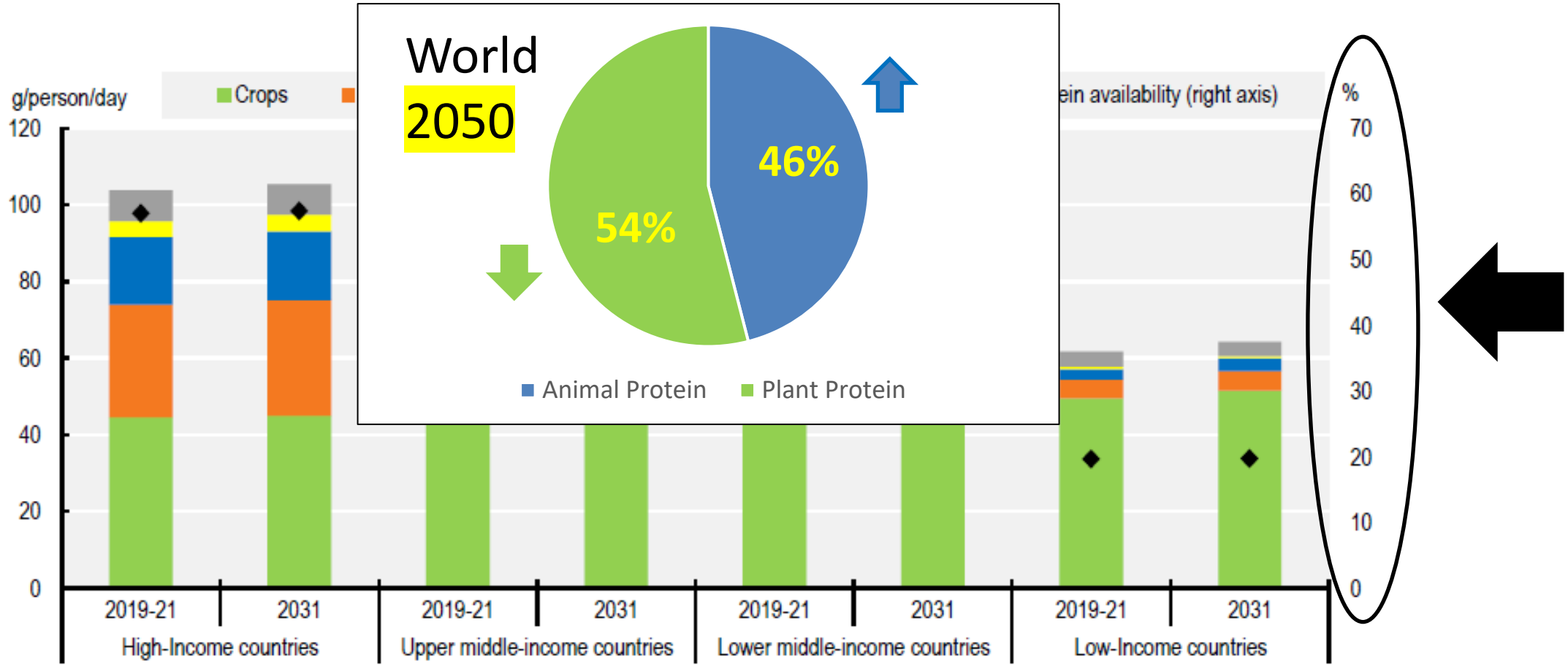

Source: FAO-OECD (2022) – and predictions from other FAO data

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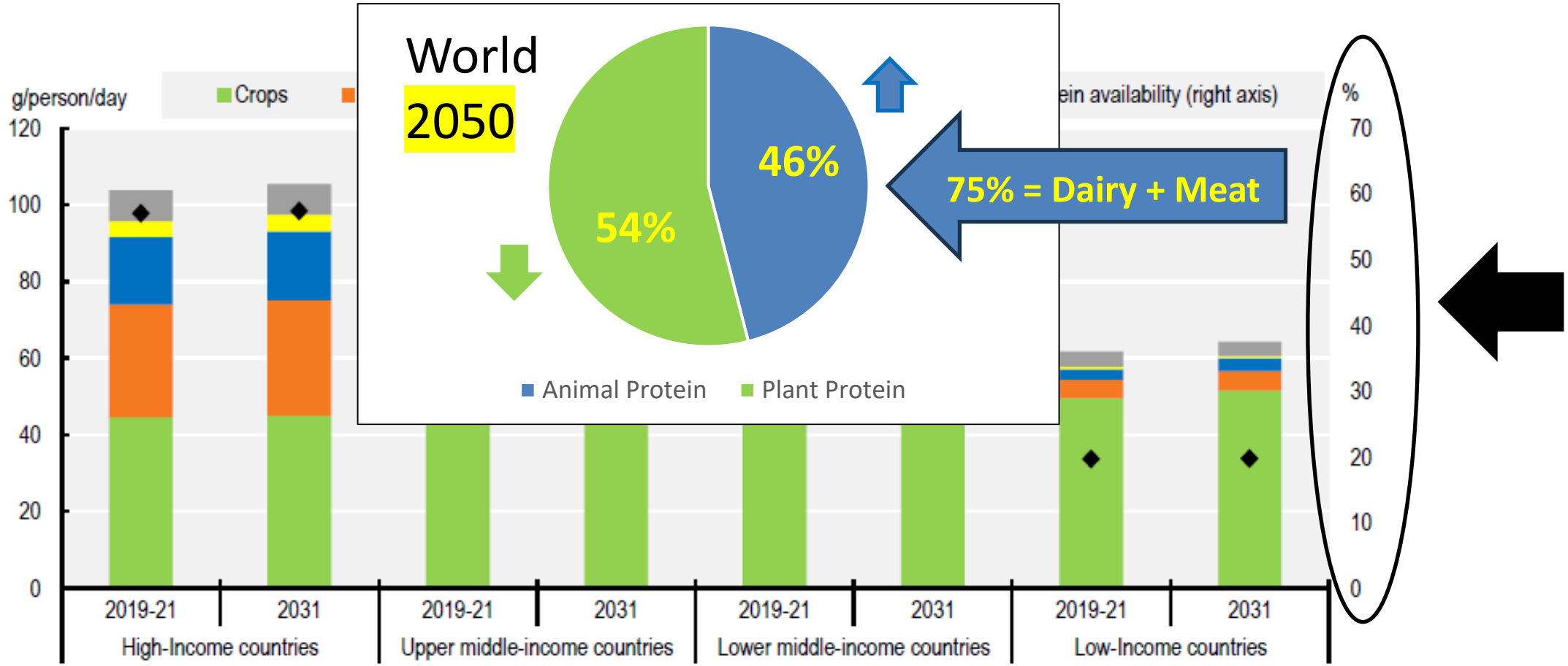
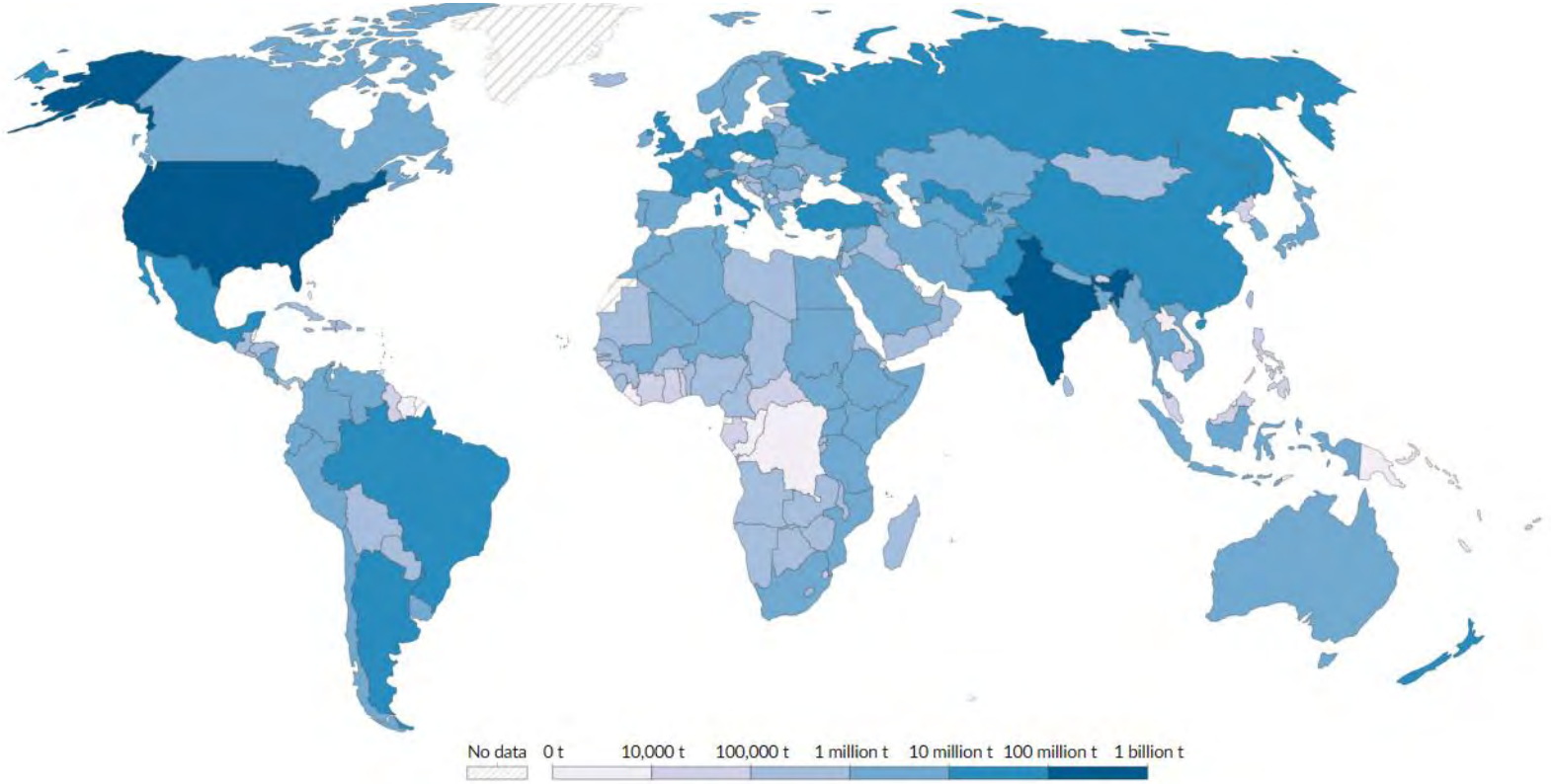


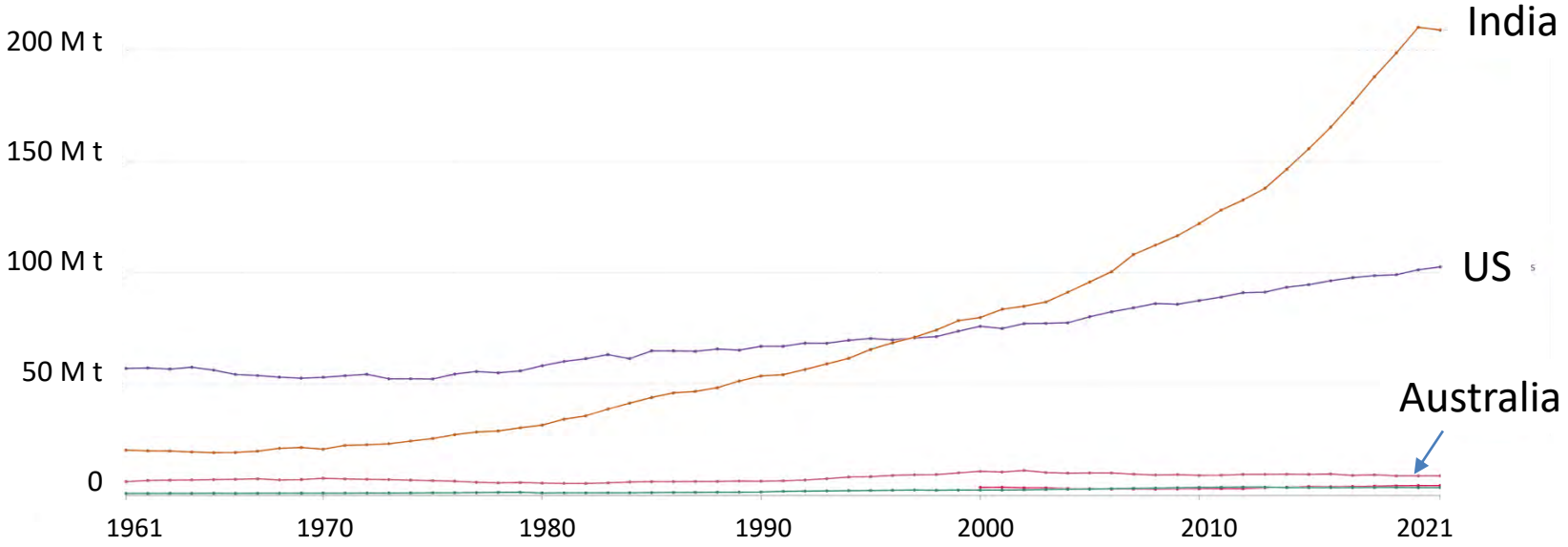
Source: FAO-OECD (2022) – and predictions from other FAO data

Le produzioni zootecniche in pillole (1)

Milk production: 2021

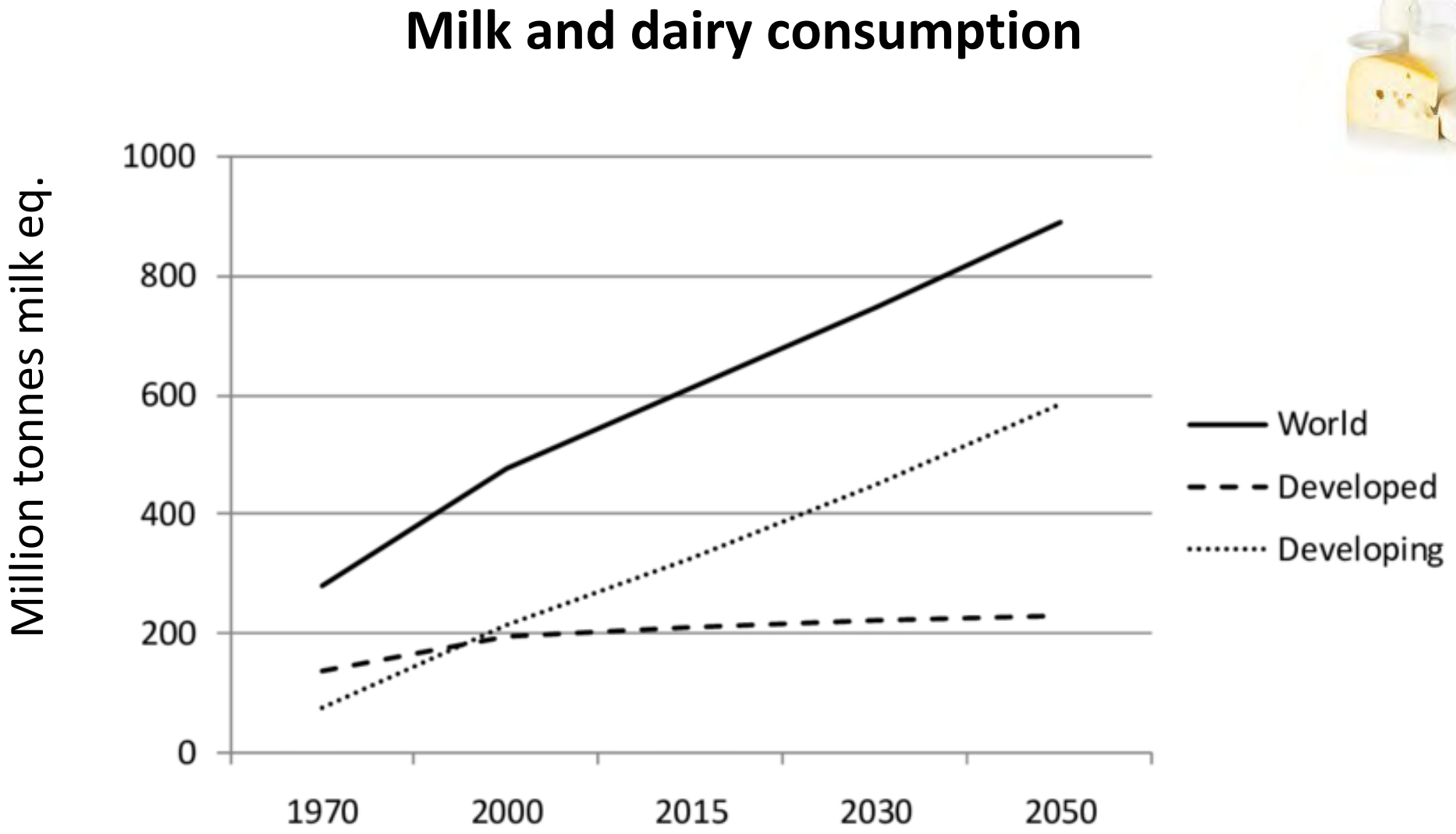


Milk production: 1961-2021



Source: FAO

Le produzioni zootecniche in pillole (1)



Source: FAO

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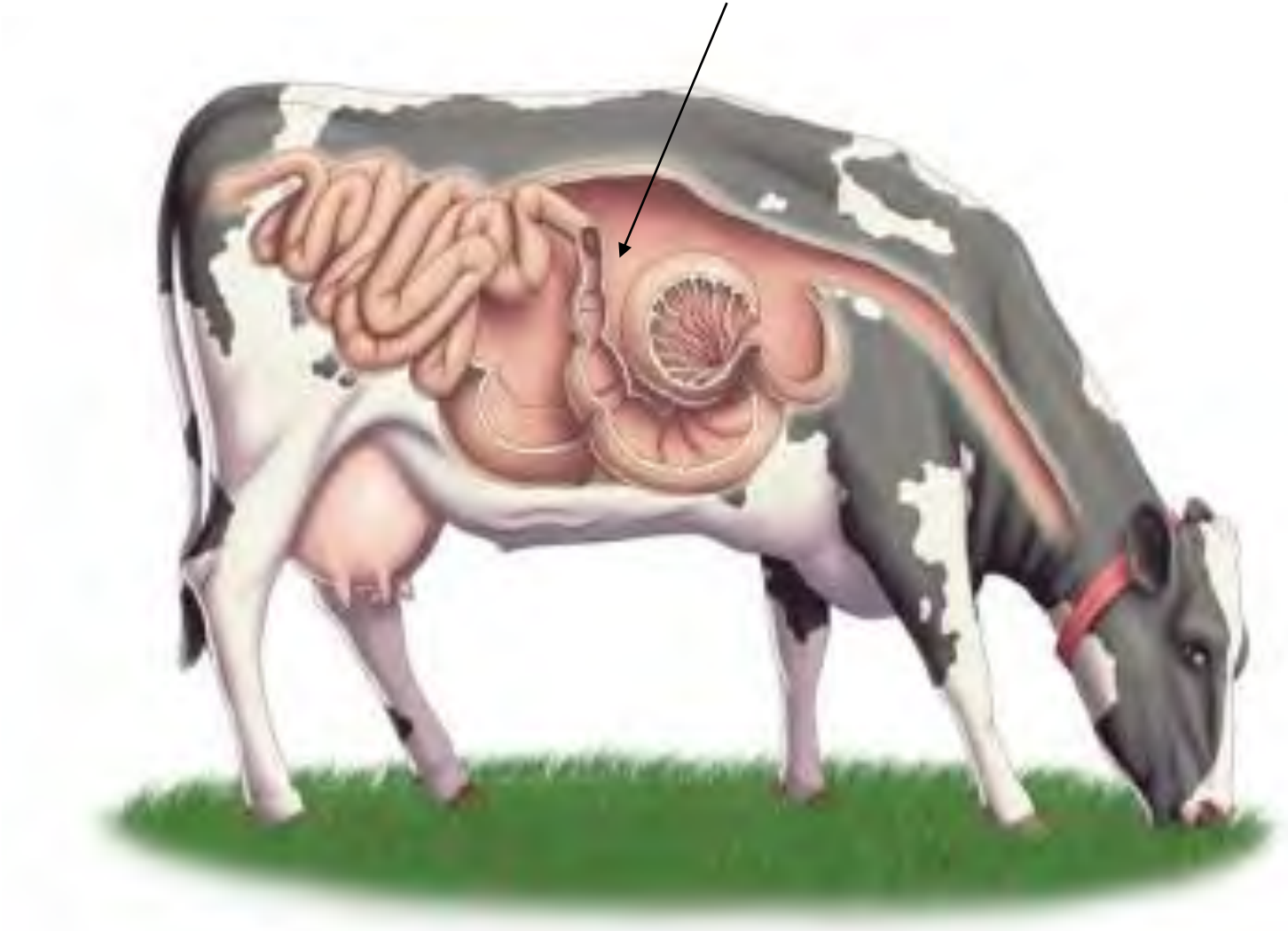
Rumen microbiota



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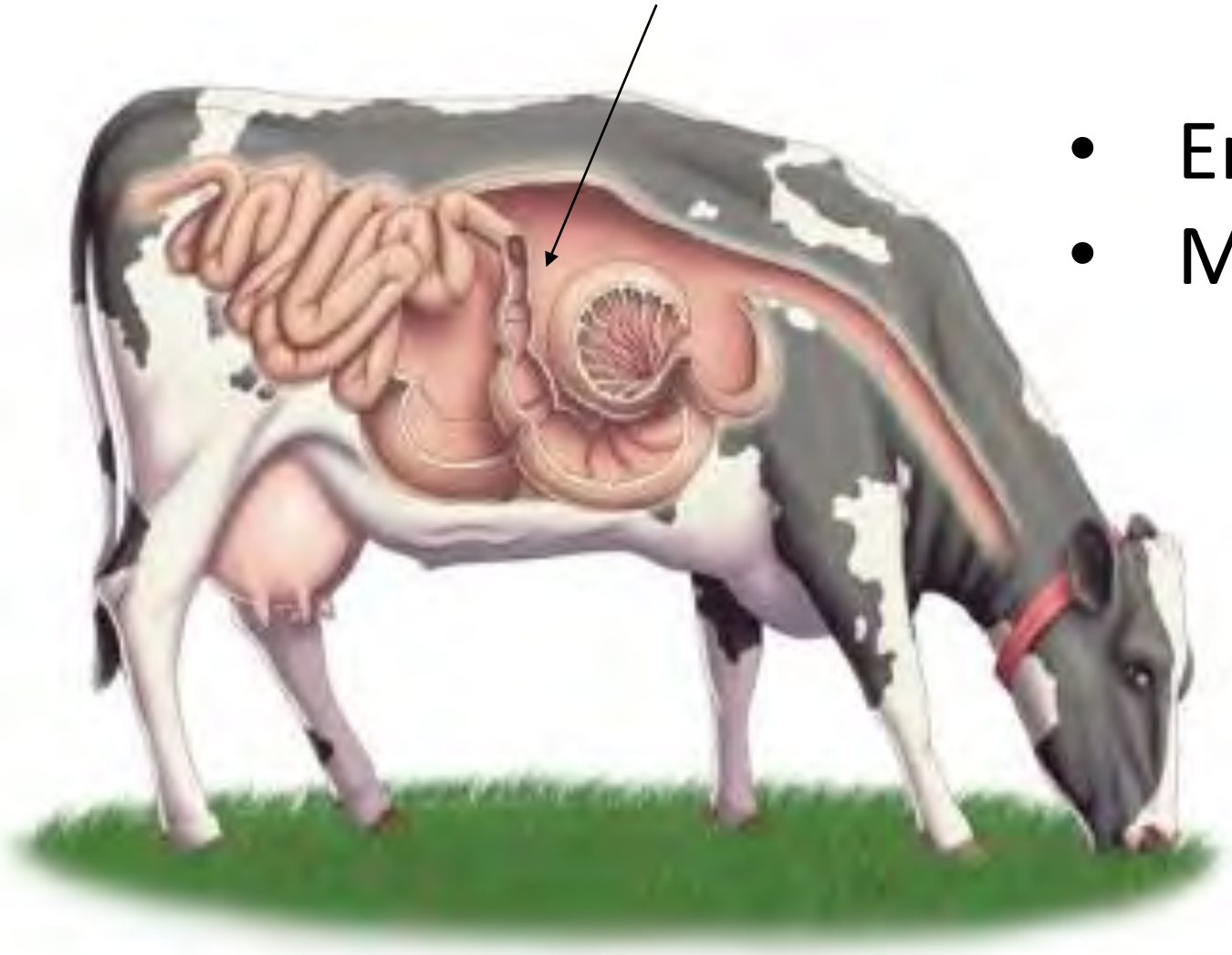
Rumen microbiota



- Emission of CH_4
- Milk production

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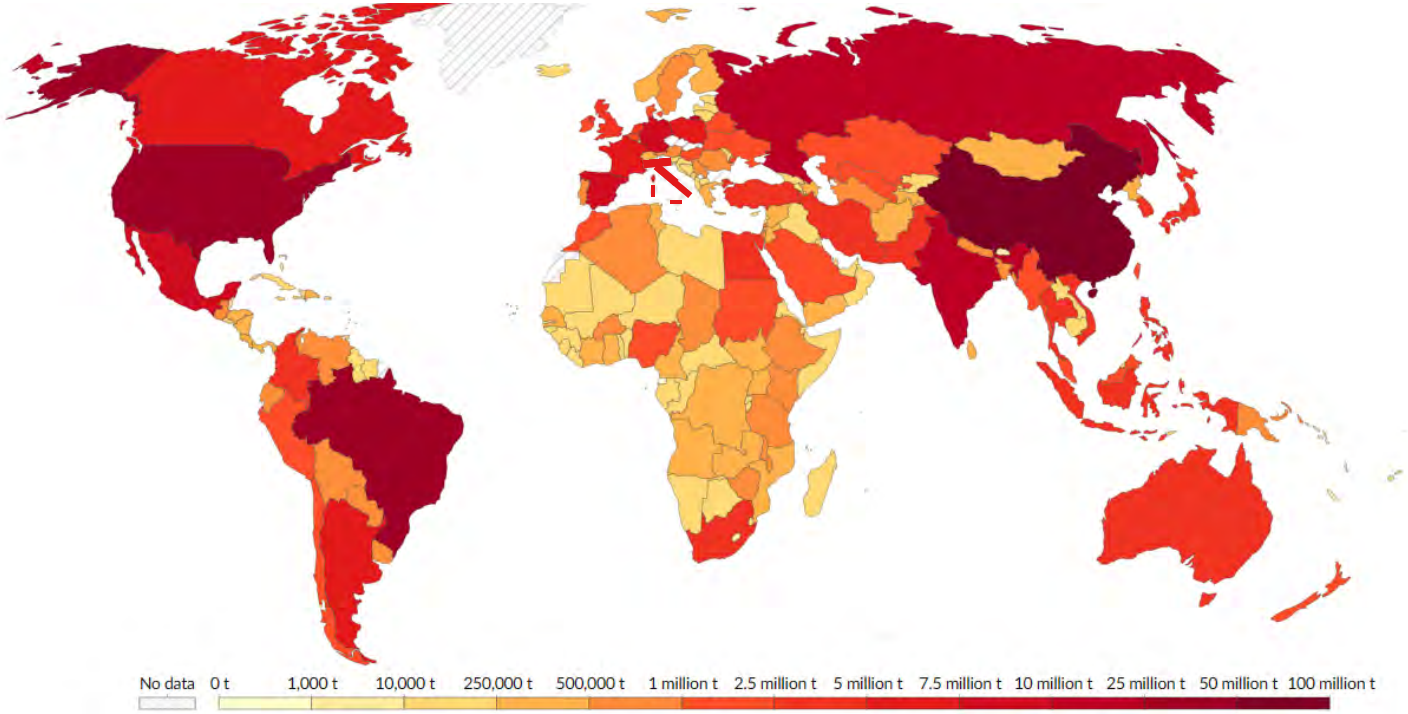
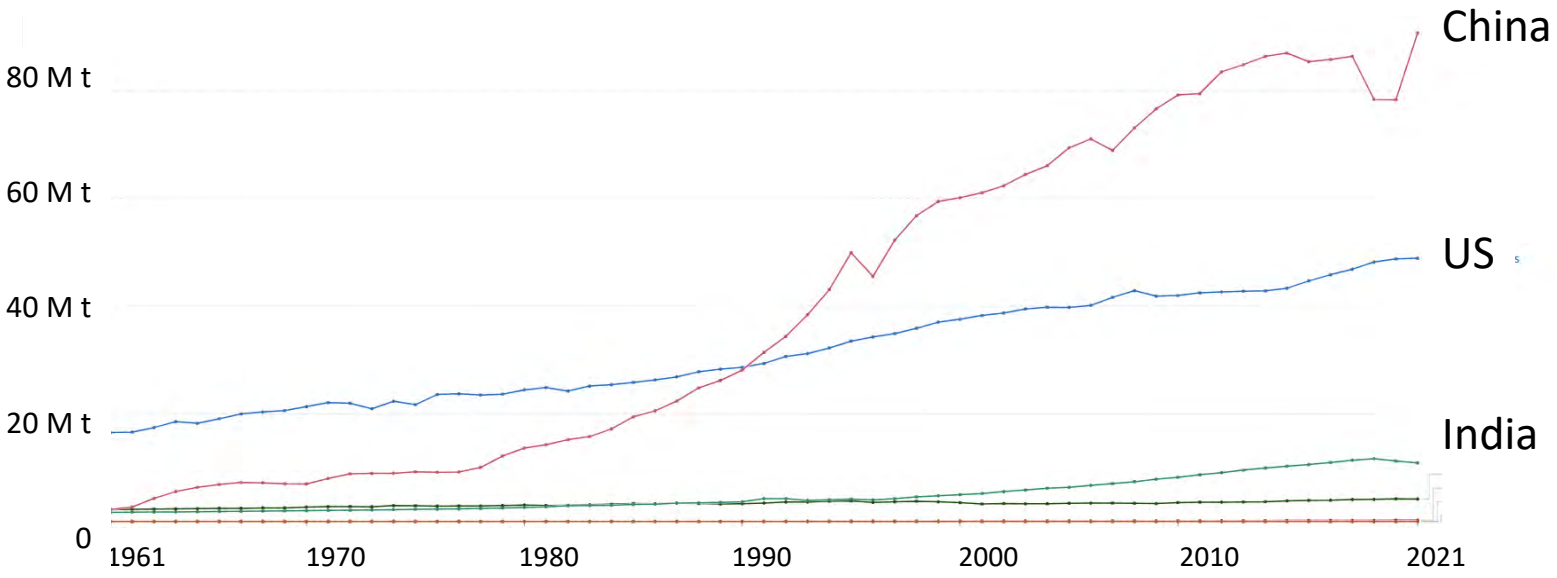
Le produzioni zootecniche in pillole (2)

Meat production: 2021



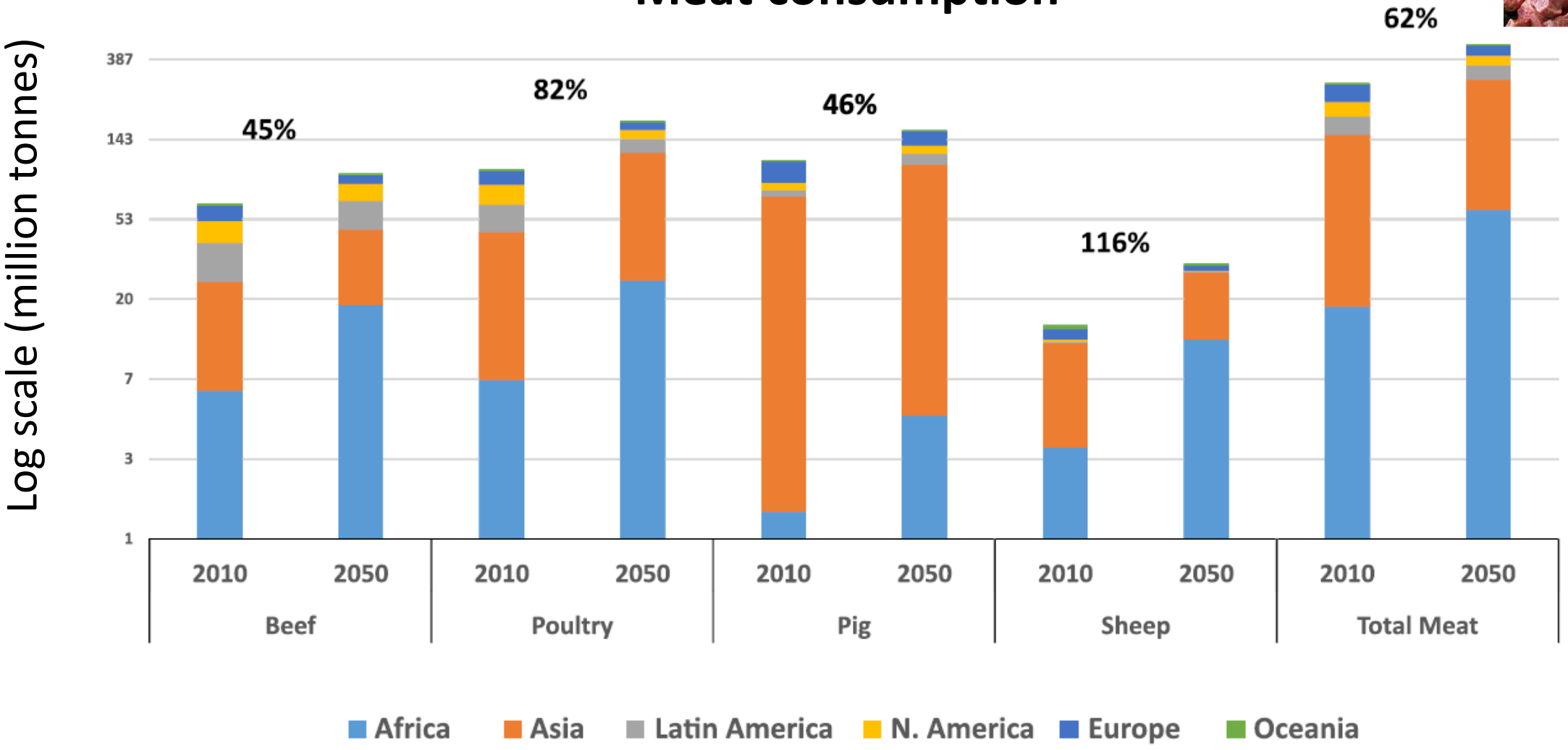
Meat production: 1961-2021



Source: FAO

Le produzioni zootecniche in pillole (2)

Meat consumption



Source: FAO – data elaborated by EAAE

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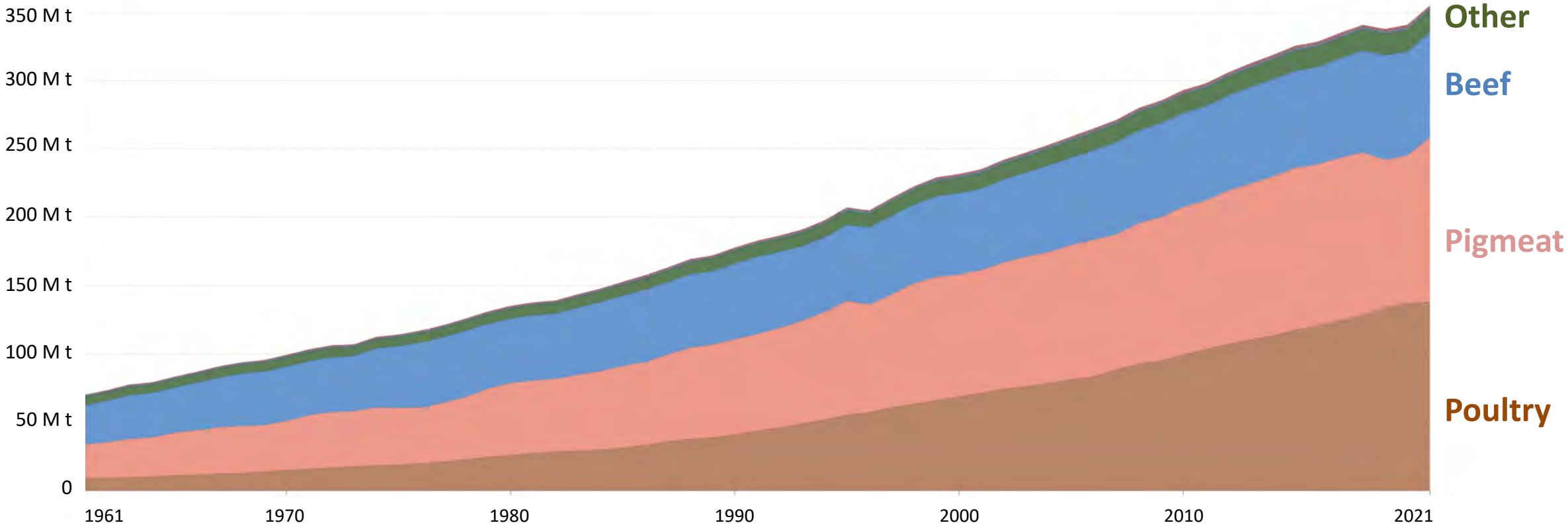
Le produzioni zootecniche in pillole (2)

Meat production



Source: FAO

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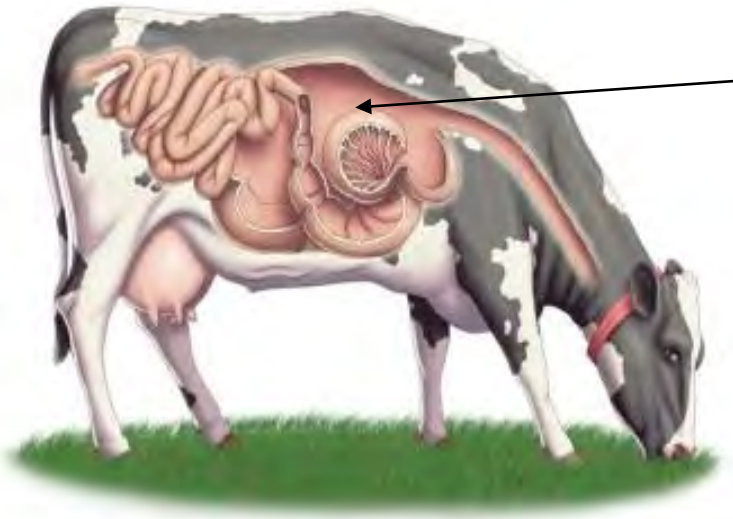
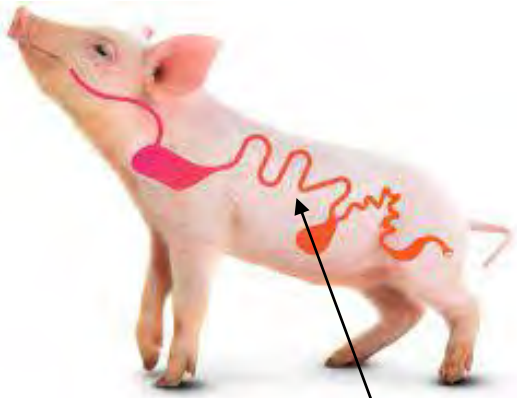


Rumen microbiota



Gut microbiota

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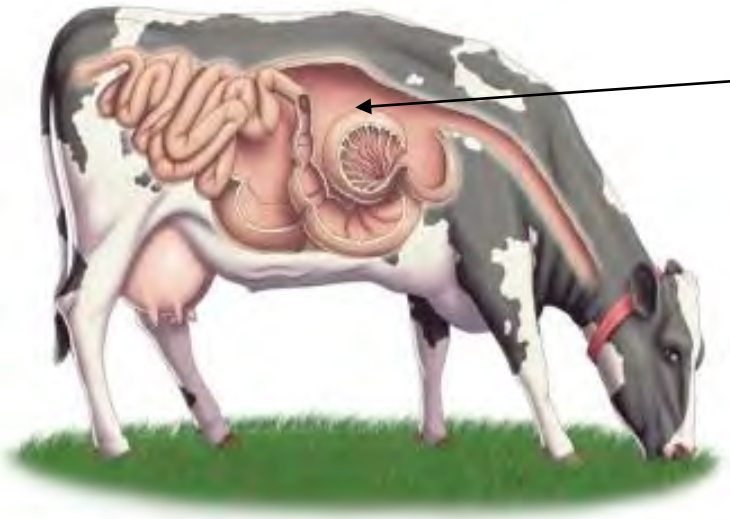
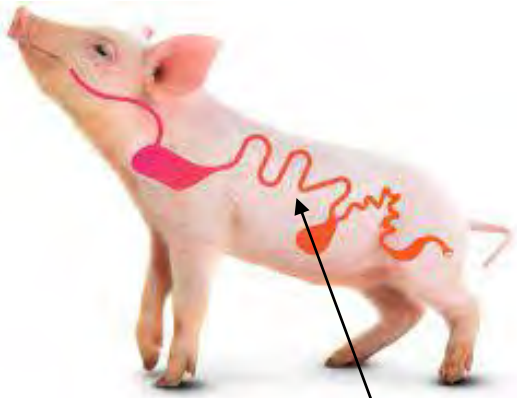
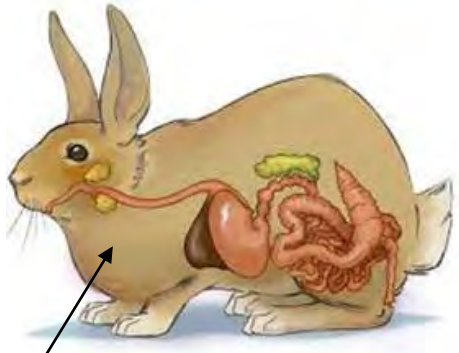


Rumen microbiota





(ciecum)

Gut microbiota

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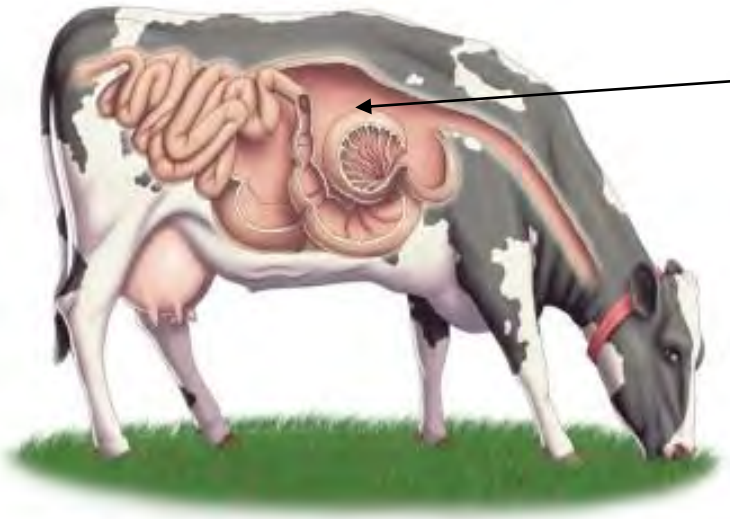
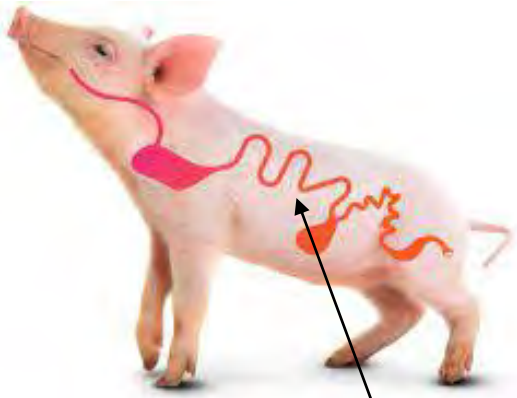
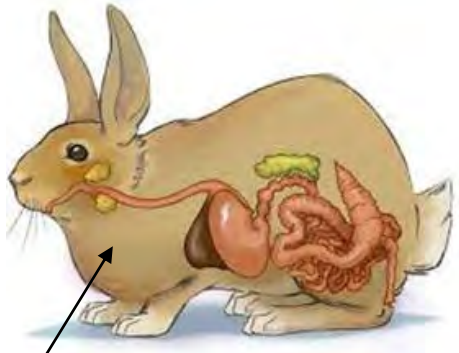


Rumen microbiota

Emission of CH_4





(ciecum)

Gut microbiota

- Feed efficiency
- Digestive disorders/diarrhoea

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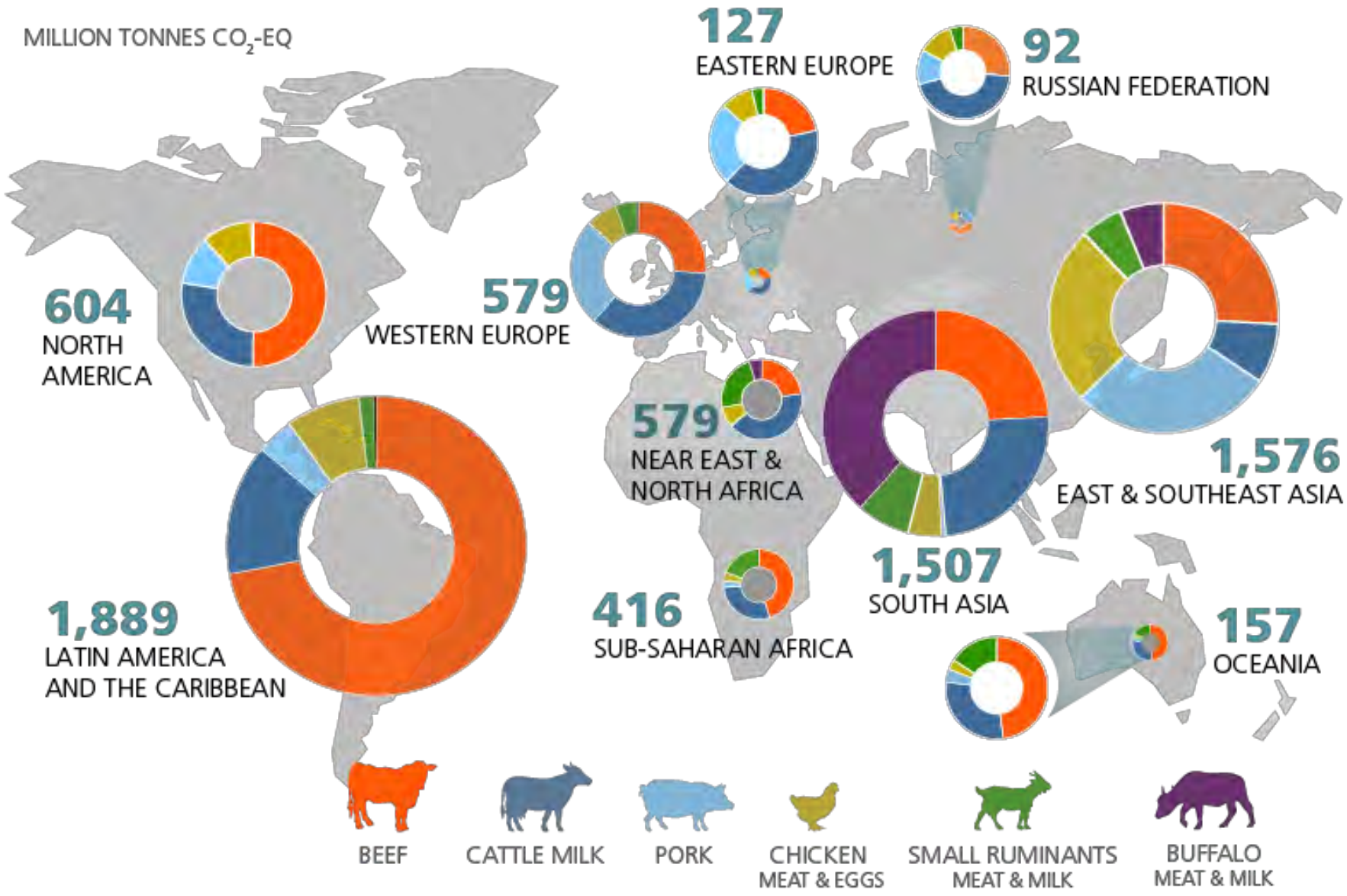
Emissioni clima-alteranti (3)



Source: FAO – GLEM 2.0

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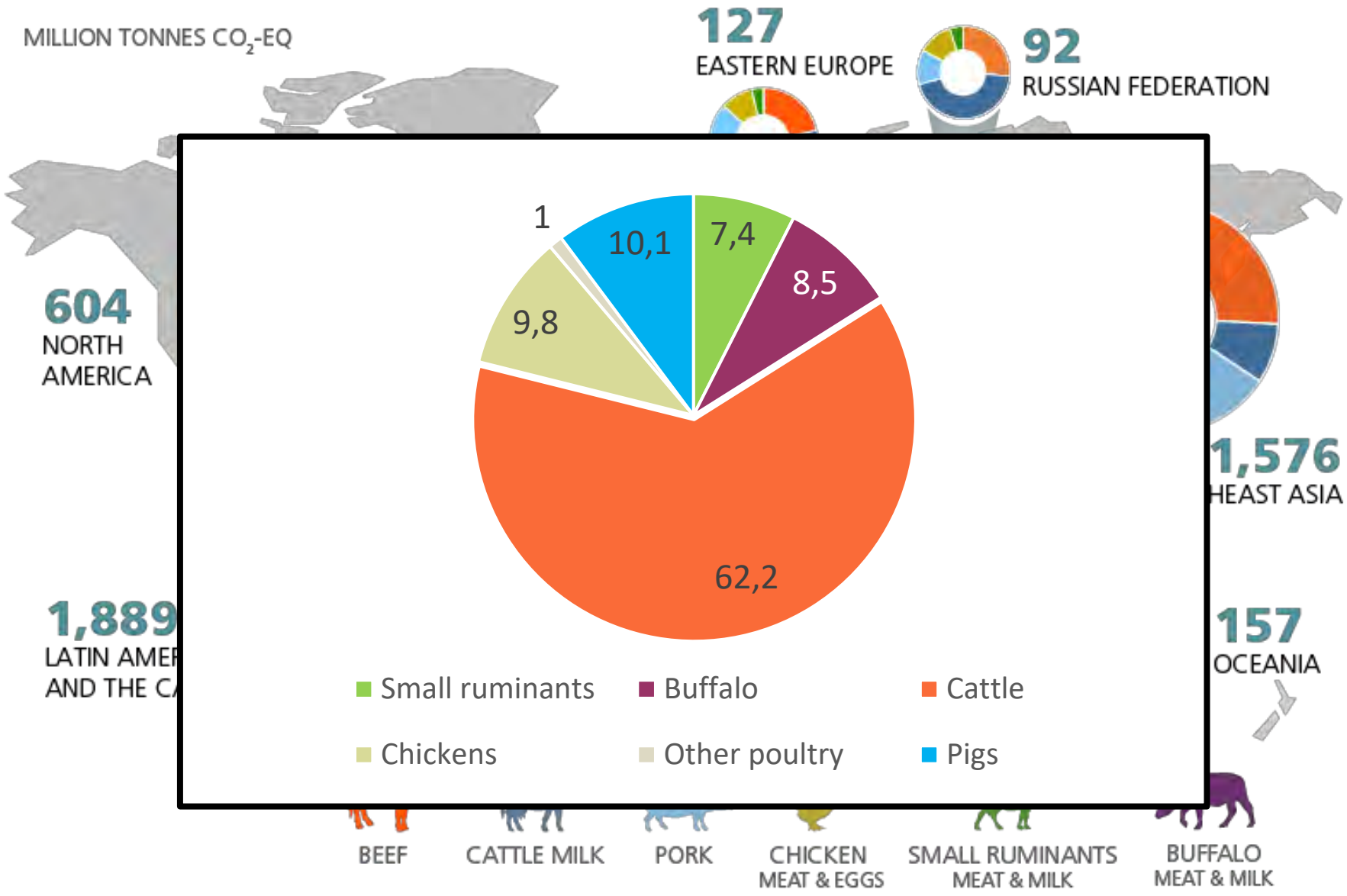
Emissioni clima-alteranti (3)



Source: FAO – GLEM 2.0

Host genetics & microbiota

(& digestive disorders)

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$$P = G + E$$

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Phenotype

Host (animal) genetics

All other factors (environment)

$$P = G + E$$

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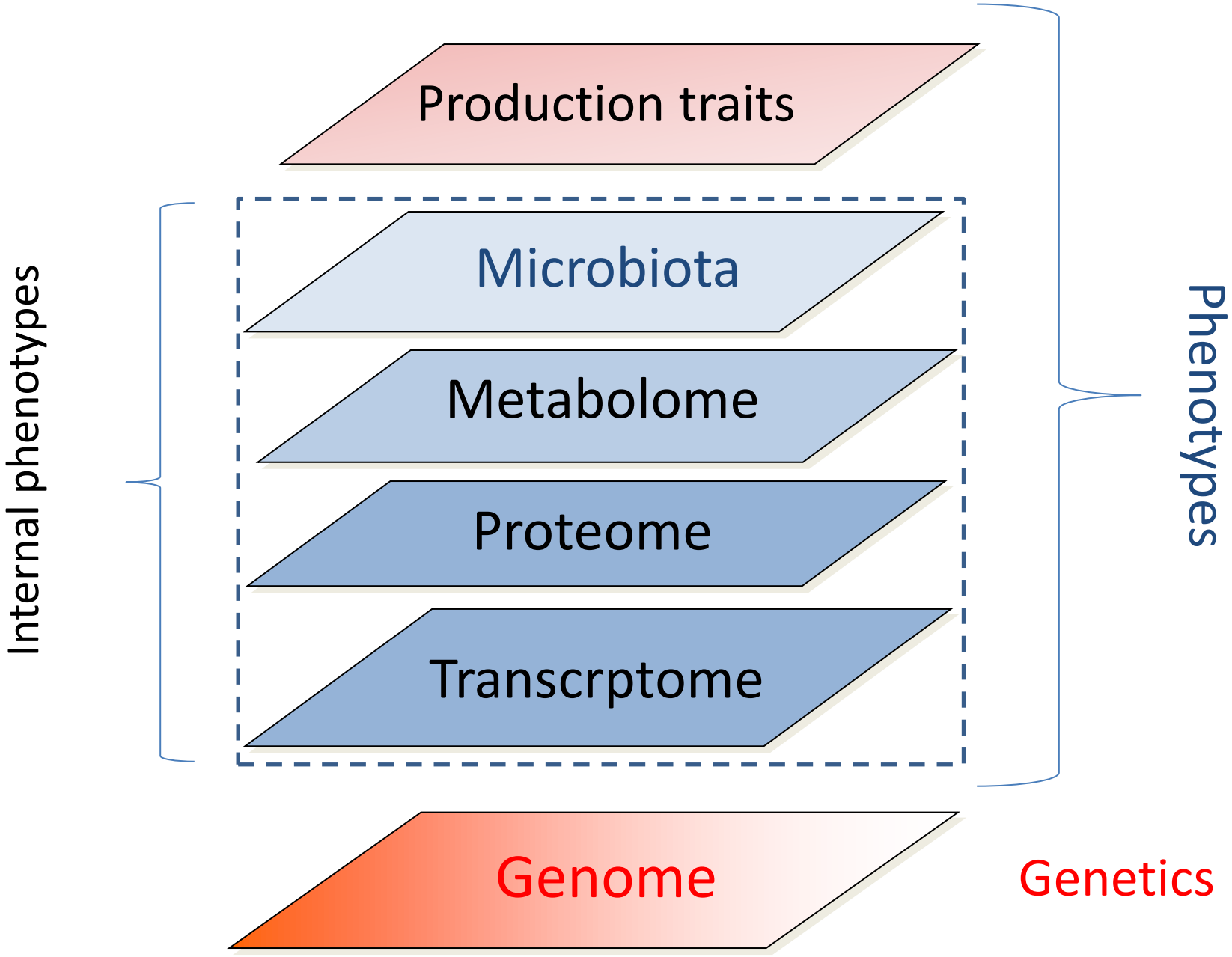

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Phenotype: microbiota (OTU)

Host (animal) genetics

All other factors (environment)

$$P = G + E$$

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Host (animal) genetics

$$h^2 = \frac{V(G)}{V(P)}$$

Phenotype: microbiota (OTU)

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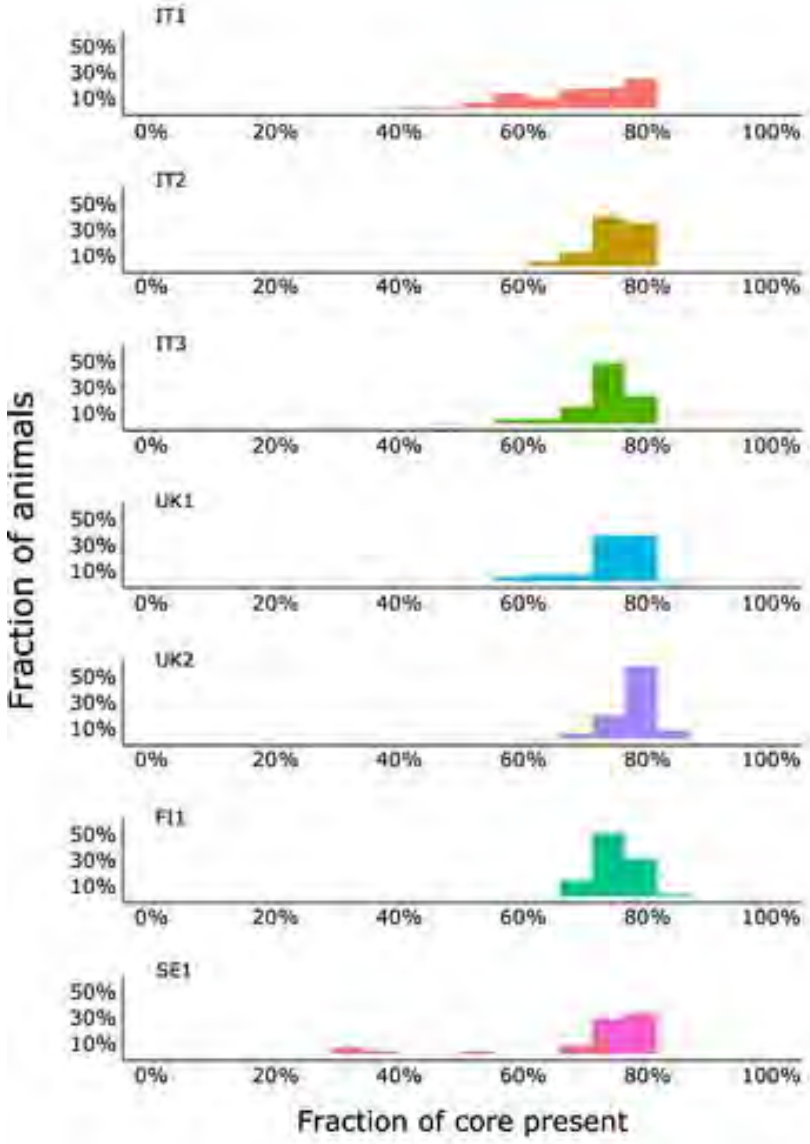
816 Holstein dairy cows +
200 Nordic Red dairy cows
(7 farms)

The core microbiota:

- 0.25% of the overall microbial species pool (512 of 250,000 OTUs)
- It is however highly abundant (30-60% of the overall microbiota)



Core microbes are highly represented within individual animals, as a high fraction of them (>50% of the core microbes) are present in >70% of the individuals.

From: Wallace et al. 2019

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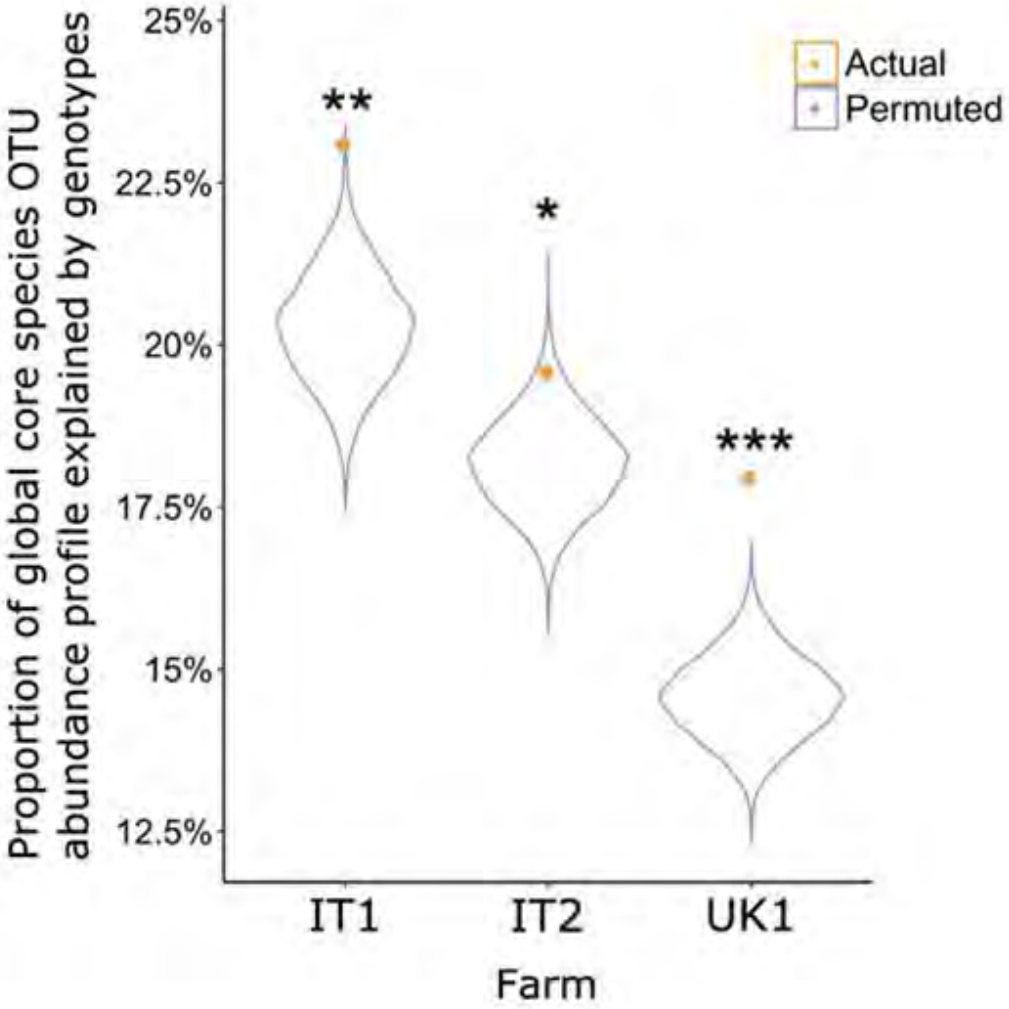

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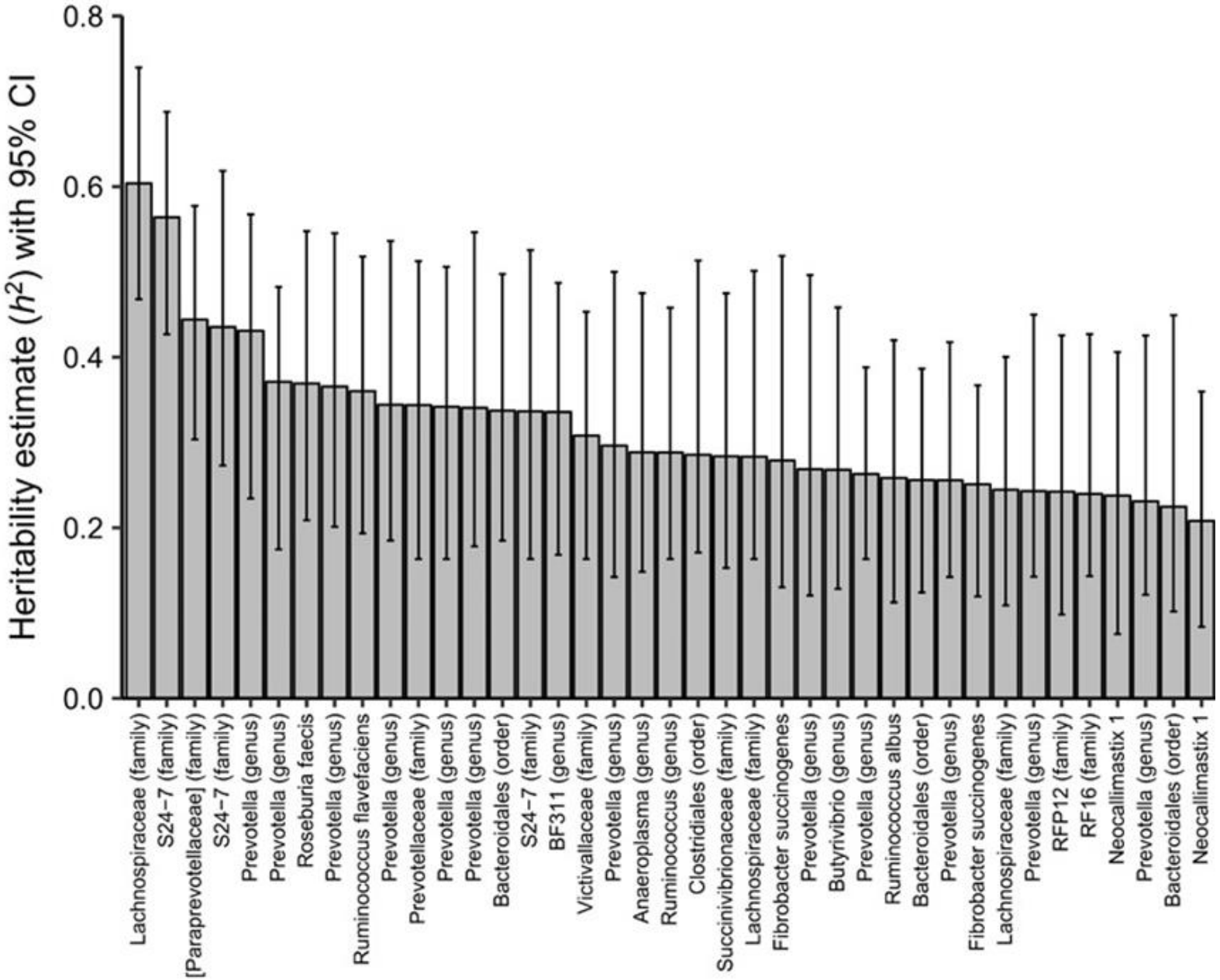

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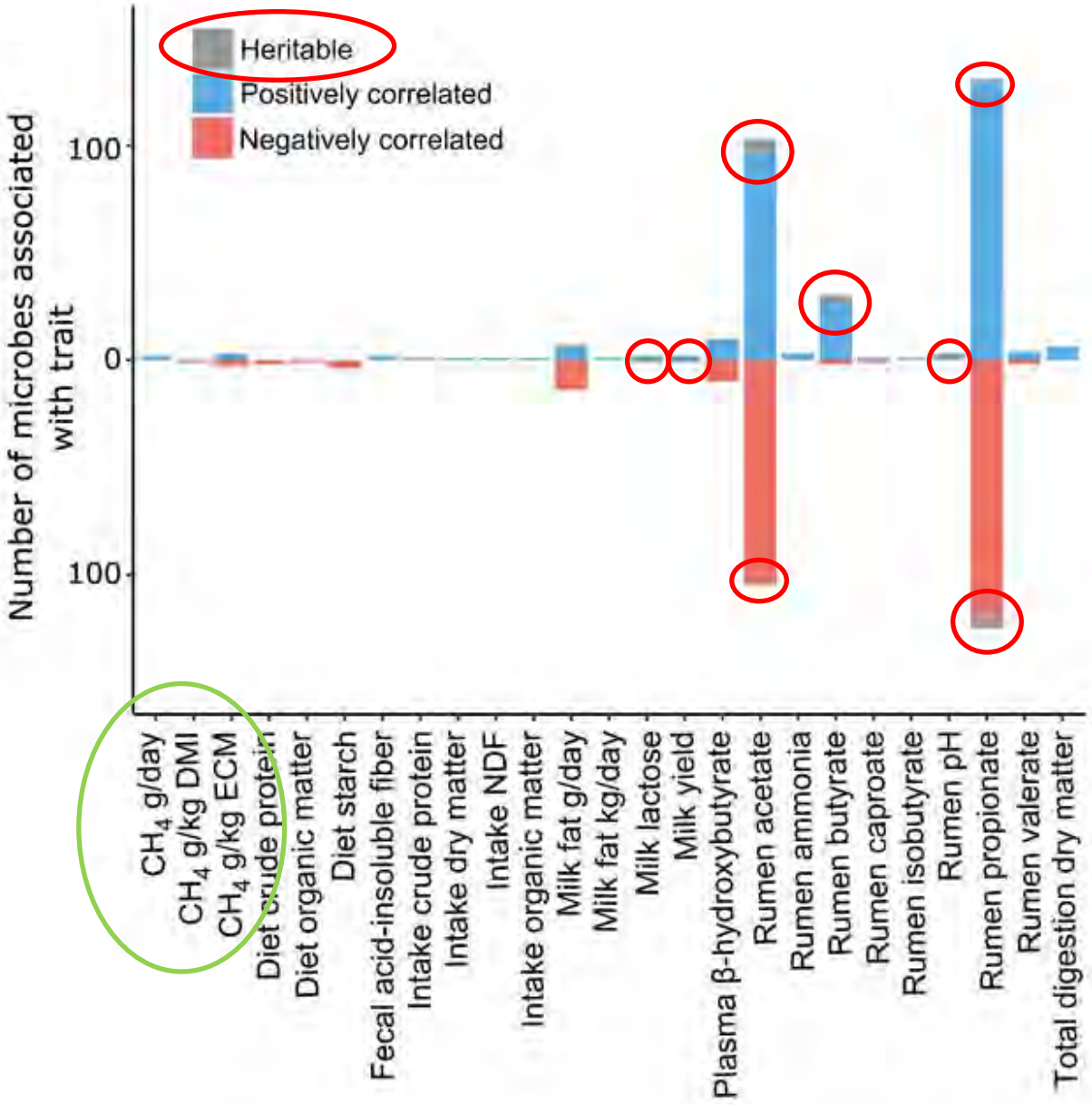

From: Wallace et al. 2019

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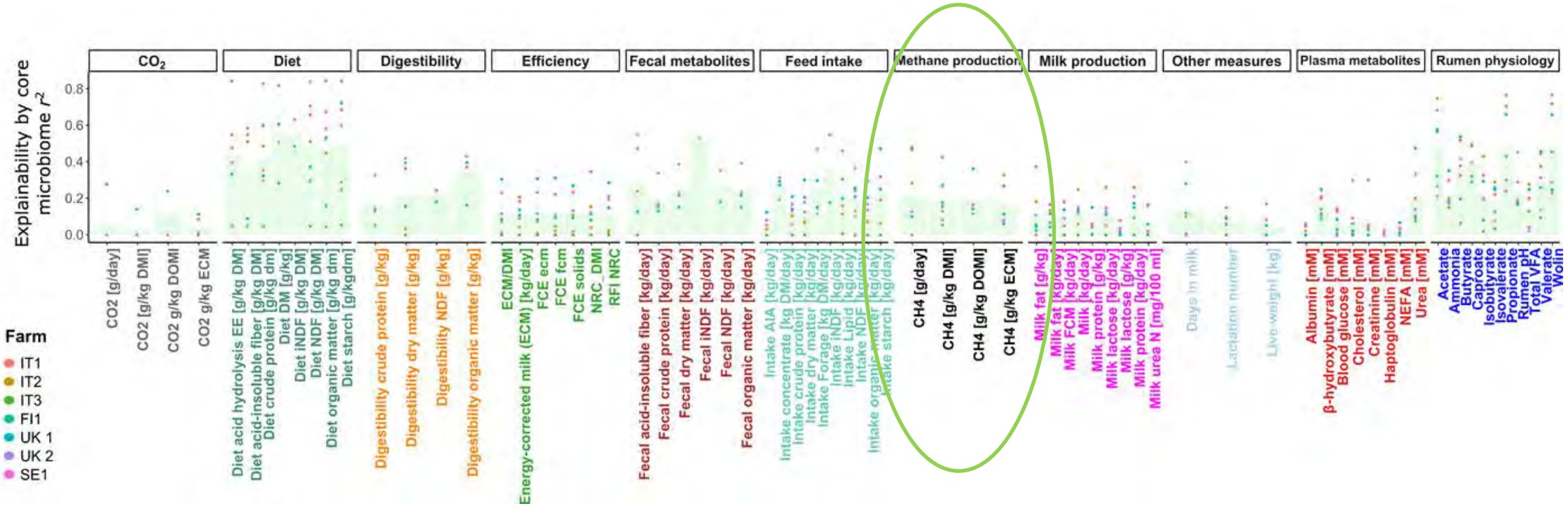
Explained variation (r^2) of different host traits as function of core microbiome composition



From: Wallace et al. 2019

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- Breeding towards low-methane emitting animals
- Breeding towards modulation of specific microbiome composition

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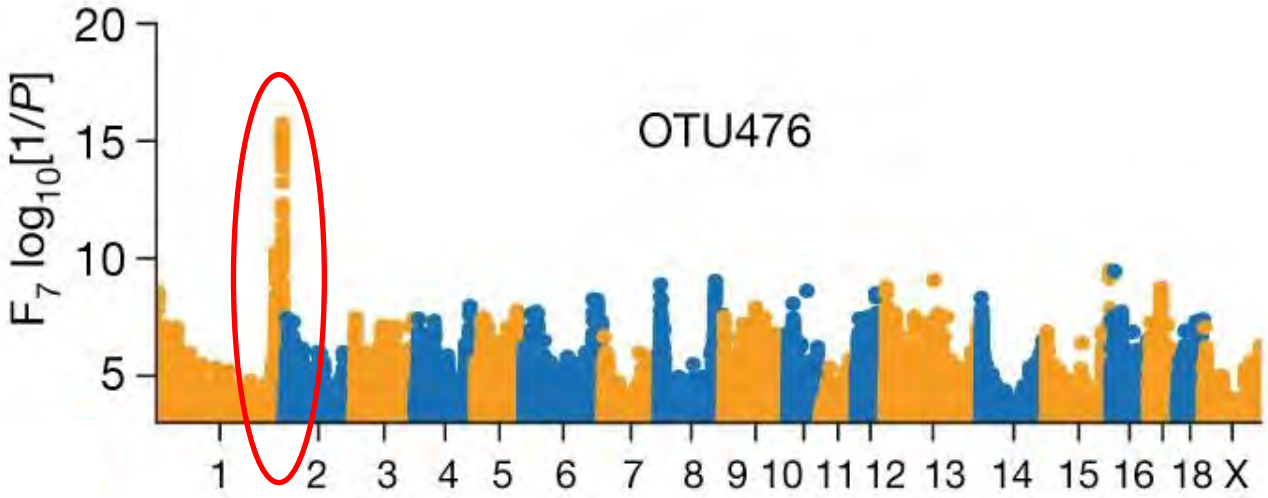
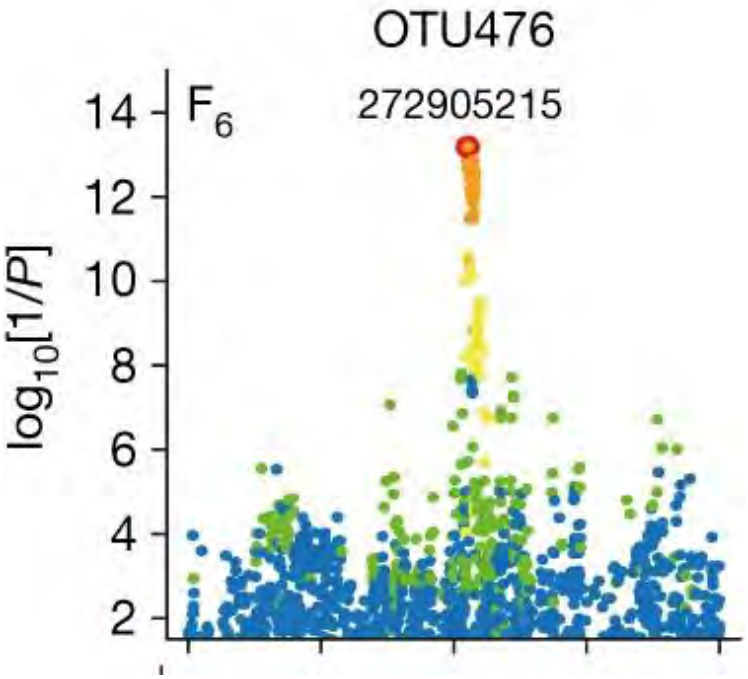
(1)

A microbiota QTL (miQTL) in pigs affecting Erysipelotrichaceae species





ABO

From: Yang et al. 2022

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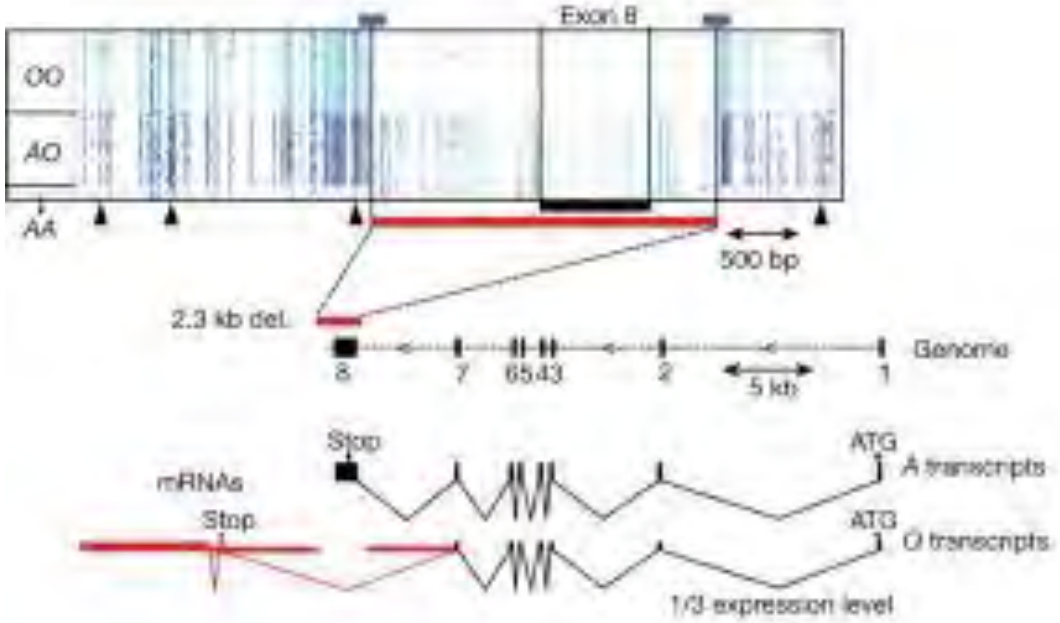
(1)

A microbiota QTL (miQTL) in pigs affecting Erysipelotrichaceae species

A 3.5-million-year-old deletion
in the pig *ABO* orthologue
causes the miQTL

A allele = wild type
O allele = with the 2.3 kb deletion in exon 8



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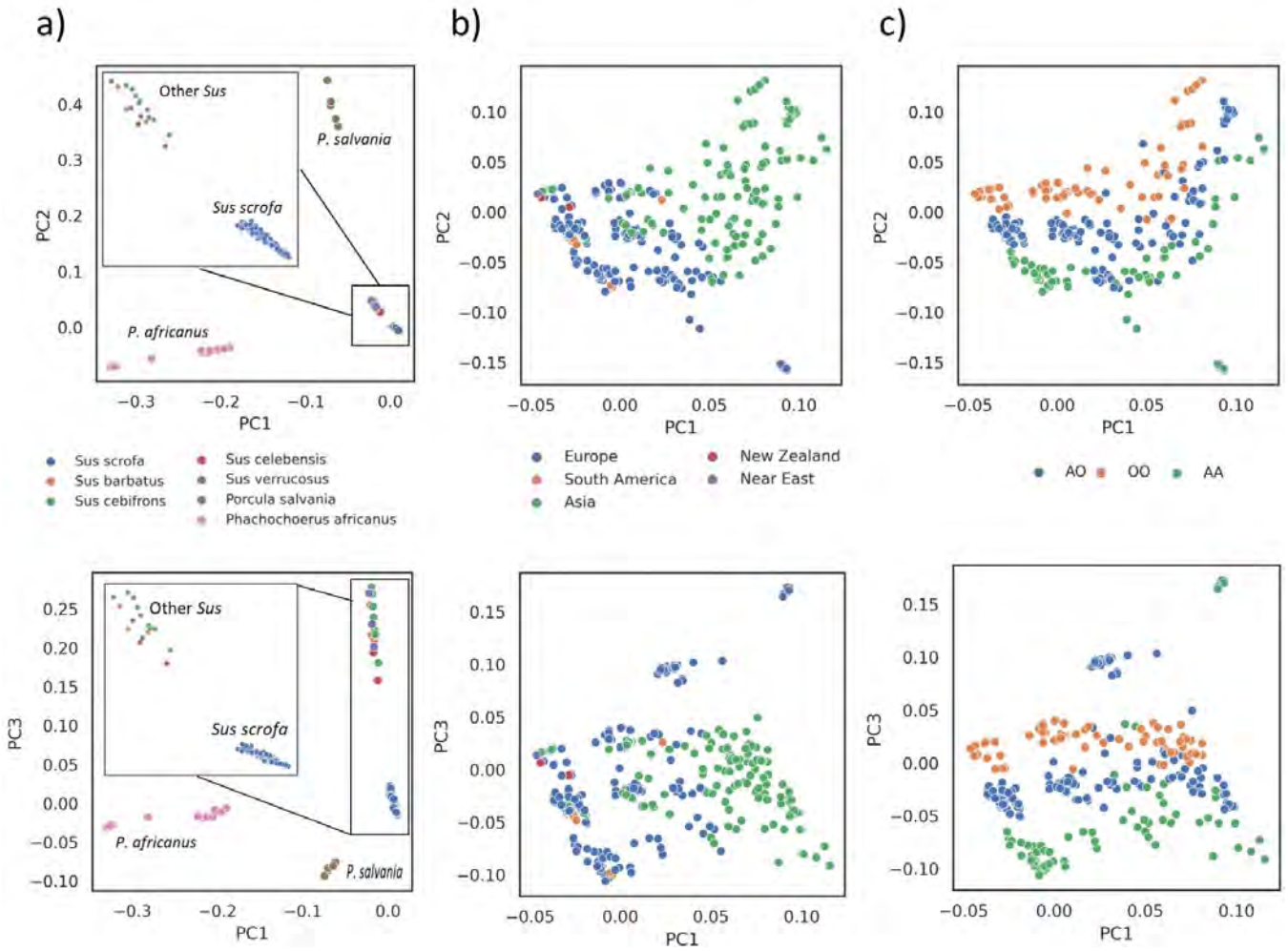

Principal Component Analysis based on Single Nucleotide Variants at the ABO gene.

(a) The analysis included all considered datasets, from different species. Datasets are coloured by species.

(b) Analysis including only *Sus scrofa* datasets. Datasets are coloured by geographic origin of the breed/population.

(c) Analysis including only *Sus scrofa* datasets. Datasets are coloured based on the ABO gene genotype (AA, AO and OO).

From: Bolner, … Fontanesi, 2023, in press

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(1)

A microbiota QTL (miQTL) in pigs affecting Erysipelotrichaceae species

- **A allele**: encodes the *N-acetyl-galactosaminyl-transferase* that adds N-acetyl-D-galactosamine (*GalNAc*, α1-3 linkage) to H and Lewis antigens present on glycan substrates, which can be used as carbon source by intestinal bacteria.

- **O allele** might reduce the concentration of *GalNAc* in the intestine, thereby reducing the growth of bacterial species that are dependent on this sugar.

From: Yang et al. 2022

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(2)

- **Piglet diarrhoea due to Enterotoxigenic *Escherichia coli* (ETEC) is an important problem in swine industry across the globe.**

- Susceptibility to ETEC is thought to be caused by attachment of *Escherichia coli* fimbria on single or multiple receptors in the piglet's small intestine.

- The F4 and F18 are the most important fimbrial subtypes in ETEC.

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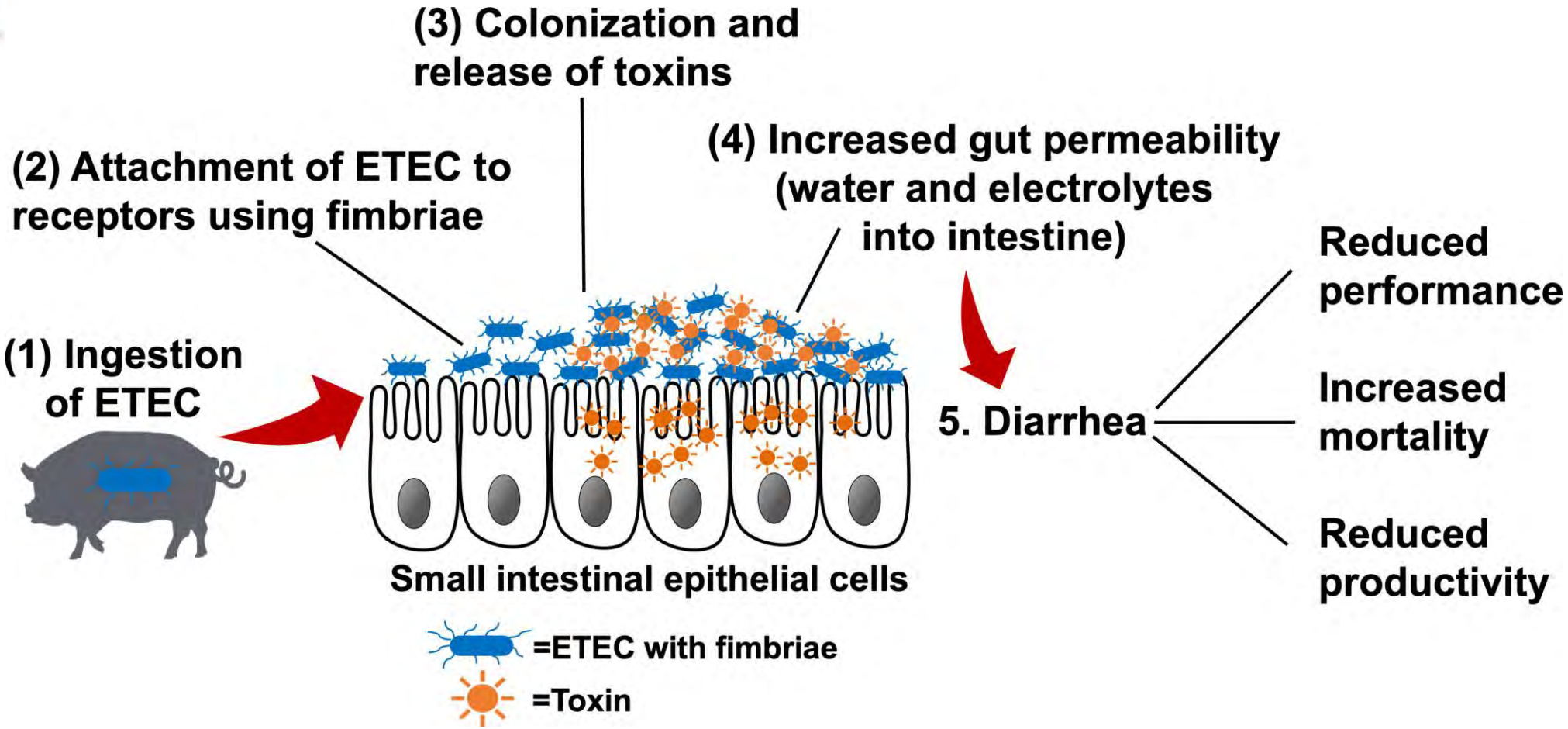
(2)



From: Kim et al. 2022

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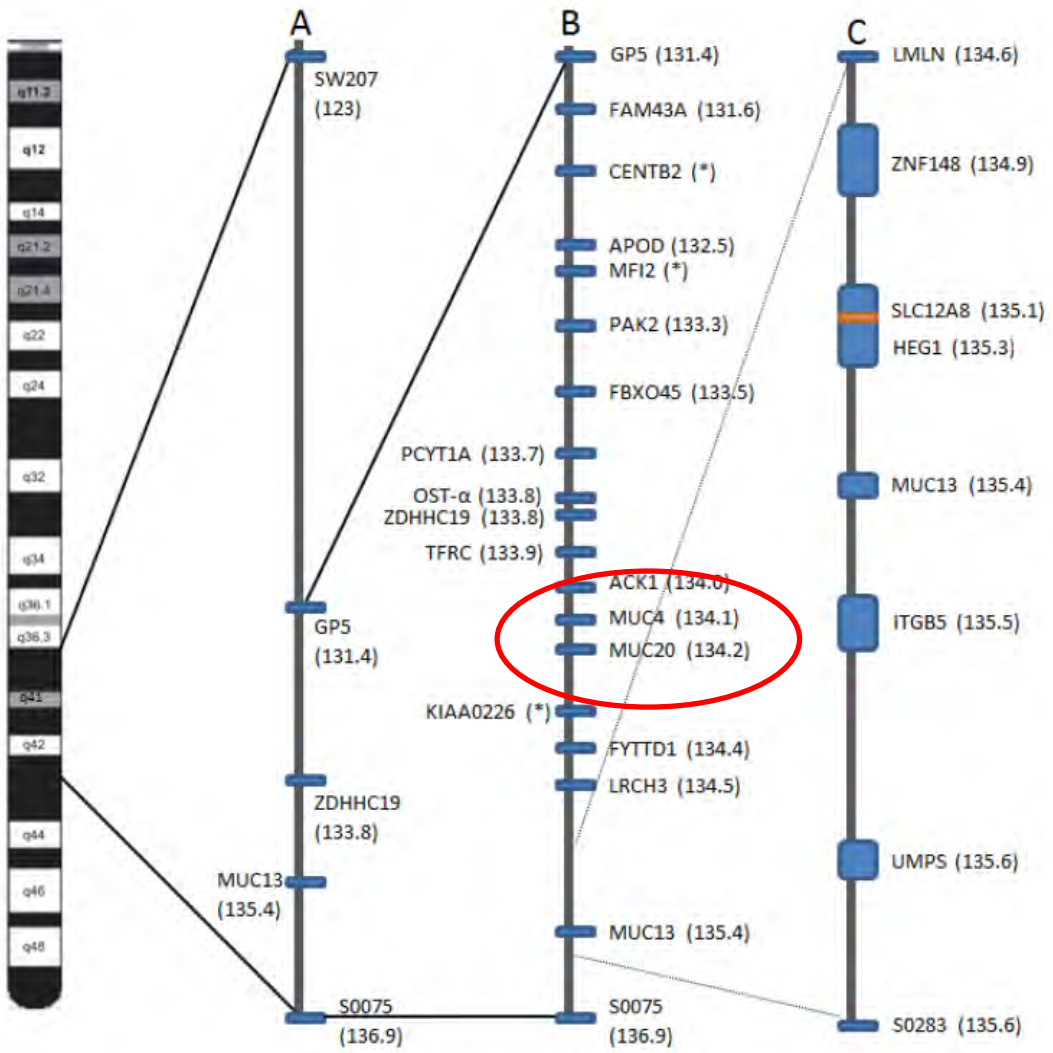
(2)



SSC13

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(2)

- Breeding towards more resistant pigs to F4ac ETEC

- We have implemented a MAS based on in Italian heavy pigs

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Submitted:

Bovo, … Fontanesi

Genome-wide association studies for diarrhoea outcomes identified genomic regions affecting resistance to a severe enteropathy in suckling rabbits

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Genome-wide association studies for diarrhoea outcomes identified genomic regions affecting resistance to a severe enteropathy in suckling rabbits

- Breeding towards more resistant rabbits to diarrhoea

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Conclusioni

- Il genoma dell'animale «condiziona» in parte anche il suo microbiota.

- Il microbiota (microorganismi patogeni) condiziona l'espressione del fenotipo dell'animale, se suscettibile (ad es. diarrea).

- E' possibile selezionare gli animali usando come fenotipo il microbiota per aumentare la sostenibilità delle produzioni zootecniche.

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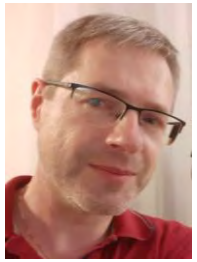

Luca Fontanesi
Full Professor

Francesca Bertolini
Associate Professor

Stefania Dall'Olio
Associate Professor

Paolo Zambonelli
Associate Professor

Samuele Bovo
Junior Assistant Professor
Bioinformatics – data analysis

Anisa Ribani
Junior Assistant Professor
Molecular genetics

Giuseppina Schiavo
Junior Assistant Professor
Bioinformatics – data analysis

Mohamad Ballan
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Bioinformatics

Matteo Bolner
PhD student
Bioinformatics

Valeria Taurisano
Post-doc
Molecular genetics
Data analysis

Jacopo Vegni
Post-doc
Data analysis

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