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Microbiome research at FiBL

FiBL Open Day – Organic transformation of food systems

Valentin Gfeller (valentin.gfeller@fibl.org), 27. November 2024

FiBL
OPEN DAY
Organic transformation
of food systems

Introduction of speakers

Valentin Gfeller
Crop Sciences

Introduction
Moderation

Anja Logo
Crop Sciences

Compost microbiome

Geoffrey Mesbahi
Livestock Sciences

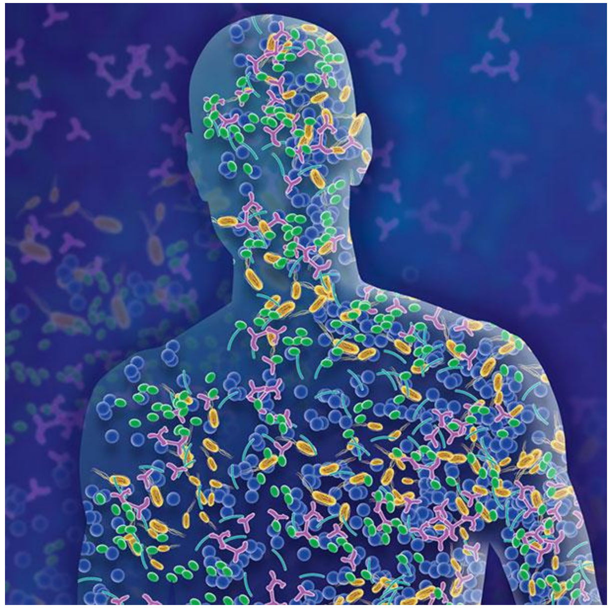
Calf microbiome

Natacha Bodenhausen
Soil Sciences

Soil microbiome

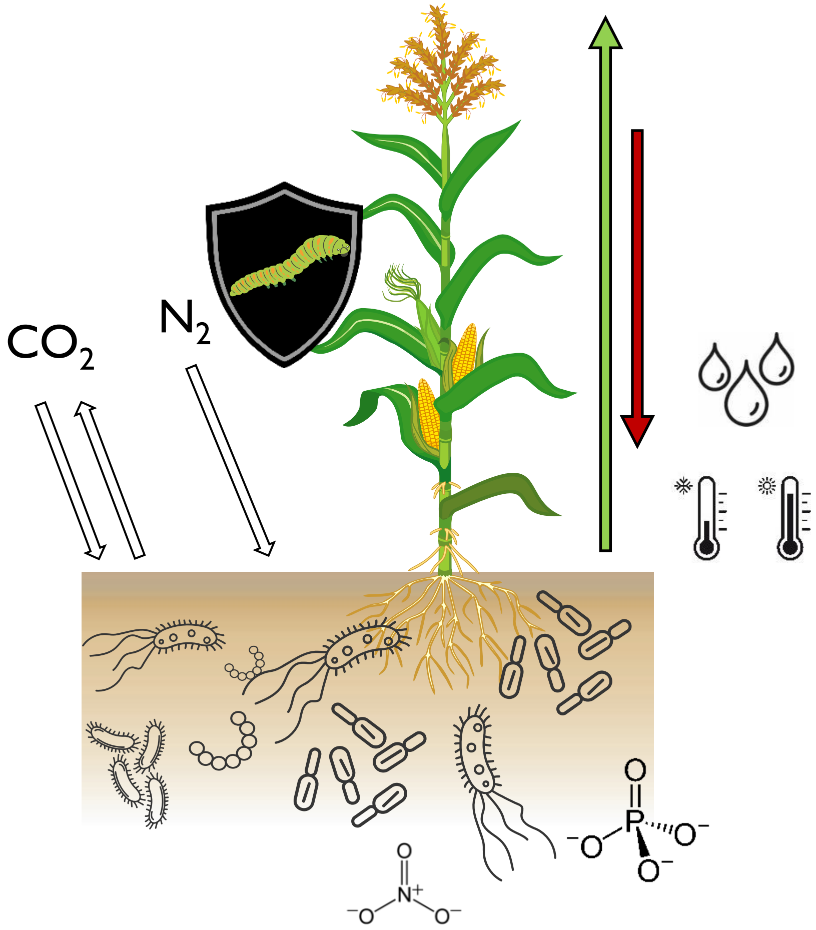
What is the microbiome?

The community of microorganisms that can be found living together in any given environment.



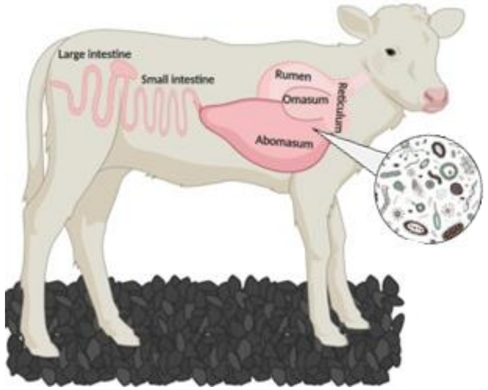
Anthony et al. 2023,
dceg.cancer.gov

Why is studying the microbiome important?



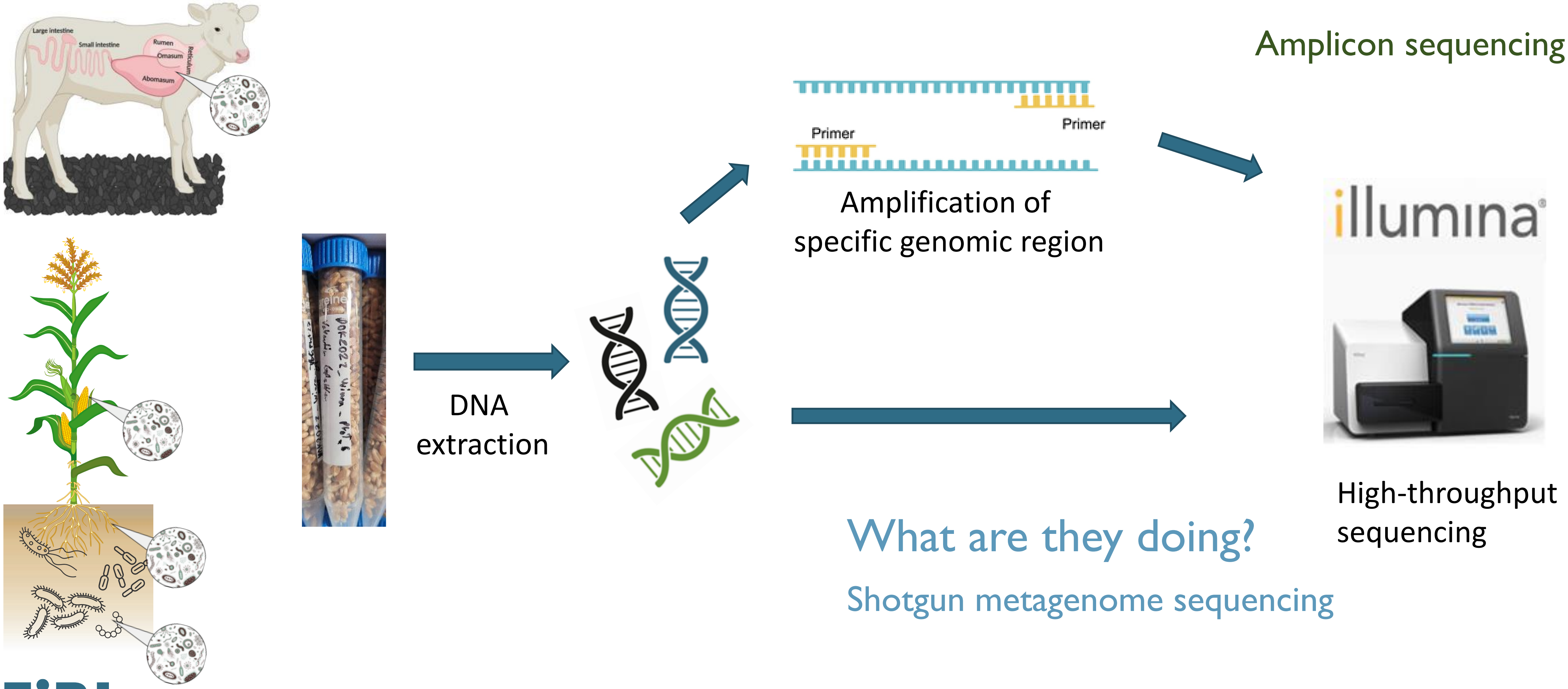
Functions of the microbiome

- Climate regulation
- Nutrient cycling/availability
- Regulation of growth
- Regulation of defense
- Regulation of resilience



Banerjee et al. 2022, Fierer 2017, Amin et al., 2021, Trivedi et al. 2020

How can we study the microbiome?



DNA extraction

Amplification of specific genomic region

Who is there?

Amplicon sequencing

High-throughput sequencing

What are they doing?

Shotgun metagenome sequencing

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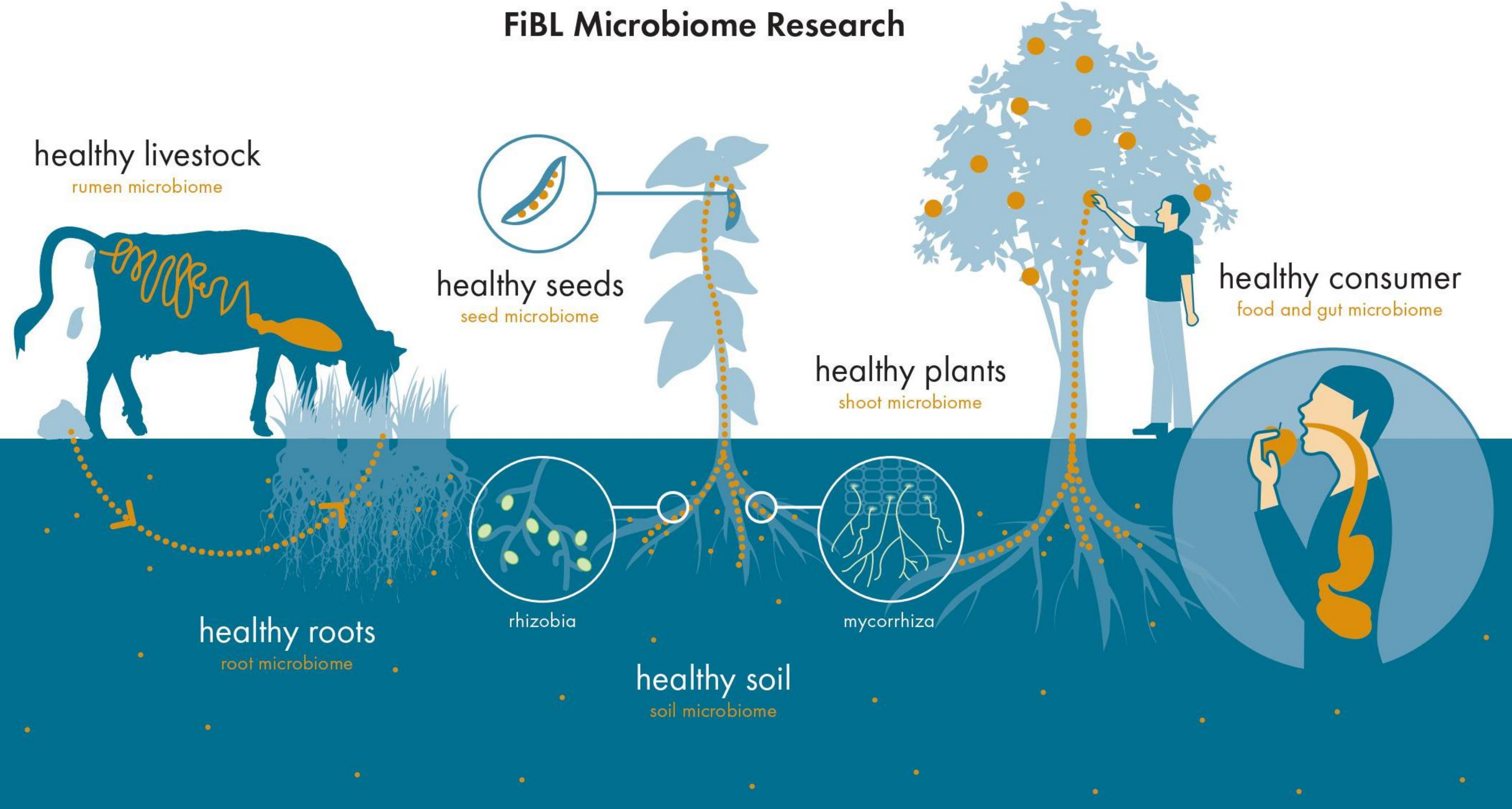
Amin et al., 2021

FiBL Microbiome Research



Questions? We would like to hear from you.

At the end of each presentation, we will have time for 1-2 questions.

After the presentations, there will be more time for questions/discussion.

How to interact?

- You can click the "Raise Hand" button, and we will give you permission to speak.
- You can also use the chat for your questions.

Bacterial and fungal communities associated with disease-suppressive composts across pathogen-plant systems

Anja Logo[123], Barbara Thürig[2], Thomas Oberhänsli[2], Jacques Fuchs[2], Franco Widmer[1], Monika Maurhofer[3], Pascale Flury[4] & Johanna Mayerhofer[1]

[1] Agroscope [2]FiBL (Forschungsinstitut für biologischen Landbau) [3]ETH Zürich [4]University of Basel

Open FiBL Day 2024, 27.11.24, Online

Background

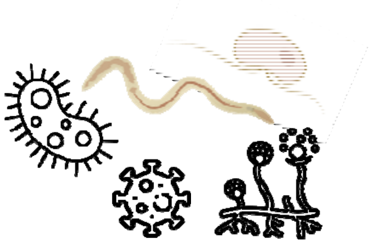
Management of soilborne plant diseases

Environemental concerns
Healthy soil microbiome

Direct control
Soil fumigation
Soil sterilization
…

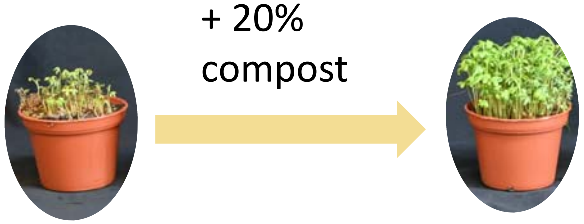
Indirect control
Crop rotation
Hygiene
Cultivar selection
…

Soilborne diseases
Can cause large yield loss
Root rots, wilts, damping-off
…



Caused by
Fungi
Oomycete
Bacteria
Nematodes
Viruses

Compost application
ecological & sustainable control strategy?



+ 20% compost

Globisporangium (Pythium) ultimum in cress

Pictures sources: growingproduce.com, www.flaticon.com, vectra.io

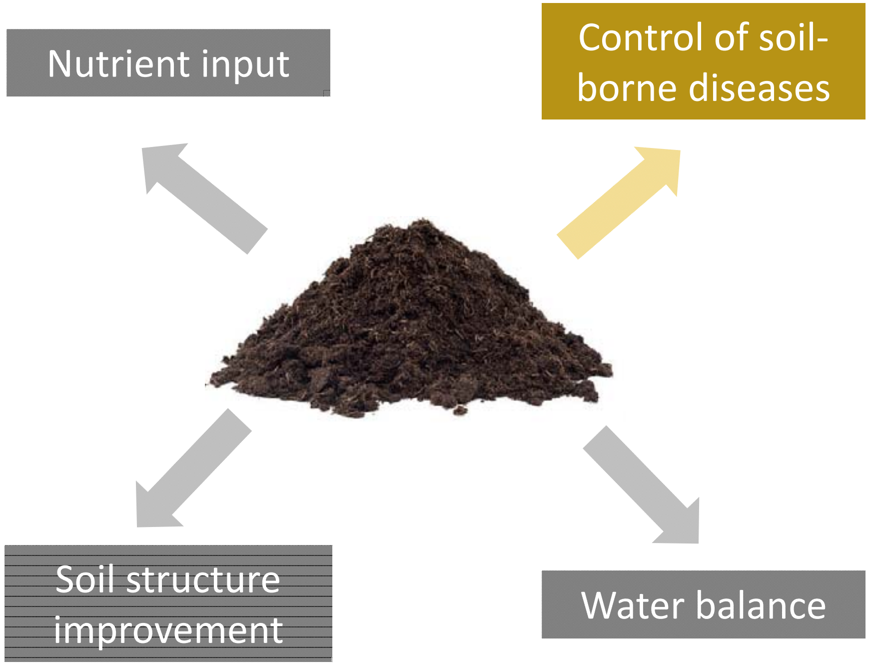
Background

Compost use to control soilborne diseaes

Composting

Biological degradation of organic material under controlled **moist**, **self-heating** and **aerobic** conditions

(Harrisons 2008)

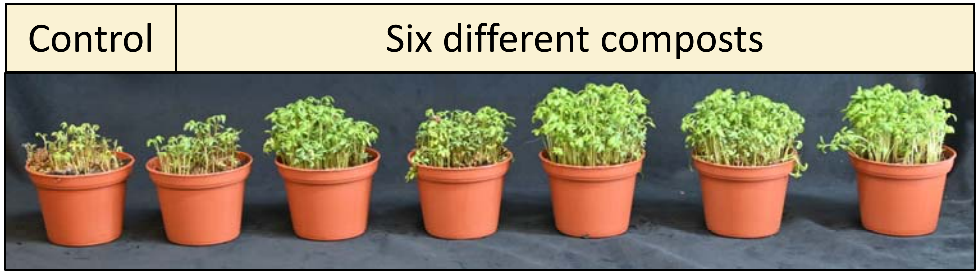


Nutrient input

Control of soil-borne diseases

Soil structure improvement

Water balance



- **Challenge***:* Effectiveness varies among pathogens, compost batches (Termorshuizen et al. 2006) and can change over time (Danon et al. 2007)
- **Reliable indicators needed** for a more targeted use of composts for plant protection (Diagnostic tool)

Background

Microbiome research to identify indicators for disease-suppressive composts

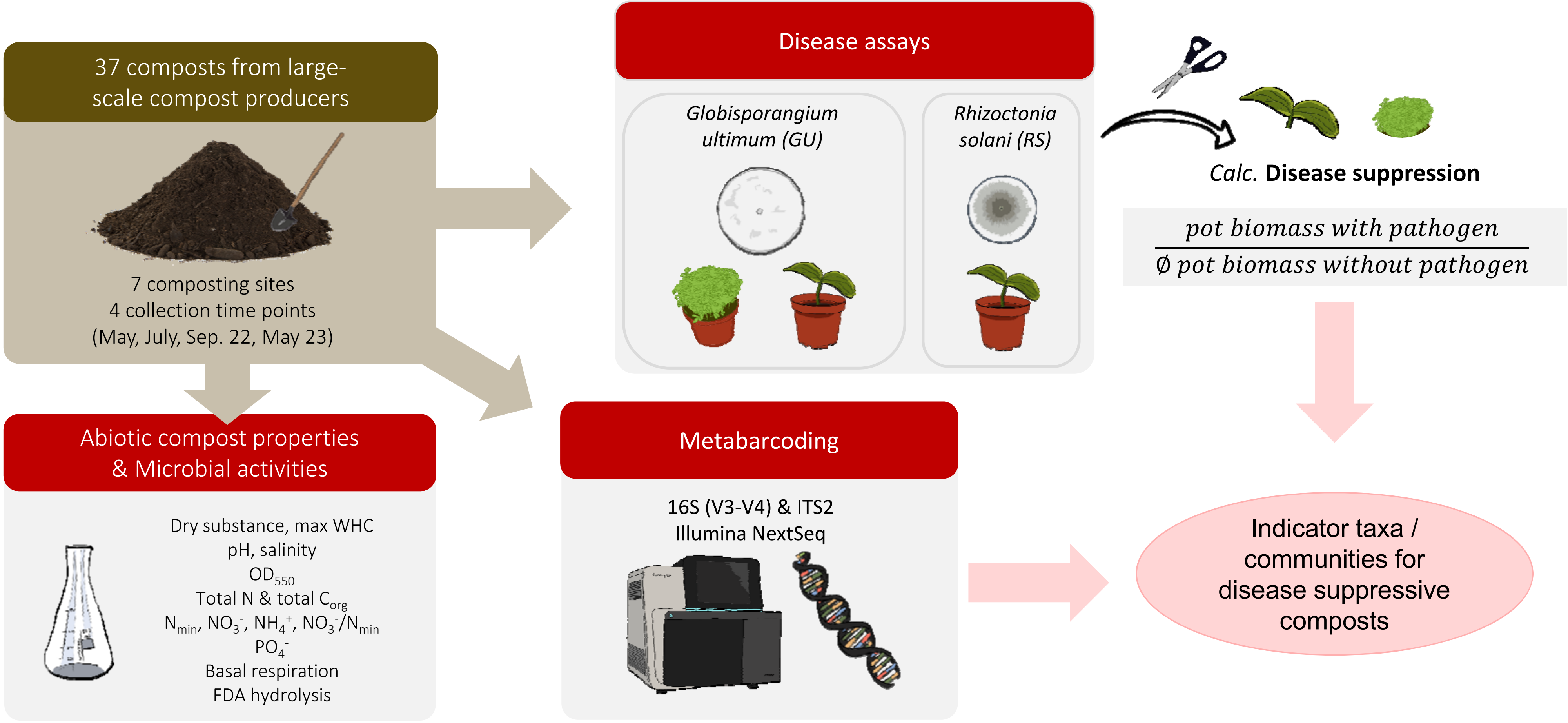
- **Compost microbes** play and **important role** in disease suppression by composts (Bonanomi et al. 2010, De Corato et al. 2016, Lutz et al. 2020)
- **NGS* technologies** to identify **microbial groups** enriched in suppressive composts (Blaya et al, 2016, Yu et a. 2015, Scotti et al. 2020, Mayerhofer et al. 2021)

Main research question

Are there bacterial or fungal taxa/communities that are indicative for disease-suppressive composts?

*Next-Generation-sequencing

Experimental Design



37 composts from large-scale compost producers

7 composting sites
4 collection time points
(May, July, Sep. 22, May 23)

Abiotic compost properties & Microbial activities

Dry substance, max WHC
pH, salinity
OD_{550}
Total N & total C_{org}
N_{min}, NO_3^-, NH_4^+, NO_3^-/N_{min}
PO_4^-
Basal respiration
FDA hydrolysis

Disease assays

Globisporangium ultimum (GU)

Rhizoctonia solani (RS)

Calc. **Disease suppression**

$$\frac{pot\ biomass\ with\ pathogen}{\emptyset\ pot\ biomass\ without\ pathogen}$$

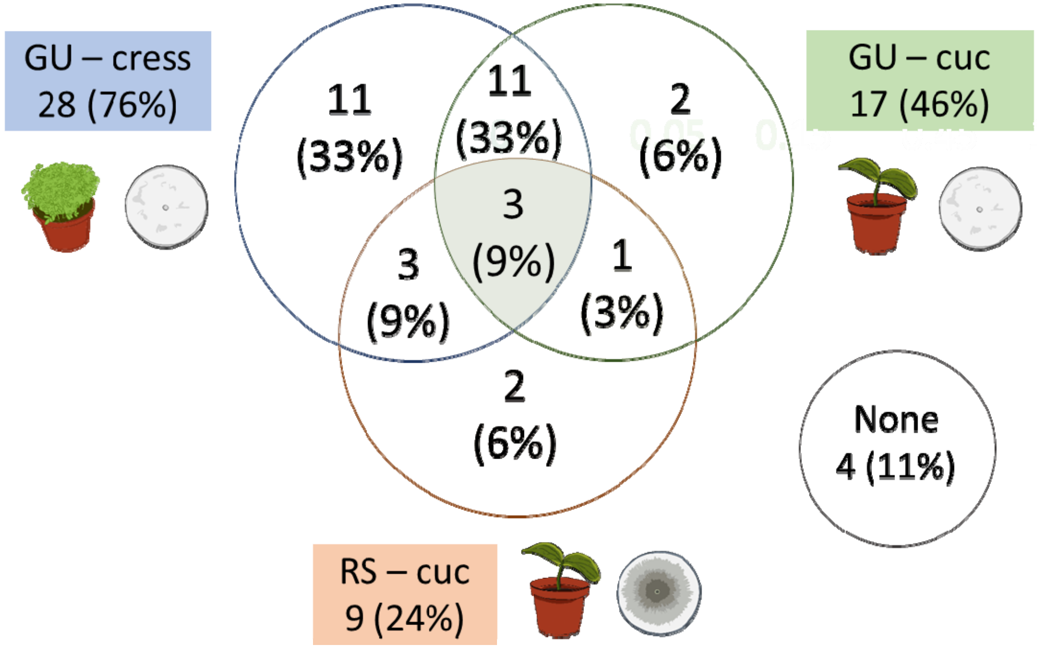
Metabarcoding

16S (V3-V4) & ITS2
Illumina NextSeq

Indicator taxa / communities for disease suppressive composts

Results

Disease suppression depends on the pathogen-plant system



- Majority of 37 composts (89%) showed suppressive activity

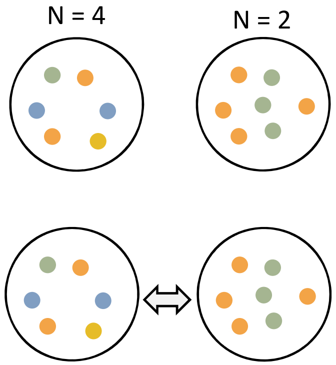
- Disease suppression depends on pathogen-plant systems
  - Pathogen > Host plant

Venn-diagram: Number of significantly suppressive composts
GU: *Globisporanigum ultimum*, RS: *Rhizoctonia solani,* cuc: cucumber

Results

Major patterns in the patterns of the bacterial and fungal communities do not explain disease suppression

Disease suppression	*G. ultimum*-cress	*G. ultimum*-cucumber	*R. solani*-cucumber
14 Physico-chemical properties Spearman's correlation	✗	✗	✗
Microbial activity Basal respiration, FDA Hydrolysis Spearman's correlation	✗	✗	✗
Fungal/Bacterial alpha diversity Spearman's correlation	✓ Bacteria ✗ Fungi	✗	✗
Fungal/Bacterial community structure PERMANOVA	✗	✗	✗

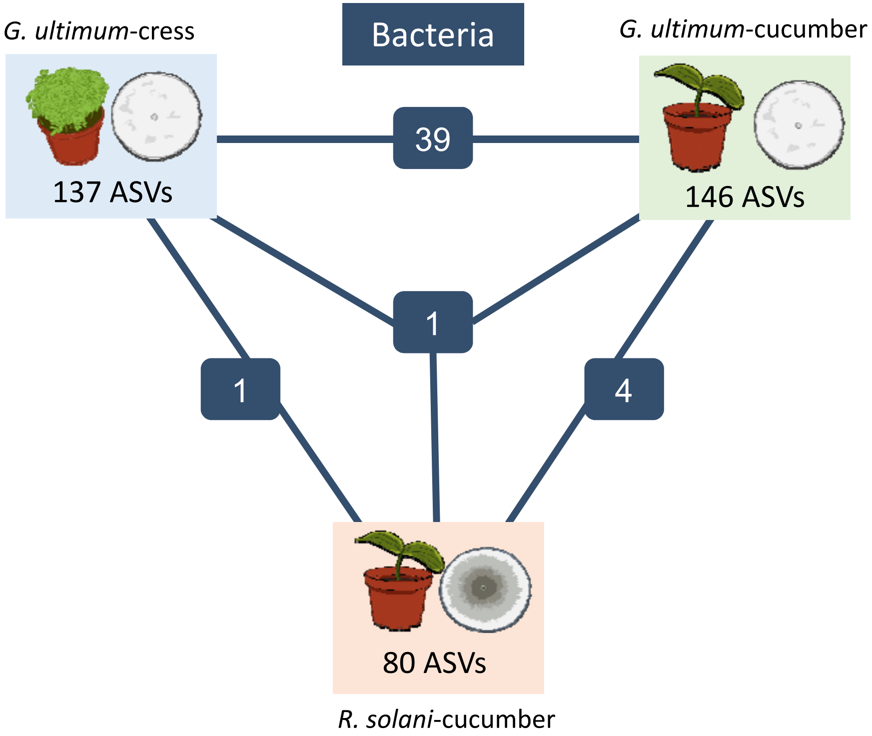


✓ Significant association ($p < 0.05$, $rho > 0.4$)

✗ No significant association

Results

Bacterial indicators for disease-suppressive composts



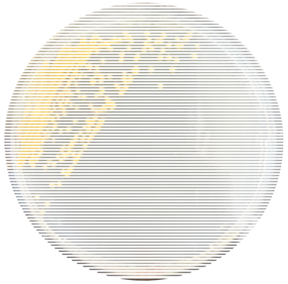
ASV = Amplicon Sequent variant, bioinformatical proxy for a taxon

- 9 top vs. 9 flop composts for each pathogen-plant system
- Bacteria more promising indicators
- Most pathogen-plant specific
- Largest overlap between systems with same pathogen
- Taxonomic classification, isolation, investigating their role in disease suppression
- Isolates with match to ASV
    - *Genera: Sphingopyxis, Algoriphagus, Sphingobacterium, Flavobacterium*

Conclusions

Microbiome-based indicators for disease-suppressive composts

- Disease-suppression by compost is **pathogen(-plant)-specific**
- **Physico-chemical properties, microbial activity, major patterns** of bacterial and fungal communities **cannot explain disease suppression**
- **Promising bacterial taxa** identified which are indicative for the most suppressive composts
- **Outlook**: Isolating interesting taxa and investigating their role in compost disease suppression



Thank you!

BLW compost microbiology project

Support in the lab:

- *Students & interns*: Oriana Gasser, Malgorzata Glowala, Benedikt Boppré, Eva Burgunder, Monica Camareno Rodriquez
- *Lab technicians*: Tabea Koch, Nadine Peter, Sonja Reinhard

Groups:

- Molecular Ecology, Agroscope
- Phytopathology, FiBL
- Plant Pathology, ETH Zürich
- Plant-Microbe Interactions, University of Basel

- Bundesamt für Landwirtschaft for financial support
- Compost producers for cooperation

Compost microbiome team excursion June 2024

Contact: anja.logo@fibl.org

Agroscope FiBL ETH zürich University of Basel

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Re-Livestock: Determinants and impacts of the calf digestive microbiome in four grass-based fattening systems

Dr. Geoffrey Mesbahi (he/him)

FiBL Open Day – 27 November 2024

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Why study microbiota in livestock science?

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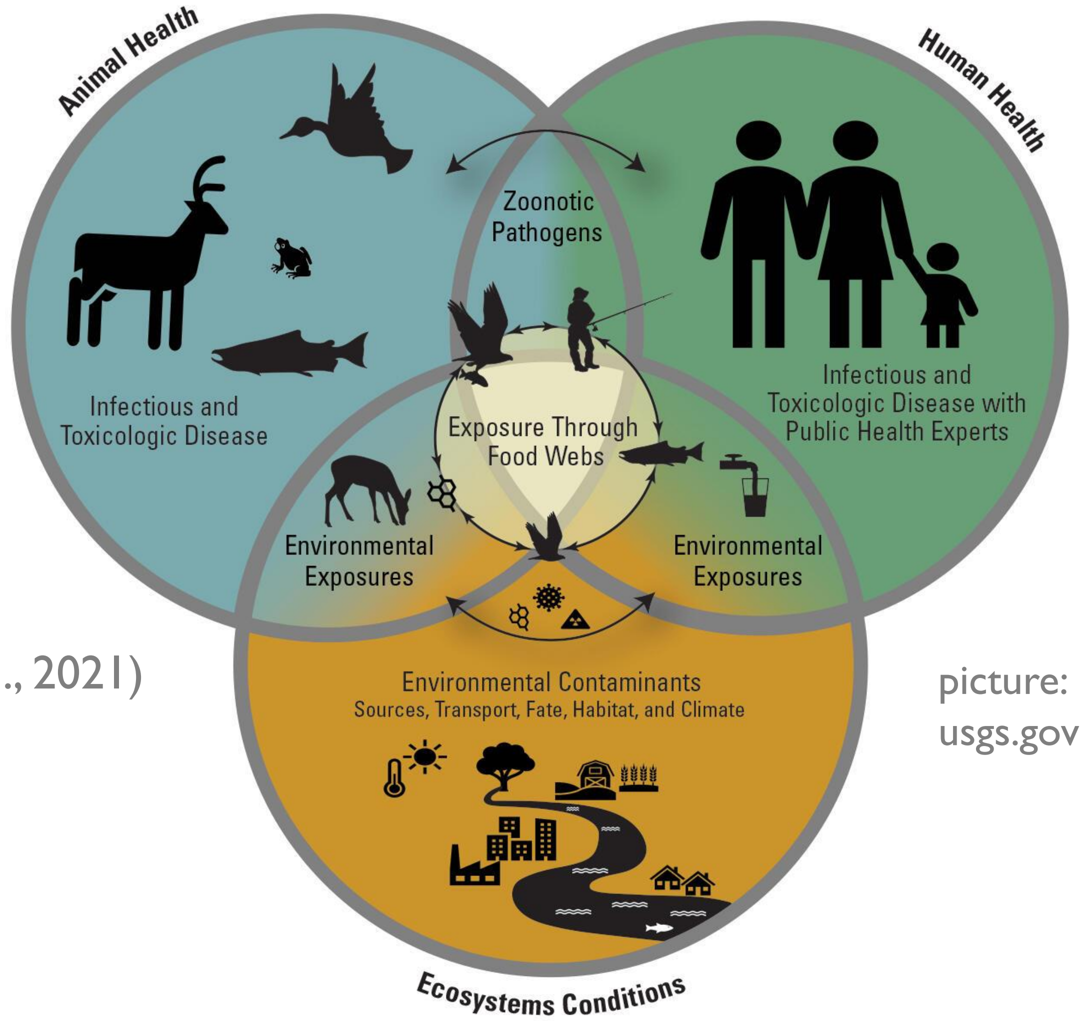
Why study microbiota in livestock science?

- One Health

58% of human pathogens are zoonotic and cause diseases in both humans and animals (Woolhouse and Gowtage-Sequeria, 2005)

Transfers animal – human – animal (Berthet et al., 2021)

Antibiotic resistance
(Catry et al., 2023; Van den Honert et al., 2018)



picture: usgs.gov

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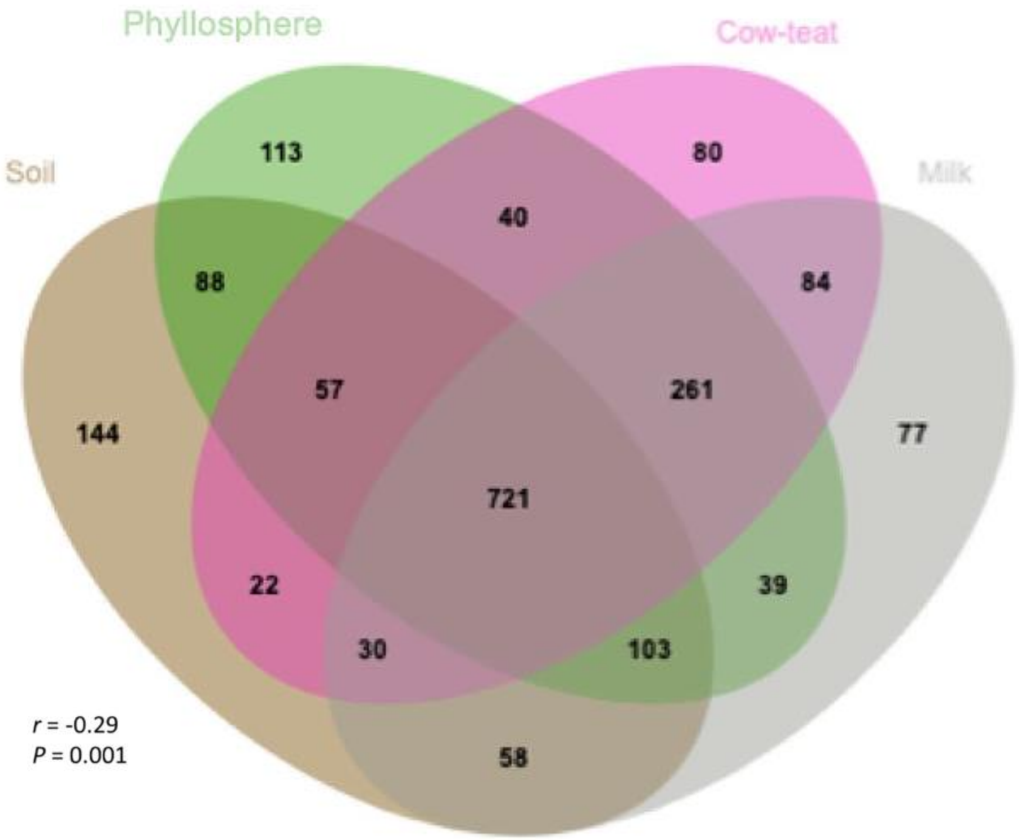
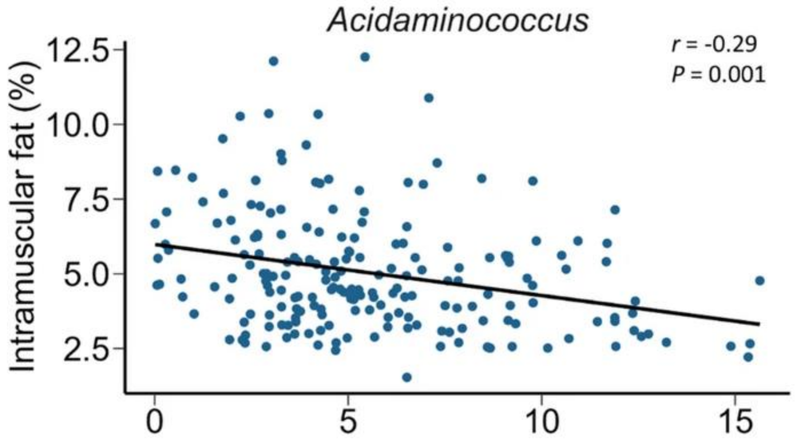
Why study microbiota in livestock science?

- One Health

- Food quality
  - Cheese properties
    Chemidlin Prévost-Bouré et al., 2021



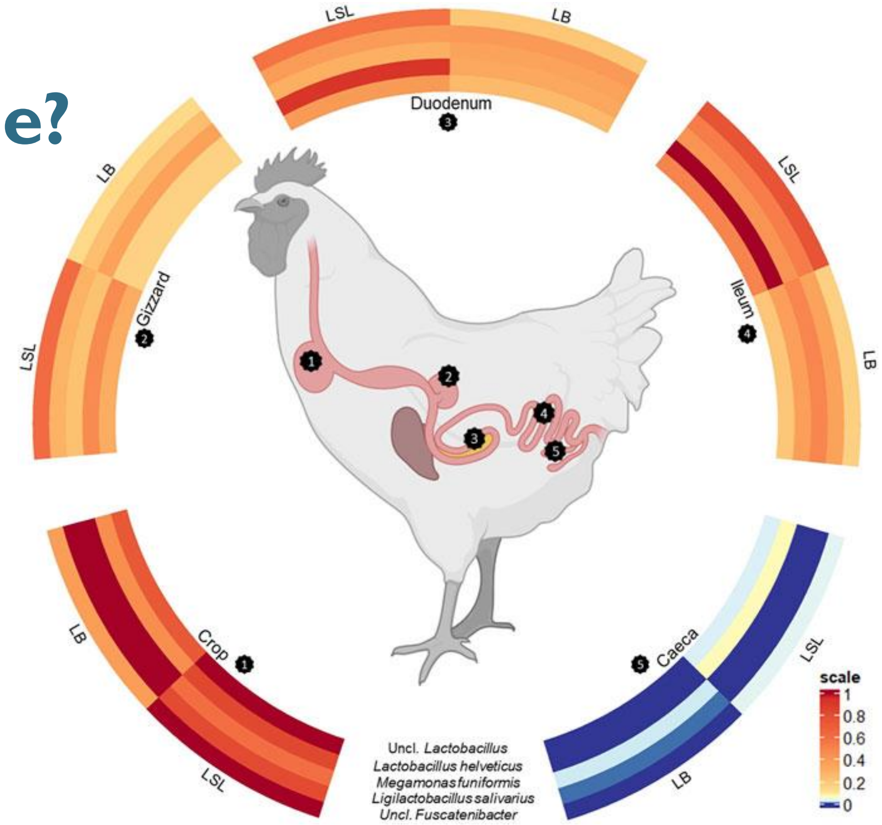
  - Meat properties
    Holman et al., 2024



Why study microbiota in livestock science?

Christoph Roth

Dr. sc. agr.



- One Health
- Food quality
- Nutrition
  - Monogastrics

    ex: effect gastrointestinal tract microbiota on mineral absorption in laying hens (Roth et al., 2022)
  - Ruminants

    digestive system depends on microbial fermentation

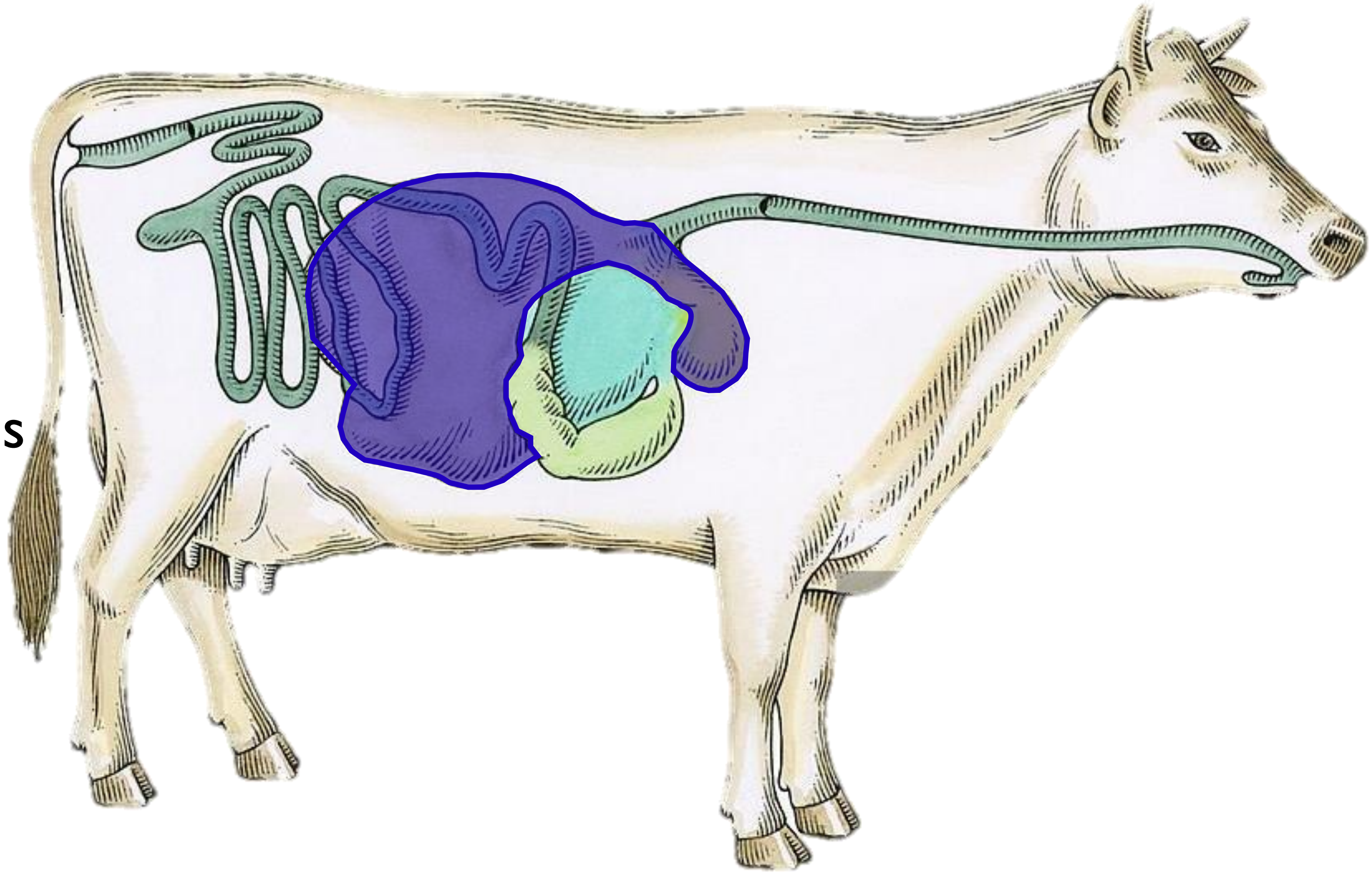
The digestive microbiota of ruminants

The digestive microbiota of ruminants

- Rumen (+ reticulum)

  Main site of microbial activity in ruminants

  Microbiota degrades feeds
  - volatile fatty acids
  - CO_2
  - CH_4



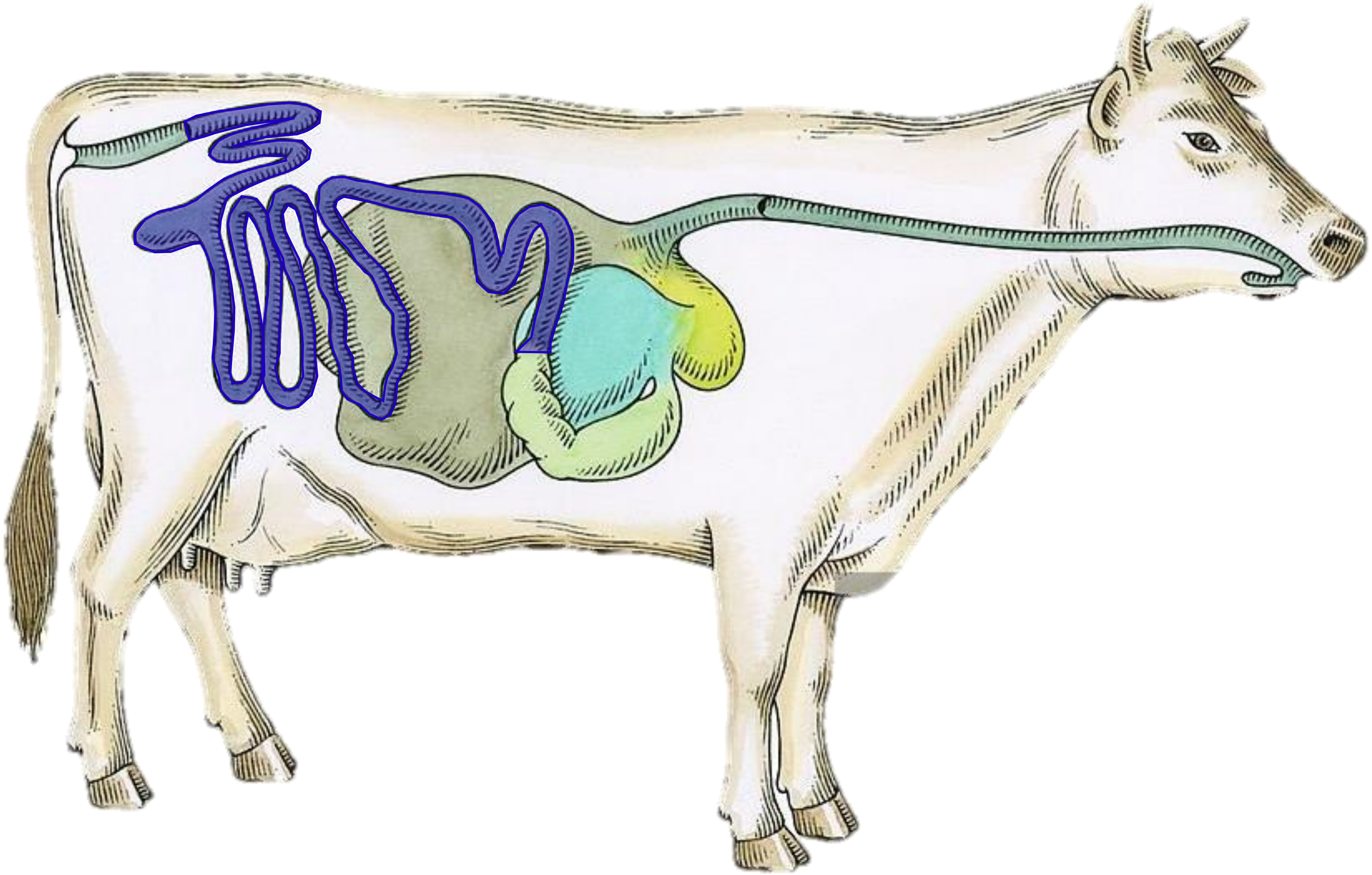
The digestive microbiota of ruminants

- Intestines

  Second digestion

  Absorb protein

  The protein comes from
  - feed
  - rumen microorganisms



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The methane issue

- Rumen
  10^{10} cells/mL

  bacteria (60-90 %)

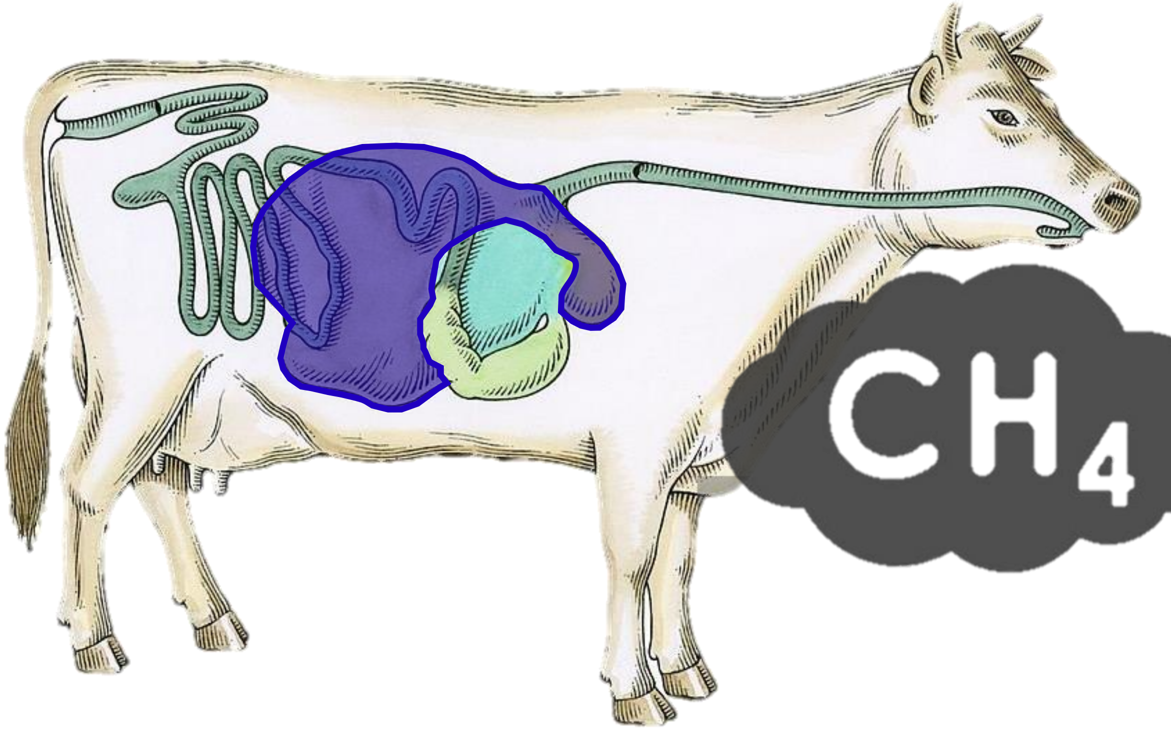
  protozoa (20-40 %)

  fungi (5-10 %)

  archaea (3-5 %)

  viruses (< 1 %)

- Intestines
  10^3 to 10^{12} cells/mL



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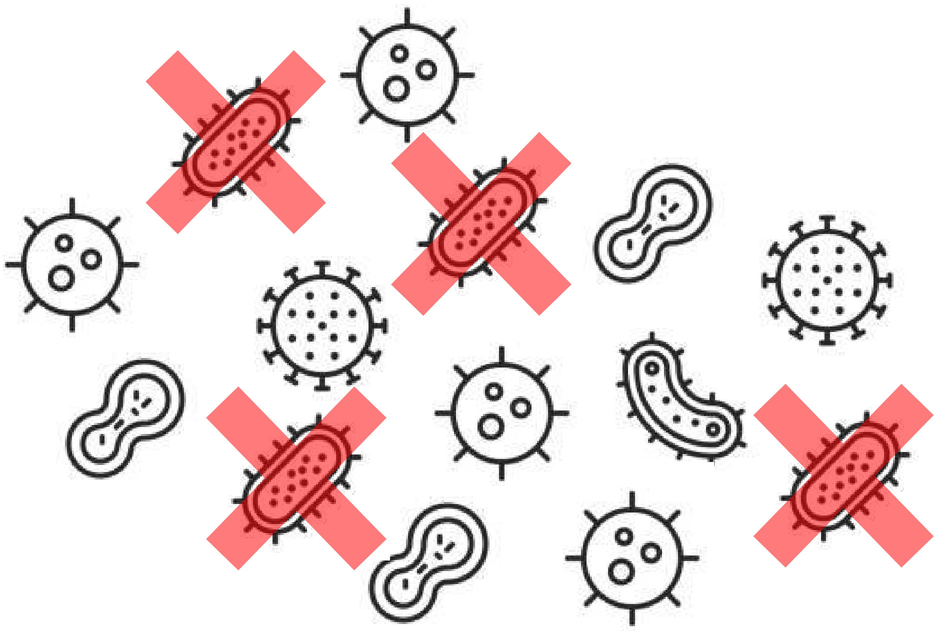
The methane issue

- How to reduce it?



Decrease methanogens activity

Disfavored the conditions that promote methanogenesis

$$\cancel{CO}_2 + \cancel{4H}_2 \rightarrow CH_4 + 2H_2O$$

Increase feed digestibility

Animal genetic selection

Honan et al., 2022
Beauchemin et al., 2022

The methane issue

- How to reduce it?

Decrease methanogens activity

Disfavored the conditions that promote methanogenesis

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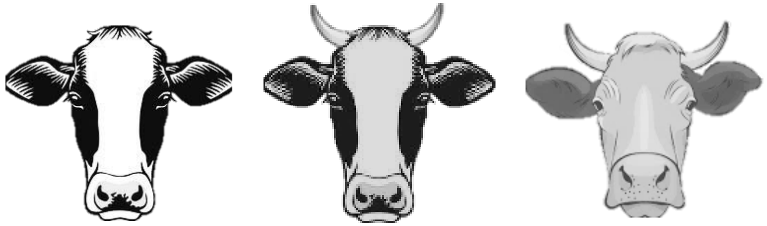

The Re-Livestock project

Re-Livestock

RESILIENT FARMING SYSTEMS

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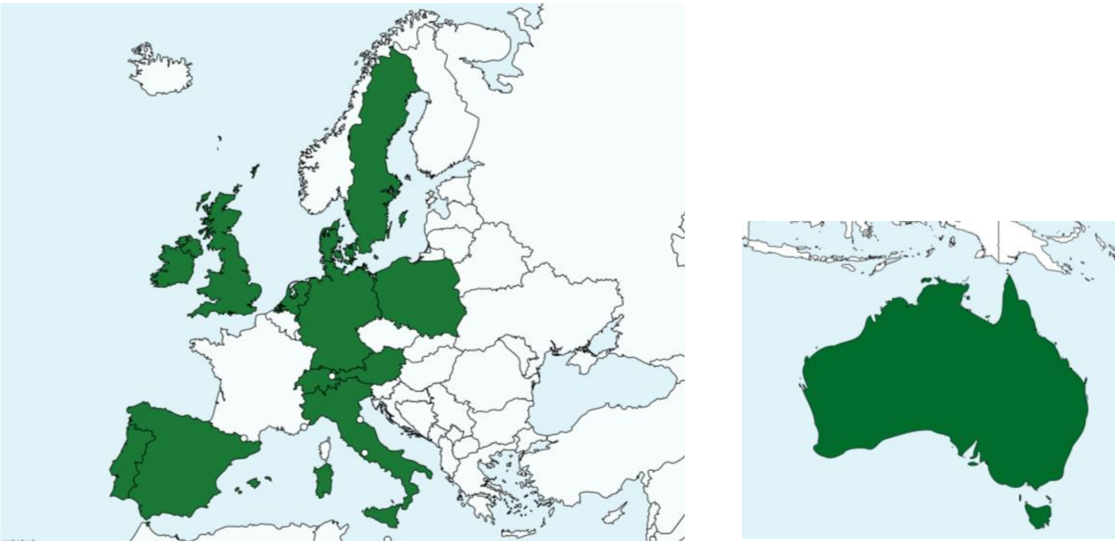
The Re-Livestock project

Re-Livestock
RESILIENT FARMING SYSTEMS



- Our project:
  - Interplay of **genotype and grass** composition on **meat** production and **methane** emissions in calves
  - Focus on the microbiota, since it affects productivity and methane emissions

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The Re-Livestock project

- Experimental set up

Dairy (n=6)
Brown Swiss

Crossed (n=6)
Limousin x Brown Swiss

Dual purpose (n=6)
Swiss Fleckvieh

Pasture

Hay

Pellets + concentrates

≈ 2000 m a.s.l
alpine grasslands

≈ 1000 m a.s.l
permanent grasslands

≈ 400 m a.s.l
temporary grasslands

≈ 400 m a.s.l
indoor control

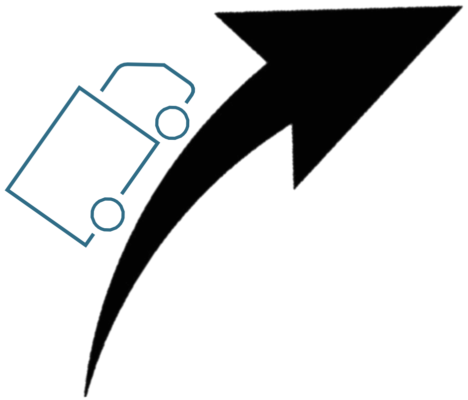
Prof. Dr. Jana Seifert

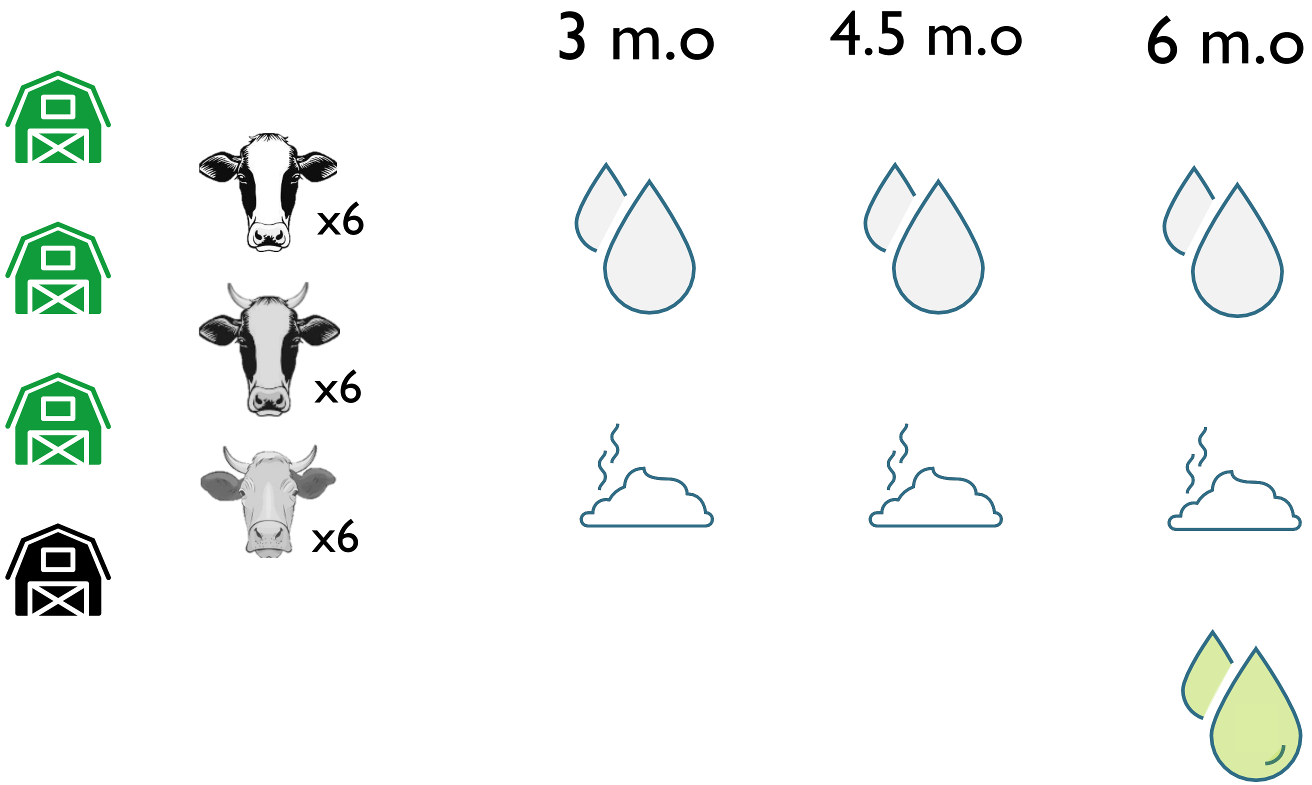
HoLMiR
Hohenheim Center for Livestock Microbiome Research

UNIVERSITY OF HOHENHEIM

The Re-Livestock project

- Microbiota sampling





4 farms * 3 genotypes * 6 calves * 3 dates
= 216 saliva samples

4 farms * 3 genotypes * 6 calves * 3 dates
= 216 faeces samples

4 farms * 3 genotypes * 6 calves * 1 date
= 72 rumen fluid samples

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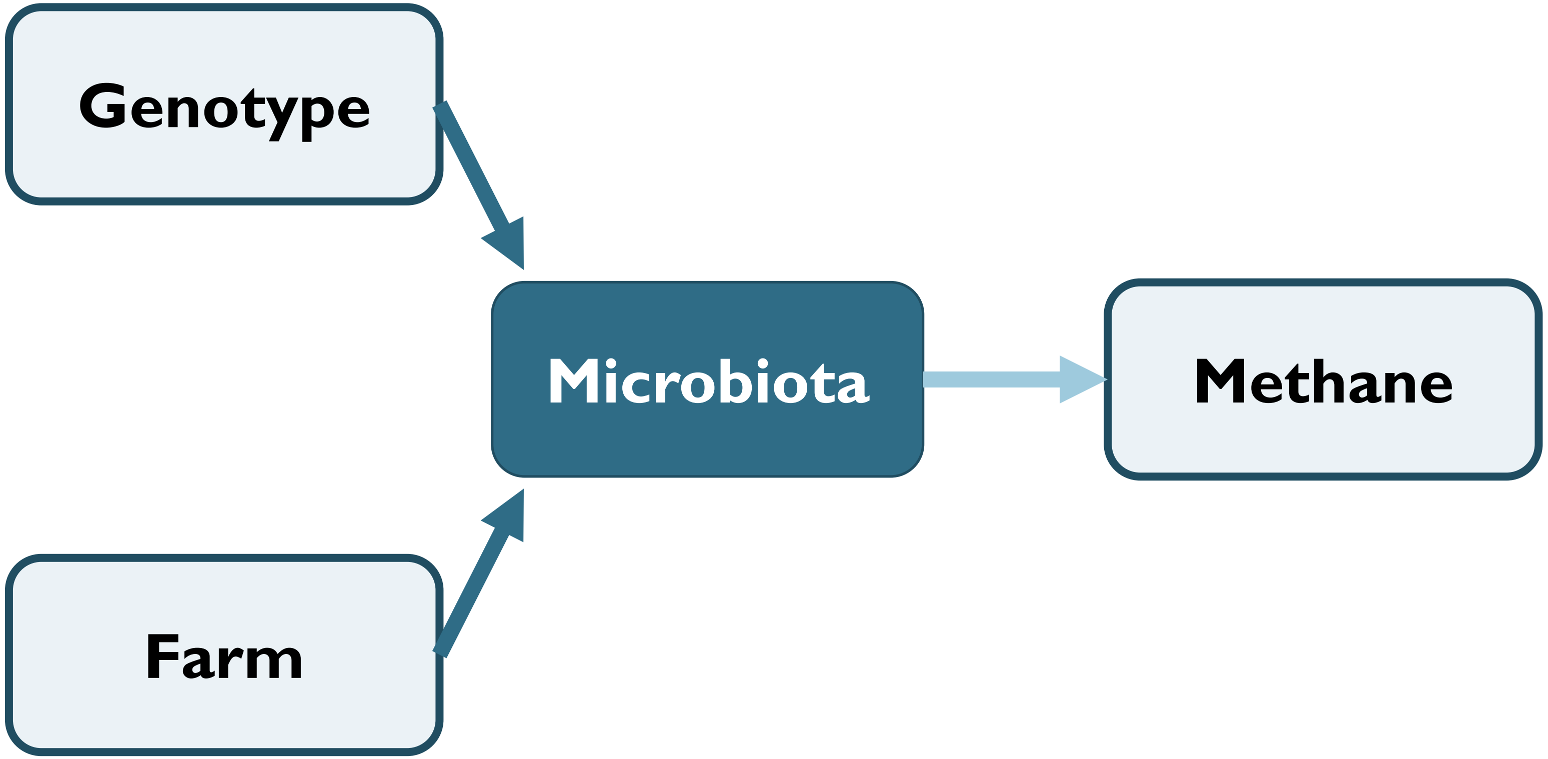
Hypothesis

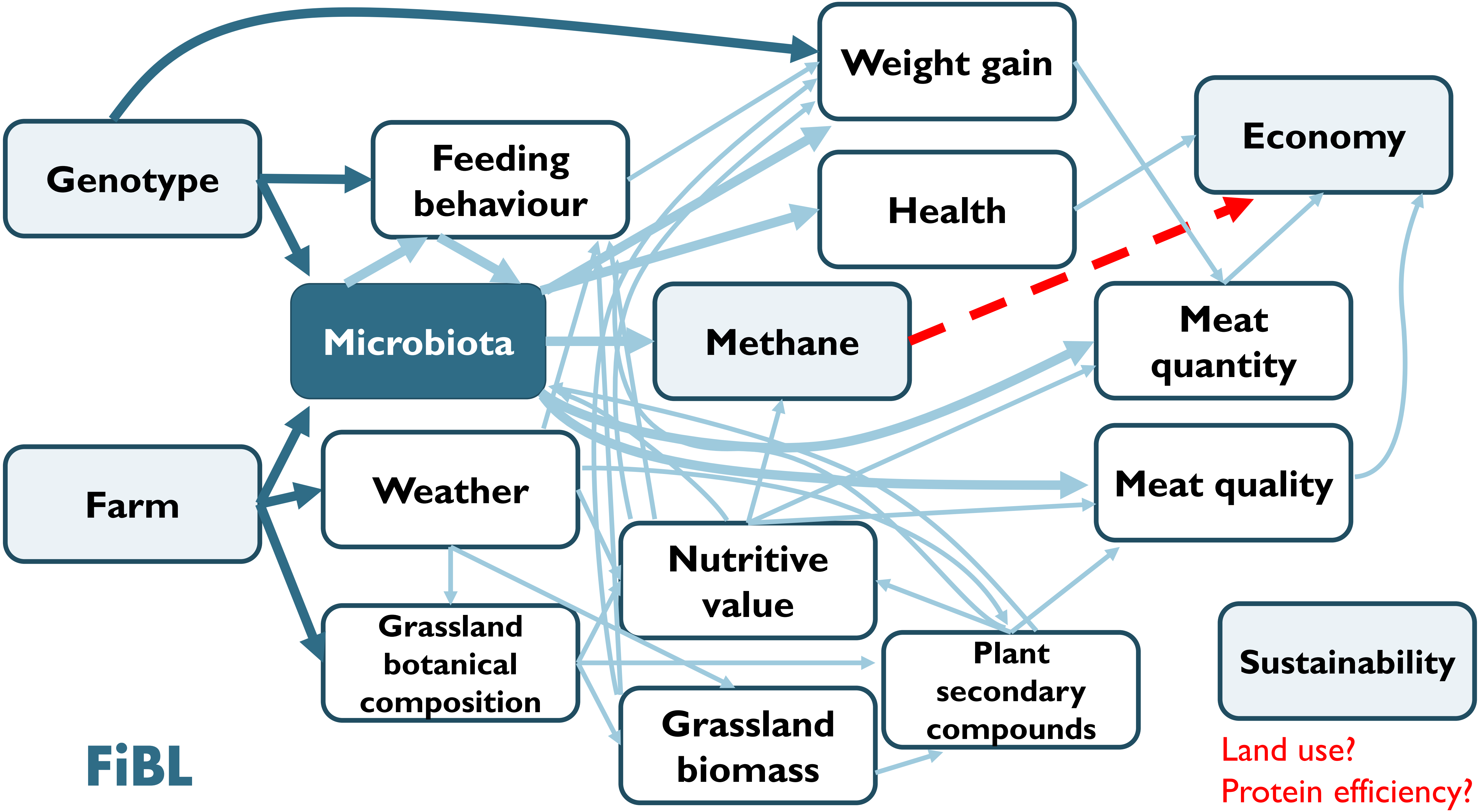


Genotype

Microbiota

Methane

Farm



Genotype

Feeding behaviour

Microbiota

Farm

Weather

Grassland botanical composition

Nutritive value

Grassland biomass

Plant secondary compounds

Methane

Weight gain

Health

Economy

Meat quantity

Meat quality

Sustainability

Land use?

Protein efficiency?

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Conclusion

- Microbiota is a keystone of the livestock production systems
- The Re-Livestock project improves knowledge about the calves' microbiota
- Understanding the drivers and the consequences of livestock microbiota is a challenge still in progress

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- The Re-Livestock project improves knowledge about the calves' microbiota
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Acknowledgement

Thanks to all the persons involved in this project

FiBL strickhof UNIVERSITY OF HOHENHEIM

This project is funded by the European Union

Funded by the European Union

Re-Livestock
RESILIENT FARMING SYSTEMS

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Beauchemin et al., 2022 – Invited review: Current enteric methane mitigation options

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Catry et al., 2023 – Antimicrobial resistance in livestock

Chemidlin Prévost-Bouré et al., 2021 – Microbial transfers from permanent grassland ecosystems to milk in dairy farms in the Comté cheese area

Holman et al., 2024 – Associations between the rumen microbiota and carcass merit and meat quality in beef cattle

Honan et al., 2022 – Feed additives as a strategic approach to reduce enteric methane production in cattle: modes of action, effectiveness and safety

Roth et al., 2022 – The active core microbiota of two high-yielding laying hen breeds fed with different levels of calcium and phosphorus

Van den Honert et al., 2023 – Importance and implications of antibiotic resistance development in livestock and wildlife farming in South Africa : a review

Woolhouse and Gowtage-Sequeria, 2005 – Host Range and Emerging and Reemerging Pathogens

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Microbiome indicators to predict inoculation success with biofertilizers

Natacha Bodenhausen, Soil Sciences Department

November 27, 2024

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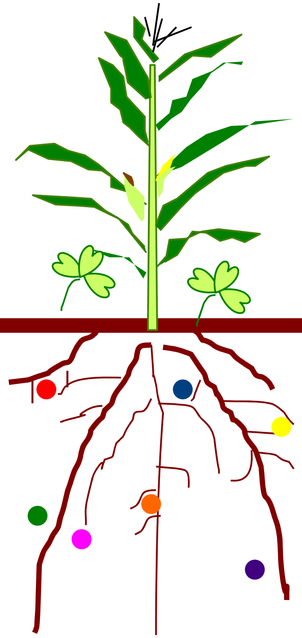
How to increase microbial diversity?

Soil management
- low till
- mulching
- compost (Anja Logo)

Picture: Jacques Fuchs



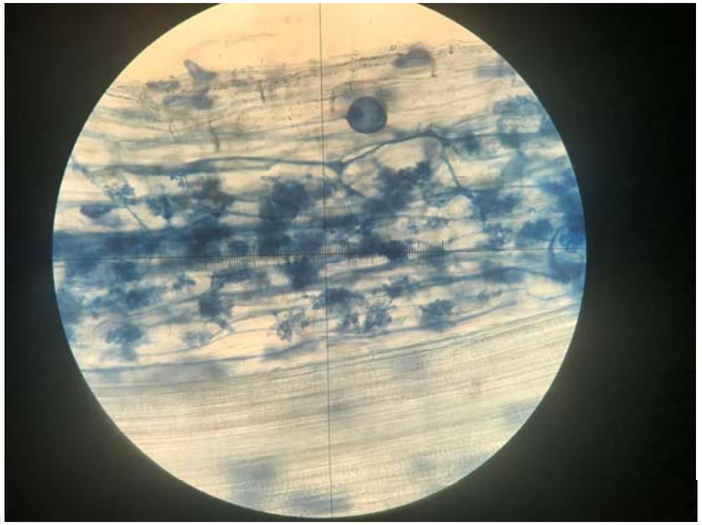
Plant choice
- Enhanced crop diversity
- Intercropping
- Living mulch
- Plant breeding

Picture: Hansueli Dierauer

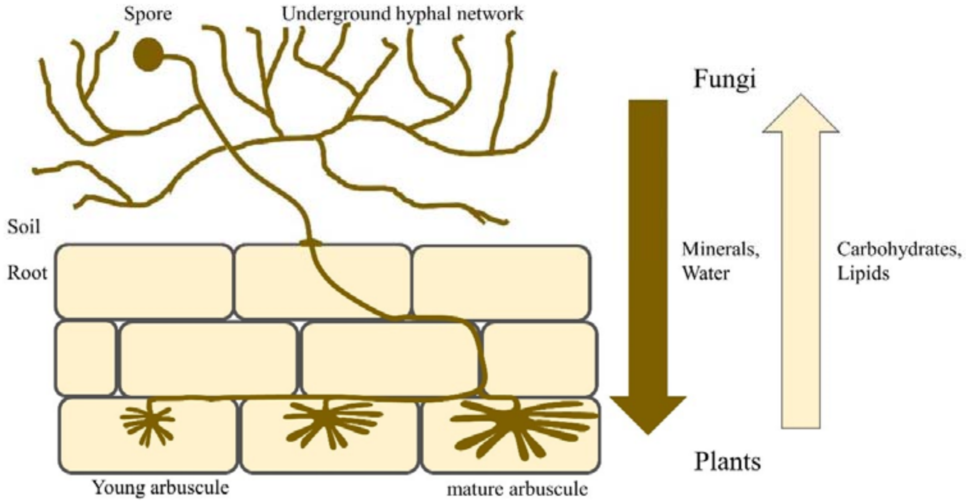
Microbiome level
- Inoculation with beneficial soil organisms

Inoculation with Arbuscular Mycorrhizal Fungi (AMF)

- Phylum Glomeromycota
- Symbiosis with 80% plant species
- Exchange of carbohydrates for nutrients including phosphorous
- Characteristic arbuscule



Picture: Julia Hess



Florence Sessoms

Inoculation with mycorrhiza promotes plant growth in greenhouse experiments…

Picture : Franz Bender

control

inoculated

but results are more variable in field experiments!

New Phytologist

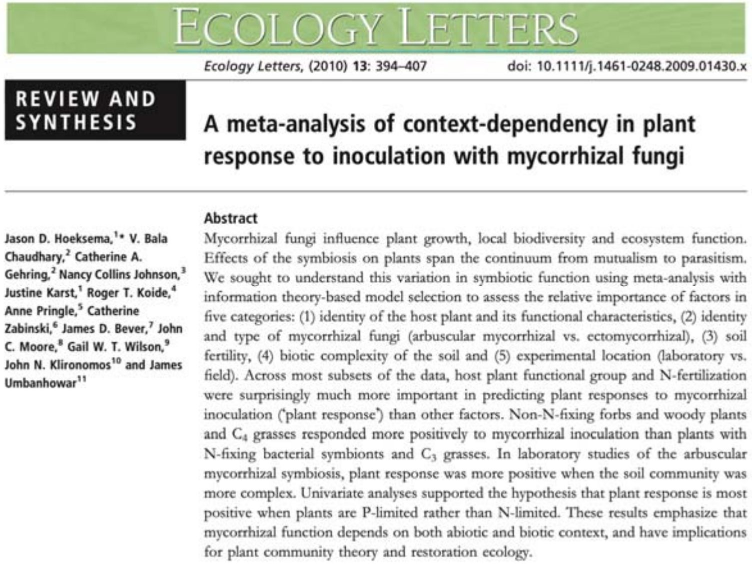
Research

Arbuscular mycorrhizal fungi increase grain yields: a meta-analysis

Shujuan Zhang[1], Anika Lehmann[2,3], Weishuang Zheng[4], Zhaoyang You[1] and Matthias C. Rillig[2,3]

[1]College of Urban Construction, Nanjing Tech University, Puzhu Road(S) 30, Nanjing, China; [2]Institut für Biologie, Plant Ecology, Freie Universität Berlin, Altensteinstr. 6, D-14195 Berlin, Germany; [3]Berlin-Brandenburg Institute of Advanced Biodiversity Research (BBIB), D-14195 Berlin, Germany; [4]College of Marine Science, Shandong University, Wenhua West Road 180, C-

Microbiome diagnostics



ECOLOGY LETTERS

Ecology Letters, (2010) 13: 394–407 doi: 10.1111/j.1461-0248.2009.01430.x

REVIEW AND SYNTHESIS

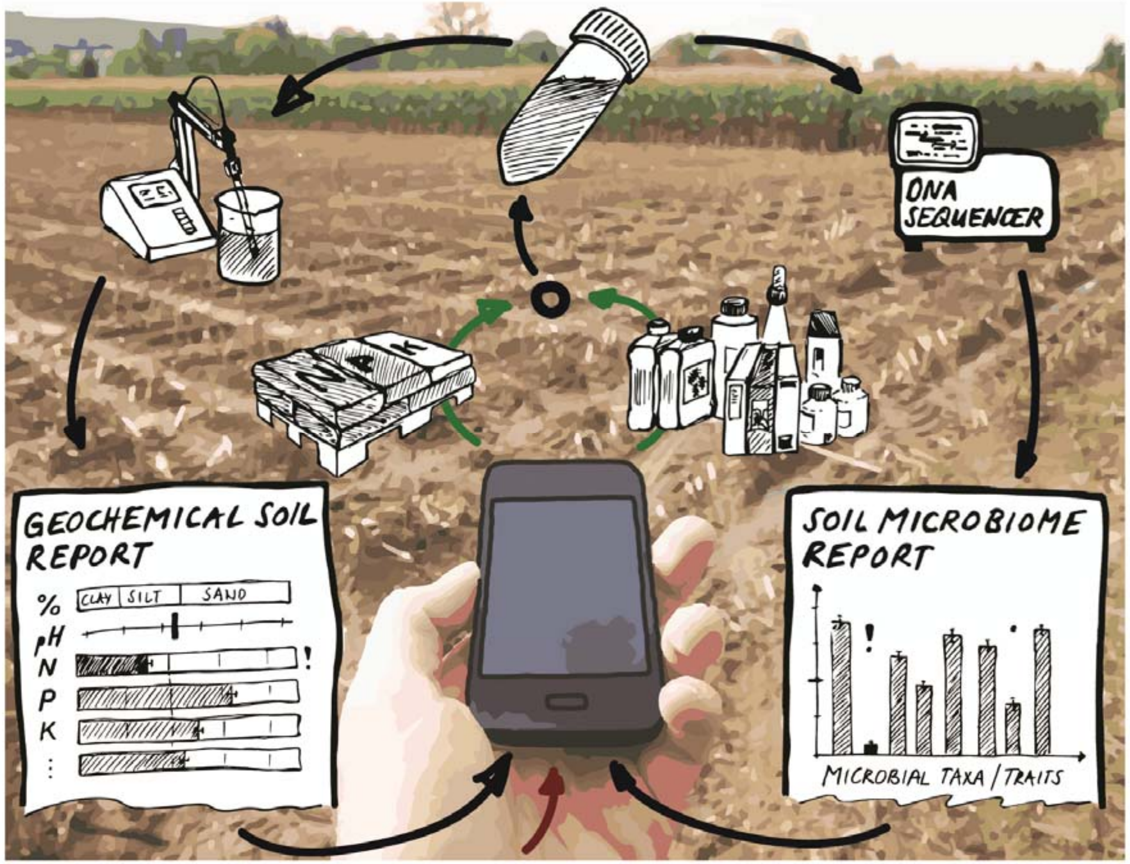
A meta-analysis of context-dependency in plant response to inoculation with mycorrhizal fungi

Jason D. Hoeksema,[1]* V. Bala Chaudhary,[2] Catherine A. Gehring,[2] Nancy Collins Johnson,[3] Justine Karst,[1] Roger T. Koide,[4] Anne Pringle,[5] Catherine Zabinski,[6] James D. Bever,[7] John C. Moore,[8] Gail W. T. Wilson,[9] John N. Klironomos[10] and James Umbanhowar[11]

Abstract

Mycorrhizal fungi influence plant growth, local biodiversity and ecosystem function. Effects of the symbiosis on plants span the continuum from mutualism to parasitism. We sought to understand this variation in symbiotic function using meta-analysis with information theory-based model selection to assess the relative importance of factors in five categories: (1) identity of the host plant and its functional characteristics, (2) identity and type of mycorrhizal fungi (arbuscular mycorrhizal vs. ectomycorrhizal), (3) soil fertility, (4) biotic complexity of the soil and (5) experimental location (laboratory vs. field). Across most subsets of the data, host plant functional group and N-fertilization were surprisingly much more important in predicting plant responses to mycorrhizal inoculation ('plant response') than other factors. Non-N-fixing forbs and woody plants and C_4 grasses responded more positively to mycorrhizal inoculation than plants with N-fixing bacterial symbionts and C_3 grasses. In laboratory studies of the arbuscular mycorrhizal symbiosis, plant response was more positive when the soil community was more complex. Univariate analyses supported the hypothesis that plant response is most positive when plants are P-limited rather than N-limited. These results emphasize that mycorrhizal function depends on both abiotic and biotic context, and have implications for plant community theory and restoration ecology.

1. identity of plant host
2. identity of the fungi
3. soil fertility
4. biotic complexity of the soil



Picture credit: Schlaeppi and Bulgarelli 2015

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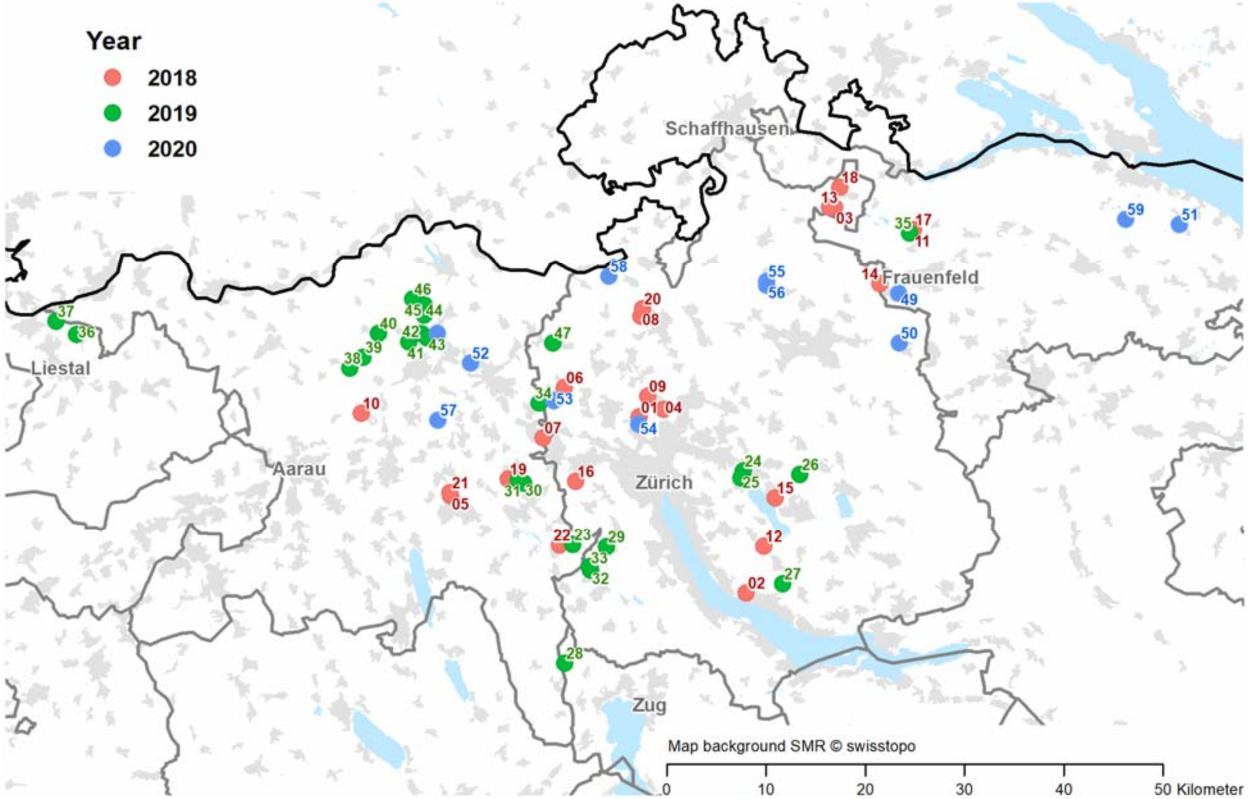
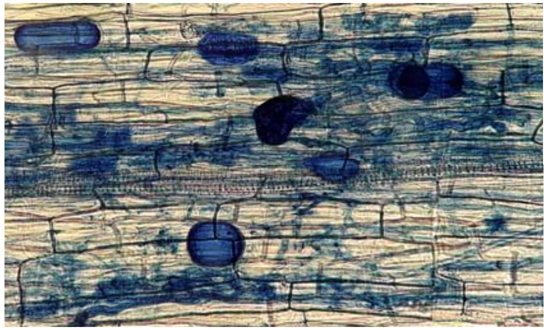
Microbiome diagnostics



Map background SMR © swisstopo

Rhizoglomus irregulare SAF #22



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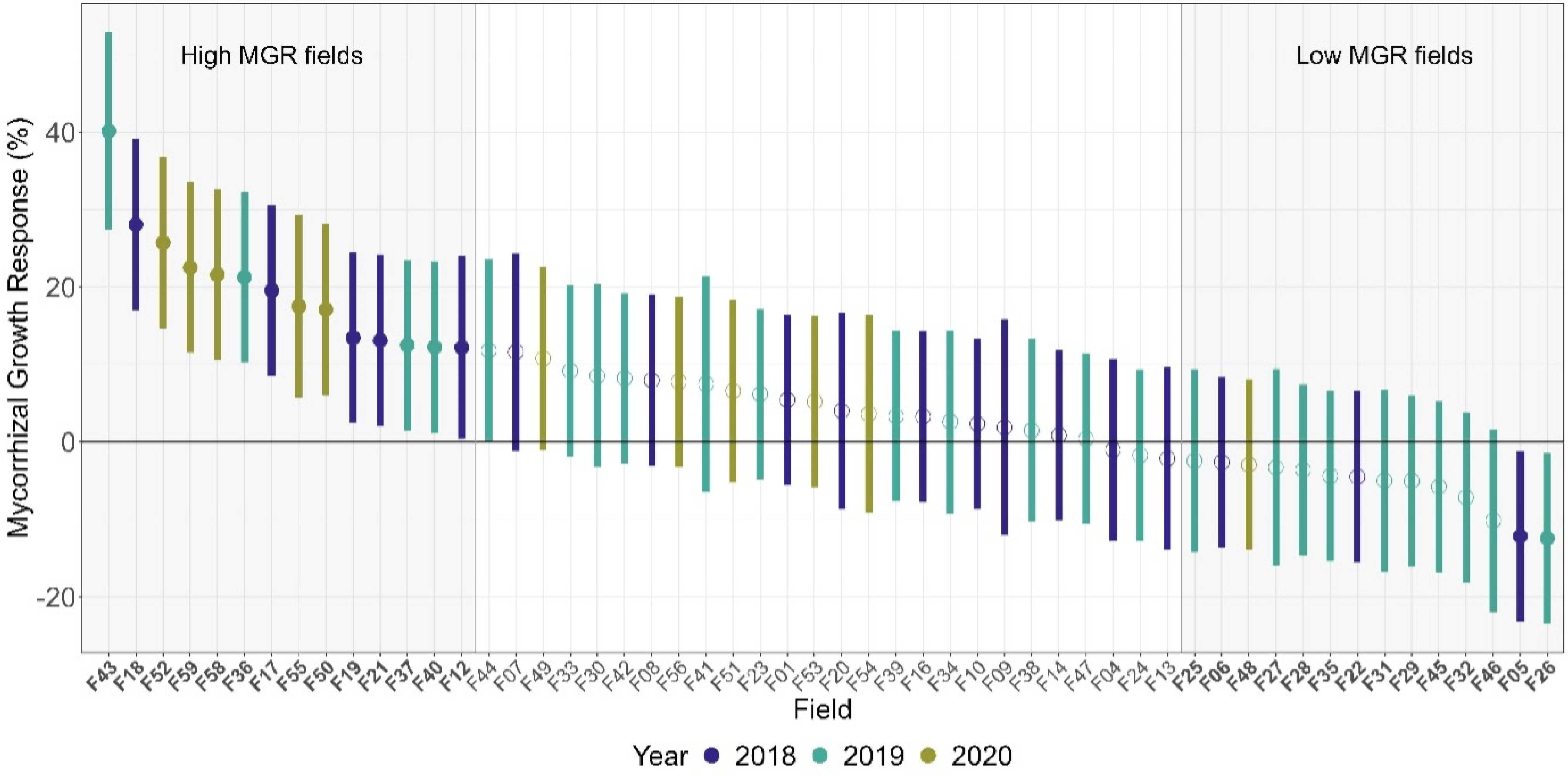
25% of the fields have positive mycorrhizal growth response

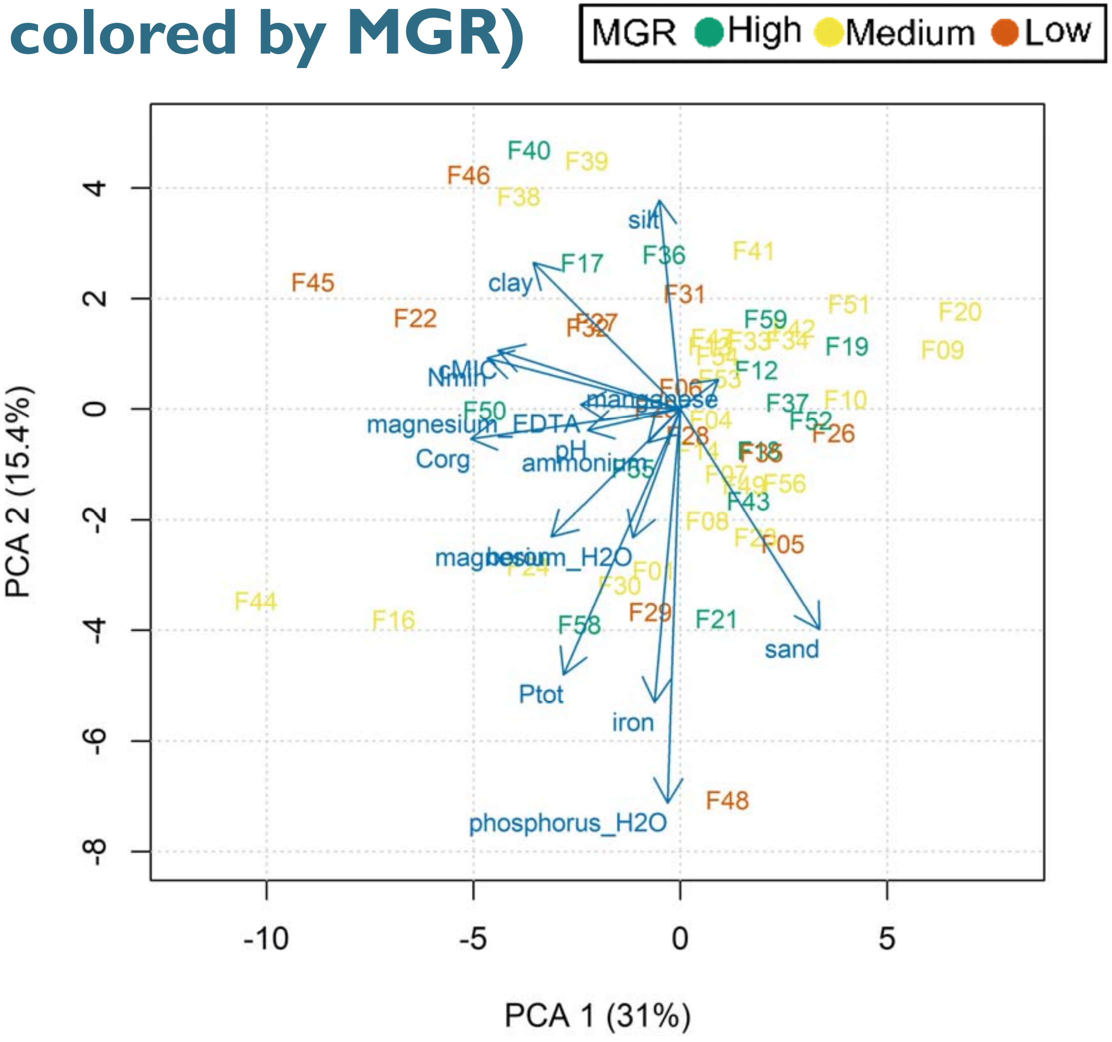


Does response to inoculation depend on soil parameters ?

physical	chemical	biological
soil texture	pH	microbial biomass
water holding capacity	extractable nutrients (P, N, K, ..)	respiration
soil structure	soil organic matter (humus)	

PCA of 15 soil variables (field colored by MGR)

Similar fields (in terms of chemistry) have **different** response to mycorrhiza



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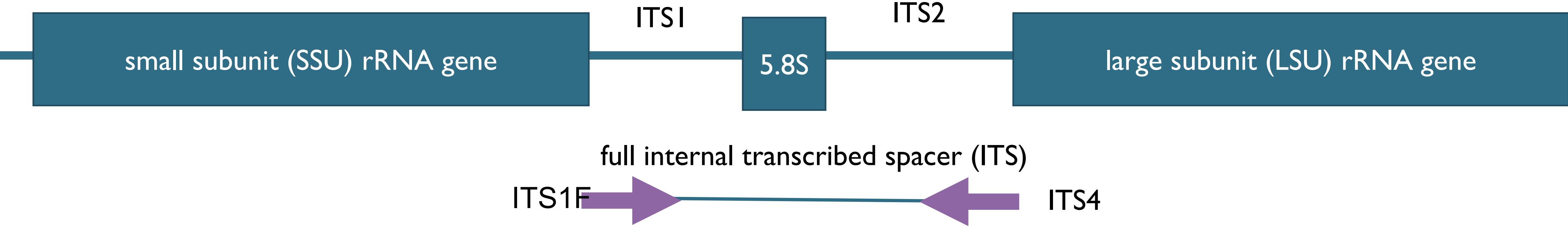
Does response to inoculation depend on soil microbiome ?


small subunit (SSU) rRNA gene

ITS1

5.8S

ITS2

large subunit (LSU) rRNA gene

full internal transcribed spacer (ITS)

ITS1F

ITS4

- size of ITS varies depending on the fungal species (500-700 bp)
- amplicons are barcoded during PCR
- Pacbio Sequencing Sequel II

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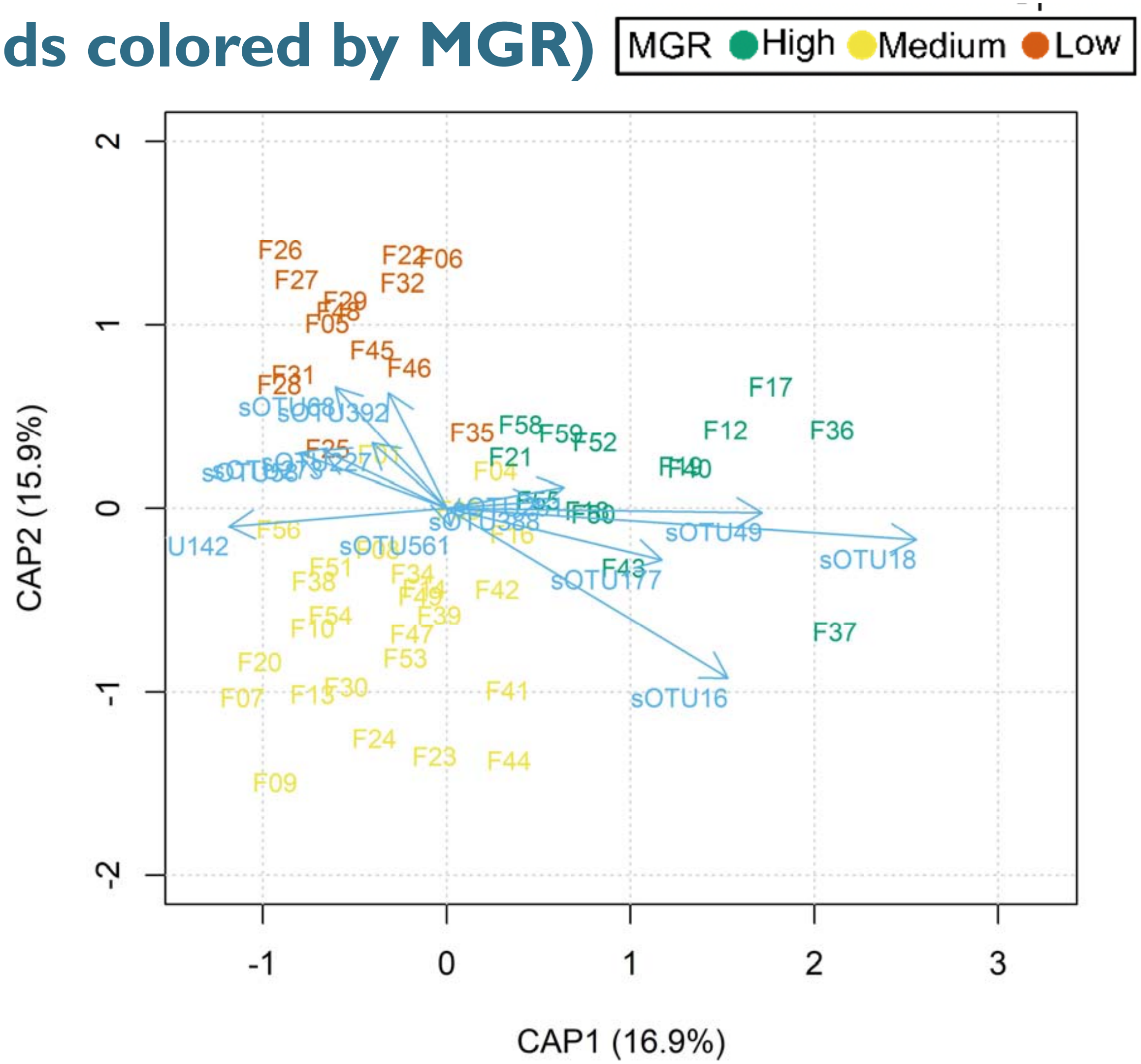
Community composition (fields colored by MGR)

Similar fields (in terms of microbiome) have **similar** response to mycorrhiza



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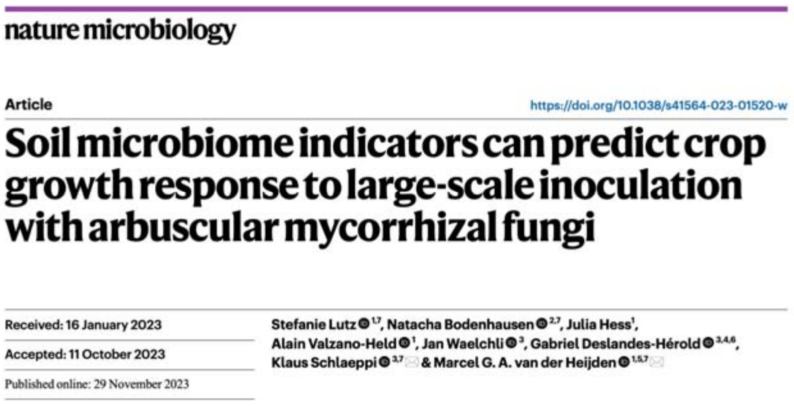
Microbiome is a good predictor of the response to biofertilizer

and soil properties are less important.



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Soil microbiome indicators can predict crop growth response to large-scale inoculation with arbuscular mycorrhizal fungi

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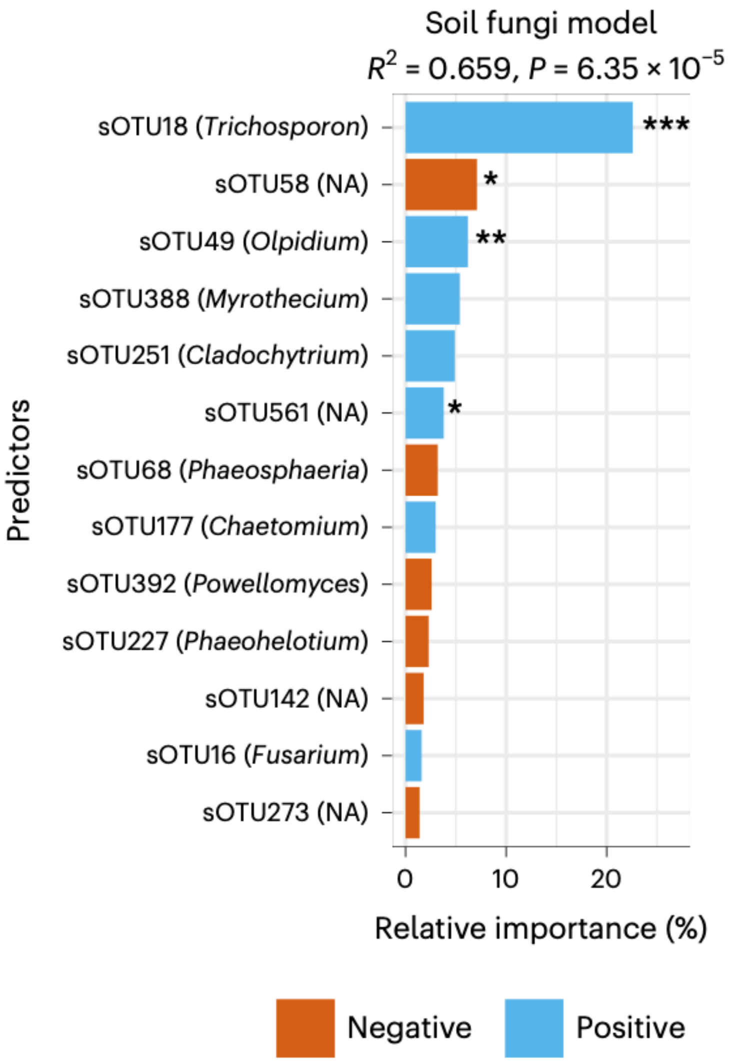

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