

Uncovering rhizosphere microbial resilience and potential to support plant growth

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Helmholtz Centre for Environmental Research



What are the services and disservices provided by microbiomes?

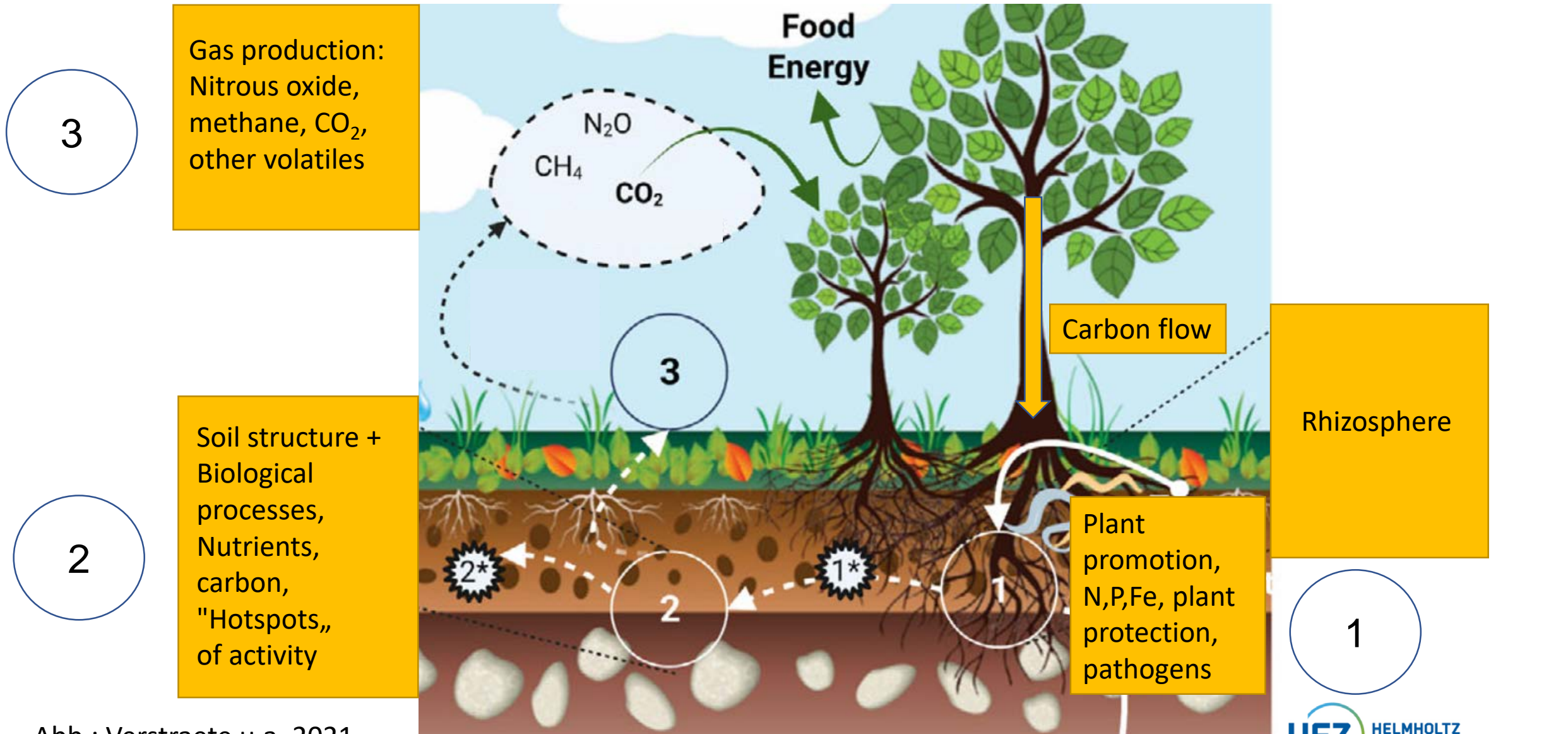
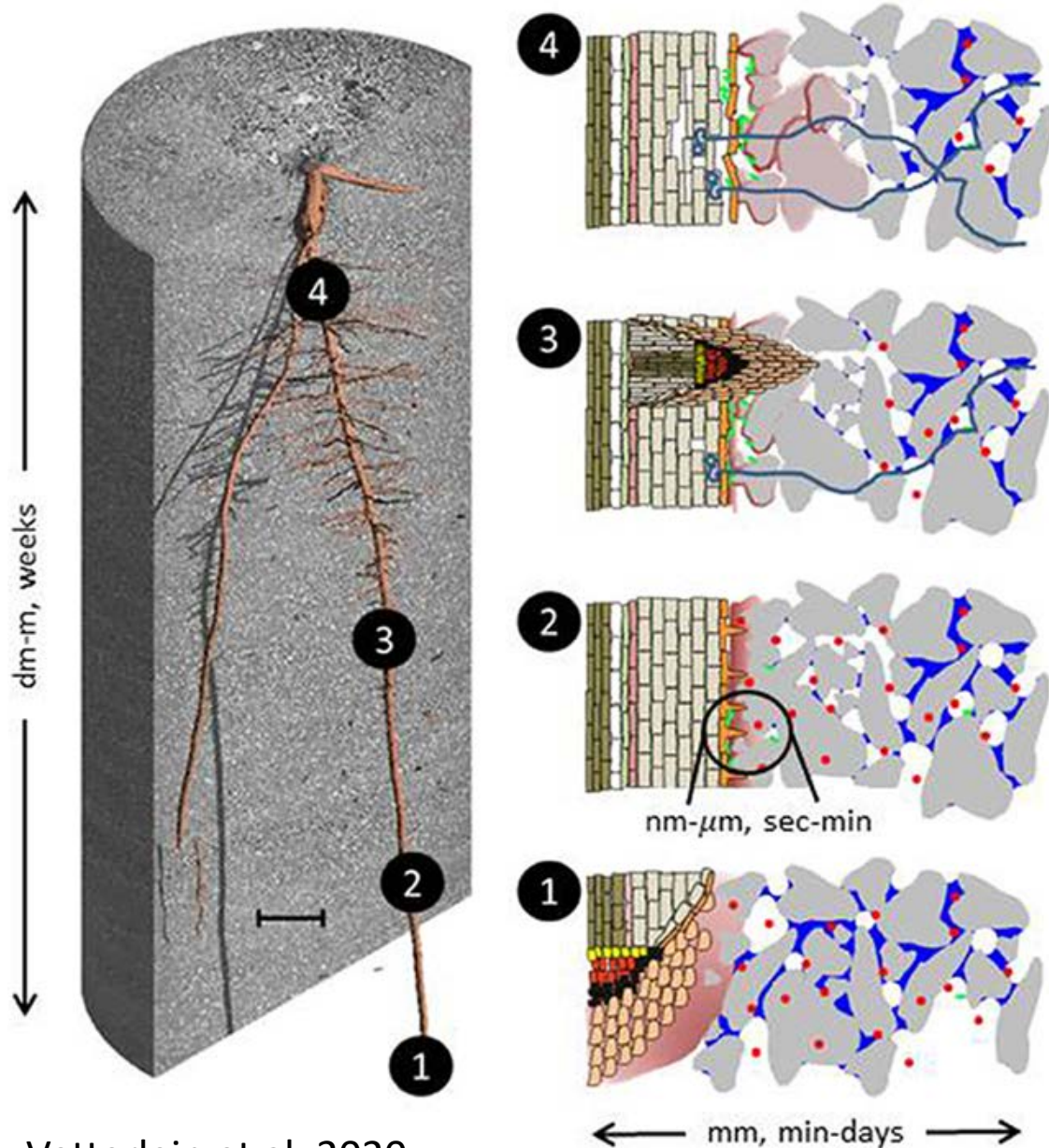


Abb.: Verstraete u.a. 2021

Rhizosphere research to support plant growth and health



Vetterlein et al. 2020

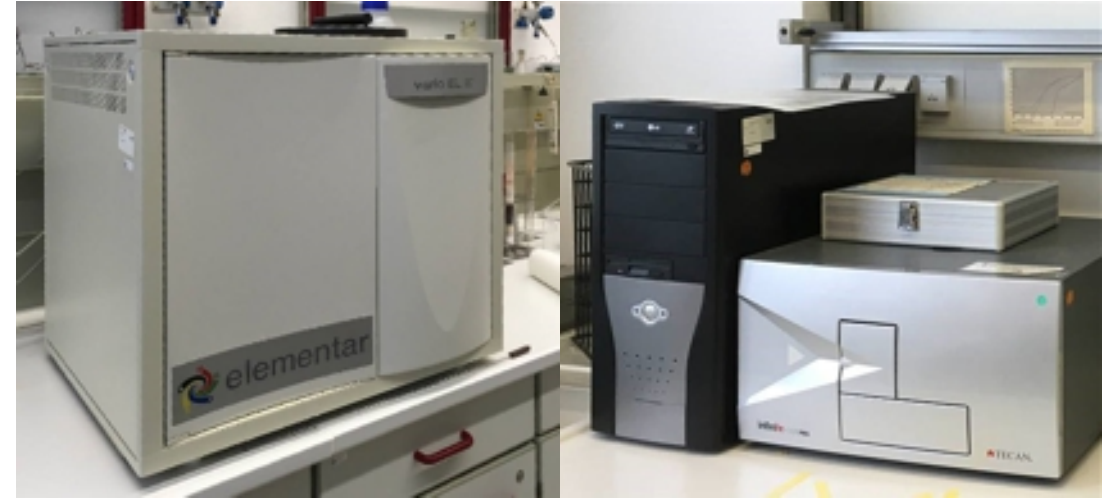
- Rhizosphere: the soil influenced by living roots
- Rhizosphere forms as the root grows
- Rhizodeposits select for certain microorganisms
- Dynamic and stress-affected compartment of the soil

How can we record diversity and functions of rhizosphere microbiomes?

Parameters for the whole community

Analytic Pipeline of Soil Eco-indicators (APPLE)

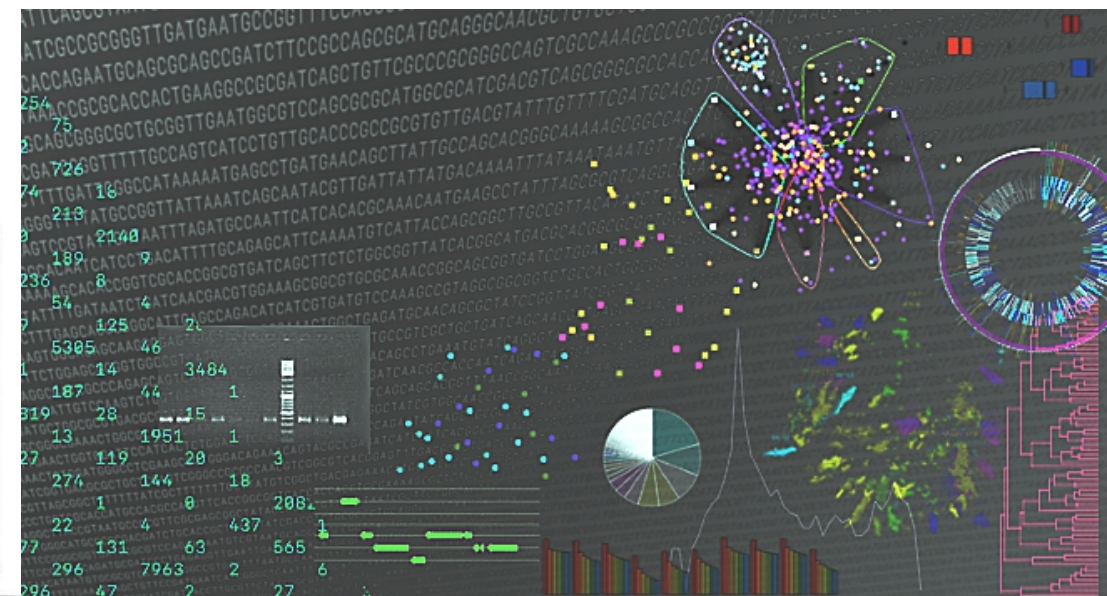
Biomass, respiration, growth, enzyme activities, biomolecules, isotopic composition



Parameters for the whole community with species composition

Meta Omics Pipeline

Diversity and functions by high-throughput molecular-analyses at gene and gene product levels



Rhizosphere formation

Minh Ganther

Lioba
Rüger

Bunlong
Yim



INRAE



ESA
EUROPEAN SOCIETY FOR AGRONOMY



Plant-microbe
interplay

Water acquisition

Nutrient acquisition

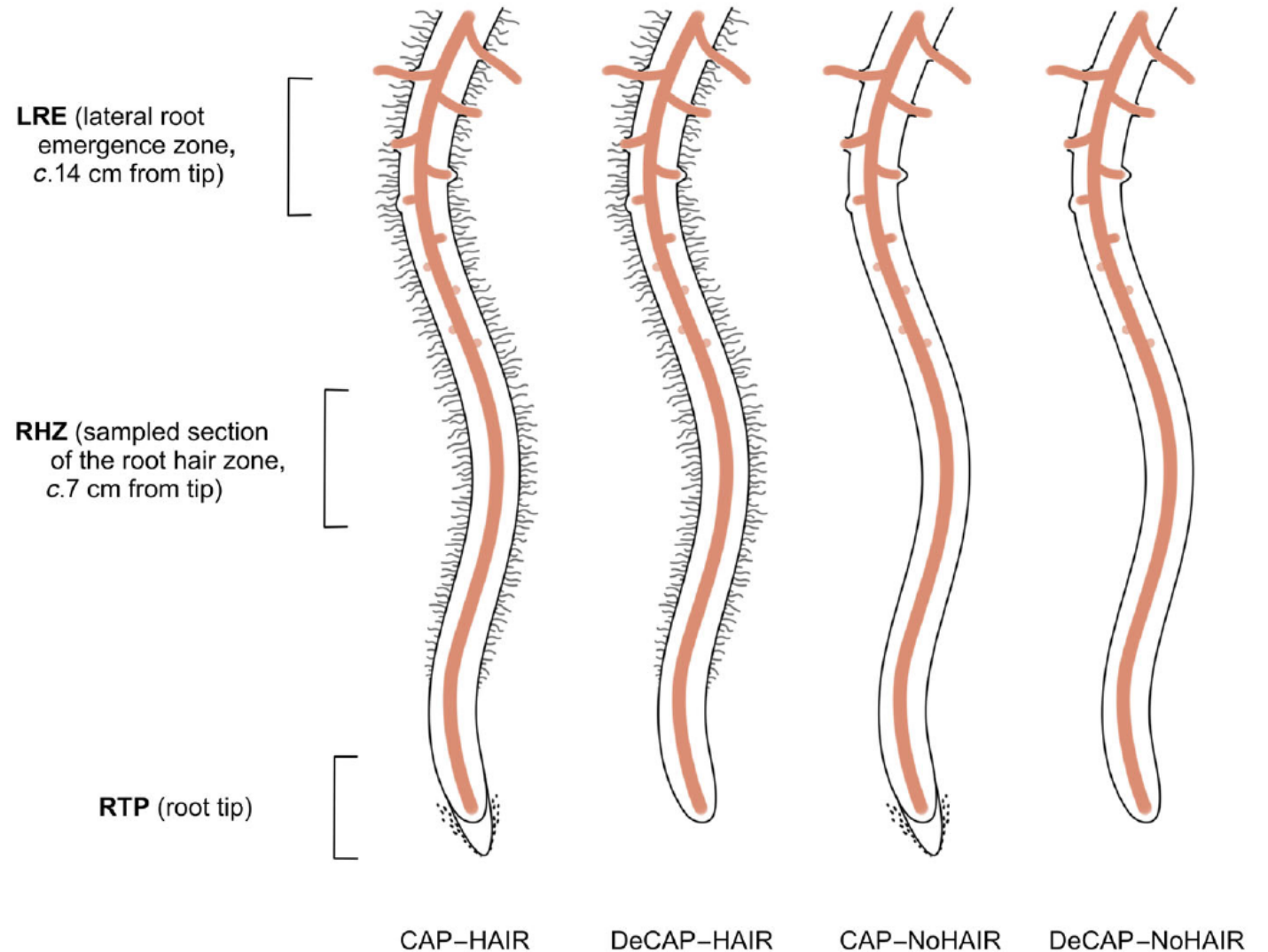
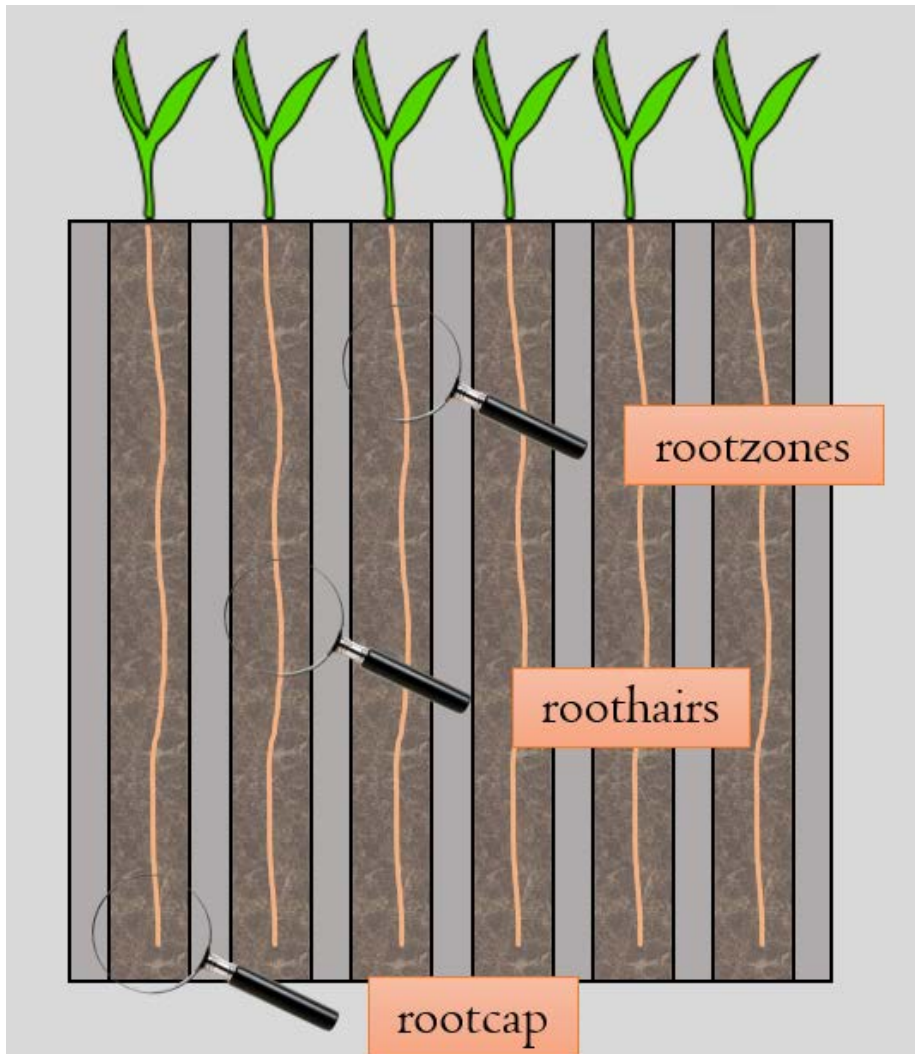
Soil structure
Carbon flux

Vetterlein et al. 2020 *Front Agron*

Vetterlein et al. 2021 *J Plant Nutr Soil Sci*

Formation of the rhizosphere: from the root cap to lateral root zone

The effects of root zones and root cap removal on maize gene expression and prokaryote and protist community composition



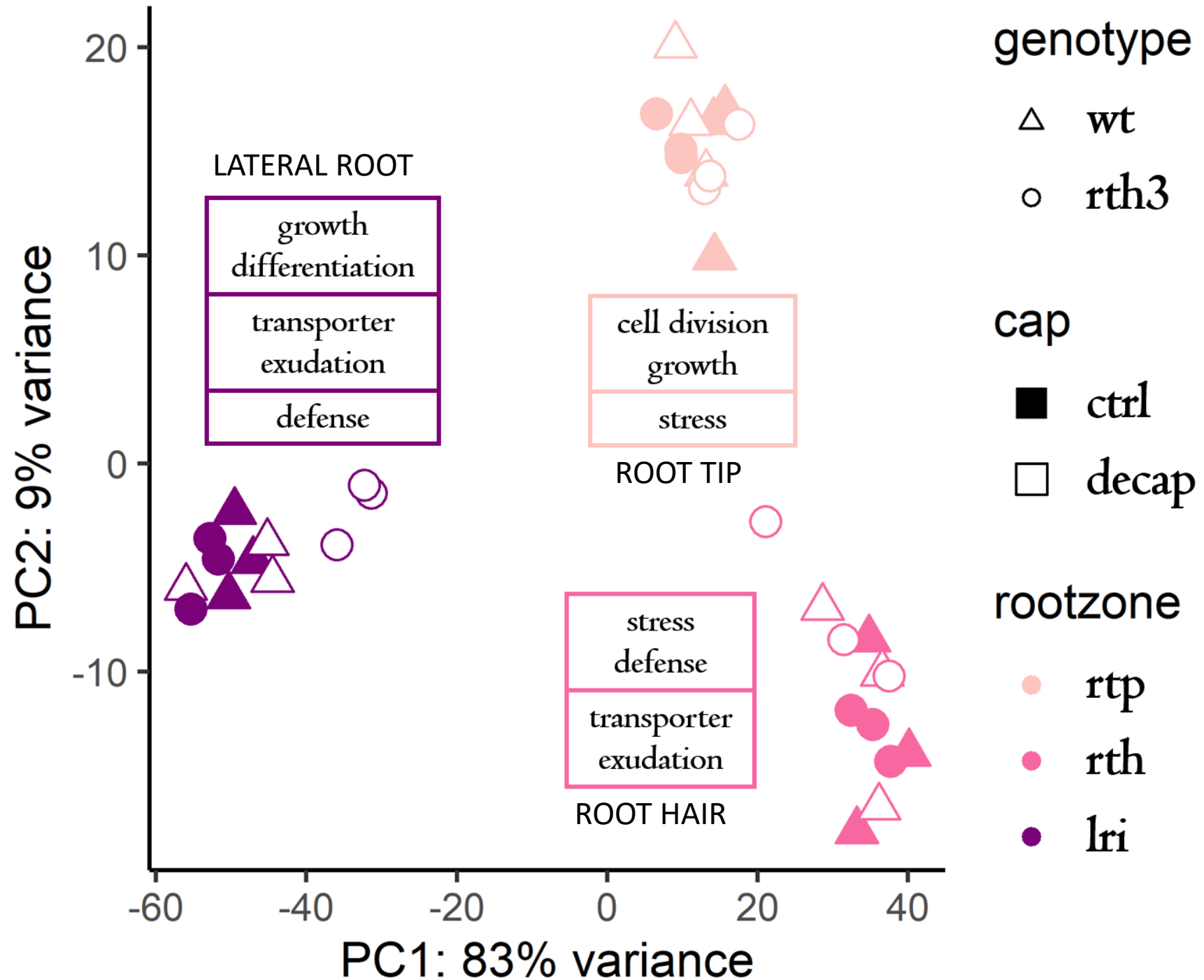
Maize root gene expression

Root parts are different,
but root cap removal or
absence of root hairs (rth3)
have a low
effect

RNA sequencing
of maize roots

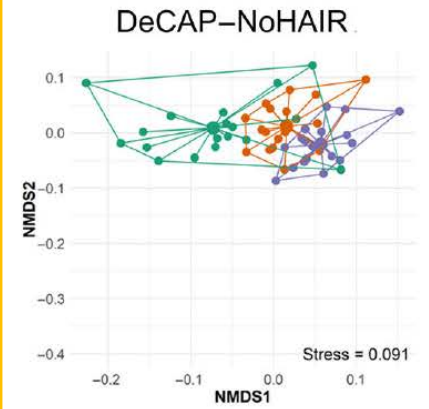
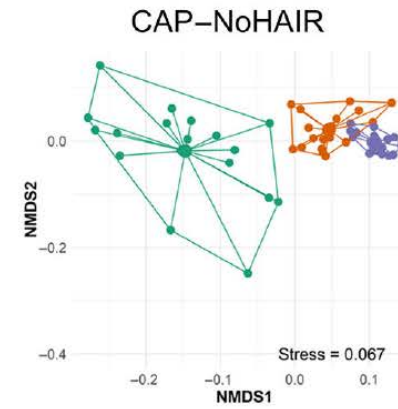
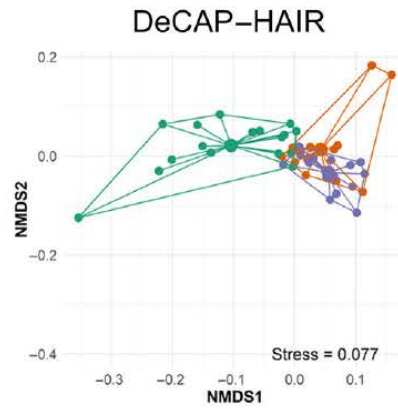
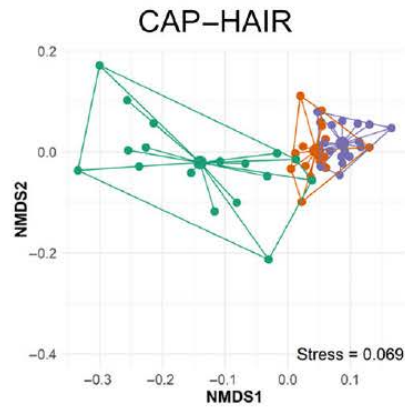
Functions: enriched
gene ontology terms
(functions based on gene
expression)

Principal components
analysis

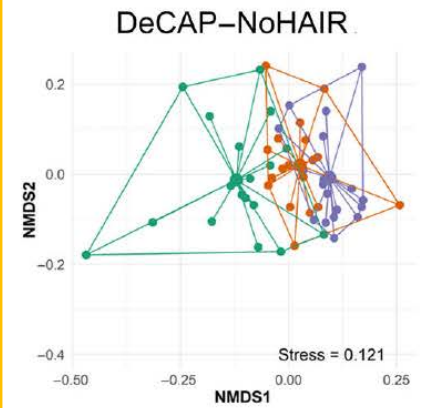
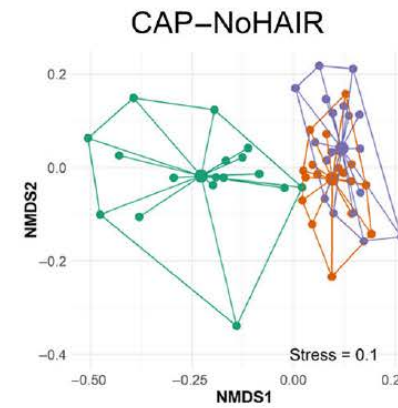
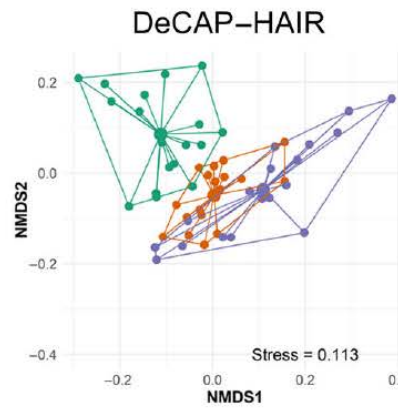
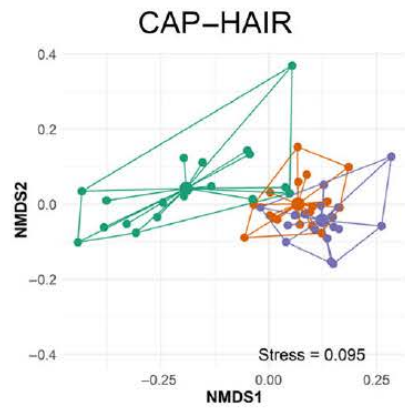


DeCapping (no root cap) leads to reduced differentiation of the rhizosphere microbiome

PROKARYOTES: bacteria and archaeobacteria



PROTISTS: unicellular eukaryotes that feed on bacteria



Root zones

TIP HAIR LAT R

Community compositions of the microorganisms

The root tip community composition is similar to those in the root hair zone and lateral root forming zone!

Maize gene categories

- transport
- growth
- immunity

Correlations between maize root gene expression and prokaryote abundance levels are related to the zone of the root

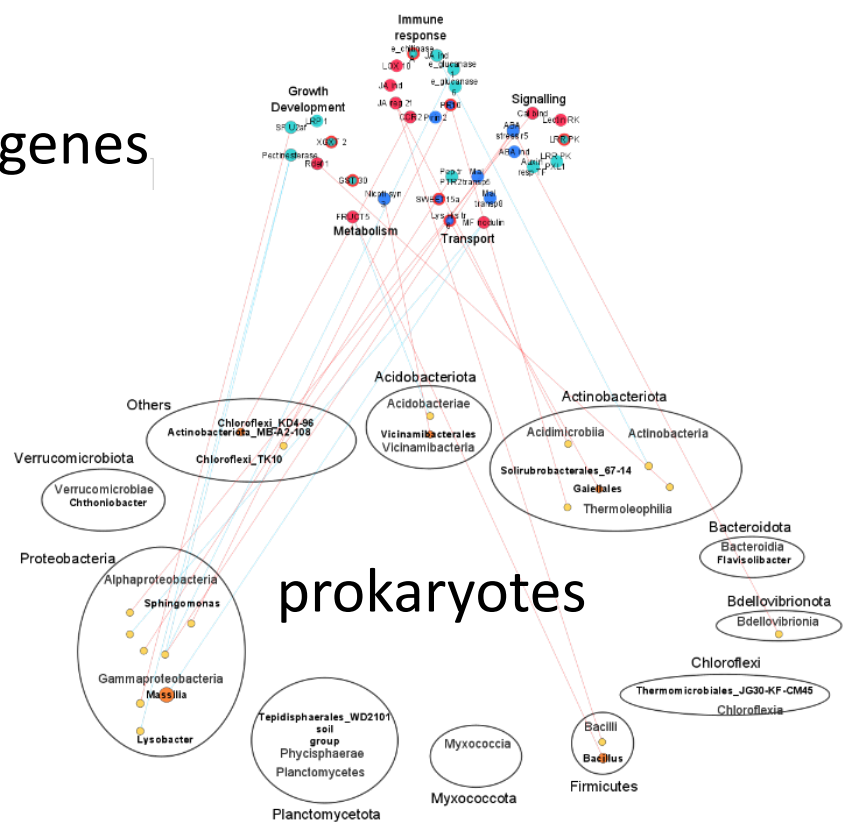
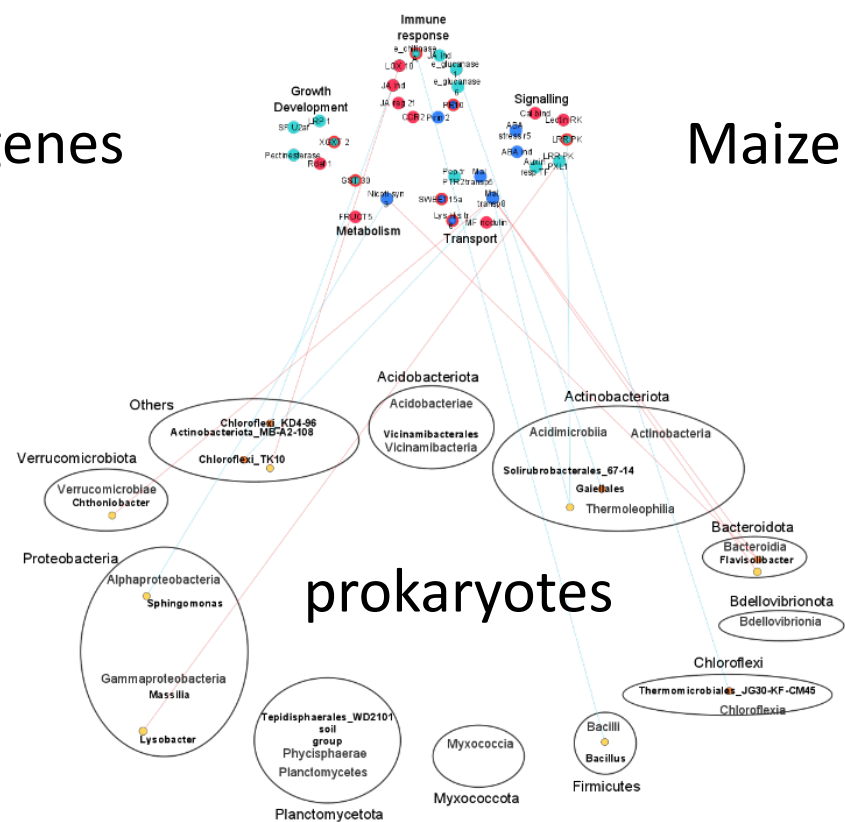
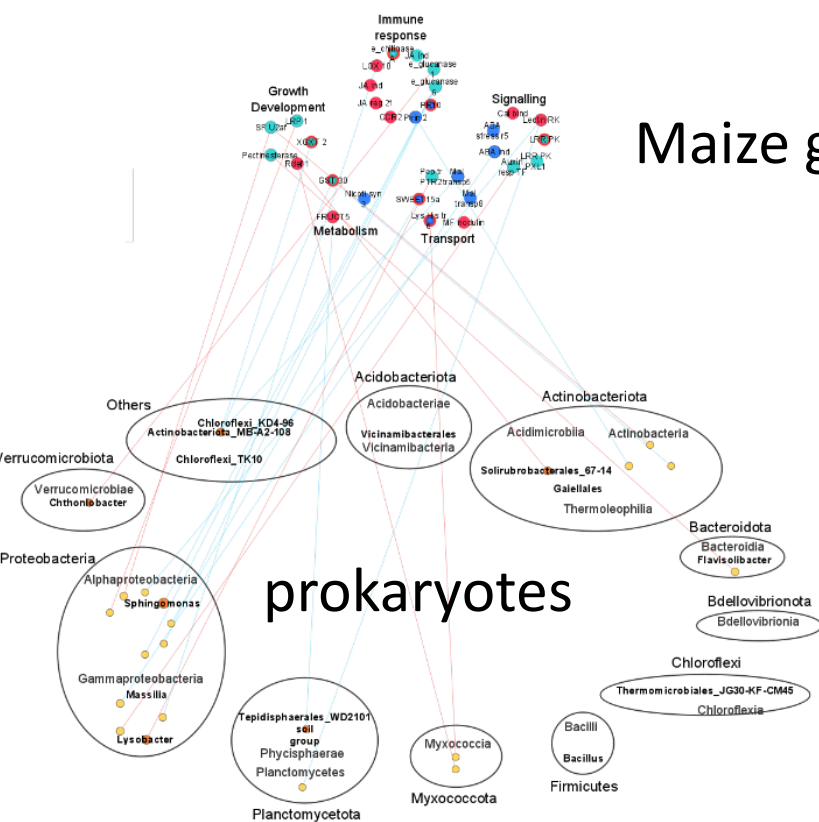
Root tip

Root hair forming zone

Lateral root forming zone

Maize genes

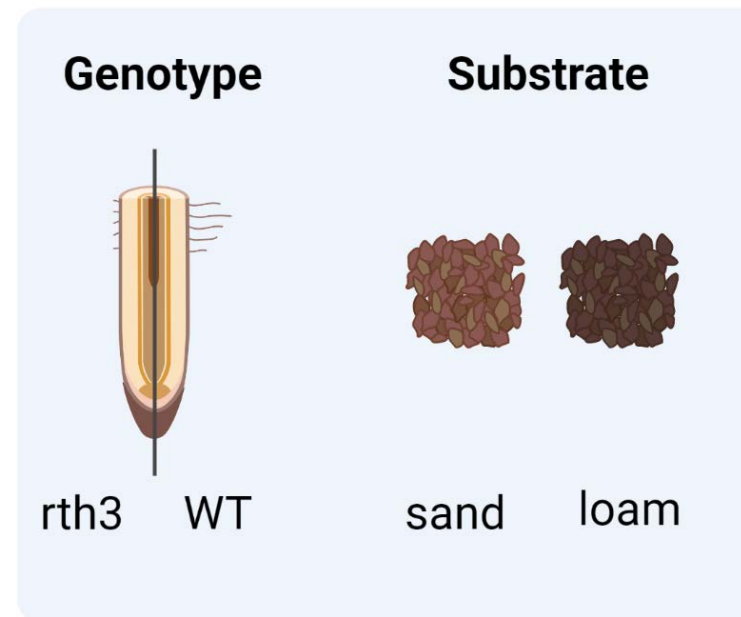
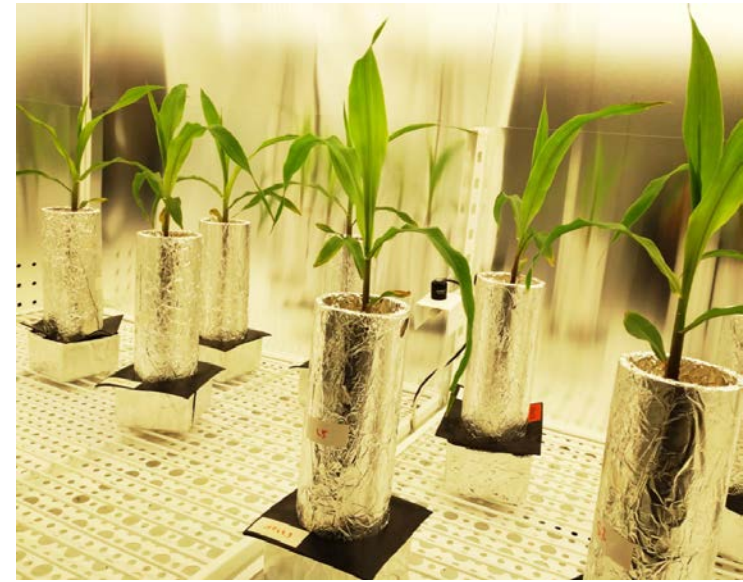
Maize genes



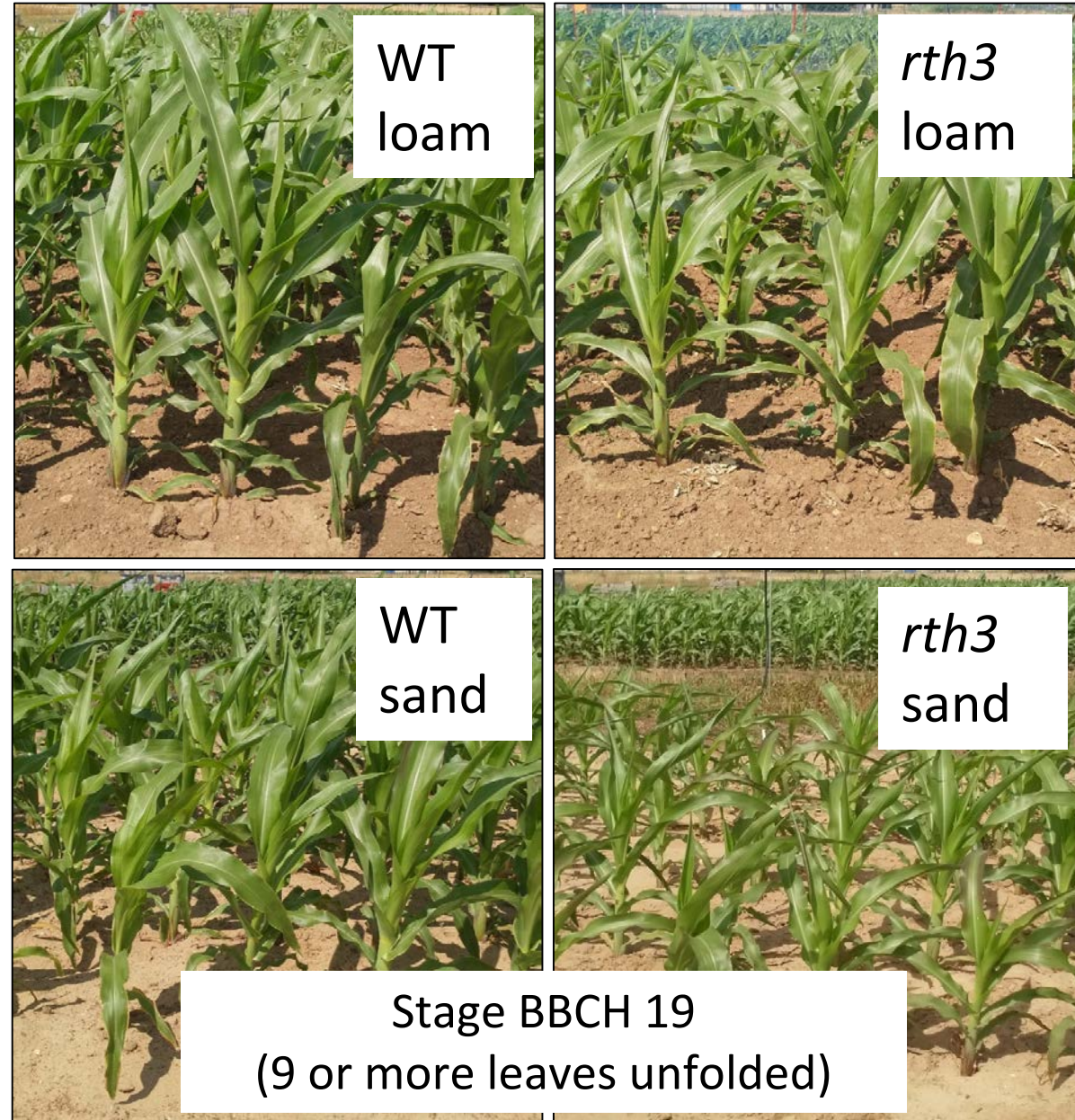
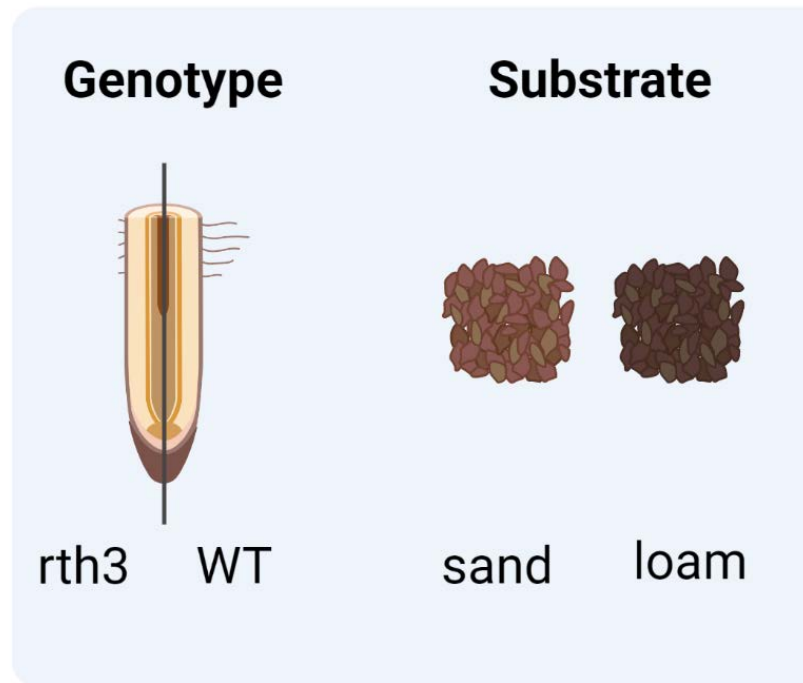
Formation of the rhizosphere: soil properties and depth

The effects of soil type and column depth on maize gene expression, prokaryote community composition, and plant beneficial *acdS* carrying prokaryote community composition

- Soil type greatest effect
- Depth of the columns a strong effect
- Presence of root hairs had minimal effect



Maize field experiment



Rhizosphere microbiomes

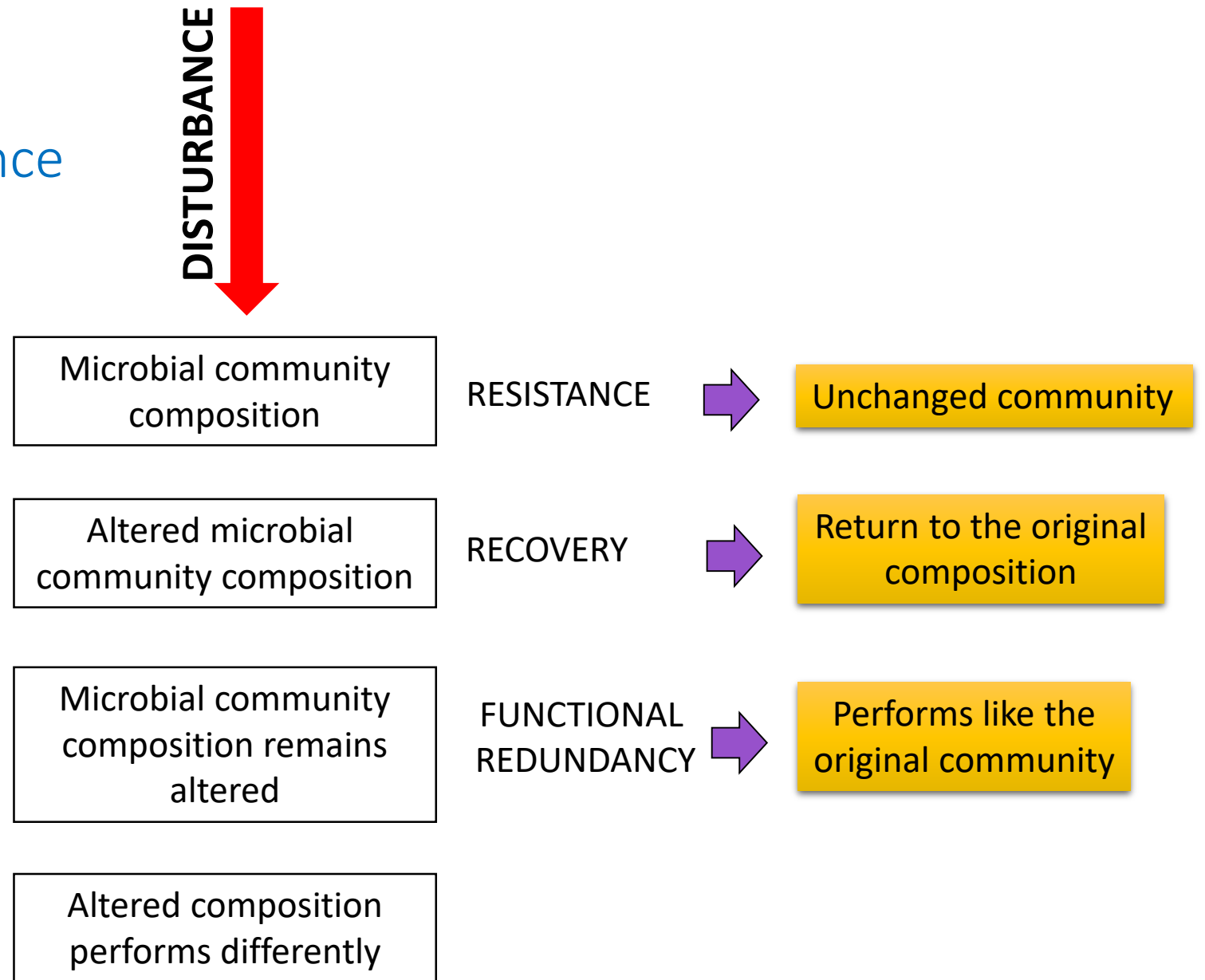
- arise from soil microbiomes that are diverse
 - soil type is the reservoir for microorganisms, soil depth modifies the community, and plant developmental stage has a strong impact on them
- rhizosphere formation is a well organized process
 - root cap-derived cells and secreted mucilage offer first control
 - secondary controls occur at older root parts by root exudates and plant defense

Resilience

18th Congress of the European Society for Agronomy in Rennes, France

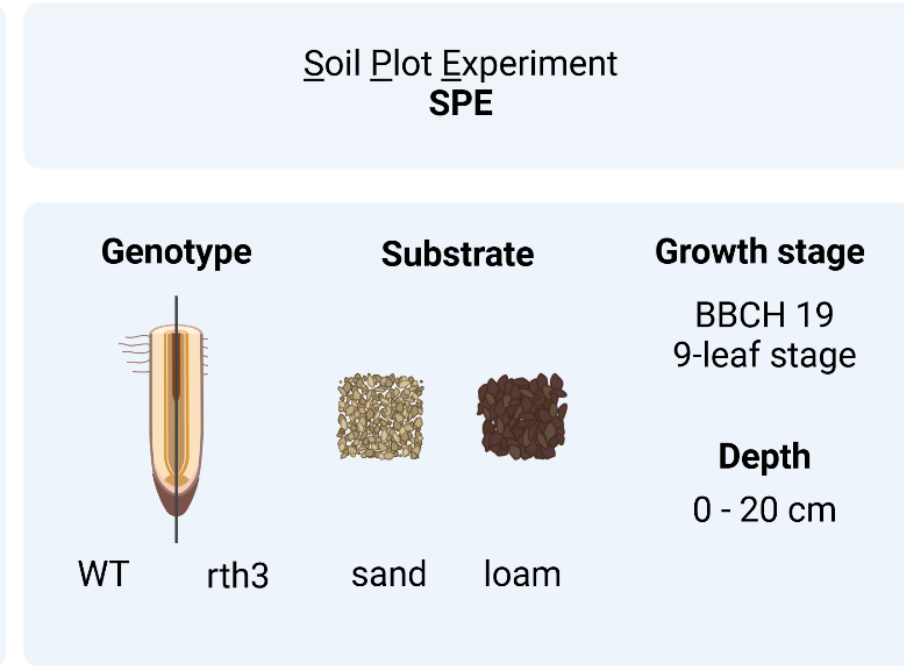


How disturbance changes the structure and performance of microbial communities





Maize field experiment



Sampling campaigns we joined:

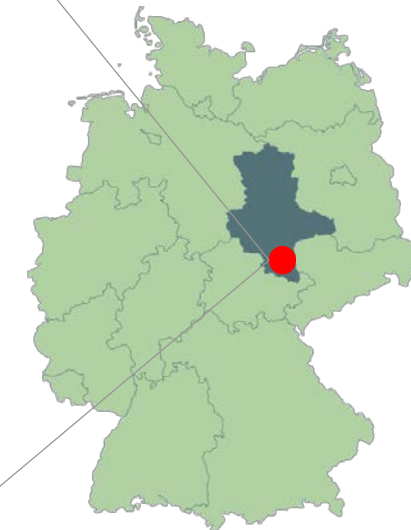
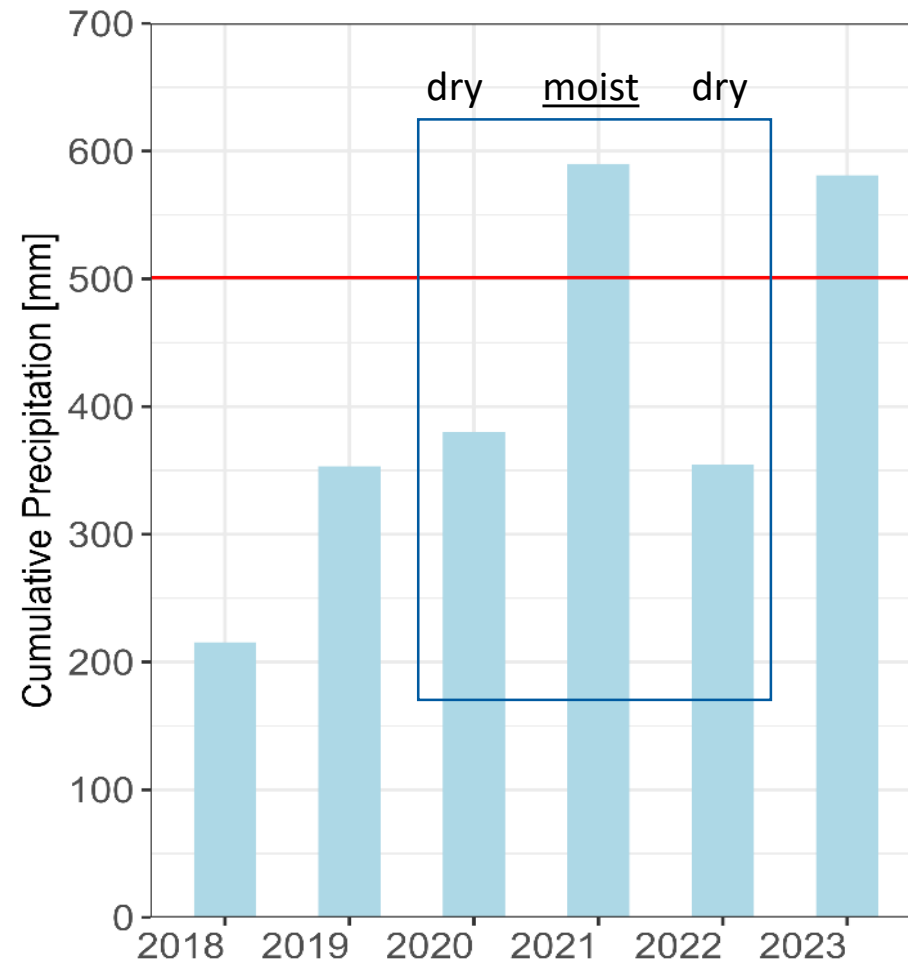
- 2019: BBCH14, -19, -59
- 2020: BBCH19
- 2021: BBCH19
- 2022: BBCH19
- 2023: BBCH19

- Loam, WT
- Sand, WT
- Loam, rth3
- Sand, rth3

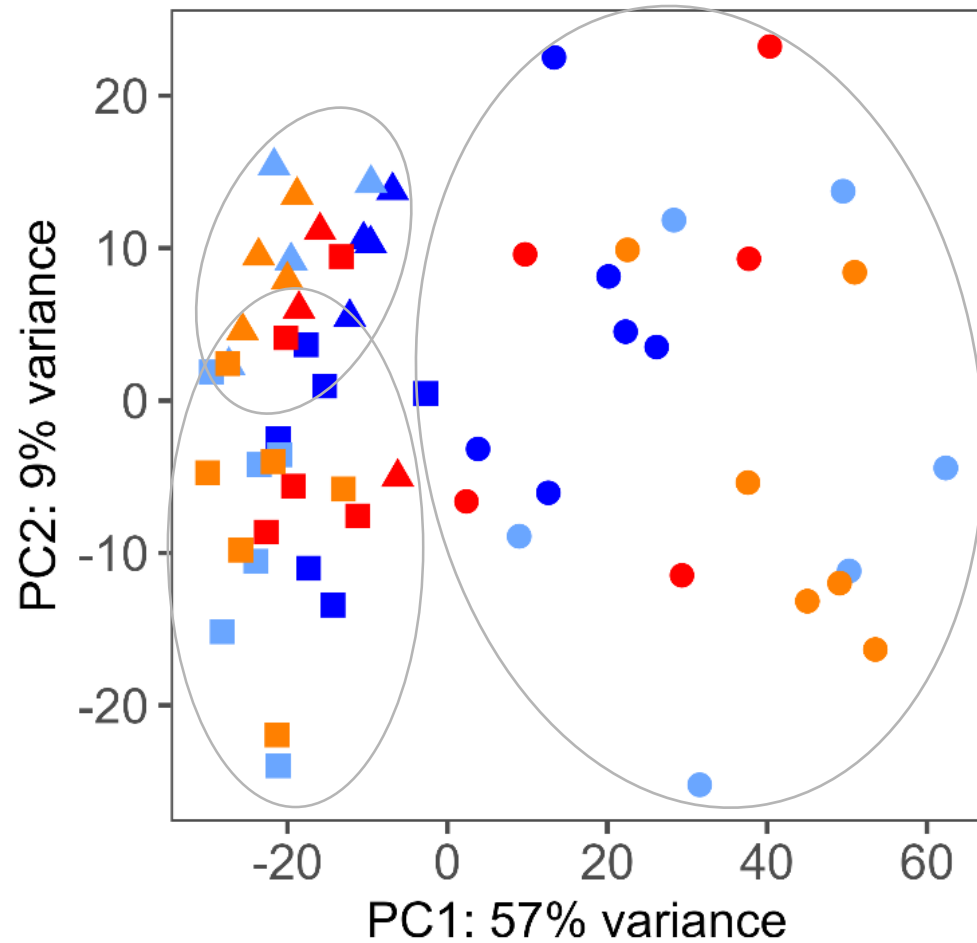
Climate in Bad Lauchstädt



“2018 – 2020 & 2022 dry years in Germany”



Maize root gene expression



- year
- ▲ 2020
 - 2021
 - 2022
- treatment
- L_rth3
 - L_WT
 - S_rth3
 - S_WT

	R^2	
Year	0.34	***
Genotype	0.02	.
Substrate	0.03	**
Substrate:year	0.06	**
Residuals	0.57	

Maize gene expression: Effects of year and substrate

2020 vs. 2021

	R^2	
Year	0.18	***
Substrate	0.09	***

2022 vs. 2021

	R^2	
Year	0.32	***
Substrate	0.04	*

Differential Expression Analysis

~ 1500 genes



~ 3000 genes

2020 (dry)

	R^2	
Substrate	0.16	**

2021 (moist)

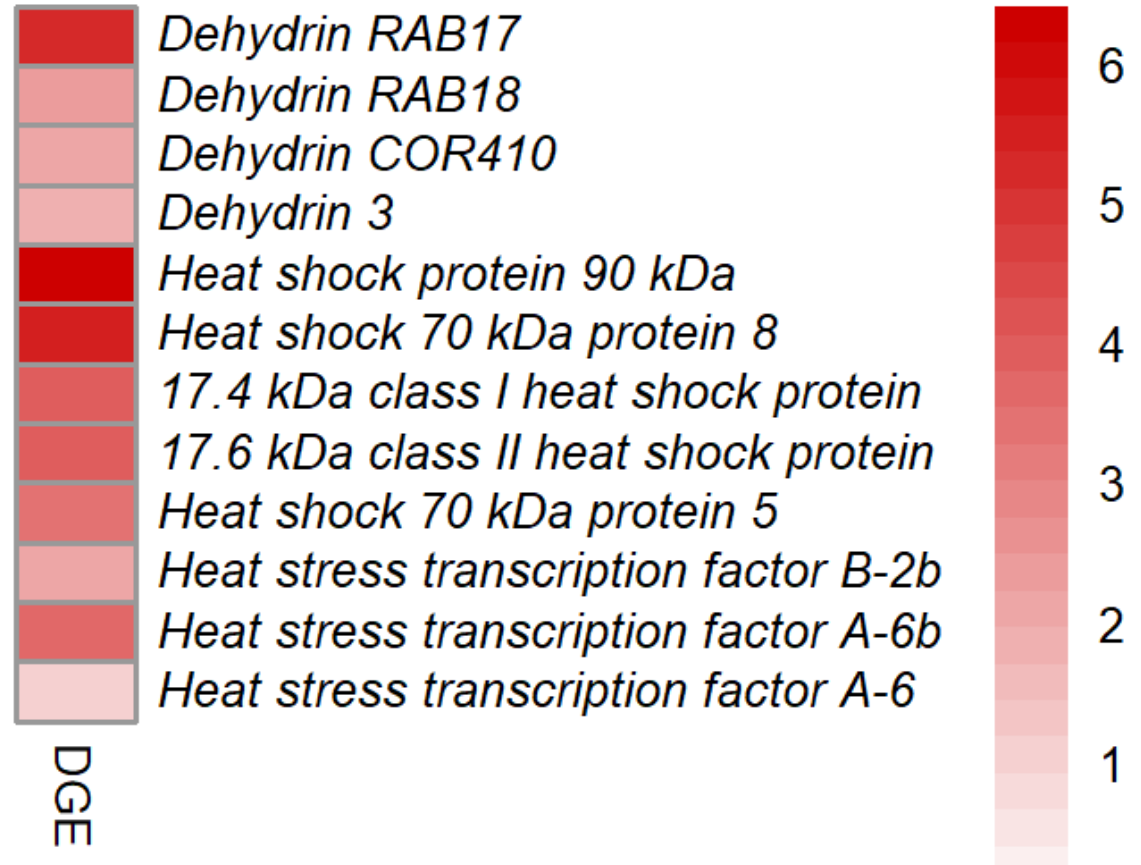
	R^2	
Substrate	0.13	***

2022 (dry)

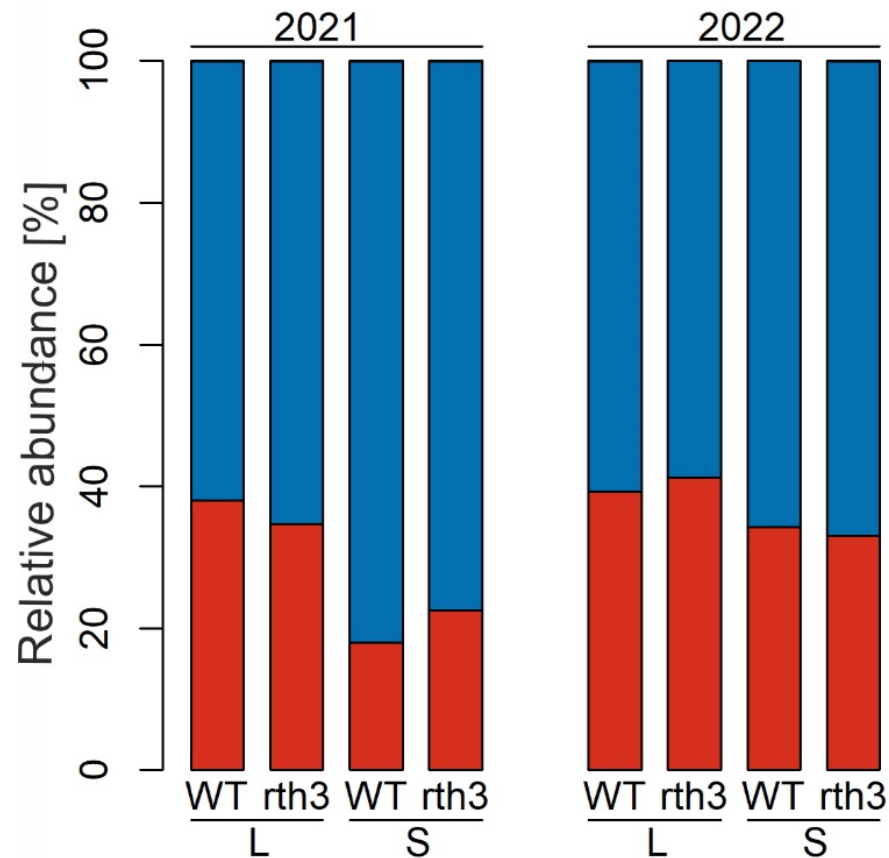
	R^2	
Substrate	0.15	**

Drought response related genes are more highly expressed during dry years

The genes were also differentially expressed in a column experiment with drought application



acdS gene carrying plant stress releasing bacterial community changes with characteristic drought related groups increased



Y **
S ***
G n.s.

Bacteria

- unclassified
- Actinobacteria
- Proteobacteria

	R^2	
Year	0.09	***
Genotype	0.02	
Substrate	0.24	***
Substrate:year	0.05	**
Residuals	0.57	

	2021		2022	
	R^2		R^2	
Genotype	0.03		0.03	
Substrate	0.35	***	0.27	***
Rest	0.59		0.67	

Dry and wet years in the maize experiment confirmed that drought is a driver of prokaryote community diversity

- Dry years led to changed maize gene expression and rhizosphere prokaryote community composition
- The magnitude of effect of drought depends on the „drought legacy“: how dry were the years before?



GCEF: Climate experiment with roofs and 5 types of land use in Bad Lauchstädt, Central Germany

Crop rotation

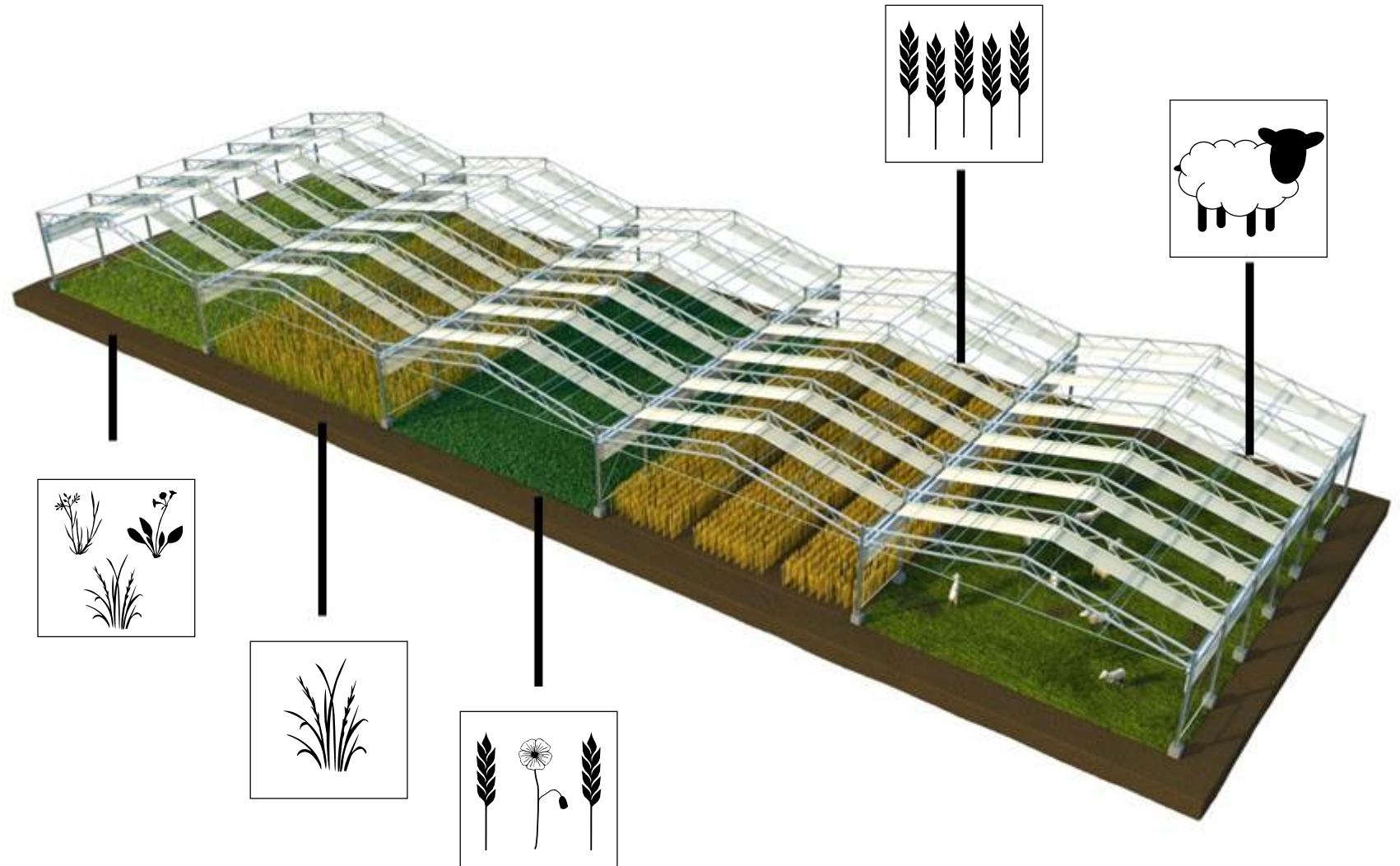
Intensive farming
Organic farming

Grasslands

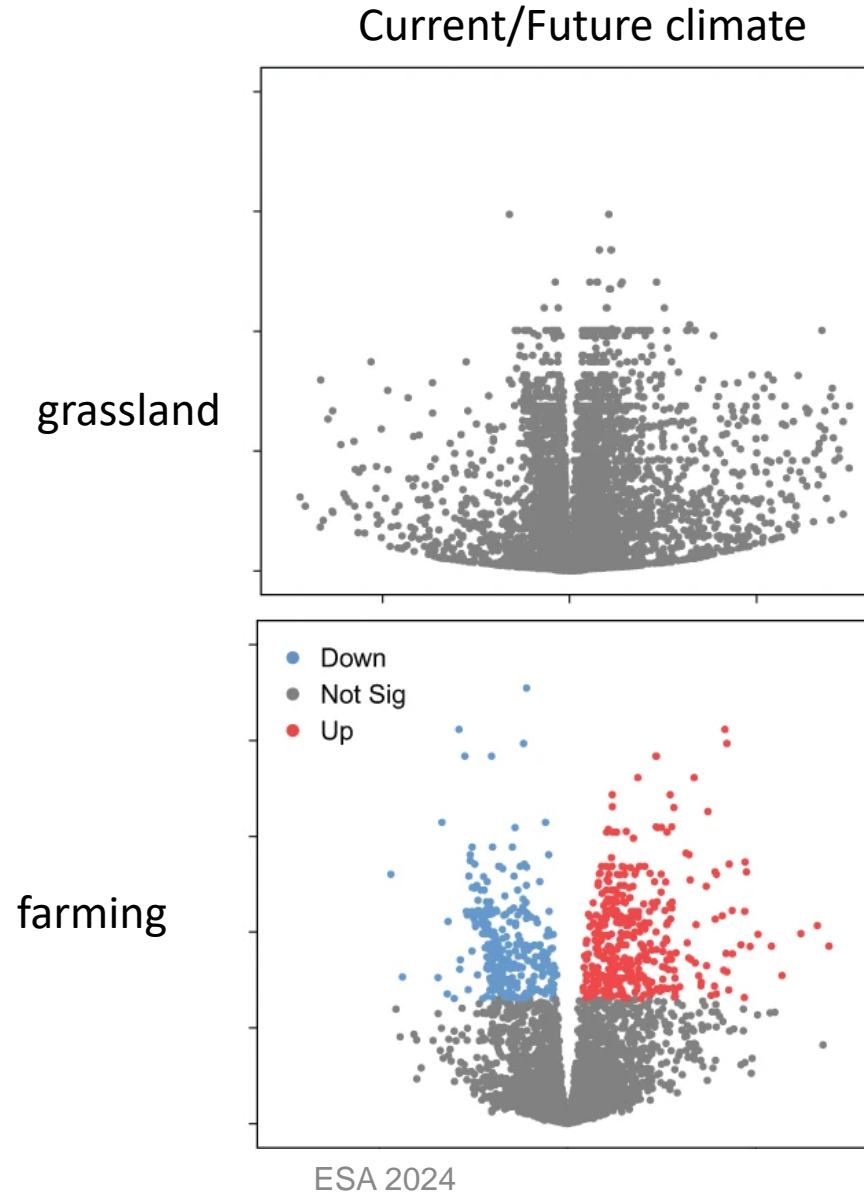
Intensive
Extensive
Extensive with grazing

Climate treatment: roofs

More rain in winter,
Less rain in summer



Climate treatment predominantly affects crop microbiomes



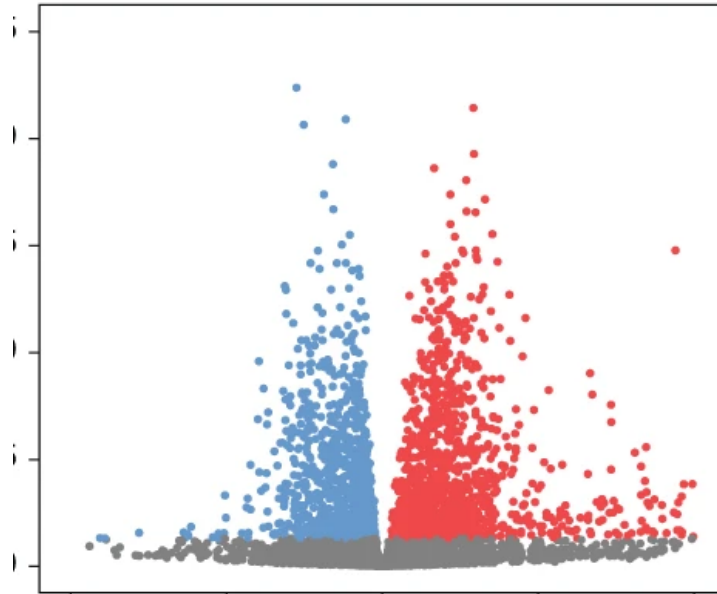
Prokaryote community changes by climate treatment in farming

- Groups that increase in future climate
- Groups that decrease in future climate

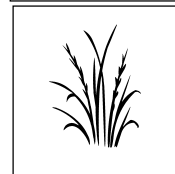
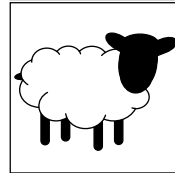
Bei et al. 2023 *ISME J*

Dry years 2018 and 2019 had a major impact

BACTERIAL DIVERSITY Normal/extremely dry years



Grass-
land

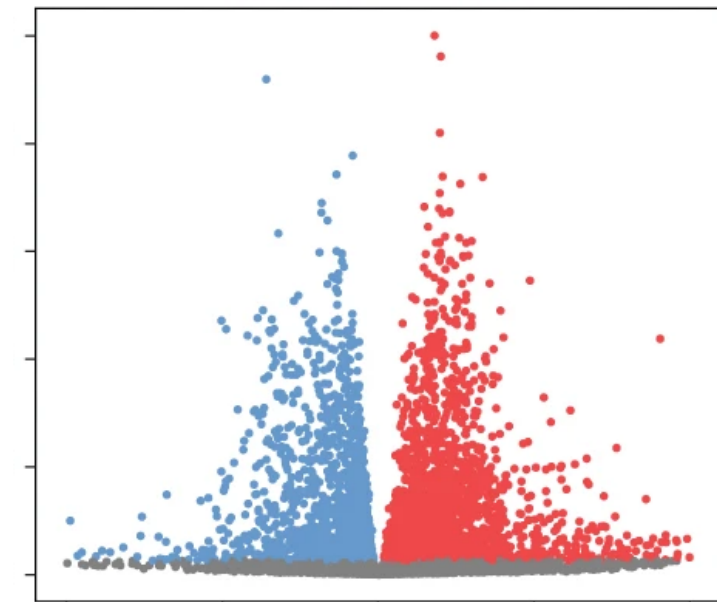


Bacterial diversity has changed considerably in both grassland and cropland as a result of the dry years.

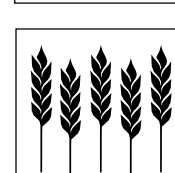
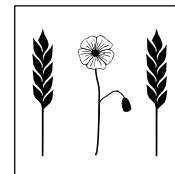
- Bacteria groups that have increased in the extreme years 2018 and 2019
- Bacterial groups that have decreased in the extreme years 2018 and 2019

The changes have functional significance:
Strong reduction of soil enzyme activities

Untargeted soil gene (metagenome) analysis:
Changes in the abundance of C and N uptake
and metabolism genes



Crop-
land



Bei et al. 2023 *ISME J*

Resilience of the rhizosphere microbiomes

- Community composition changes drastically when a stress is prolonged or caused by multiple stressors simultaneously.
- Resilience results from high functional redundancy between microorganisms (for key functions)
- The potential risk of loss of functions for specific responses (e.g. pesticide degradation, production of certain secondary metabolites) remains.
- In the future, we should find markers of essential soil biodiversity, to be used for modelling purposes

Bei et al. 2023 *ISME J*, Rillig et al. 2023 *Nat Climate Change*, König et al. 2023 *Eur J Soil Sci*

Benefits for plant growth



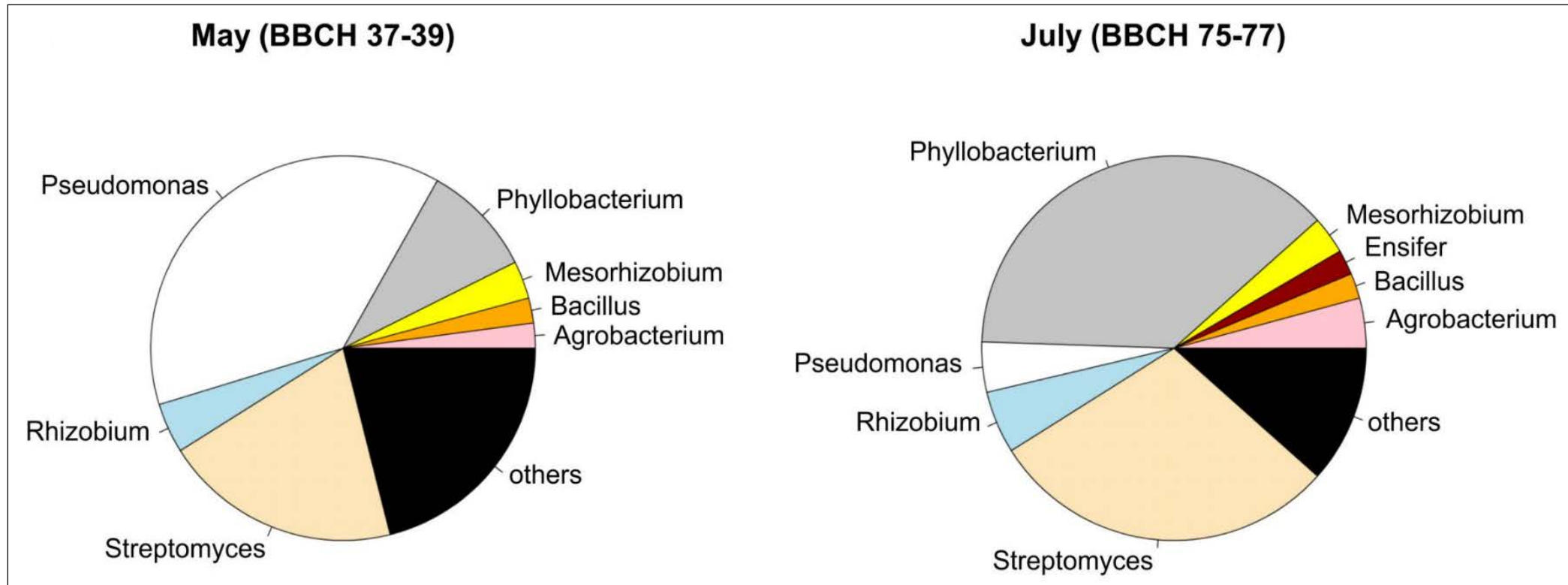
Collections of rhizosphere bacteria from wheat and barley rhizospheres

Claudia
Breitkreuz



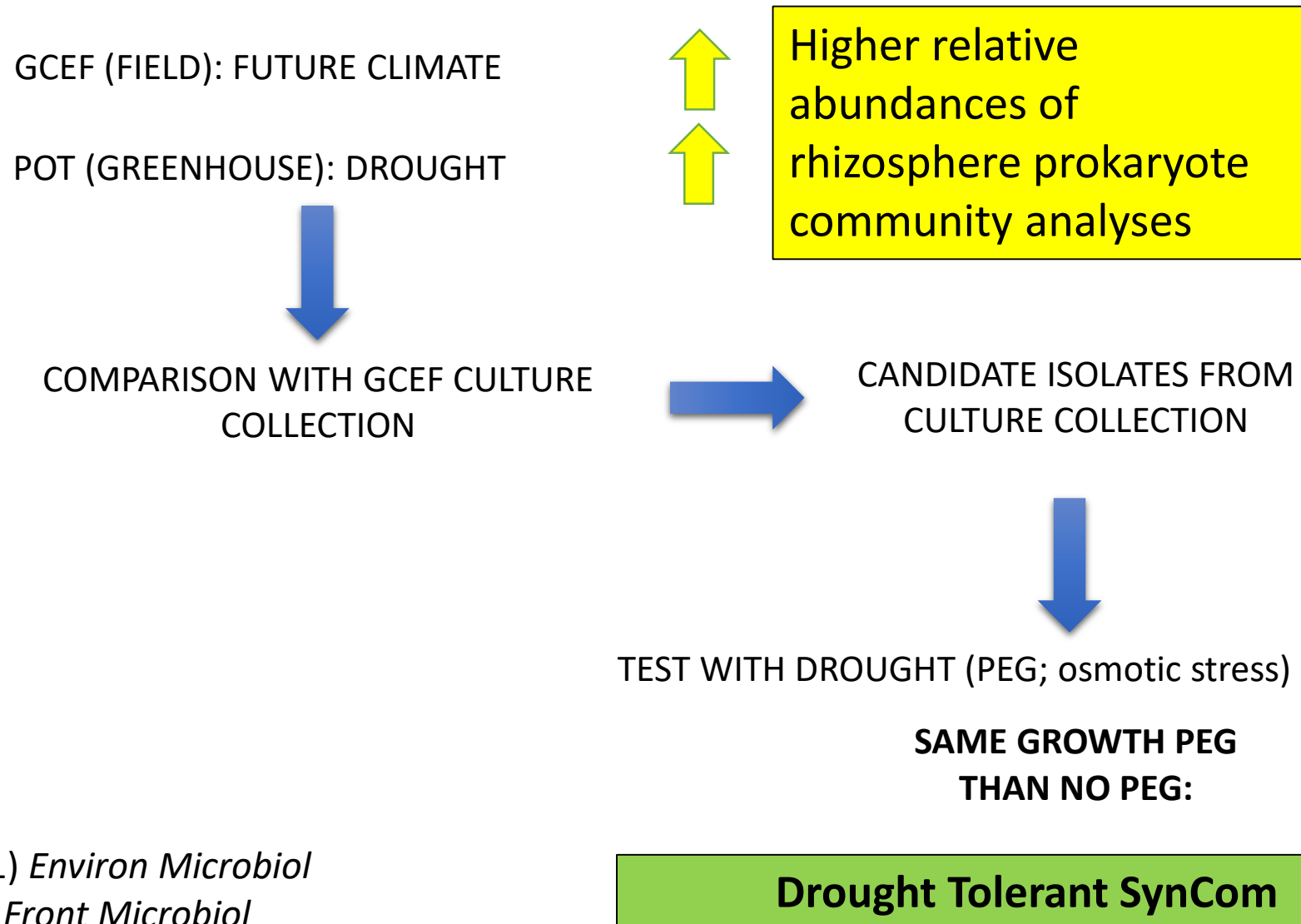
Schädler et al. 2019 *Ecosphere*
Photo: Andre Künzelmann

Seasonal change in P-solubilising bacteria from wheat rhizosphere during the growing season - from *Pseudomonas* to *Phyllobacterium*

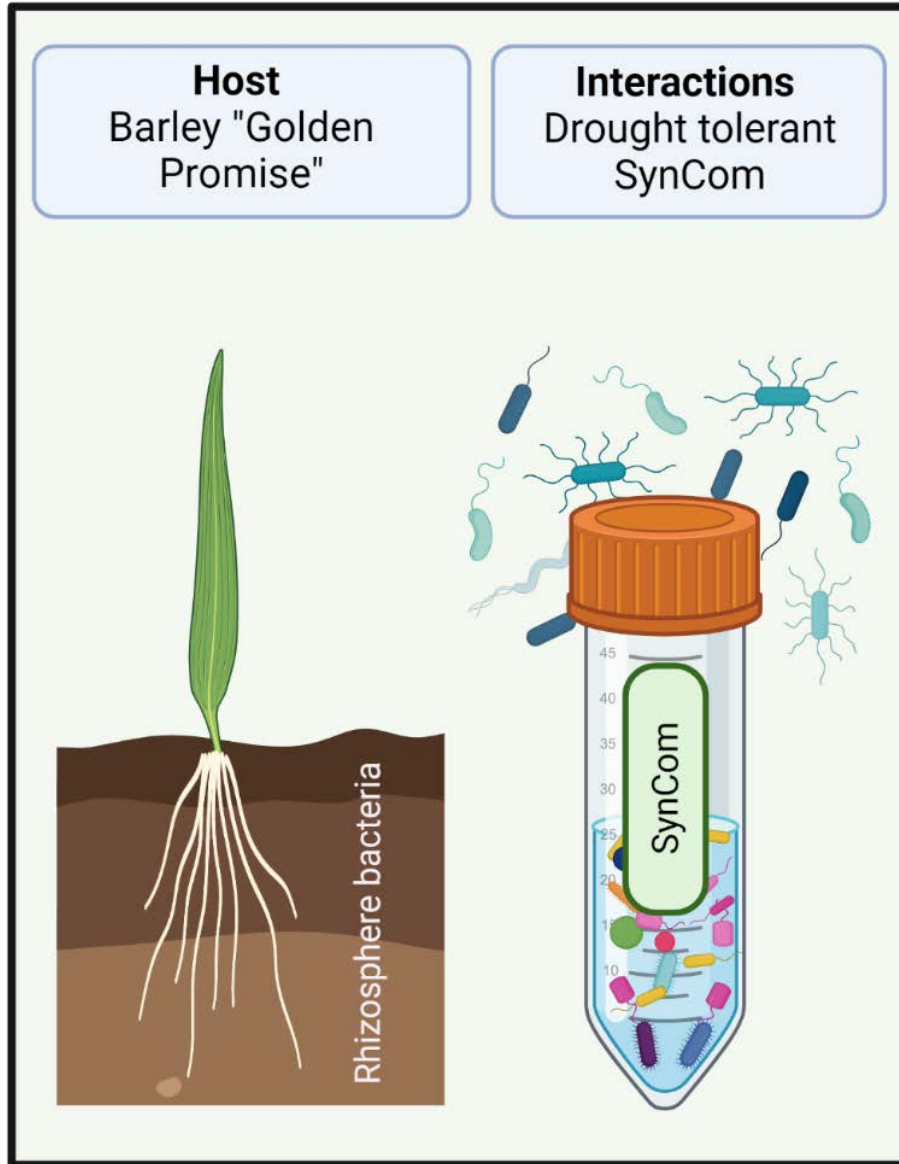


In total 817 mineral P-solubilising bacterial Isolates from wheat rhizosphere

Selection of drought-tolerant members for synthetic communities from barley and wheat rhizospheres



Benefits for the host plant?



Community analyses and cultivation of rhizosphere microorganisms to assess their potential to increase the stress tolerance of plants

Linda Rigerte

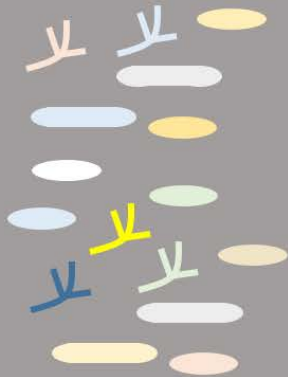
Host
Barley
„Golden
Promise“



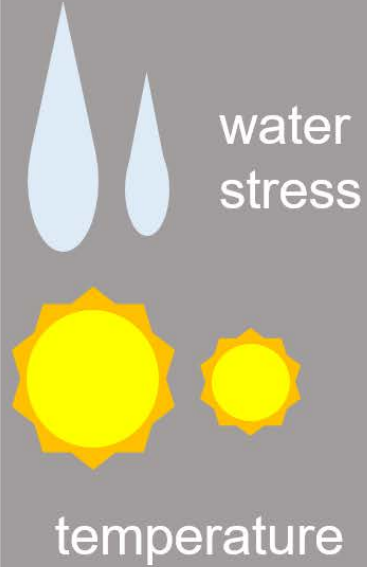
Rhizosphere bacteria

Interactions

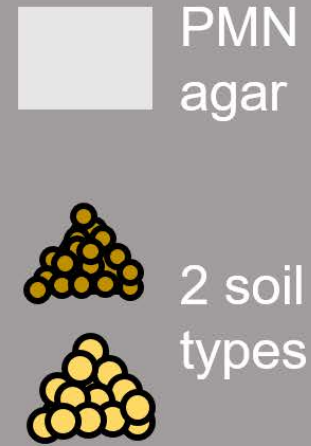
Drought tolerant
DT-SynCom



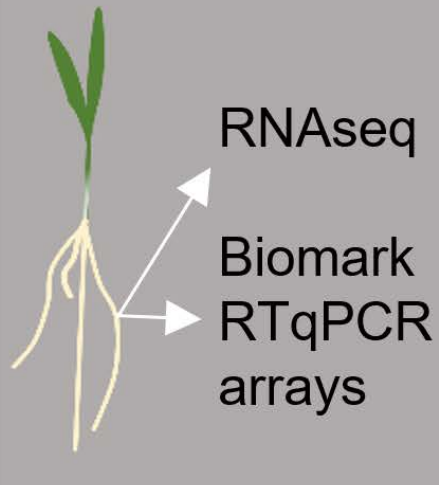
Treatments



Substrates

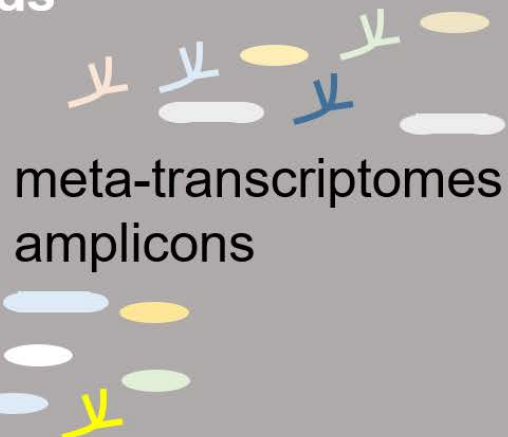


Methods



RNAseq

Biomark
RTqPCR
arrays



meta-transcriptomes
amplicons

Approach: To assess interactions between bacteria and their influence on barley under drought, high temperature and plant disease

Aim: To elucidate bacterial community factors involved in plant drought tolerance.

Product: Plant stress tolerance-enhancing bacterial community

Isolating and enriching plant beneficial microorganisms

- Strategies for finding beneficial plant growth promoting bacteria and ensuring their functionality in the field are under intensive analysis
- Approaches to support the beneficial members of plant microbiome are to
 - apply stress (drought, pathogen)
 - change management (crop rotation, cover crops, soil amendments, intercropping)
 - change plant variety (plant selects for beneficial microbes /plant responds to them)

Integration between disciplines



Integration at national level

German Science Foundation (from 2024):

Permanent Senate Commission on the Transformation of Agricultural and Food Systems

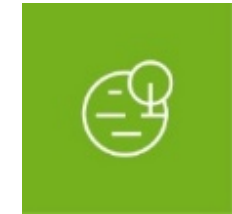
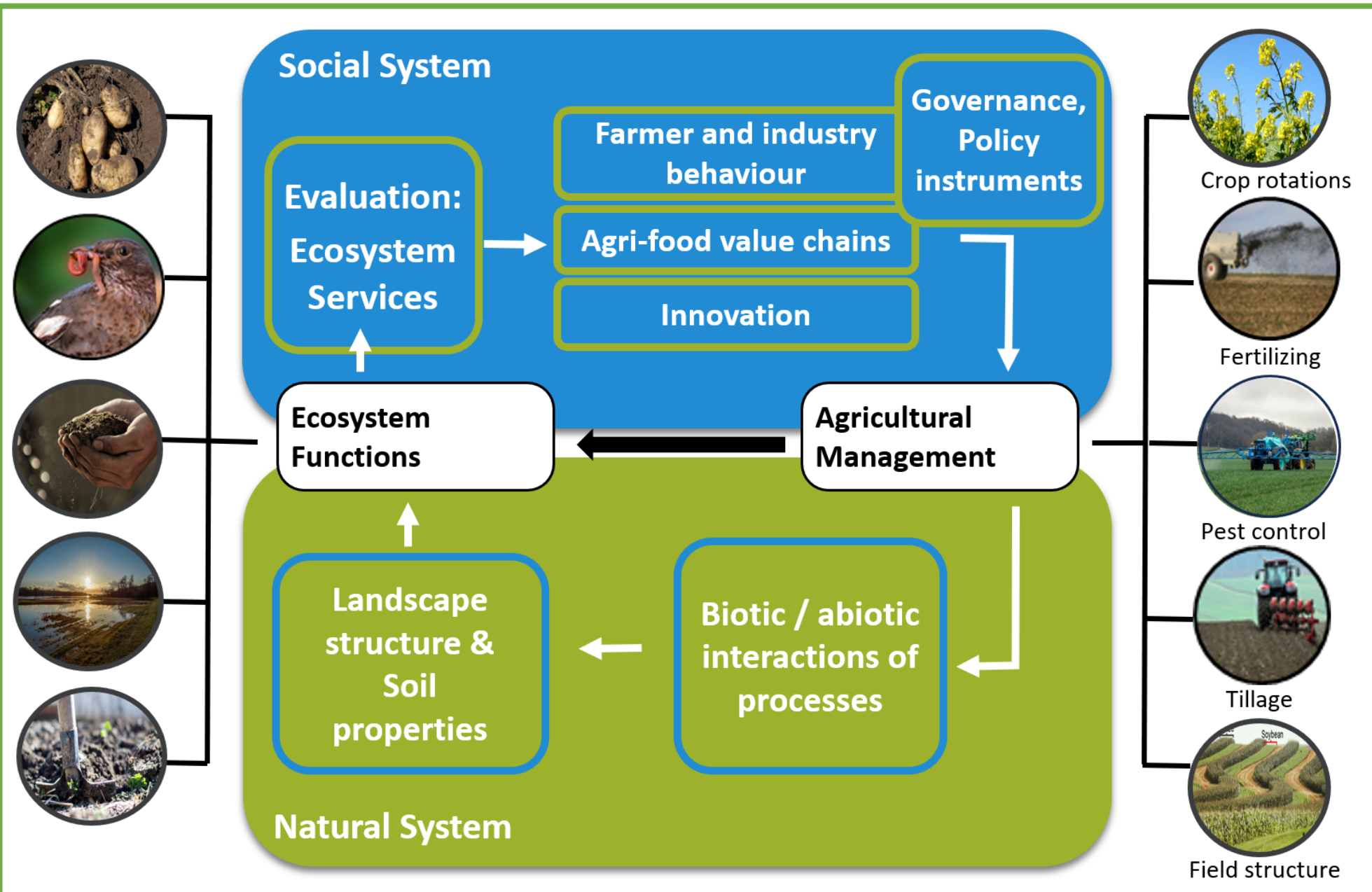
advises various target groups in politics, research and society on developments relating to upcoming transformations in agricultural and food systems

- ways of achieving food security within planetary boundaries
- ways of diversifying the cultivation of crops
- ways of bringing about a societal transformation in the production and consumption of meat and animal products.

Chair: Doris Vetterlein



Integration at research programme level of an interdisciplinary institute



Thematic area
Ecosystems of
the Future

Vogel,
Rode,
Möckel,
Tarkka



Figure:
Hans-Jörg Vogel

At which level do soil scientists, microbiologists, landscape ecologists and sociologists meet?

ECOSYSTEM FUNCTIONS (processes to maintain life) and SERVICES (for human beings)

Provisioning Services

Food Production, Fiber and Raw Materials

Regulating Services

Climate Regulation, Water Regulation,
Pollination, Pest and Disease Control

Supporting Services

Soil Formation, Nutrient Cycling, Biodiversity Maintenance

Acknowledgements

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Bunlong Yim

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Lioba Rüter

Eva Oburger

Michael Santangeli

Corina Vlot Schuster

Deutsche
Forschungsgemeinschaft

DFG



UFZ HELMHOLTZ
Zentrum für Umweltforschung