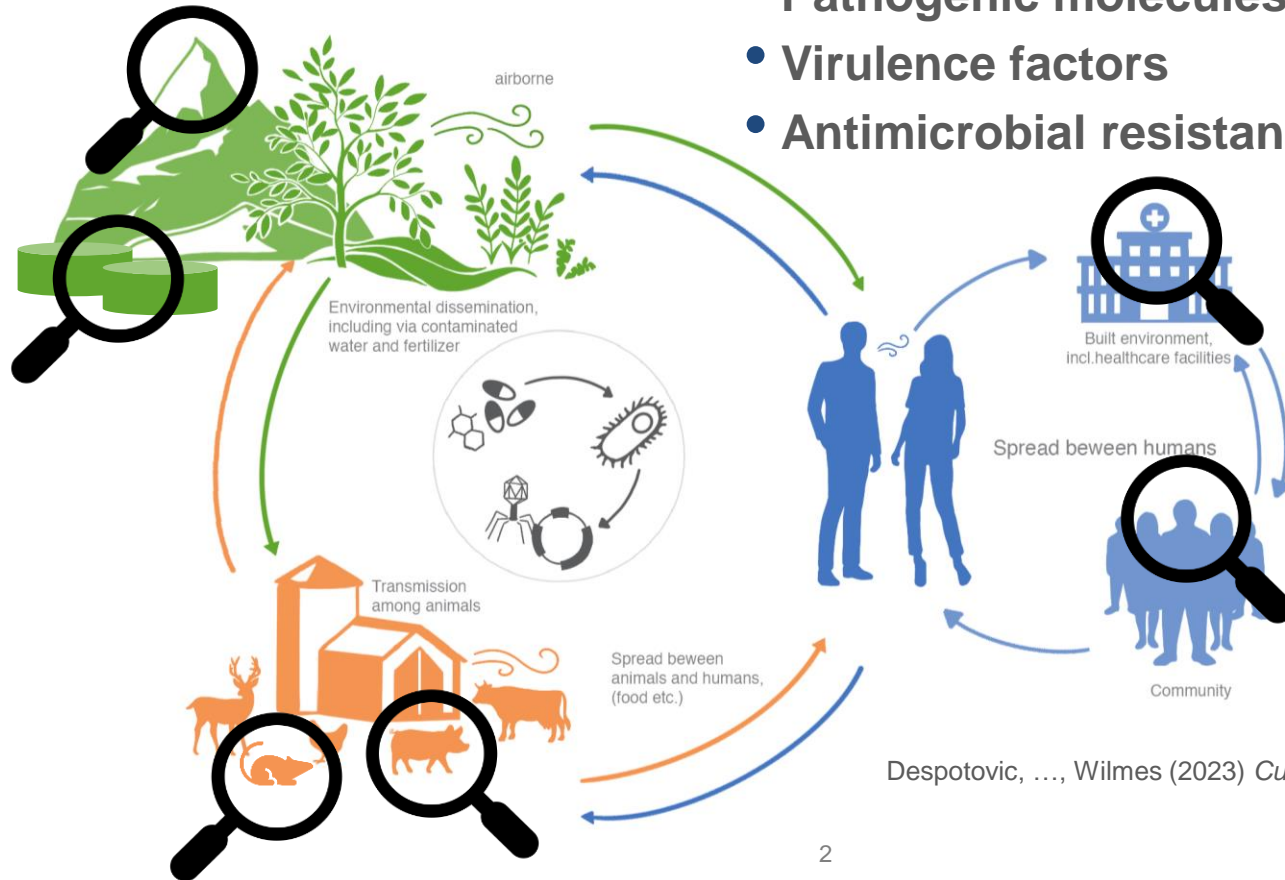


**One Health: Systematically
resolving infective competence in
microbiome reservoirs to
understand organismal and
functional transfer across biomes**

Microbiome exposures in One Health

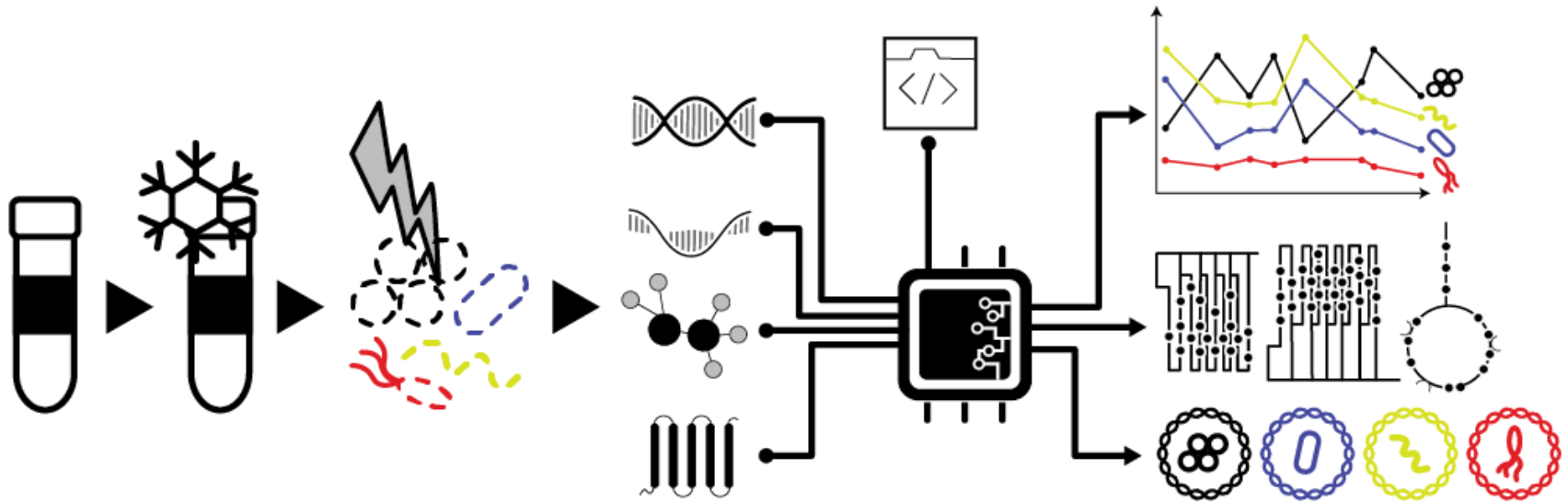


- Pathogenic molecules
- Virulence factors
- Antimicrobial resistance

Infective competence

Despotovic, ..., Wilmes (2023) *Current Opinion in Microbiology* **73**:102291.

Integrated multi-omics

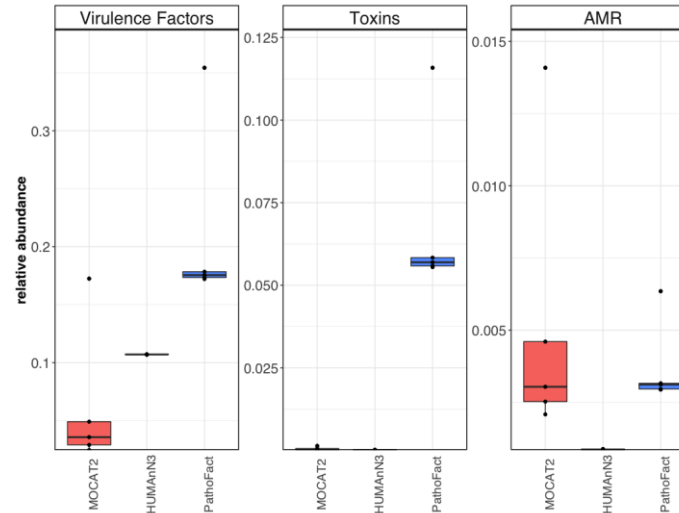
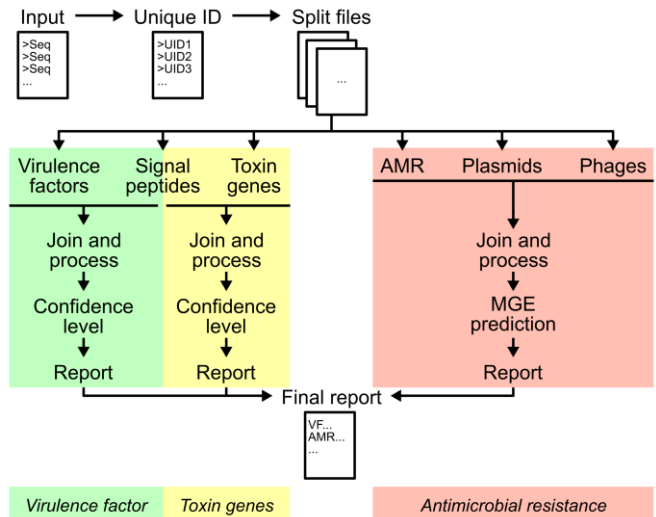


Roume, ..., Wilmes (2013) *The ISME Journal* **7**:110–121.
Muller, ..., Wilmes (2013) *Trends in Microbiology* **21**:325–333.
Roume, ..., Wilmes (2013) *Methods in Enzymology* **531**:219–236.
Muller, ..., Wilmes (2014) *Nature Communications* **5**:5603.

Roume*, Heintz-Buschart*, ..., Wilmes (2015) *npj Biofilms and Microbiomes* **1**:15007.
Heintz-Buschart, ..., Wilmes (2017) *Nature Microbiology* **16180**:1-12.
Heintz-Buschart & Wilmes (2018) *Trends in Microbiology* **26**:563-574.
Herold, ..., Wilmes (2020) *Nature Communications* **11**:5281.
Martinez-Arbas*, Narayanasamy*, ..., Wilmes (2021) *Nature Microbiology* **6**:123–135.

PathoFact

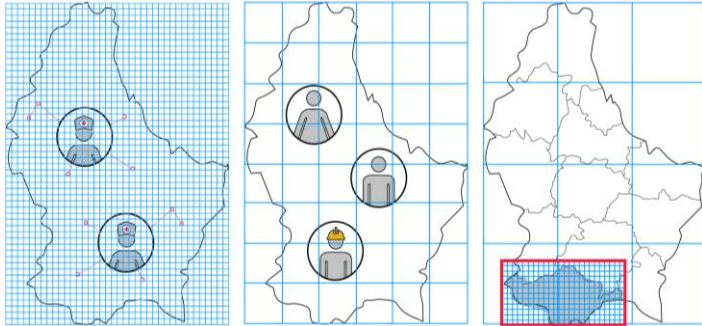
Pipeline for the prediction of **virulence factors & antimicrobial resistance genes** in metagenomic data



<https://pathofact.lcsb.uni.lu>

Community - Impact of COVID-19

Mass screening in Luxembourg

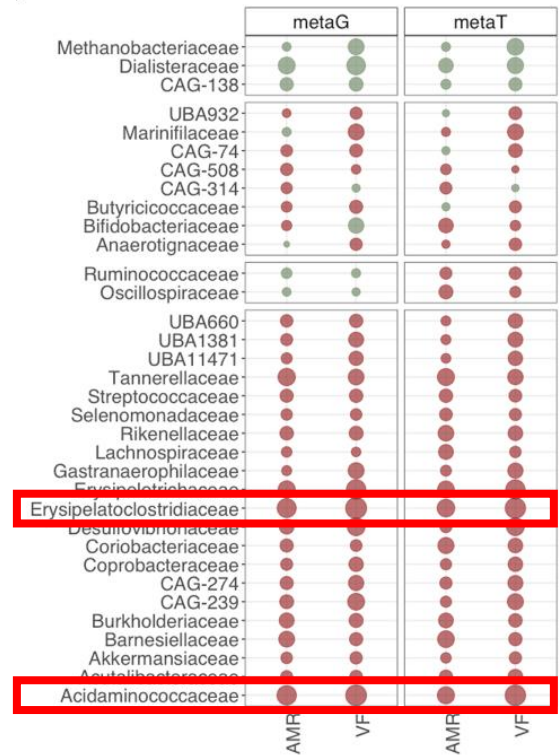


Legend:
 — Targeted testing zone
 ○ Focus on population group

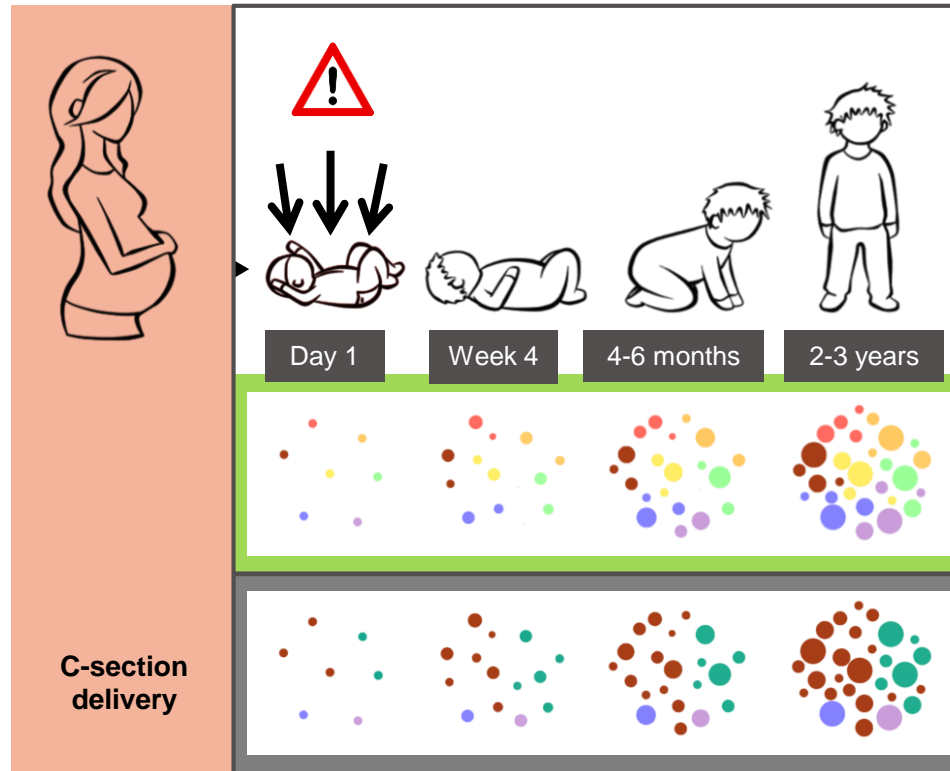
Wilmes et al. (2021) *The Lancet Regional Health – Europe* 4:100056.

Wilmes et al. (2021) *The Lancet Regional Health – Europe* 5:100116.

- Increase in abundance and expression of **virulence factors & antimicrobial resistance genes** in COVID-19
- **Infected competence** ↑
- Genes encoded & expressed by **commensal taxa**
- Enrichment in the expression of **betaherpesvirus & rotavirus C genes**

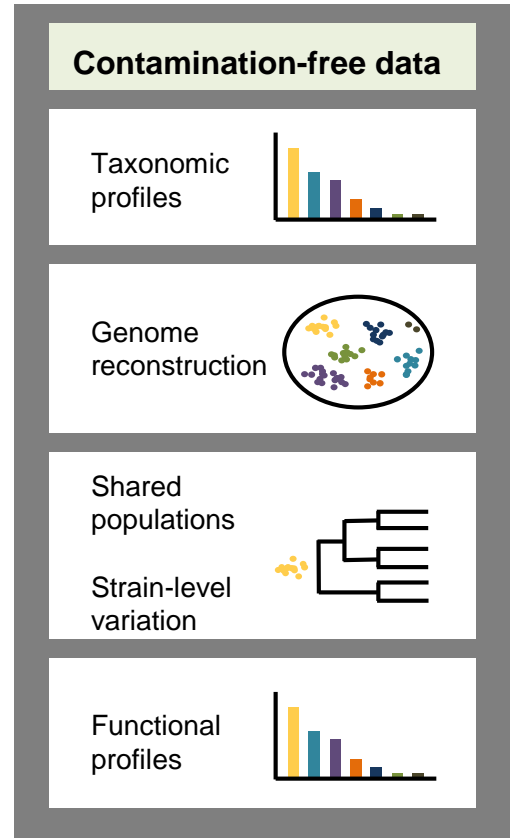
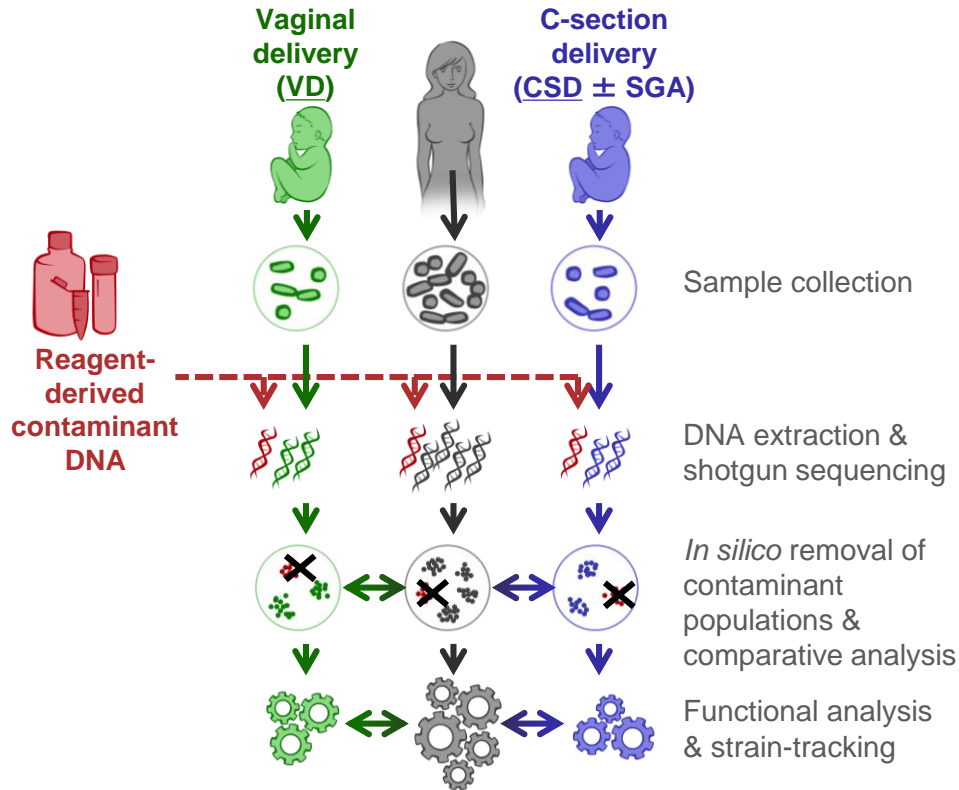


Humans & built environment - Earliest exposures



- Qualitative & quantitative **differences** for **bacteria, archaea & microeukaryotes**

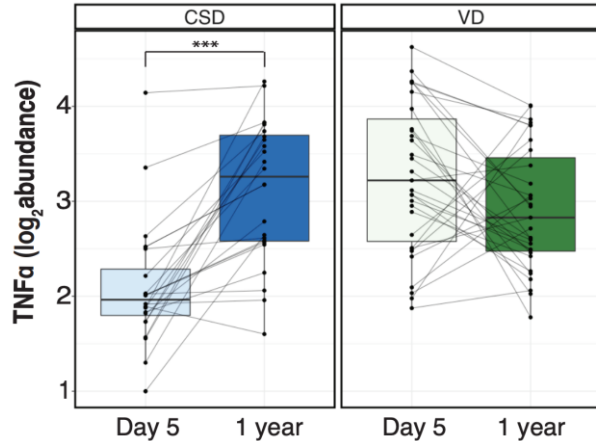
Artefact-free high-resolution metagenomics



Wampach*, Heintz-Buschart*, Fritz*, ..., Wilmes (2018) *Nature Communications* 9:5091.

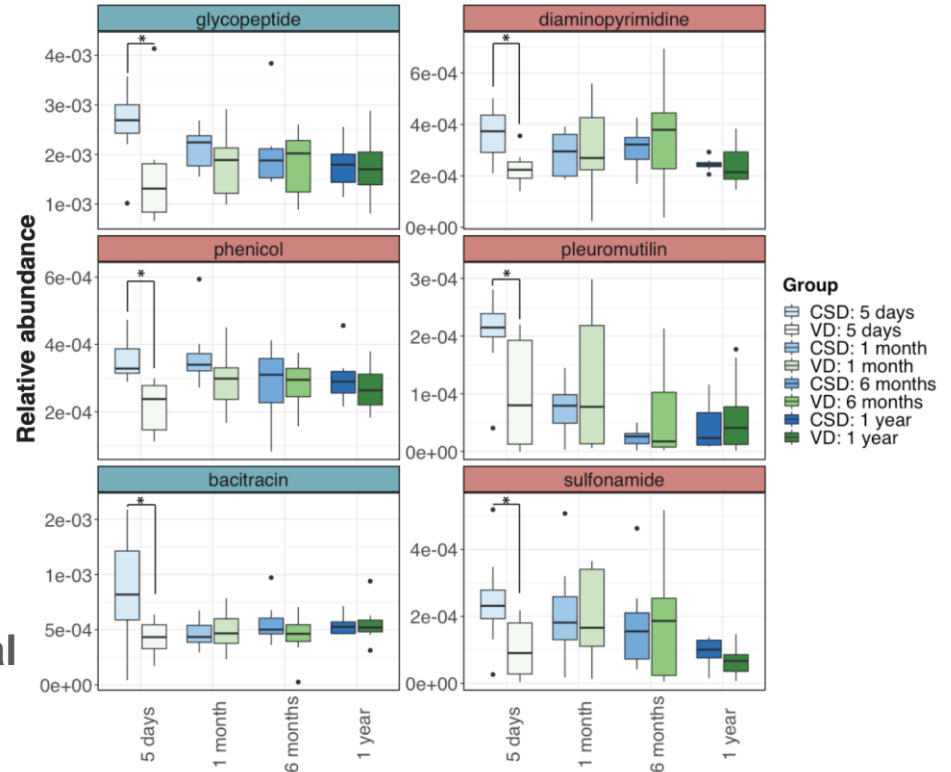
Humans & built environment – Phage-mediated AMR

TNF α levels

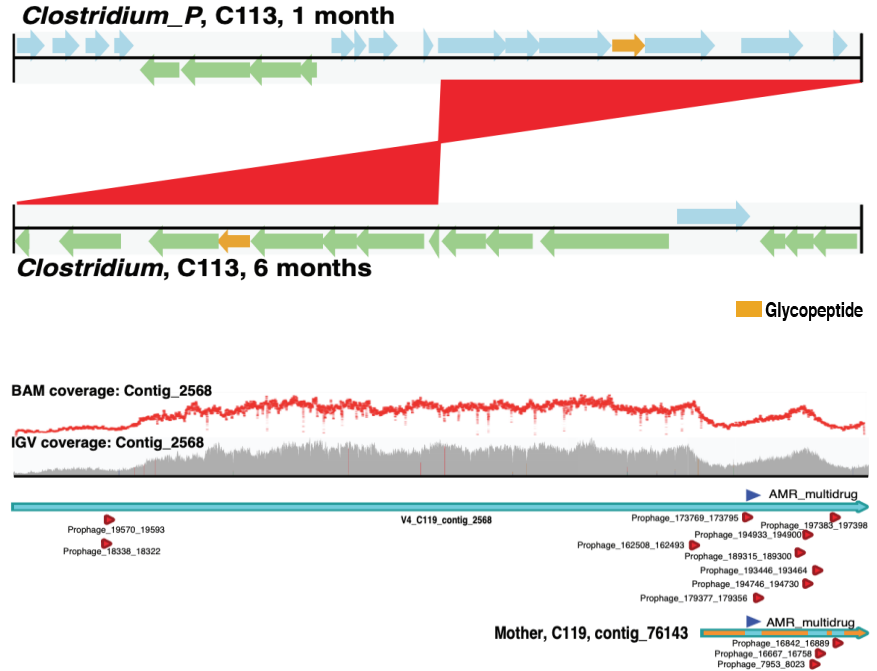
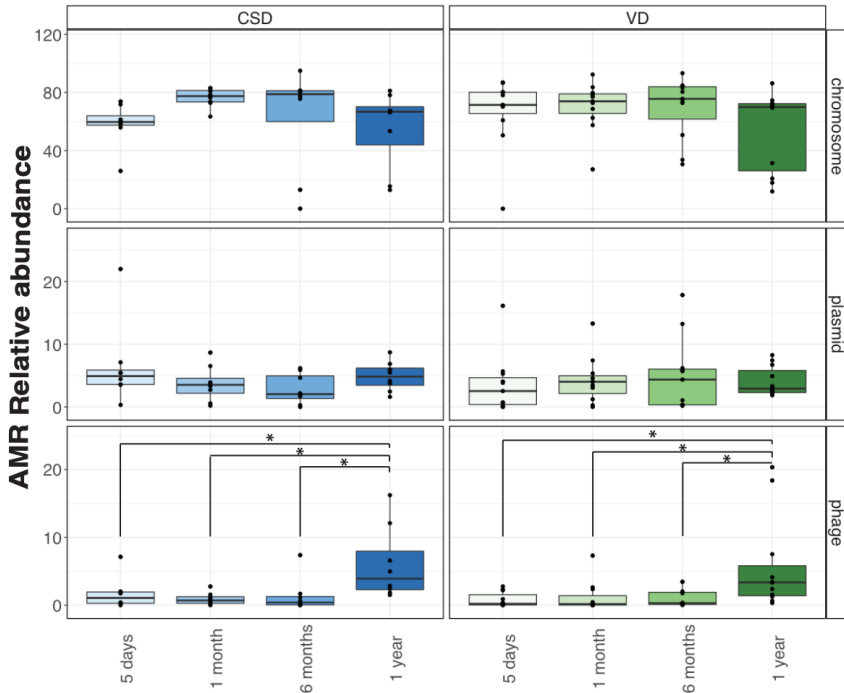


- **Differential abundances in TNF α** over time (CSD) linked to LPS exposure
- **Differential abundance of antimicrobial resistance at 5 days** after birth

Antimicrobial resistance

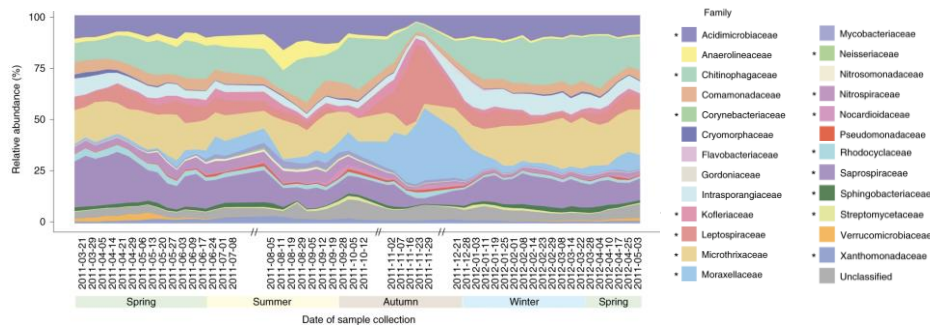


Humans & built environment – Phage-mediated AMR

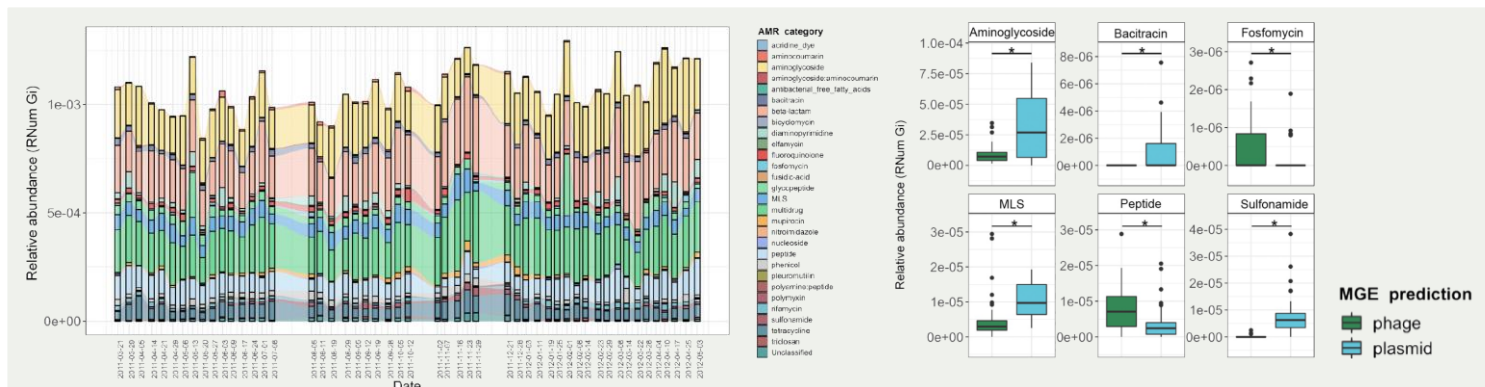


- Mobile genetic element-mediated AMR (bacteriophages & plasmids)
- Horizontal gene transfer of AMR

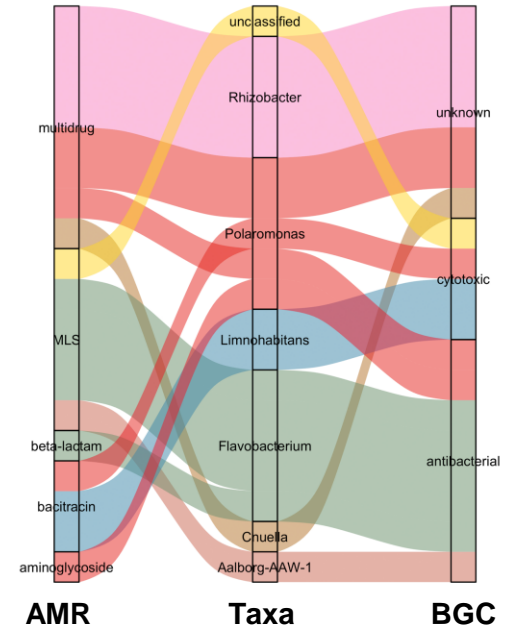
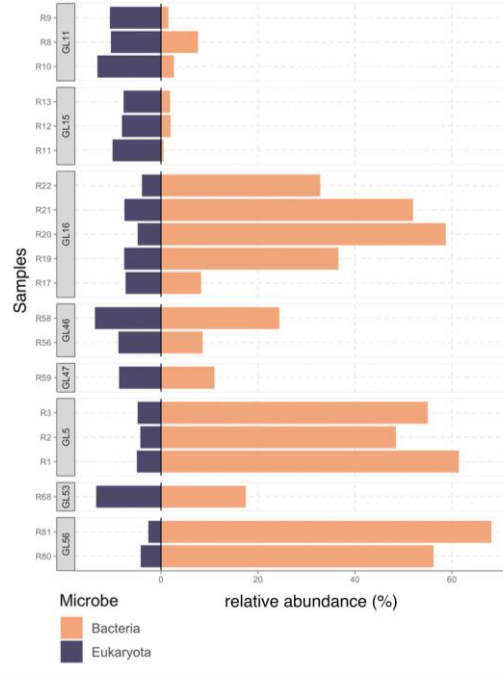
Environment – Mobile resistance in wastewater



- Mobilome-mediated **segregation of antimicrobial resistance**
- **Exclusivity or clear enrichments** in specific antimicrobial resistance genes in taxonomic clades
- Links to ESKAPEE pathogens

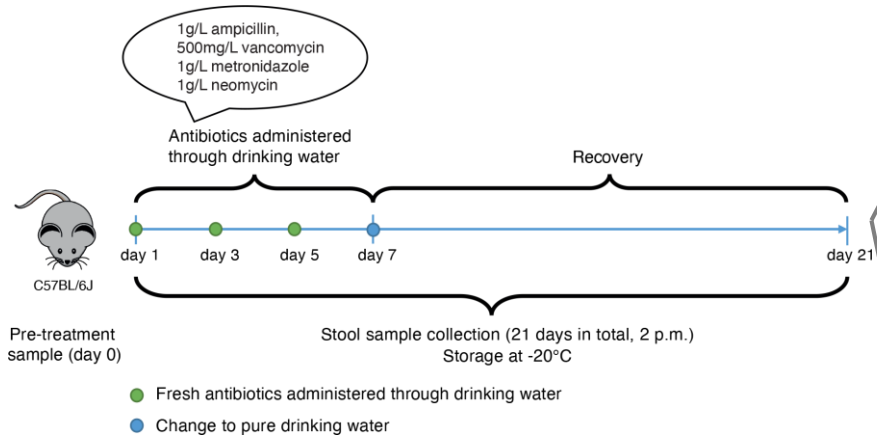


Environment – AMR in a pristine environment

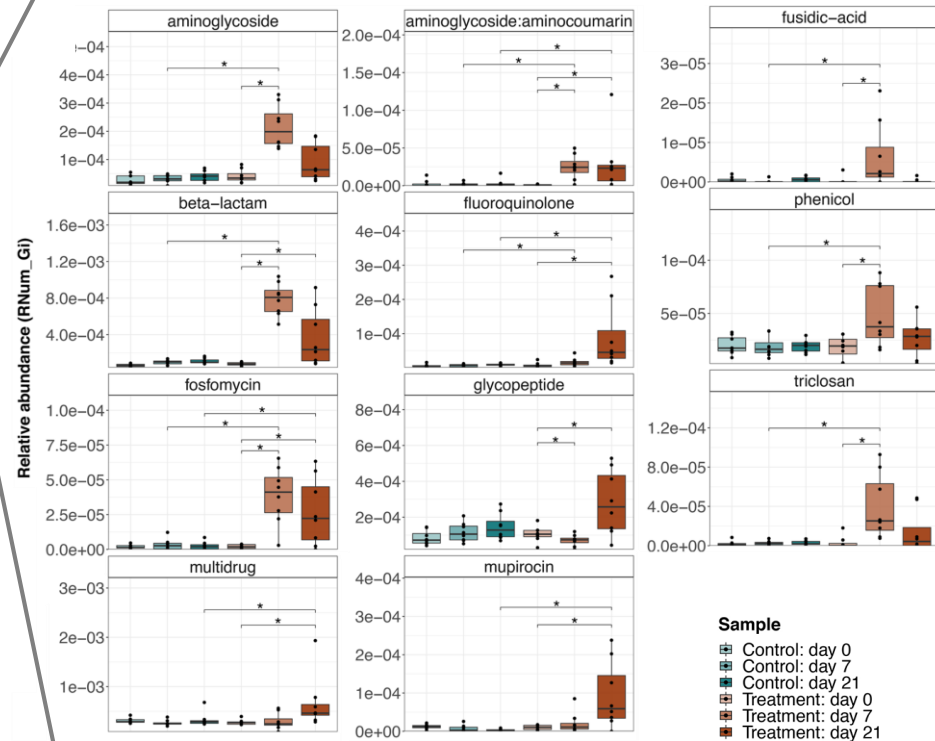


- Link: **AMR & biosynthetic gene clusters (BGCs)**
- Predominantly encoded by **bacteria**

Animals – Rapid evolution of AMR



- Significant **longitudinal differences** in various antimicrobial resistance gene categories
- **Integron-driven antimicrobial resistance** linked to reconstructed genomes of *Akkermansiaceae* and *Enterobacteriaceae*



Controlling microbiomes circulations for better food systems



Coordinator:
Prof. Marco Candela (University of Bologna)



Start: 1. Nov.
2018

31 public &
private partners

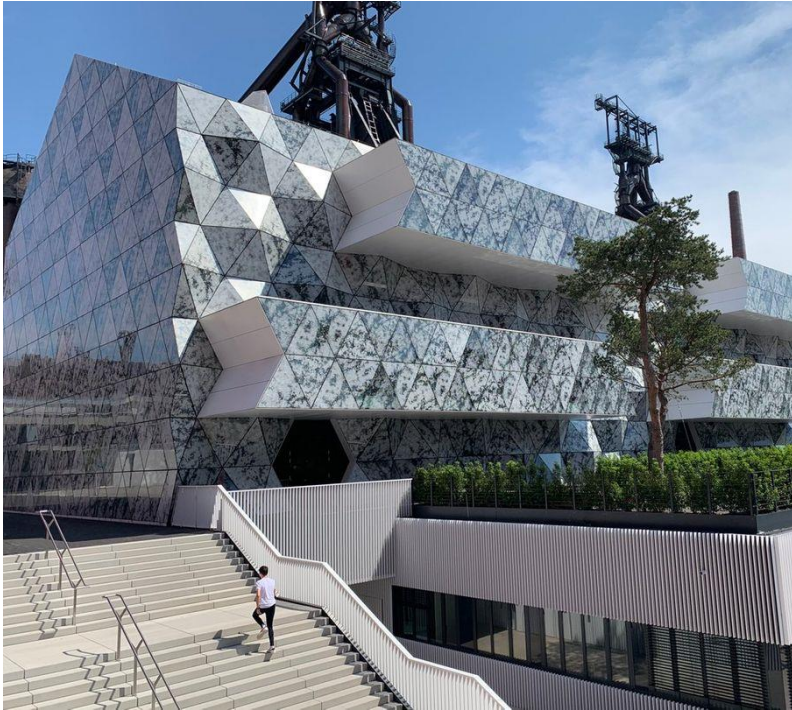
10 Mio €

5,000
metagenomes
planned

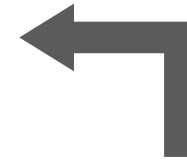
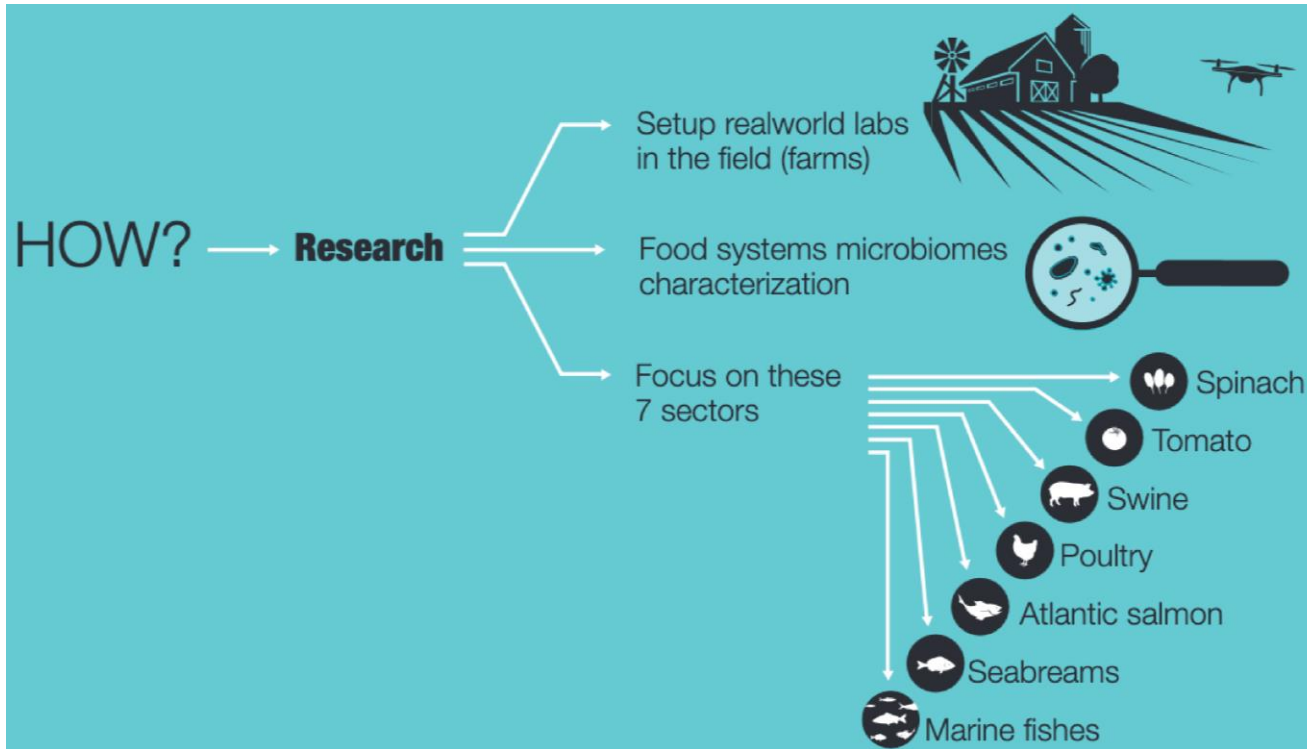
CIRCLES aims to discover and translate **innovative microbiomes-tailored circular actions** into concrete applications that will ultimately enhance EU food system performances and their overall sustainability.

Grant agreement ID: 818290

Reminder - What is metagenomics?



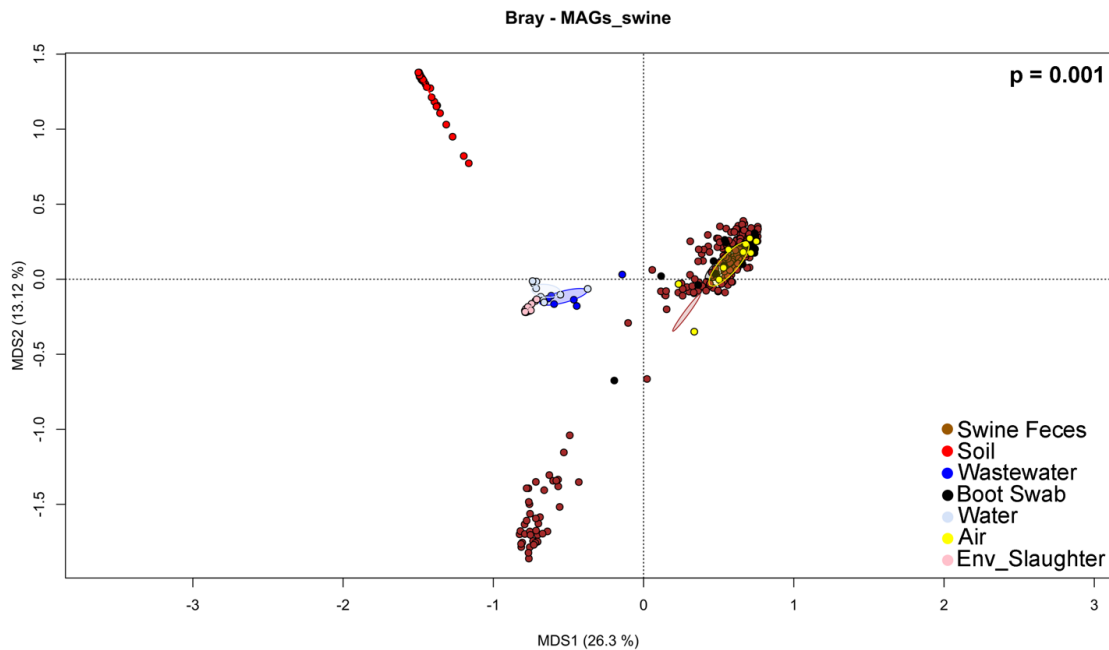
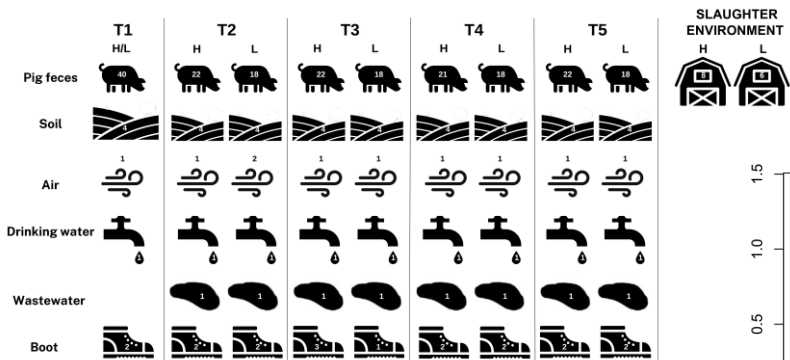
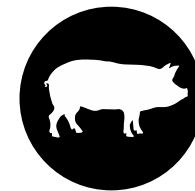
Improving food quality & sustainability



Smart
Microbiome
Modulators

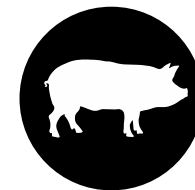


ARBs & AMR transmission from swine farm to the environment

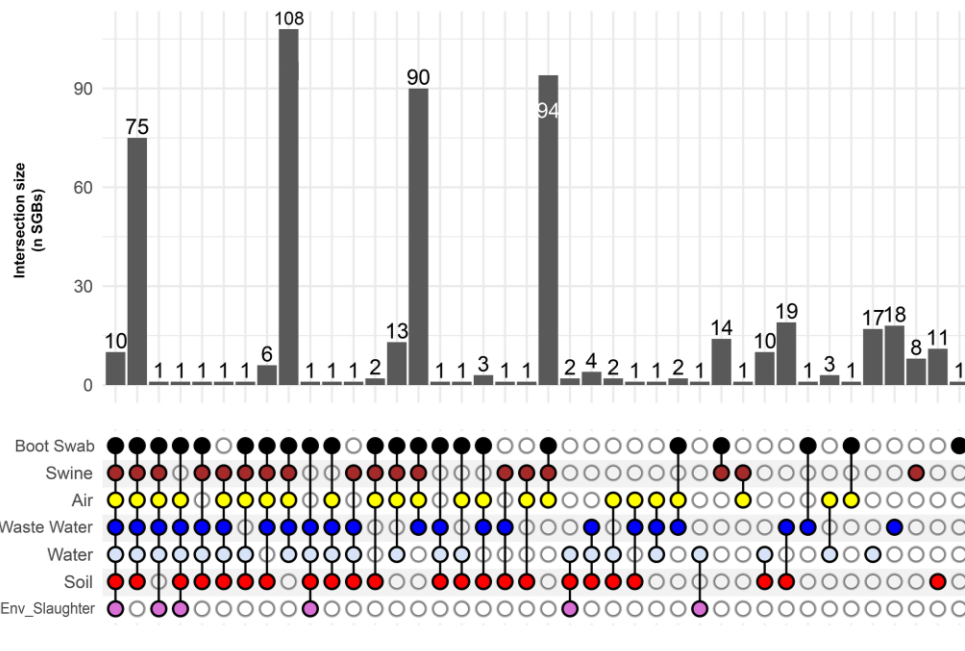


Scichitano *et al.* (2023); submitted

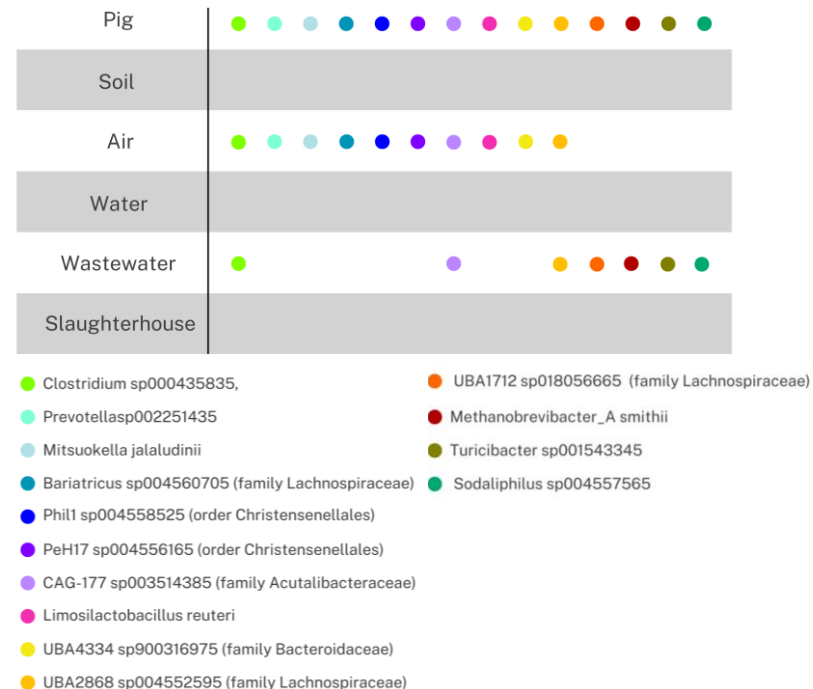
ARBs & AMR transmission from swine farm to the environment



Shared species

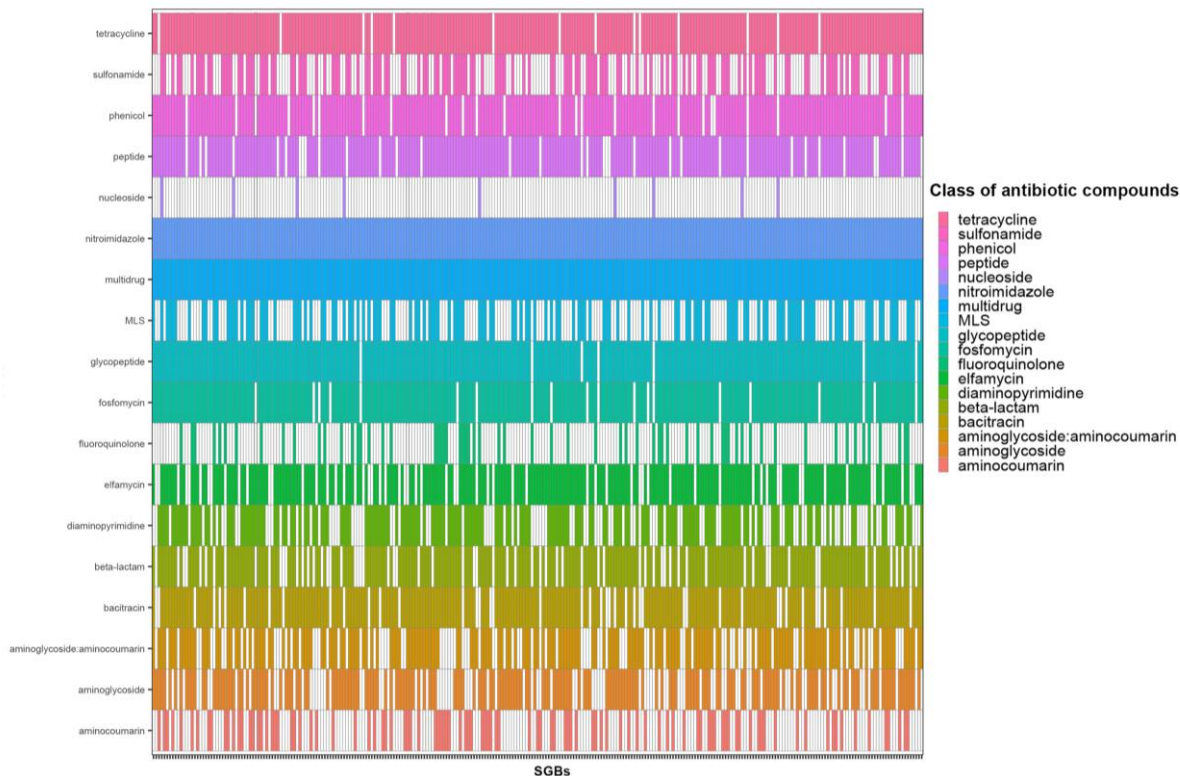
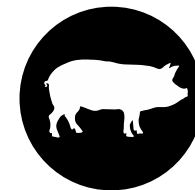


Shared strains



Scichitano *et al.* (2023); submitted

ARBs & AMR transmission from swine farm to the environment



Scichitano *et al.* (2023); submitted

Nitroimidazole,
glycopeptide, fosfomycin
classes **most frequent**

Nucleoside,
fluoroquinolone,
aminocoumarin classes
least frequent

10% located on **mobile
genetic elements (MGEs)**

Core resistome of 6.8%;
not predicted on MGEs

Conclusion

- **Interconnectivity** of infective competence & biomes
- Need to better **understand gene flows** in view of One Health, pandemic preparedness, health & disease
- Understanding and **modulating microbiomes** requires systems-level study
- **Meta(gen)omics** hold large potential in improving food quality and sustainability
- **Transmission tracking** of ARBs & AMR needs to be extended
- CIRCLES' **intervention phase** analysis ongoing

Acknowledgements

Velma Aho, Susheel Busi, Jordan Caussin, Laura de Nies, Charlotte De Rudder, Francesco Delogu, Milena Despotovic, Léa Grandmougin, Benoit Kunath, Laura Lebrun, Tuesday Lowndes, Mara Lucchetti, Polina Novikova, Kristopher Schmit, Catherine Sedrani, Melanie Thomas, Manuel Buttini, Janine Habier, Rashi Halder

Carine de Beaufort, Patrick May, Jochen Schneider, Alex Skupin, Laurent Mombaerts, Atte Aalto, Jorge Goncalves, Enrico Glaab, Christian Jäger, Michel Mittelbronn, Reinhard Schneider, Rejko Krüger, Emma Schymanski, Anne Grünewald, Serge Haan, Elisabeth Letellier, Rudi Balling, Michael Heneka



Ulf Nehrbaas
Frank Glod
Jasmin Schulz
Jacques Zimmer
Chantal Snoeck
Markus Ollert

Joël Mossong



Romain Martin
Bruno Rodrigues



Marie-Louise Uwizeye
Joachim Hansen



Emilie Muller



Andreas Michalsen
Daniela Liebscher
Etienne Hanslian



Frederic Zenhausern
Matthew Barrett
Brett Duane
Matthew Estes



Eric Martens
Stefanie Widder



Karoline Faust
Anna Heintz-B.



Brit Mollenhauer
Sebastian Schade



Andreas Otto
Dörte Becher



Paul Keim
Jim Schupp
Dave Engelthaler



Christian-Albrechts-Universität zu Kiel

Ruth Schmitz-Streit



Wolfgang Oertel



Helmholtz-Zentrum POTSDAM

Jens Kallmeyer



Marco Candela

EPFL
Massimo Bourquin
Hannes Peter
Tom Battin



Kenya Honda
Toshimori Kitani
Haruhiko Koseki



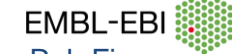
David Galas
David Huang



Sebastian Schmidt
Peer Bork



Bob L. Hettich



Rob Finn
Juan Vizcaino



Christine Moissl-Eichinger



Nico Jehmlich



Phil Bond

Funding:



**Postdoc & PhD
positions
available**

**Thank you very much
for your attention!**

paul.wilmes@uni.lu
cedric.laczny@uni.lu



[@wilmeslab](https://twitter.com/wilmeslab)



LUXEMBOURG
SOCIETY FOR
MICROBIOLOGY



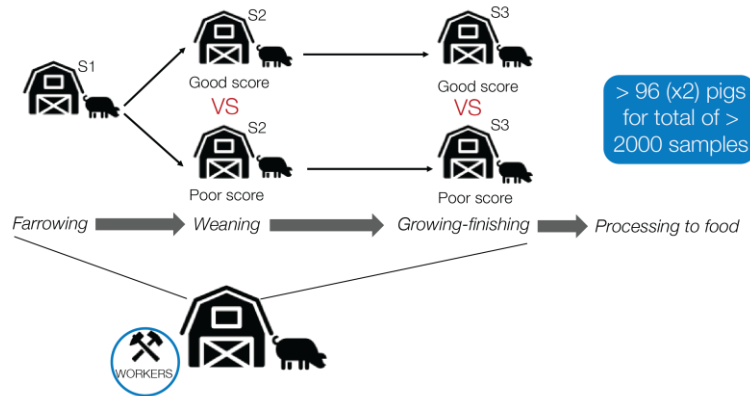
7th Luxembourg Microbiology Day

Save the date

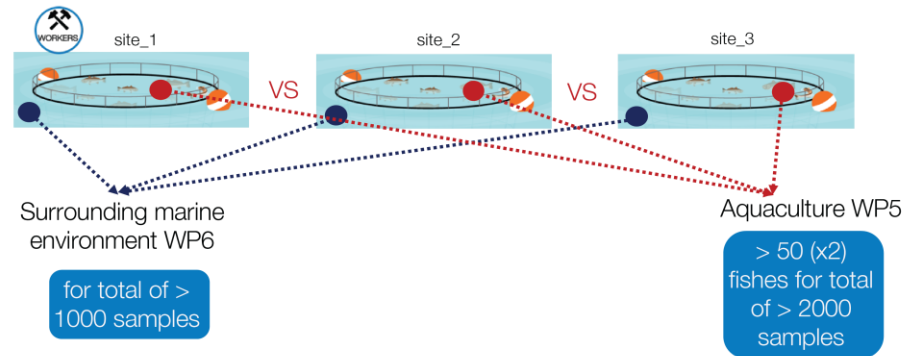
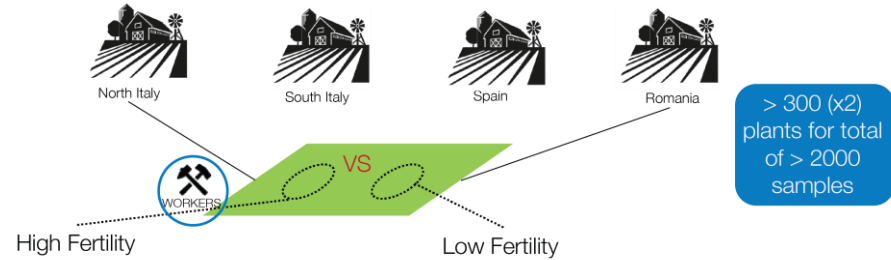
May 16th 2024 | Venue - TBC

www.microbiology.lu

CIRCLES Goal 1 - Improving food quality



> 120 (x2) birds for total of > 2000 samples



Increasing microbiome awareness in the general public



CIRCLES TURNS BLUE: marine microbiome stories at the Ancona Blue Life Fest

July 27th, 2021

written by Grazia Quero After its kick start in Rimini, the initiative [...]

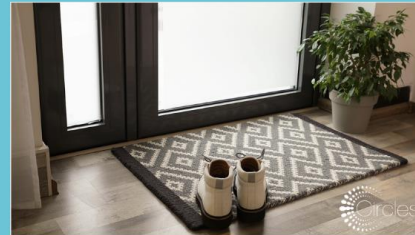


Citizens of Bologna explore the microbiome

October 12th, 2022

Scroll down for the Italian version & images of skin microbiome During this [...]

[Read More >](#)



Map the house-floor microbiome space in the city of Bologna

October 11th, 2022

How does the microbial life look like on our house floors? How is it [...]

[Read More >](#)



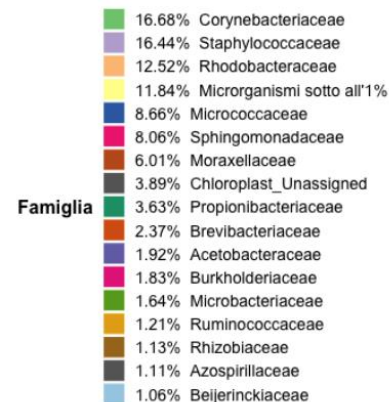
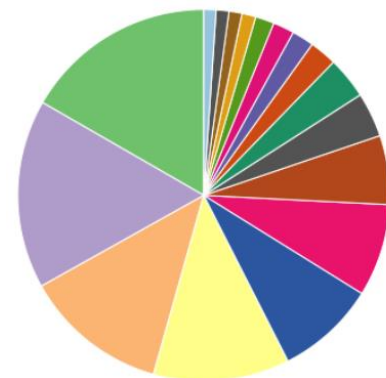
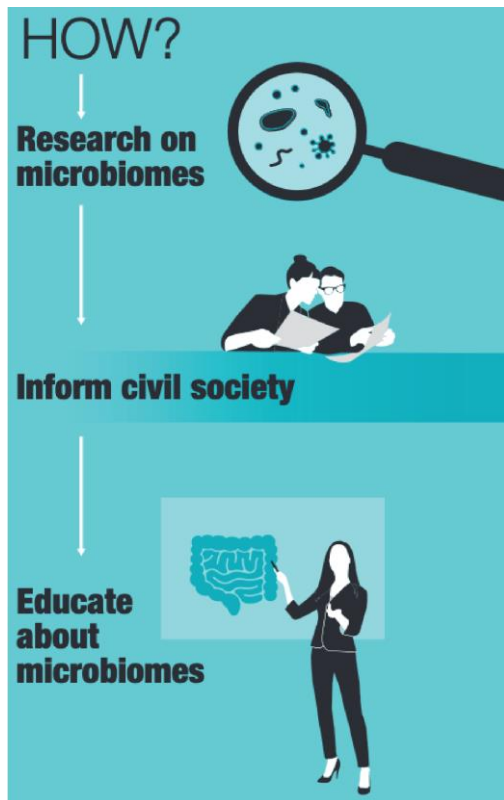
Citizens of Helsinki explore their house-floor microbiome

November 25th, 2022

How does the microbial life look like on the entry of your house? How [...]

[Read More >](#)

CIRCLES Goal 2 – Improving human life



First EU map of the variation of the house floors microbiome (Bologna, Mazara del Vallo, Helsinki and Bruxelles)

