Detailed programme

Microbiomes in soil, plant, animal and human health.

One Health Summer School

11.–16. August 2019, University of Bern

Keynotes and workshops for PhDs and Postdocs researching soil, plant and gut microbiomes and their links to host and environmental health. **Speakers:** Thomas Clavel (DE), Viviane Cordovez (NL), Noah Fierer (US), Gilbert Greub (CH), Corné Pieterse (NL), Paul Schulze-Lefert (DE), Emma Wetter Slack (CH), Shinichi Sunagawa (CH), Jean-Claude Walser (CH)

www.onehealth.unibe.ch/summerschool

Universität Bern
Interfaculty Research Cooperation
One Health

UNIVERSITÄT BERN

General information

WELCOME !

The Interfaculty Research Cooperation «One Health: Cascading and Microbiome-Dependent Effects on Multitrophic Health» unifies nine research groups from the Faculties of Natural Sciences, Medicine and VetSuisse of the University of Bern. Together we investigate how environmental chemicals and microbiomes impact the health of soils, plants, animals and humans (see www.onehealth.unibe.ch).

On the topic of Microbiomes and One Health, we organize an International Summer School, which will take place from the 11. – 16. August 2019 in Bern. This event is designed for PhD and postdoctoral researchers from the fields of biology, environmental sciences, medicine, chemistry and bioinformatics.

The program of the first two days consists of conceptual keynote lectures (about soil, plant and gut microbiomes and their links to environmental health) and a poster session where participants present and discuss their own research with the attendees. The other three days offer hands-on activities on the following topics: microbiota analysis (amplicon data), microbiome analysis (shotgun metagenomic data), scientific visualization and advanced graphics, ordination and network analysis. Two workshops are related to graphics and data analysis in R and the two other workshops cover command line based microbiota and microbiome analyses. It is important that participants are comfortable with some form of coding language. You do not have to be fluent in R but you need to be able to understand basic R code. The program is rounded with social events on the topics of 'Women in Science' (Sunday) and 'Microbes and Games' (Wednesday).

Klaus Schlaeppi, Alban Ramette, Siegfried Hapfelmeier, Adrien Mestrot, Matthias Erb

Contacts:
…for questions concerning content: **Zoe Bont**, zoe.bont@ips.unibe.ch
…for questions concerning organization: **Nichole Wetter**, nichole.wetter@ips.unibe.ch

@OneHealthUniBe @unibern #PhD #Postdoc #summerschool #microbiome #onehealth

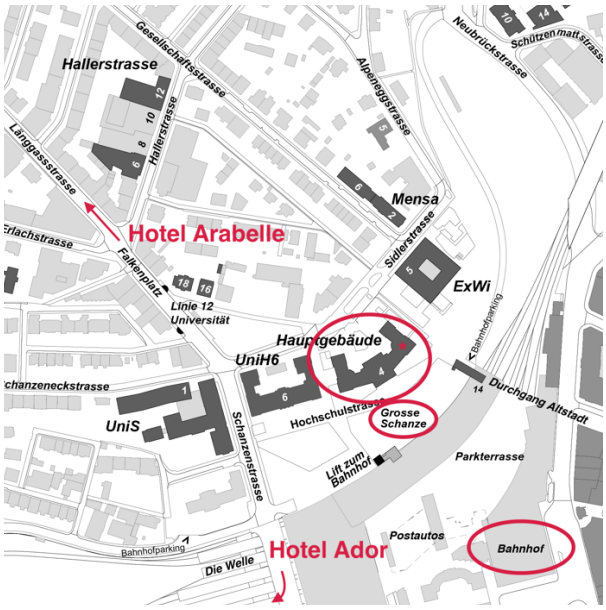
Venue

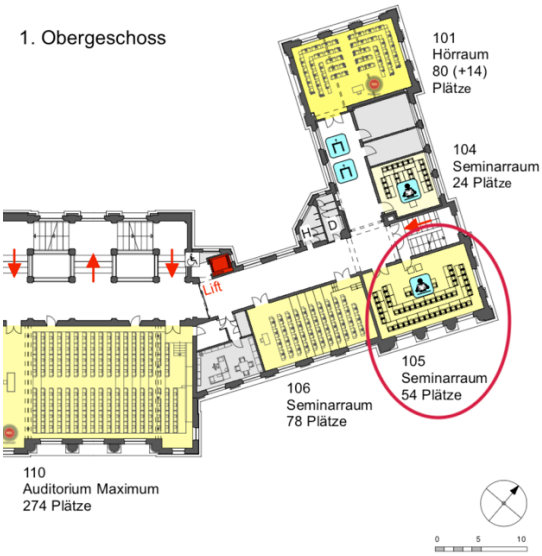
The summer school takes place in and around the main building of the University of Bern (=Hauptgebäude; indicated on the map below). The address of the main building is Hochschulstrasse 4 in 3012 Bern. It can be reached in a 5 min walk from the train station (=Bahnhof).

The scientific program including lectures, discussions, poster sessions and workshops will take place in the main building in the seminar rooms 104, 105 and 106 (**first floor**, East wing *).

Our social dinner events on Sunday and Wednesday evenings will take place at the restaurant Grosse Schanze (indicated on the map below; www.grosseschanze.ch).

Coarse directions to the speaker and student hotels Ador (Laupenstrasse 15) and Arabelle (Mittelstrasse 6) are also indicated on the map below.





Program

Overview

	11.08.19	12.08.19	13.08.19	14.08.19		15.08.19		16.08.19
	SUN	MO	TUE	WED		THU		FR
Locations:	Grosse Schanze	Hauptgebäude, 105	Hauptgebäude, 105	104	105	104	105	104 and 105
Chairs	Klaus/Adrien	Alban/Klaus	Klaus	Adrien	Klaus	Alban	Klaus	Klaus
09:00		Noah Fierer	Thomas Clavel			Microbiota analysis in R, Jean-Claude Walser	Microbiome analysis, Shinichi Sunagawa	Exerscience! Practical application with template data, Jean-Claude Walser
09:30				Scientific visualization, Mirjam Quick	Microbiota analysis using QIIME2			
10:00		Coffee	Coffee					
10:30		Viviane Cordovez	Emma Slack					
11:00								
11:30		participant talks	participant talks					
12:00								
12:30		LUNCH	LUNCH	LUNCH		LUNCH		LUNCH
14:00		Matthew Agler	discussion groups 105, 104, 106	Scientific visualization, Mirjam Quick	Microbiota analysis using QIIME2	Microbiota analysis in R, Jean-Claude Walser	Microbiome analysis, Shinichi Sunagawa	Exerscience! ...
14:30								
15:00		Paul Schulze-Lefert	synthesis					
15:30			Poster odd					**Synthesis**
16:00		Coffee						Closure with Apéro
16:30	registration and	participant talks	Coffee					
17:00	welcome drink		Poster even					
17:30	welcome note							
18:00	**Women in Science**			Grosse Schanze				
18:30	DINNER	**Sessions:**		DINNER (Zoe)				
19:00		The soil microbiome and links to One Health						
19:30		The plant microbiome and links to One Health						
20:00	**Women in Science**	The gut microbiome and links to One Health		Gilbert Greub				
20:30	podium discussion	Microbiomes and their links to One Health		**Playing microbe games**				
21:00	Bar							

Sunday 11.8.2019

@Grosse Schanze

16:30 Registration and welcome drink (Zoe Bont, One Health UniBE)

17:30 Welcome note – **Prof. Matthias Erb** (One Health UniBE)

Chairs: Dr. Francesca Ronchi and Prof. Adrien Mestrot (One Health UniBE)

Women in Science

17:45 **Prof. Britta Engelhardt** – Clinical Neuroscience, University of Bern and representing the equal opportunity commission
www.neuroscience.unibe.ch/about_us/personen/prof_dr_engelhardt_britta

Women in Science: Passion wins over prejudice

Prof. Susanne Reffert – Theoretical Physics, University of Bern
www.reffert.itp.unibe.ch

Women in theoretical physics – My experience

18:30 Dinner

Chairs: Dr. Francesca Ronchi and Prof. Adrien Mestrot (One Health UniBE)

20:00 **Panel discussion** with **Profs. Britta Engelhardt, Susanne Reffert** and…

Prof. Heike Meyer – Economic Geography, University of Bern
www.geography.unibe.ch/about_us/staff/prof_dr_mayer_heike

Dr. Christelle Robert – Chemical Ecology, University of Bern
www.ips.unibe.ch/research/plantphys/chemecol

21:00 Bar

Monday 12.8.2019

@Main building, seminar room 105

Chair: Dr. Alban Ramette (One Health UniBE)

The soil microbiome and its links to One Health

9:00 Keynote lecture

Prof. Noah Fierer – University of Colorado, US
www.fiererlab.org

Searching for simplicity amidst the complexity of the soil microbiome

10:00 Coffee break

10:30 Keynote lecture

Dr. Viviane Cordovez – Netherlands Institute of Ecology, NL
www.nioo.knaw.nl/nl/employees/viviane-cordovez-da-cunha

Microbiome of disease suppressive soils: microbiology and chemistry at the plant-soil interface

11:30 Participant talks introducing their science and advertising their poster (presented on TUE afternoon) in 3'-speed talks:

P1 - Blaschkauer Mihal
P2 - Caggìa Veronica
P3 - Cazzaniga Sara
P4 - Drabesch Sören
P5 - Guan Hang
P6 - Kozjek Katja
P7 - Lusley Pauline
P8 - Malpica Nachelli
P9 - Paddock Kyle
P10 - Rogivue Aude
P11 - Sikder Maniruzzaman

12:30 Lunch break **@ Mensa, Gesellschaftsstrasse 2**

@Main building, seminar room 105

Chair: Dr. Klaus Schlaeppi (One Health UniBE)

The plant microbiome and its links to One Health

14:00 Keynote lecture

Dr. Matthew Agler – Friedrich Schiller University Jena, DE
https://sites.google.com/view/microbiosis

Microbiota-mediated disease resistance in plants

15:00 Keynote lecture

Prof. Paul Schulze-Lefert – Max Planck Institute for Plant Breeding Research, D
www.mpipz.mpg.de/schulze-lefert

Reductionist approaches to explore plant microbiota establishment and functions

16:00 Coffee break

16:30 Participant talks introducing their science and advertising their poster (presented on TUE afternoon) in 3'-speed talks:

P12 - Darbon Geoffrey
P13 - Emonet Aurélia
P14 - Gfeller Valentin
P15 - Medina Paz Francisco
P16 - Perez-Bernal Santiago
P17 - Richards Luke
P18 - Schandry Niklas
P19 - Silva Gutierrez Federico
P20 - Stalder Luzia
P21 - Stergiou-Gekenidis Maria
P22 - Thönen Lisa
P23 - van Bentum Sietske

until ca. 17:30

Tuesday 13.8.2019

@Main building, seminar room 105

Chair: Prof. Siegfried Hapfelmeier (One Health UniBE)

The gut microbiome and its links to One Health

9:00 Keynote lecture

Prof. Thomas Clavel – University Hospital Aachen/TU Munich, DE
www.ukaachen.de/kliniken-institute/institut-fuer-medizinische-mikrobiologie/forschung/ag-clavel

Host specificity of gut microbiomes

10:00 Coffee break

10:30 Keynote lecture

Prof. Emma Wetter Slack – ETH Zurich, CH
foodimmunology.ethz.ch

Immunity and the gut ecosystem

11:30 Participant talks introducing their science and advertising their poster (presented on TUE afternoon) in 3'-speed talks:

P24 - Christensen Sandro
P25 - Dhawan Aditi
P26 - González de Chávez Capilla Teresa
P27 - Kalbermatter Cristina
P28 - Misztal Steven
P29 - Mukherjee Mohana
P30 - Notter Dias Matheus
P31 - Sattari Zahra
P32 - Uddin Wasim
P33 - Warryn Louisa

Setup of Posters

12:30 Lunch break **@ Mensa, Gesellschaftsstrasse 2**

@Main building, seminar rooms 104, 105 and 106

Chair: Dr. Klaus Schlaeppi (One Health UniBE)

Microbiomes and their links to One Health

14:00 Discussion groups:

- What are the emergent questions in your research field?
- What did you learn from the other fields?
- Links of 'your' microbiome to One Health?
- Areas of collaboration?

@104: Soil group and keynote speakers with Dr. Alban Ramette
@105: Plant group and keynote speakers with Dr. Klaus Schlaeppi.
@106: Gut group and keynote speakers with Prof. Siegfried Hapfelmeier

15:00 @105: Synthesis
Discussion groups bring their key points into the plenary discussion

15:30 Poster session – odd numbers

PhDs and Postdocs introduce their research to the keynote speakers and the other participants. The session is split in two (even and odd numbers) so that participants have time to present their work and to discuss the work of others.

Coffee will be served around 4 pm.

16:30 Poster session – even numbers

17:30 Closing of the day

Wednesday 14.8.2019

NOTE: In parallel we host the public International One Health Symposium. It is not possible to attend both the Summer School and the Symposium ;-(

Workshop 1 - Scientific visualization
Dr. Miriam Quick, miriamquick.com
In this workshop you will learn the basic principles of scientific data visualization using the R package ggplot2. It will cover topics such as visual variables, design thinking, choosing the right chart, tidy data principles and how to make readable charts. This workshop is advanced graphics using R.

Blaschkauer Mihal, Darbon Geoffrey, Dhawan Aditi, Drabesch Sören, Gfeller Valentin, González de Chávez Capilla Teresa, Guan Hang, Notter Dias Matheus, Richards Luke, Sattari Zahra, Schandry Niklas, Stalder Luzia, Warryn Louisa

Workshop 2 – Microbiota analysis using QIIME2
Drs. Aeriel Belk and Claire Duvallet, qiime2.org
QIIME2 is a software environment that covers all analysis steps from raw DNA sequence to data analysis including visualization and statistical testing. In this workshop you will learn how to process amplicon sequence data (e.g. 16S rRNA gene fragments) to OTU tables and first analyses.

Caggìa Veronica, Cazzaniga Sara, Christensen Sandro, Emonet Aurélia, Kalbermatter Cristina, Kozjek Katja, Lusley Pauline, Malpica Nachelli, Medina Paz Francisco, Misztal Steven, Mukherjee Mohana, Paddock Kyle, Perez-Bernal Santiago, Rogivue Aude, Sikder Maniruzzaman, Silva Gutierrez Federico, Stergiou-Gekenidis Maria, Thönen Lisa, Uddin Wasim, van Bentum Sietske

	seminar room 104	**@Main building seminar room 105**
	Chair: Adrien Mestrot	Chair: Alban Ramette
9:30 *	Workshop 1 **Scientific visualization**	Workshop 2 **Microbiota analysis using QIIME2**
12:30	Lunch break	**@ Mensa, Gesellschaftsstrasse 2**
14:00 *	Workshop 1 **Scientific visualization**	Workshop 2 **Microbiota analysis using QIIME2**

until ca. 18:00
* Coffee will be served for individual breaks

@Grosse Schanze

18:30 Dinner

Chair: Dr. Klaus Schlaeppi (One Health UniBE)

Microbes and games

20:00 Keynote lecture

Prof. Gilbert Greub - University of Lausanne, CH
www.chuv.ch/en/microbiologie/imu-home/research/research-groups/gilbert-greub

Playing with microbes : science education and outreach

20:30 **Playing microbe games**

Thursday 15.8.2019

Workshop 3 – Microbiota analysis in R
Dr. Jean-Claude Walser, ETH, www.gdc.ethz.ch/the-gdc
This workshop combines theoretical aspects with practical exercises to better understand your microbial data. You learn the basics in microbial ecology and you will be able to explore and analyse microbiota datasets in R in a reproducible manner. Besides the basics we will have a closer look at cluster analysis and we will touch network analysis

Caggìa Veronica, Cazzaniga Sara, Christensen Sandro, Dhawan Aditi, Drabesch Sören, Gfeller Valentin, González de Chávez Capilla Teresa, Guan Hang, Kalbermatter Cristina, Malpica Nachelli, Misztal Steven, Mukherjee Mohana, Notter Dias Matheus, Paddock Kyle, Rogivue Aude, Sikder Maniruzzaman, Stalder Luzia, Stergiou-Gekenidis Maria, Thönen Lisa, Uddin Wasim

Workshop 4 – **Microbiome analysis using mOTUs**
Prof. Shinichi Sunagawa, ETH, www.micro.biol.ethz.ch/research/sunagawa
The mOTU-tool (motu-tool.org) processes shotgun sequencing data and enables to define the taxonomic profile of metagenomes, to quantify metabolically active members in metatranscriptomes and to quantify differences between strain populations using single nucleotide variation profiles. mOTUs functions with a database of mOTUs presenting operational taxonomic units that are based on 10 single copy protein- coding phylogenetic marker genes that delineate prokaryotes reliably at the species level. In this workshop, you will learn how to use the different functionalities of the tool.

Blaschkauer Mihal, Darbon Geoffrey, Emonet Aurélia, Kozjek Katja, Lusley Pauline, Medina Paz Francisco, Perez-Bernal Santiago, Richards Luke, Sattari Zahra, Schandry Niklas, Silva Gutierrez Federico, van Bentum Sietske, Warryn Louisa

	seminar room 104	**@Main building seminar room 105**
	Chair: Alban Ramette	Chair: Klaus Schlaeppi
9:00 *	Workshop 3 **Microbiota analysis in R**	Workshop 4 **Microbiome analysis using mOTUs**
12:30	Lunch break	**@ Mensa, Gesellschaftsstrasse 2**
14:00 *	Workshop 3 **Microbiota analysis in R**	Workshop 4 **Microbiome analysis using mOTUs**

until ca. 17:30
* Coffee will be served for individual breaks

Friday 16.8.2019

@Main building, seminar room 104 and 105

Chair: Dr. Klaus Schlaeppi (One Health UniBE)

9:00	Workshop 5 – **Exerscience!** **Dr. Jean-Claude Walser** (ETH, CH) www.gdc.ethz.ch/the-gdc It is time to apply the learned skills from the separate workshops. In groups of two – mixing attendees of different workshops – you will process a microbiota/microbiome data set from count tables to the graphic visualization. Each group produces an exemplified template code for one type of analysis (e.g., taxonomy profile, diversity analysis, co-occurrence patterns...) with the goal to make these code chunks as markdown files available for all course attendees. You will leave the course with code examples that are ready to be applied to your data. Coffee will be served for individual breaks	
12:30	Lunch break	**@ Mensa, Gesellschaftsstrasse 2**
14:00	Workshop 5 – **Exerscience!**	
15:30	Workshop synthesis	
15:45	Feedback, Certificates	
16:00	Summer school closure with Apéro	

Practical Information

Participants
PhD students and postdoctoral scientists with a background in biology, environmental sciences, medicine, chemistry and bioinformatics

Registration
Registration functions through the online registration form and closes by May 17th, 2019. The number of participants is limited to 40. We will review the applications to build a diverse and motivated group of attendees that is balanced with regard to gender, career stage and research topics. Accepted participants are notified by end of May and thereby they receive the payment instructions. With payment until the deadline June 15th (tbc) the participants confirm their attendance. Unconfirmed participation offers are handed to people of the waiting list. After receiving the payment we will communicate the detailed information and instructions for the summer schools (bring you own laptop, preparatory work with a poster and 3' speed talk to introduce the poster).

Workshops
Workshop participation will be assigned to balance the attendees according to the specified priorities. You need your own laptop to participate in the workshops. Make sure you have R eventually as 'R studio' installed. Further software requirements for the workshops will be communicated later.

Level of English
The course language is English and participants are expected to give a detailed talk about their work and are expected to actively take part in the discussions.

ECTS Credits
Participants having successfully completed the Summer School will receive a certificate of attendance and can obtain 2 ECTS points. 2 ECTS correspond to 50 – 60 hours of work, which covers the preparatory work (reading for keynote lectures, preparation of 3'-speed-talk and poster), 3'-speed-talk and poster presentation as well as full participation during the course. Acknowledgement of the ECTS points in the study programs at home institutions other than the University of Bern is the responsibility of the participants.

Accommodation
We have secured special rates with centrally located 3* hotels, within a short walking distance of the Summer School. Rooms are available on a first come, first served basis. Applicants can indicate if they would like to share with a specific person in the application form. Alternatively applicants can arrange their own accommodation independently at their own cost and/or commute (if applicable).

Price
Single room with breakfast: 1'300 CHF*
Shared twin room with breakfast: 1'100 CHF*
Course only, no accommodation: 540 CHF**

*Included in the price: Fee for course and course material, hotel accommodation incl. breakfast for 5 nights, lunches Mon-Fri, meals on Sunday 11 August and Wednesday 14 August and Apéro on Friday 16 August.

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Travel to Bern
Bern is easily accessible by train and has its own airport (www.bernairport.ch). In addition, there are direct trains from Zurich and Geneva Airport to Bern's main station. For those travelling via Basel Airport, there is a bus to Basel's central railway station. The train ride from Basel to Bern takes roughly one hour. There is no airport pickup service available.

Insurance
Please make sure you have health and accident insurance.

Visa
You are responsible for checking whether you need a visa for Switzerland. Please start the application process early as the visa process will take several weeks to complete. The University of Bern can issue an invitation letter and a confirmation of payment for you. However, we are unable to offer any individual assistance for the application process.

Internet
Make sure your laptop is connecting with WIFI. EDUROAM users use their account to connect to the internet. Non-EDUROAM users need a mobile phone to receive SMS and register for internet access. To activate by text message, we will provide you with a valid voucher code. *Quick user guide:* Connect your device to the access point «public-unibe». Select the menu item «Guest Login» and register with your mobile number and voucher code. You will receive your access code by text message (SMS).

Abstracts

The soil microbiome and its links to One Health

P1 - Blaschkauer Mihal - Elucidating the two-way relationships between soil bacteria and plant roots in wild and domesticated wheat.

Wild plants possess various mechanisms that enable their survival in unpredictable surroundings, differently from domesticated plants. Plants are able to interact with their immediate soil environment, thus modulating and improving their local growth conditions. The microbial community in the rhizosphere has also been recognized as an important player in the plant-soil interaction and plants have been found to affect it through exudation of primary and secondary metabolites along the ability to form symbiotic relationships with bacteria in order to improve their mutual environment. In this study, I elucidate some aspects of the two-way relationship between soil bacteria and plant roots in wild and domesticated wheat. Wild emmer and domesticated wheat genotypes in different densities were sown in the field, harvested and analyzed for its bacterial metagenome (Illumina MiSeq, two-step PCR) as well as their primary and secondary metabolites composition (HPLC) along building a novel system for in vivo analysis and comparison of root volatiles, which will then be used checked for its effects on the rhizosphere. In addition, I've studied the effects of wheat domestication trough comparison of root structures (hydroponic growth in rhizoslides), nitrogen fixation and photosynthetic rates. Next, I will move on to laboratory/greenhouse experiments in order to clarify the exact molecular basis for the observed differences in the plant's root phytobiome using gene silencing and other molecular biology methods.

P2 - Caggìa Veronica - Soil: the foundation of our food chain

One Health is an important framework looking at the connections between different biomes for the wellbeing of the entire environment. Among the groups investigating on cascading and microbiome-dependent effects on multitrophic health, I am focusing on soil and plant-soil interactions. I will investigate how common environmental chemicals (herbicides, arsenic, benzoxazinoids) affect microbiomes diversity and functioning and how these changes impact microbiome-mediated health of soils.

P3 - Cazzaniga Sara - Cover crops-associated microbiome to promote soil resilience to plant pathogens

Conventional food production is often accompanied by elevated nutrient inputs, intense pesticide applications and frequent tillage. The negative environmental implications of these practices include soil erosion and biodiversity loss. A number of promising systems are being developed to make agricultural production sustainable. Among these, cover cropping is a green and cost-efficient practice that can contribute to this goal. Cover crops are non-economic crops grown between cropping seasons to improve soil nutritional status, soil fertility and structure. Cover crops also have the potential to improve soil health by boosting microbial life.

This project is based on the hypothesis that combinations of cover crops species can promote diversity and activity of plant-beneficial soil microorganisms while deterring plant pathogens. Therefore, we will first compare the effect of individual cover crops species to that of mixtures on the soil microbiome. Furthermore, we aim to pinpoint cover crop-associated microbiomes which increase soil resilience to soil-borne pathogens.

Cover crop-associated resident (total, not necessarily active) and active fractions of microbial and metazoan communities will be investigated by amplicon-based metagenomic sequencing of ribosomal DNA and RNA. Data will be retrieved from a combination of field trials featuring different soil managements and controlled greenhouse experiments to allow ecologically valid results.
This project is supported by the Dutch government and sponsored by end users and cover-crop breeders. At completion, this project will provide them information allowing optimal use of cover crops, in line with the EU requirements for reduced reliance on chemical inputs.

P4 - Drabesch Sören - Impact of cadmium on agricultural greenhouse gas emissions
In my Bachelor and Master education, I studied Geoscience focused on Soil Science and Hydrogeology. As of April this year (2019), I started my PhD studies within the Geomicrobiology group of the University of Tübingen. The aim of my work is to identify the impact of cadmium on agricultural, microbially produced greenhouse gas emissions.
Cadmium is a highly toxic heavy metal and enters agricultural soils gradually due to the application of phosphate mineral fertilizers as cadmium is able to substitute calcium within phosphatic minerals. Because of climate change the bioavailability of cadmium in soils may change as for example a rise in temperature may reduce the binding strength of cadmium to mineral surfaces, and thus, may render cadmium more mobile in the environment. Hereby, the potential of cadmium to interact with the greenhouse-gas producing microbial community is enhanced. Cadmium may exert more toxicity on the existing soil microbiome thereby reducing greenhouse gas emissions or shifting the emission of individual greenhouse gases if certain chemical or metabolic transformations are favored over others.
Until now it is not clear how the changes in climatic conditions (elevated atmospheric CO2-concentration and temperature) will influence the biogeochemistry of cadmium in soils.
In climate controlled greenhouses, I will quantify temporally resolved greenhouse gas emissions from agricultural soils and link this emission to different climate conditions (temperature and CO2-concentration) and Cd bioavailabilities. How these two environmental stress factors will influence the dynamics of the soil microbial community in my experiments will be investigated by different omics approaches (amplicon sequencing and metagenomics/transcriptomics). The overreaching goal is to develop a mechanistic understanding of how soil microorganisms affects microbial greenhouse gas emissions from agricultural soil under combined cadmium and climate stress.

P5 - Guan Hang - Cascading health effects of arsenic at the soil-plant-human interfaces
To investigate the effect of As on the health of soil, plant and human, we investigate the cascading effects of As speciation and the contributions of involved microbes across the trophic levels. We have conducted initial experiments to be ready for the As main experiment. We spiked soils with As and incubated the soil. We analyzed the As concentrations and speciation in soil solutions to assess how long is needed until As in the pore water stabilizes. Results showed that soil incubation needs 5 weeks. The percentages of total inorganic As reached up to 94.91%, with As(V) being the predominant species. DMA(V) was the only organic species, representing 0.29 - 5.09% of the total As. After the incubation, we grew maize in the soils to assess whether maize can survive at a high As level.
We currently conduct a main experiment in which we have nine experimental groups: three soil treatments (normal soils, sterilized soils and first-sterilized soils reconditioned with microbes), and three As concentrations (0, 100 and 200 ppm). In each treatment, 10 pots with maize plants and three pots without maize will be incubated. We analyze As concentrations and speciation, trace elements and general chemical parameters such as ions, pH, DOC in pore water and soil samples. Together with other research groups, we will furthermore investigate arsenic effects on soil microbes, soil microbial functioning, and plant health.

Afterwards, the maize grains will be used to perform studies on the next trophic level to analyze As cascading health effects.

P6 - Kozjek Katja - Functional diversity of soil microorganisms

Soil ecosystem is one of the most diverse and complex ecosystems of all. It contains different microorganisms with several thousand complex functional capabilities. The functional diversity of microorganisms defines the diversity and abundance of functional genes.

Extreme climate events and changing land use influence the soil microbial community and key players behind the decomposition of organic material in soils. Due to the complexity of microbial communities in soils and lack of methods, previously it has not been feasible to study functions by soil microorganisms involved in the carbon cycle. Novel approaches, such as targeted metagenomics approach, allow us to study functional genes that regulate carbon dynamics. Functional genes are very diverse and form a very small part of the total nucleic acid pool. With so-called, sequence capture technique, where custom-designed, hybridization-based oligonucleotide probes are used, we are able to enrich and capture functional genes of interest. In this study, we aim to target functional genes that are coding for extracellular enzymes and consequently responsible for decomposition of organic matter in soils. By assigning each functional gene to a taxonomic group we are able to elucidate which groups of microorganisms are performing a particular function in the soil carbon cycle. Patterns of functional genes are crucial to understand climate change effects on future soil health and agriculture.

P7 - Lusley Pauline - Soil and cover crop: a potential resource of biocontrol agents against pea root rot caused by Aphanomyces euteiches

Leguminous present several benefits, as the reduction of nitrogen inputs because of the symbiosis with nitrogen-fixing soil bacteria. So, leguminous are strongly encouraged by the European Union Common Agricultural Policy. In Normandy, pea represents one of the major plant protein sources. However, pea is particularly susceptible to Aphanomyces euteiches, a soilborne oomycete, which can lead to the total loss of the harvest. Currently no treatment is available to counteract this pathogen, whose sexual form can survive in soil up to twenty years. Recently intensive research is focused for developing new crop protection alternatives. Some of them are based on the use of beneficial microorganisms coming from soil microbiome which can stimulate plant growth and manage plant health. Such microbes are commonly known as biocontrol microbial agents (BCAs). Furthermore, soil microbiome diversity has been shown to be influenced by many factors, particularly the plant species used as cover crop. The aim of this study was to research and isolate potential soilborne BCAs to manage pea root rot. In this goal, one hundred and forty nine bacterial strains were isolated from Normandy soils under three cover crops: pea (susceptible host) and rapeseed (non host) from one plot, and faba bean (non-susceptible host) from a second plot.

In vitro confrontation tests between A. euteiches and isolated strains revealed seventeen potential BCAs. All biocontrol strains were isolated only under rapeseed (9 strains) and faba bean (8 strains) covers. Interestingly, no BCA was found under pea cover, despite of being adjacent to rapeseed cover on the same field. Isolated BCAs have been consequently identified by 16S ADNr sequencing and characterized biochemically. In parallel, a complete analysis of the microbiome diversity under the three crops has been assessed by DNA metabarcoding analysis.

Our results revealed the importance of cover crop, as a determining factor for selection of potential beneficial microorganisms of interest and also confirm the role of crop rotation patterns as an agronomic levers of interest for the protection of crops against soil-borne pathogens.

P8 - Malpica Nachelli - Effect of biochar on soil microbial communities including AMF, in association with the yield of organic orange trees

To retain a productive and healthy horticulture orchard fertilizing is essential. Organic Orange Orchards in Mexico receive much less fertilizer input than conventionally managed ones as mineral fertilizers are forbidden and organic fertilizers are hardly available. A healthy, well-managed soil exhibits a better nutrient cycling what results in a better plant residue mineralization as well as plant nutrient uptake. This supports plant health and increases it resistance against diseases. To maintain plant productivity in low input soils soil water household, pH and soil microbiology are crucial. Biochar application could be a simple and possibly effective solution to improve soil health locally at plant roots.

The application of biochar effectively changes the physical and chemical properties of soil. The high porosity of biochar reduces the soil bulk density and increases its water holding capacity and aeration (Tryon, 1948; Laird et al., 2010). During pyrolysis Ca, Mg and K accumulate in biochar and are supposed to be responsible for soil pH elevation after biochar application (Laird et al., 2010; Van Zwieten et al., 2010). Biochar decompose very slowly in soil, with residence times of a few hundred years to millennia (Lehmann and Joseph, 2009; Zackrisson et al., 1996). The micropores of biochar may serve as niches that protect plant beneficial microorganisms such as arbuscular mycorrhiza (AMF) (Saito and Marumoto, 2002). In addition, reports confirm that biochar alters the soil microbiome and soil function (Jenkins et al., 2017).The results mentioned above suggest a significant role of biochar for beneficially altering soil properties in citrus orchards.

In the proposed project we want to assess the application possibilities of biochar in organic orange orchards in Mexico to improve plant health. We want to test locally available biochars on their effect on soil microbial communities, AMF root colonization, plant nutrient status and yield.

P9 - Paddock Kyle - Microbial Community Response to Bt in Bt-Resistant and -Susceptible Western Corn Rootworms

Bacillus thuringiensis (Bt) is a soil bacterium that exhibits insecticidal properties in a diverse set of insect pests. The crystal proteins (Cry) produced by the bacteria disrupt the peritrophic membrane of the insect gut which leads to death. Previous studies have shown the microbiota is crucial for susceptibility to Bt in Lepidopteran species, but the specific role hasn't been investigated in Coleopteran species. The western corn rootworm, Diabrotica virgifera virgifera Leconte, is capable of evolving resistance to Bt in as little as three generations. To investigate the role of the microbiome in Bt resistance, we surveyed rootworm microbiota using 16S rRNA amplicon sequencing. We compared microbial communities associated with larvae from a Bt (eCry3.1Ab) resistant colony to a susceptible control colony while feeding for 1, 3 and 5 days on Bt-expressing corn or its near-isoline analogue as a control. Microbiota richness was significantly lower in resistant insects compared to susceptible insects. The majority of insects were dominated by Wolbachia sp., yet microbial communities associated with resistant and susceptible colonies were significantly different. Feeding on Bt for one day significantly affected the community structure of susceptible insects, while no differences were seen in the resistant insects in response to Bt. These findings suggest resistant larvae may be better able to contain pathobiont infection after ingesting Bt. Identification of bacteria associated with Bt-resistance will aid in the development of new resistance management techniques and technologies.

P10 - Rogivue Aude - The Swiss alpine cheese resistome

The environment, humans, and livestock are the major sources of antimicrobial resistant microorganisms and genes. These resistances are likely transferred to human pathogens through the food chain. In this project, we focus on the resistome of Swiss alpine cheese. This cheese is unusual because it is made of raw milk and the traditional cheese-making facilities

on the alps differ from the industry in terms of hygiene. The aim of this study is to obtain a complete picture of the resistome by investigating the alpine cheese-making environment (soil, water, and manure), its fabrication chain (the milking and cheese-making equipment, the milk and the young cheese) until the mature product, to assess the risk of this foodstuff for consumers. We will couple traditional microbiology techniques with shotgun metagenomics sequencing to characterize the resistance, and better understand its prevalence among the bacterial community. Moreover, we will study how it has evolved along the cheese making production chain. The potential spread of the antimicrobial resistance genes will be assessed by the characterization of the mobile elements encoding resistance genes: the mobilome.
This applied One Health project will provide a complete picture of the antibiotic resistant bacteria and their genes including mobile genetic elements to estimate the hazard of alpine cheese as a reservoir of antimicrobial resistance.

P11 - Sikder Maniruzzaman - Are we ready to use metabarcoding to study nematode communities in agriculture?
Recent advances in next generation sequencing has accelerated the research in microbial ecology. While nematodes are the most abundant soil metazoa, the ecology of this group of organisms is poorly elucidated. One of the major reasons for nematode studies lagging behind is the lack of a reliable and validated sequencing strategy with sufficient taxonomic resolution. There are some reports on partial success on metabarcoding using DNA of nematodes extracted from soil, but nematologists fail to use this technique on environmental samples. In this study, we are validating three earlier reported and a new primer combinations for successful amplification of nematodes. We have tested the applicability of the primer sets on 26 samples of individual nematode species, 20 mock communities, 20 soil mock communities, 20 soil samples, and 10 infected plant root samples. We have successfully amplified 96 samples with four different primer combinations for Illumina MiSeq sequencing. This study will give us the most suitable primers to study nematode community in agriculture and natural environment. Based on results of this experiment, we will determine community structure on different Arabidopsis thaliana accession and different maize lines.

The plant microbiome and its links to One Health

P12 - Darbon Geoffrey - Inoculation with plant growth promoting microbes: community shifts in the potato rhizosphere.
Inoculation with plant growth promoting microbes (PGPM) is a promising strategy to improve plant resistance to water and nutrient stresses. As impressive results in controlled conditions (greenhouse, growth chambers) were obtained, the field inoculation assays have often been inconsistent in terms of results. One of the major factors explaining this is the presence of an established microbial community that will compete with the introduced microbes. This results in mitigated implantation success in many cases. With our research, we are seeking to decipher community shifts of the potato rhizosphere microbial community that were caused by inoculum application. Not only will we perform community analysis via sequencing, but also tracing of inoculants via qPCR. The aim is to associate particular community modifications with improved implantation success. We will perform these analyzes on soil from our potato field that I located in Prangins (VD). We also have another potato field in Conthey (VS) which was not inoculated with PGPMs but rather cultivated in rotation with either rye or soybean. We will monitor with our partners from Fibl how the microbial community structure is affected by rotation with these crops.

P13 - Emonet Aurélia - Spatio-temporal compartmentation of defences in A.thaliana roots

Plants can raise defences against biotic threats such as pathogens through the recognition of specific Pathogen-Associated Molecular Patterns (PAMPs), inducing the so-called “PAMP-triggered immunity” (PTI) both in shoots and roots. However, the rhizosphere contains also an extensive number of commensal and beneficial, all of them potentially detected by the roots, and it is so far unclear how plants manage to discriminate friend from foe. Such discrimination is crucial since plants also need to limit the energetic cost of defences and balance the opposing need of defence and growth. It is therefore fundamental to understand how plants regulate their immune responses in roots. This work describes the spatial confinement of defence responses and investigate whether restriction to endangered or vulnerable areas, e.g. root parts devoid of endodermal barriers or damaged sections, can explain how roots can utilize PAMP perception but avoid its constitutive activation.

P14 - Gfeller Valentin - Secondary metabolite mediated plant-soil feedbacks and their effects on health

Plant-soil feedbacks (PSFs) are known to strongly influence plant growth in diverse environments. In maize, the benzoxazinoids (BXs), a class of plant secondary metabolites, have been shown to trigger PSFs on growth and defense in a root microbiome-mediated way. But very little is known about the impact of PSFs on food quality. In a crop rotation field study, we currently investigate the maize BXs dependent microbiome-mediated PSF effects on wheat performance and grain quality. Further, feeding experiments with mice will shed light on PSF effects on consumer health. The obtained knowledge can help to promote health in soils, plants and humans.

P15 - Medina Paz Francisco - Domestication effect on the root-associated bacterial microbiota of the common bean plant

Overall, I'm interested on integrating molecular and bioinformatic tools into field ecological work to understand mechanisms that determine plant-microbe interactions under natural conditions. Particularly, my current research is about the effect that the domestication process might have had on the capacity of the bean plant to recruit its root-associated microbiota. In this work we hypothesize that common bean cultivars' (cultivated varieties product of domestication and inbreeding processes) microbiota might have a lower taxonomical and/or functional diversity than the wild common bean populations. We are currently exploring the use of different omic" approaches to address the previously mentioned hypothesis including metataxonomics and metatranscriptomics, while performing experiments under native field conditions. Currently, we are working on the development of a novel and very promising microbial mRNA enrichment method for the study of the functional and taxonomical diversity of bacterial root endophytes. In addition, we have already set up a methodology to analyze, through 16S rRNA gene amplicons, the assemblage of the endophytic bacterial community of the roots of the common bean plant.

P16 - Perez-Bernal Santiago - Mycorrhiza-faciliated bioirrigation in intercropping systems in dryland agriculture

Increasing food production in semiarid agricultural zones imposes a challenge due to rising drought events. In developing countries, intercropping is a common practice to improve yields and tackle water scarcity. A remarkable aspect of intercropping systems is Deep-rooted plants lift water from bottom soil layers which can then be utilised by shallow-rooted plants. The effective transfer of lifted water between deep and shallow roots plants could be enhanced through mycorrhizal associations. The aim of my project is to study the bioirrigation potential of common mycorrhizal networks in intercropping systems.

P17 - Richards Luke - Using microbial community dynamics to shape beneficial plant root microbiomes

With global populations constantly on the rise and most of the earth's arable land already in use, increased agricultural productivity and efficiency is one of the most important problems facing humanity. In addition, challenging public opinion and government regulation means that commercializing GM products is becoming increasingly difficult. In light of this, it is incumbent on research to explore other avenues for crop improvement.

The soil microbial community plays a major role in plant development, providing vital nutrients to roots and possibly even warding off pathogens. Understanding the effects that a given microbial community composition has on growth and development will be of great importance in the future of agriculture. Many studies have considered the molecular cross-talk between plant and microbe and how microbial communities are shaped by edaphic factors.

We aim to understand how the microbiome is affected by exogenous microbe application in order to take a step towards building a stable assemblage of microbes that act synergistically to promote plant growth.

Can a small assemblage of bacterial partners (a mini-microbiome) be compiled to promote plant growth? Does this mini-microbiome require customization depending on crop species? How does introducing an artificial microbiome affect the pre-existing soil community?

P18 - Schandry Niklas - Microbes in plant-plant interactions

Grassy crop species, including corn, wheat or rye, release secondary metabolites of the benzoxazinoid (Bx) family into soil. Bx act as allelochemicals, meaning that they reduce growth of neighbouring target plants. Bx are converted by soil-inhabiting microbes into molecules that display a higher phytotoxicity and also have antimicrobial properties. The root microbiome, in turn, is an important factor in plant fitness, as it contributes for example to the nutritional state of the plant.

I investigate to which degree the detrimental effects of Bx on target plants can be attributed to modulations of the root microbiome, and if these effects can be alleviated using defined communities. On the one hand, I use natural soils conditioned by Bx-releasing plants or by a Bx-synthesis deficient mutant. To assess genetic factors that shape susceptibility, we use these soils to grow and phenotype several hundred genotypes of the model target plant Arabidopsis thaliana. I will sequence the root microbiome of a subset of genotypes to understand its contribution to the plant phenotype. In a second approach, I make use of a collection of genome-sequenced, culturable bacteria isolated from A. thaliana roots. Screening this collection against two naturally occurring Bx, we found contrasting growth behaviours among strains and genera. Using these strains, I could to show that the allelochemicals shape synthetic communities in vitro in reproducible trajectories. Currently, I am testing if specifically designed SynComs can modulate Bx effects on target plants.

P19 - Silva Gutierrez Federico - Root microbiome dynamics in response to systemic defense activation

Interactions of plants and their surrounding microbes matters for plant health. We hypothesize that (i) root microbiota dynamically enriches specific members in response to biotic attack. Using next generation sequencing we determine bacterial composition in roots and we compare control with defense activated plants. We activate plant defenses in the systemic leaf tissue so the immune trigger is not confounding the response i.e. that microbiota shifts are plant mediated. We simulate leaf pathogen attack by spraying the defense-inducing peptide flg22, which presents the minimal epitope of flagellin (being a MAMP = microbe-associated molecular pattern). We confirmed our experimental system that flg22 foliar spray induces defenses in roots using marker gene analysis. Also, result suggests that plants re-structure their root microbiota in response to systemic defense activation. Overall, this work will

elucidate whether plants “cry for help" when being attacked and if they recruit protective microbiome members in a targeted manner.

P20 - Stalder Luzia - The functional ecology of plant microbiome interactions between Pseudomonas and the fungal plant pathogen Zymoseptoria tritici

Plants are exposed to a wide range of pathogenic bacteria and fungi. It has been shown that the outcome of individual interactions between pathogen and plant cannot be understood in isolation, as the presence of other microorganisms can act synergistically or antagonistically in the disease progression. Yet, the understanding of complex, i.e. at least tripartite interactions is largely missing. We will establish a new microbiome interaction model using tripartite interactions of bacteria, fungi and plants. For this, we focus on wheat, Zymoseptoria tritici, the major fungal pathogen of wheat, and the bacteria Pseudomonas, a dominant member of the phyllosphere. We will characterize how intra-specific variation in a fungal pathogen determines microbial activities in the phyllosphere using genome-wide association mapping. In addition, we will characterize how differential gene expression of the fungus and the bacteria influences the outcome of bacterial-fungal competition. Our results will provide insights into the mechanism of competitive exclusion in the plant microbiome. We will generate knowledge of the exact loci that fungi evolved as defenses against Pseudomonas. The identification of such previously unknown loci will likely promote the description of new antimicrobial compounds that could be assessed for agricultural and even human applications.

P21 - Stergiou-Gekenidis Maria - Tracking antibiotic resistance from the environment to the food chain

The overall aim of this project is to understand how antibiotic resistance (AR) transfers from environmental reservoirs to the start of the plant-based food chain, and then to identify which of the resistant bacteria and genes are capable of surviving on the lettuce (Lactuca sativa L.) used as a model plant, over its complete growth period.

First, an extensive field study was conducted under practice conditions in which lettuce was grown under different regimes: in soil with or without manure, and irrigated with native or UV-treated river water. The different regimes were combined to result in four treatments. Lettuce, soil, and water samples were then analyzed in a culture-dependent approach to determine presence of various AR-bacteria: ESBL-producing and carbapenem-resistant Enterobacteriaceae, multidrug-resistant Pseudomonas spp. and Acinetobacter spp., vancomycin-resistant Enterococcus spp., and fluoroquinolone-resistant E. coli and Klebsiella spp. Bacterial colonies were identified using MALDI-TOF biotyping.

After the field study, a 16S microbiome study was conducted for the different environments (plant, water, soil, manure) from the four treatment regimes, and metagenomic shotgun sequencing will be performed to unravel the resistome of the different samples at selected time points.

Finally, a controlled greenhouse experiment recreating the chain of events at the interface between environment and plant is currently performed using an ESBL-producing E. coli strain.

P22 - Thönen Lisa - Functioning of plant microbiomes in multi-trophic health

The aim of my PhD project (which is part of the One Health project) is to investigate the functioning of plant microbiomes in multitrophic health, specially focusing on the impact of benzoxazinoids, arsenic and pesticides on the plant microbiome and plant health. Using synthetic communities (selection of isolated maize root bacteria) in a controlled plant growth system, we seek to elucidate the role of single or combinations of bacterial strains plant health promotion in response to the above named environmental chemicals.

P23 - van Bentum Sietske - Selecting soybean-specific beneficial microbes for sustainable yield improvement

The demand for higher crop yields and sustainable agricultural practices calls for innovative solutions. In this endeavor, the use of plant-beneficial microbes that sustain plant health is a viable alternative. It was recently demonstrated that the model plant species Arabidopsis thaliana can adjust its root microbiome upon pathogen infection and specifically recruits a group of disease resistance-inducing microbes. In this project, we will study such microbiome-shaping capacities in soybean and aim to select soybean-specific consortia of beneficial microbes. The ability of soybean to recruit specific microbes upon infection with different pathogens will be investigated both under controlled and field conditions. The microbes that are recruited by diseased soybean plants will be isolated and assessed for their ability to protect soybean plants from diverse attackers. To explore the mechanisms of beneficial microbe recruitment, metabolite profiles in soybean roots and root exudates of control and infected plants will be analyzed. Combining metabolite profiling and microbiome data is expected to lead to effective industrialization of soybean-specific microbes, thereby providing soybean growers with a novel, stable biocontrol product applicable in the field.

The gut microbiome and its links to One Health

P24 - Christensen Sandro - Establishing a 2D Mouse Enteroid Monolayer Culture System to study the microbiota-host interactions

In my medical thesis project, I am trying to establish a 2D mouse enteroid monolayer to have a screening tool of bacterial metabolites derived from an E.coli mutant called E.coli HA107, which is an auxotrophic strain that enables scientist to set up a reversible colonization system in germ-free mice. With the establishment of a 2D mouse enteroid monolayer, we want to gain insights in the mechanisms of how bacterially produced metabolites influence the gene expression profiles of the intestinal epithelial layer and affect the innate immune response. For that, we will use different methods as quantitative polymerase chain reaction (qPCR) to measure gene expression, chromatin immune precipitation to elucidate the regulation of gene expression as well as others.

P25 - Dhawan Aditi - Temperature sensing mechanism in M.tuberculosis and its role in pathogenesis

Rise in ambient temperature has shown to increase bacterial pathogenesis and disease burden in populations. This indicates that bacteria can respond to an external cue like temperature. Many pathogenic bacteria modulate their virulence and persistence-governing genes in response to increase in temperature. Thus, with increasing global temperature it is crucial to understand the role temperature can play in pathogenesis. We are using Mycobacterium tuberculosis (Mtb) as a disease model to study temperature-mediated pathogenicity and progression of tuberculosis. In particular, we aim to analyse the molecular mechanism governing temperature-regulating genes to develop a gene-regulatory network. Presently, we have analysed gene expression in response to temperature shift in mycobacterial heat shock proteins like clpB, hsp70, groEL1 and groEL2 by real time-qPCR and identified a transcriptional reporter that responds linearly to temperature. The reporter gene is sensitive to even 1? shift in temperature. Additionally, in silico analysis of post-transcriptional modifications in the Mtb transcriptome revealed 115 potential thermo-regulated genes in Mtb and four genes unique to the pathogenic strain. Finally, we will infect mammalian cell lines with Mtb to determine the role of temperature in pathogenesis. Using whole-transcriptome approach, we will analyse the differential response of the virulence genes and

host defence to temperature change. Thereby, using the Mtb transcriptome data to build a thermo-regulated gene network.

P26 - González de Chávez Capilla Teresa - Arsenolipids: A journey through the human gut

Arsenolipids are present in seaweed, fish and crustaceans and comprise a wide range of lipid soluble species including arseno-hydrocarbons and arseno-fatty acids. The use of dietary supplements as health remedies over recent decades, has led millions of people worldwide to increase their consumption of fish oil. Although fish oil has potential benefits, it is one of the main sources of arsenolipids in the human diet, with concentrations of arsenic from 0.2 to 16 mg kg-1 oil. To date, little is known about general arsenolipid metabolism, but recent publications have shown that arseno-hydrocarbons and arseno-fatty acids are toxic to human cells. In this study, the metabolism of arseno-hydrocarbons and arseno-fatty acids in humans was evaluated. The in vitro gastrointestinal digestion of the arsenolipids present in krill oil and hijiki seaweed revealed that arseno-hydrocarbons and arseno-fatty acids are likely to enter the liver unchanged. The subsequent exposure of human liver cells to arseno-hydrocarbons and arseno-fatty acids provided insight into the main metabolic products of these arsenolipids. While this study did not considered the microbiota present in the human gut, it serves as a starting point to understand the fate of these arsenic species after human consumption.

P27 - Kalbermatter Cristina - The role of maternal microbiota in durably shaping intestinal immunity and gene expression in the offspring through epigenetic mechanisms

Postnatally acquired microbes shape host immune development. However, recent findings reveal that already microbial signals of the maternal microbiota during pregnancy remarkably affect the neonatal immune system. Using an auxotrophic E. coli strain, it is possible to reversibly colonise pregnant dams during gestation and hence distinguish between the contribution of maternal microbiota from the influence of postnatal colonisation. We hypothesise that microbe-host interactions during gestation shape neonatal immunity by altering its epigenetic landscape and thus having a lifelong effect. We were able to show that the expression of enzymes, modifying histone tails or the DNA methylation pattern itself, were increased in pups born to germ-free dams compared to pups born to gestation-only colonised mice. For instance, the expression of several histone deacetylases was significantly increased in 16 day-old embryos and 14 day-old pups from germ-free mothers. These data indicate a potential influence of the maternal microbiota on epigenetic remodelling in utero, notably on histone deacetylases. We next aim to assess differences in H3K4me3 between intestinal epithelial cells isolated from offspring born to transiently colonised or germ-free dams using chromatin immunoprecipitation. We expect to observe alterations in genes important for epithelial cell homeostasis and antimicrobial peptides, which were differentially expressed in a previous RNA sequencing analysis. Our research will reveal essential insights into epigenetic mechanisms as a result of interactions between maternal microbiota, the embryo, and the neonate. It will increase the knowledge about the importance of maternal colonisation during pregnancy for neonatal health and display its durable consequences.

P28 - Misztal Steven - Mechanisms of early life host microbial mutualism

In recent years, microbiome research received high attention as the pervasiveness of microbiota effects on host constitution throughout all life stages became evident and numerous commensals were described as harmful or commercialized for probiotics. In the intestine the diversity and complexity of species interaction explodes with onset of weaning and remains highly dynamic in adults. Inevitably the question arises, to what extend the dominant initial colonisers, like Lactobacillus, direct subsequent species succession and prime immune development during this particular sensitive host period termed 'neonatal-window-of-

opportunity'. Due to the high community complexity it so far was impossible to unambiguously link single pioneer species to observed effects. To address this challenge, we constructed a Lactobacillus reuteri strain which is only able to transiently colonise the mouse intestine and the germ-free status of animals is reacquired without intervention after a defined time. We will use this model in conjecture with state-of-the-art techniques to disentangle effects of neonatal L. reuteri colonisation on a newly constructed defined microbiota, clarify underlying mechanisms from bacterial and host side contributing to observations, and elucidate the time window notably contributing. Finally, we will use this basic knowledge to test long-term implications for health.

P29 - Mukherjee Mohana - Direct and microbiota mediated effects of arsenic on mammalian host

Arsenic (As) is a metalloid widely distributed in the environment in various organic and inorganic forms. Exposure to As poses a great risk to human health, causing cancer, metabolic disorders and even death in cases of acute poisoning. Moreover, it has been classified as a Group I carcinogen by the IARC (International Agency for Research on Cancer).

Food and water constitute the most common sources of exposure of the mammalian host to this naturally occurring xenobiotic. The mammalian body has its own mechanisms to metabolize and deal with the ingested As, whereas, trillions of bacteria residing within the mammalian gut also interact with the host ingested As. There have been in vitro studies demonstrating the potential of various members of the gut microflora to metabolize As. The microbiota mediated metabolism leads to the production of various species and chemical forms of As which, in turn, affects the bioaccessibility of this metalloid at the gut epithelial surface. Hence, the gut microflora might exacerbate or mitigate the toxic effects of As on the mammalian system by producing As metabolites of variable toxic potentials. We are therefore interested to learn how the presence of microbiota might affect the As metabolism within the gut and thereby, modulating the overall toxic effects of this element on the host.

P30 - Notter Dias Matheus - Effects of Diet containing Benzoxazinoids on our Health

Through a plant-containing diet, the mammalian organism is exposed to a huge diversity of secondary plant metabolites. Secondary metabolites are overall poorly defined and our knowledge of their function for the plant is still incomplete. Apart from well characterized plant toxins, their roles as dietary components in mammalian biology and health is mostly unknown. Nonetheless many are considered to underlie health-promoting effects ascribed to plant food products. Benzoxazinoids (BXs) are a group of secondary metabolites produced by important crops plants including rye, wheat and maize, and therefore present in the daily grain based diet of most humans. It was shown that BXs that are exudated by the roots in high quantities promote plant immunity and resistance to generalist insect herbivores through modulation of the root microbiota. However, the direct effects of dietary BXs or the indirect effects of the BX-induced plant immune/resistance phenotypes on the plant eater are unknown. By comparing the effects of BX-free and BX-supplemented experimental diets, and the feeding of BX-competent and BX-deficient plant material in mice, we wish to pinpoint the direct and indirect (by changing the plant phenotype) effects of BX metabolites on gut microbiota and host intestinal immunology and health. Our experimental tool set includes gnotobiotic mouse models that allow a rigorous multi-omics approach.

P31 - Sattari Zahra - Polyfermenthealth – Linking bacterial diversity in fermented food to metabolic health

Fermented foods are highly capable of contributing to nutrient and microbial biodiversity due to an improved nutritional profile resulted from fermentation. PolyFermentHealth project intends to demonstrate that the genetic potential contained in collections of lactic acid bacteria can be translated, via fermented food, into diverse and beneficial metabolic profiles in vivo. In brief, the collection of sequenced bacteria from dairy industry available at Agroscope Liebefeld will be used for the genetic screening leading to the choice of specific strains in order to produce certain metabolites. These strains will be used for the fermentation of cow milk to produce experimental yoghurts. As the next step a combination of in vivo techniques will be applied, using axenic animal models, next generation sequencing technologies and 'Omics'-based approaches such as 16S ribosomal sequencing, metagenomics, metatranscriptomics, metabolomics and host RNA sequencing in order to discover new mechanisms involved in the interactions between the beneficial exogenous microbes, the produced yoghurts and the host organism in order to maximize the health properties of these foods. The results from Polyfermenthealth project will pave the way for the food industry to develop a new generation of products with nutritional claims. In the long term, Polyfermenthealth will contribute to a targeted use of bacterial resources and food matrices to deliver nutrients that contribute to human metabolic health and increase in the added value of dairy products

P32 - Uddin Wasim - One Health: Methodological Standardization for Microbiome Investigation Across Compartments

In order to standardize microbiome investigation across different compartments (i.e. soil, root, mouse, cow, human), we performed a comparative experiment including samples from soil, plant-root, mouse, cow and human but also defined bacterial community (mock community). Testing compartment specific DNA extraction kit against a common kit (suggested by Earth Microbiome Project) and four universal bacterial specific primer pairs, we showed that extraction kit has marginal effect compared to choice of primer pair and sample compartment on microbial alpha and beta diversity. We streamlined and validated bioinformatics pipeline (i.e. DADA2) and statistical analyses for microbiome investigation across compartments. Furthermore, our designed common microbiome response experiment against chosen factors such as arsenic, pesticide, plant secondary metabolites, is underway. In this experiment, we will test our standardized methods to understand, if chosen factors can influence the microbiome of different compartments.

P33 - Warryn Louisa - Prevention and control of Mycobacterium ulcerans infections

My current research is based on developing new immunodiagnostic tools and identifying novel treatment options for Buruli ulcer (BU). BU - or Mycobacterium ulcerans disease - is a disease of skin and soft tissue which results in chronic progressive ulceration that could lead to disabilities and possible but rare mortality from secondary infections. The polyketide toxin, mycolactone, is the key virulence factor of M. ulcerans and is responsible for the pathological features of BU. It is currently not known how BU is contracted although an environmental source of infection is strongly indicated. This knowledge gap makes prevention next to impossible, especially since there are no effective vaccines for BU. Current control measures hinge on treatment of all cases, which is contingent upon early diagnosis. Another aspect of my research is to study the ecology of M. ulcerans to try to understand transmission routes. This is, however, hampered by the extremely slow growth of the organism, which make direct isolation from environmental sources problematic. Nonetheless, identifying the environmental niche of M. ulcerans and understanding the interactions of the bacterium with the biotic and abiotic factors in this niche will help to inform prevention measures for this disease

Email

Lastname	Firstname	University/Institute	Email
Organization			
Bont	Zoe	University of Bern, CH	zoe.bont@ips.unibe.ch
Erb	Matthias	University of Bern, CH	matthias.erb@ips.unibe.ch
Hapfelmeier	Siegfried	University of Bern, CH	siegfried.hapfelmeier@ifik.unibe.ch
Mestrot	Adrien	University of Bern, CH	adrien.mestrot@giub.unibe.ch
Ramette	Alban	University of Bern, CH	alban.ramette@ifik.unibe.ch
Schlaeppi	Klaus	University of Bern, CH	klaus.schlaeppi@ips.unibe.ch
Wetter	Nichole	University of Bern, CH	nichole.wetter@ips.unibe.ch
Speakers			
Agler	Matthew	Friedrich Schiller University Jena, DE	matthew.agler@uni-jena.de
Clavel	Thomas	University Hospital Aachen/TU Munich, DE	tclavel@ukaachen.de
Cordovez	Viviane	Netherlands Institute of Ecology, NL	v.cordovez@nioo.knaw.nl
Engelhardt	Britta	University of Bern, CH	britta.engelhardt@tki.unibe.ch
Fierer	Noah	University of Colorado, US	noah.fierer@colorado.edu
Greub	Gilbert	University of Lausanne, CH	Gilbert.Greub@chuv.ch
Meyer	Heike	University of Bern, CH	eike.mayer@giub.unibe.ch
Reffert	Susanne	University of Bern, CH	sreffert@itp.unibe.ch
Robert	Christelle	University of Bern, CH	christelle.robert@ips.unibe.ch
Schulze-Lefert	Paul	Max Planck Institute for Plant Breeding Research, DE	schlef@mpipz.mpg.de
Sunagawa	Shinichi	ETH Zurich, CH	ssunagawa@ethz.ch
Walser	Jean-Claude	ETH Zurich, CH	jean-claude.walser@env.ethz.ch
Wetter Slack	Emma	ETH Zurich, CH	emma.slack@hest.ethz.ch
Quick	Miriam	Data journalist + researcher	miriamquick@gmail.com

Lastname	Firstname	University/Institute	Email
Participants			
Blaschkauer	Mihal	Ben Gurion University, IL	miblasch@gmail.com
Caggìa	Veronica	University of Bern, CH	veronica.caggia@ips.unibe.ch
Cazzaniga	Sara	Wageningen University and Research, NL	sara.cazzaniga@wur.nl
Christensen	Sandro	University of Bern, CH	sandro.christensen@students.unibe.ch
Darbon	Geoffrey	Louvain-la-neuve, BE	geoffrey.darbon@agroscope.admin.ch
Dhawan	Aditi	TERI School of Advanced Studies, IN	aditidhawan.17@gmail.com
Drabesch	Sören	University Tübingen, DE	soeren.drabesch@ifg.uni-tuebingen.de
Emonet	Aurélia	University of Lausanne, CH	aurelia.emonet@unil.ch
Gfeller	Valentin	University of Bern, CH	valentin.gfeller@ips.unibe.ch
González de Chávez Capilla	Teresa	University of Bern, CH	teresa.gonzalez@giub.unibe.ch
Guan	Hang	University of Bern, CH	hang.guan@giub.unibe.ch
Kalbermatter	Cristina	University of Bern, CH	cristina.kalbermatter@dbmr.unibe.ch
Kozjek	Katja	Lund University, SE	katja.kozjek@biol.lu.se
Lusley	Pauline	UniLaSalle, FR	pauline.lusley@gmail.com
Malpica	Nachelli	Forschungsinstitut für biologischen Landbau, CH	nachelli.malpica@gmail.com
Medina Paz	Francisco	CINVESTAV Unidad Irapuato, MX	francisco.medina@cinvestav.mx
Misztal	Steven	University of Bern, CH	steven.misztal@dbmr.unibe.ch
Mukherjee	Mohana	University of Bern, CH	mohana.mukherjee@ifik.unibe.ch
Notter Dias	Matheus	University of Bern, CH	matheus.notter@ifik.unibe.ch
Paddock	Kyle	University of Missouri-Columbia, US	paddockk@missouri.edu
Perez-Bernal	Santiago	University of Basel, CH	santiago.perezbernal@unibas.ch
Richards	Luke	University of Warwick, UK	Luke.Richards.1@warwick.ac.uk
Rogivue	Aude	Agroscope, CH	aude.rogivue@agroscope.admin.ch
Sattari	Zahra	University of Bern, CH	zahra.sattari@dbmr.unibe.ch
Schandry	Niklas	Gregor Mendel Institute of Molecular Plant Biology, AT	niklas.schandry@gmi.oeaw.ac.at
Sikder	Maniruzzaman	Aarhus University, DK	mms@agro.au.dk

Lastname	Firstname	University/Institute	Email
Silva Gutierrez	Federico	University of Bern, CH	federico.silva@ips.unibe.ch
Stalder	Luzia	University of Neuchâtel, CH	luzia.stalder@unine.ch
Stergiou-Gekenidis	Maria	Agroscope, CH	maria.stergiou@agroscope.admin.ch
Thönen	Lisa	University of Bern, CH	lisa.thoenen@ips.unibe.ch
Uddin	Wasim	University of Bern, CH	wasim.uddin@ifik.unibe.ch
van Bentum	Sietske	Utrecht University, NL	s.vanbentum@uu.nl
Warryn	Louisa	Swiss Tropical and Public Health Institute, CH	louisa.warryn@unibas.ch