

National Centre of Competence in Research Microbiomes

Phase I Overview
2020-2024



Summary

The Swiss National Centre of Competence in Research (NCCR) Microbiomes established in 2020 aims to harness microbial communities for human health, agriculture, environmental protection, and industry.

We bring together leading experts in human, animal, and plant microbiomes, genomics, computational biology, and microbial ecology to uncover the rules governing microbiome function, develop tools to assess their status, and create strategies to restore balance when disrupted.

Our research spans diverse environments from human and animal bodies to plants, soils, and industrial systems, and integrates methods from computer modelling and engineering to synthetic biology.

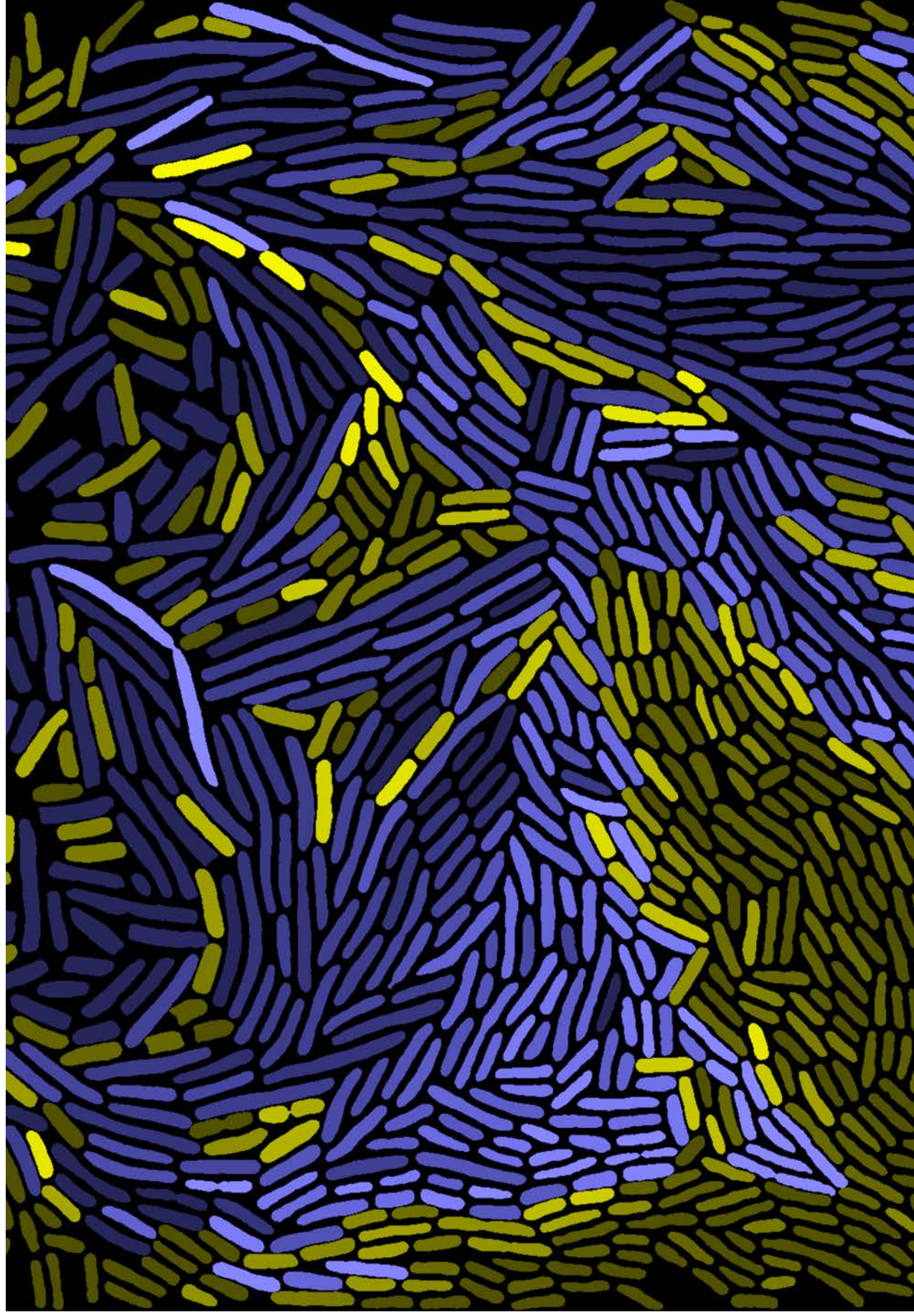
During our programme's first phase (2020-2024), we investigated the fundamental principles of microbiome engineering by examining how individual microbial species can be introduced or

eliminated from complex microbial communities. While conceptually straightforward, this targeted approach yielded profound insights into the mechanisms governing microbiome assembly and stability.

These foundational studies delivered tangible advances on multiple fronts: enhanced diagnostic capabilities, more accurate predictive modelling frameworks, and essential groundwork for microbiome interventions planned in subsequent phases.

In Phase I, the NCCR Microbiomes comprised 24 research teams in institutions across Switzerland: the University of Lausanne (leading institution), ETH Zurich (co-leading institution), EPF Lausanne, the University of Zurich, the University of Bern, and CHUV Lausanne University Hospital.

The NCCR Microbiomes is funded by the Swiss National Science Foundation.



Microscopic image analysis reveals how two different bacterial strains, yellow and blue, interact and influence each other's growth. Dal Co Lab, UNIL

Table of Contents

Directors' Message

From an Idea to a Successful Research Consortium	5
--	---

Research

Unlocking the Microbiome	9
Microbiome Formation	10
Microbiome and its Host/Environment	12
Health and Dysbiosis	15
Microbiome Engineering	17
Microbiome Diagnostic and Intervention Tools	18

Community

Shaping the Future of Microbiome Science in Switzerland	20
NCCR Women Campaign	22
Scientific Conferences	24

Innovation

Sharing Knowledge, Data, and Tools	26
Clinical Applications and Startups	28

Society

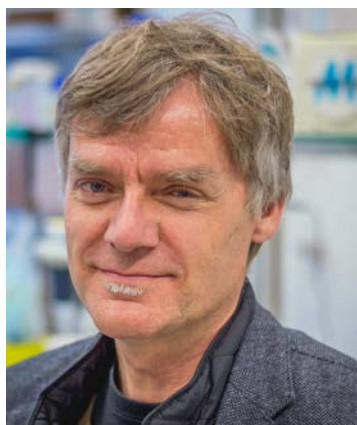
Public Health Engagement	30
Microbiology Literacy	33
Museum Exhibition: INVISIBLES. La vie cachée des microbes	35

Organisation

Directors, Management, and Principal Investigators	36
In Memoriam	39

References

Featured Publications	41
-----------------------	----



The NCCR Microbiomes directors team (clockwise from top left): Director Jan Roelof van der Meer, University of Lausanne; Co-Director Julia Vorholt, ETH Zurich; Deputy Co-Director Emma Wetter Slack, ETH Zurich; Deputy Director Philipp Engel, University of Lausanne.



The NCCR Microbiomes team

Directors' Message

From an Idea to a Successful Research Consortium

When we first considered submitting a proposal for the fifth call of the National Centre of Competence in Research (NCCR) in 2017, our goal was to enhance and unite microbiology research across Switzerland as well as strengthen collaboration between groups in the Romandie and German-speaking regions. While the term "microbiome" had been in use within the scientific community for about a decade at that time, it was just beginning to emerge more widely in public discourse, with its broader conceptual implications still developing. We recognised that microbiome research offered exceptional potential as the unifying scientific theme we sought - one that could bridge disciplinary boundaries and establish Swiss research as a prominent player in this rapidly expanding field.

Microbiologists have always known that microorganisms are all around us. Yet, traditional training emphasised studying them in isolation - in pure cultures. In contrast, microbes are almost never found alone in their natural environments. Instead, they exist within intricate communities composed of numerous different species, each influencing the others in ways we are only beginning to understand. Studying microbes in their full ecological and functional complexity, with all their intricate interactions, metabolic interdependencies, and emergent properties, remained a formidable challenge. This undertaking is too ambitious for any single research group to tackle alone. But it is precisely the kind of transformative, multidisciplinary endeavour that a large, long-term research consortium like an NCCR is uniquely positioned to address.

Studying microbiomes means working with inherently complex systems - systems composed largely of invisible life forms. To do so effectively requires advanced tools and methods that can distinguish between all microbial species in a given habitat or host, track microbial activity and interactions with each other and their hosts, and develop models that explain how these systems function and

predict future behaviour. It is also crucial to understand how microbes modify their environments through metabolic activity, and how microbiomes adapt to a changing climate.

Microbes thrive in essentially every part of our planet, even in the most hostile environments. They are found in the deep sea, in soil, on and in plants and animals, and in our own bodies. Life as we know it fundamentally depends on microorganisms. To truly understand the world, we must understand their roles and embrace the microbial perspective. Through their collective actions, microbes drive ecosystem functioning, the major elemental cycles, and the transformation of greenhouse gases on our planet. Yet, we remain disproportionately focused on the relatively small number of microbes that cause disease. While this focus is justified, it overlooks the vast majority of microbes that play beneficial, and even essential, roles in maintaining planetary health.

This broader perspective defines the mission of the NCCR Microbiomes. It is why we founded a large, well-integrated consortium with overlapping research interests to bring together all the necessary areas of expertise, and spark collaboration. We needed researchers willing to move beyond their individual disciplines, learn from one another, and create something greater than the sum of its parts.

Launching the consortium right in the midst of the lockdowns caused by the pandemic was challenging. Yet, we found innovative ways to communicate and collaborate, building an extraordinary team. A team ready to take on the complexity of microbiome research. We embarked on this journey with the vision of delivering significant benefits for human, animal, and plant health, and for the health of our planet.

Jan Roelof van der Meer & Julia Vorholt
Directors NCCR Microbiomes



Bacterial cells produce colonies when they multiply on the surface of agar plates; different species can have strikingly different colours. Daniel Garrido Sanz, Keel Lab UNIL

24

Research Groups

53

Research Projects

Institutional Collaborations

Across 6 partner institutions
the University of Lausanne (leading house), ETH Zurich (co-leading house),
EPF Lausanne, the University of Zurich, the University of Bern,
and Lausanne University Hospital (CHUV)

118

Researchers

31.2 MCHF

Total Phase I Funding
16.1 MCHF from SNSF

Gender Balance

45% of NCCR Microbiomes PhD students
were women

33% of the PIs were women

2 Spin-off Projects

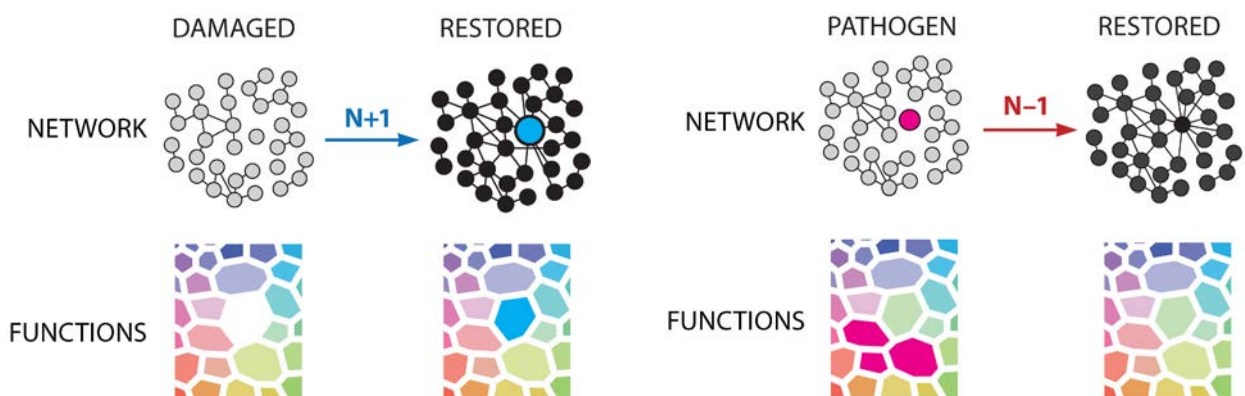
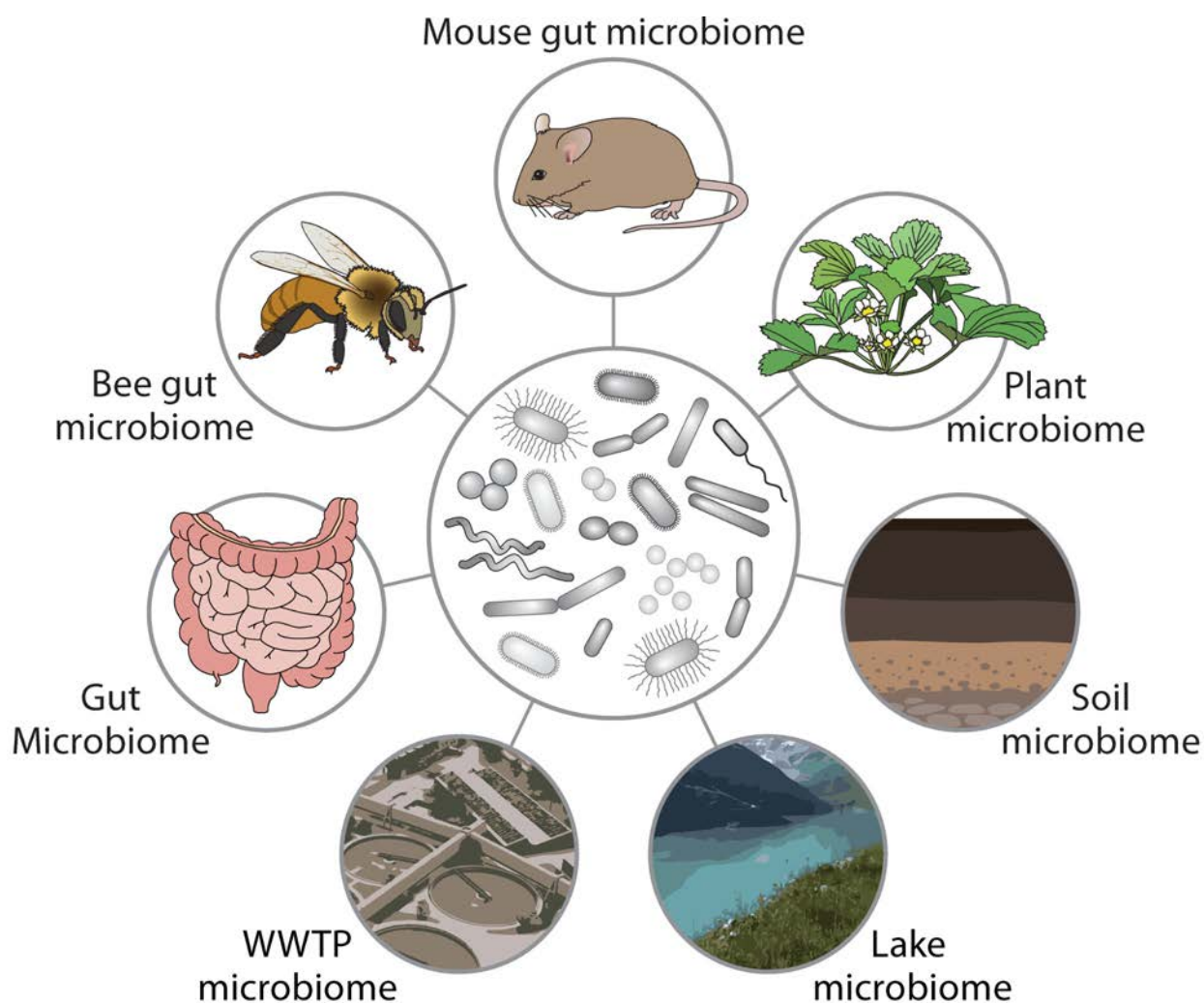
Created and supported

Open Science

133 Publicly shared datasets

86 Publications

Major peer reviewed articles
Freely accessible to all



Top: All habitats (environments and hosts) are occupied by microbiota, different assemblages of microbial cells and species, collectively forming the microbiomes. WWTP: Wastewater treatment plant.

Bottom: Examples of specific applied N+1/N-1 intervention goals during Phase I research. Left: N+1 seeks to complement (blue) microbiome functions in case of damage. Right: N-1 seeks to restore microbiome functioning by reducing pathogen loads (pink).

Image adapted from [1].

Unlocking the Microbiome

From microbiome composition to functional engineering, one step at a time

Microbiomes are the diverse communities of microorganisms such as bacteria, fungi, viruses, protists, and archaea, that inhabit all environments ranging from the human body to soil, plants, and animals.

These microbial communities are crucial for maintaining the health and functionality of their host systems, influencing processes like digestion, immune function, disease resistance, and nutrient cycling. Microbiomes also play essential roles in non-host systems such as soil, water, and engineered environments, where they contribute to biogeochemical cycles, pollutant degradation, and ecosystem productivity. While mostly invisible to the naked eye, microbiomes play an essential role in shaping biological systems and ecosystems.

Microbial communities are dynamic, constantly adapting in response to their environment, and can either promote system stability or be subject to disruptions, such as in dysbiosis, an imbalance in the microbiome often linked to disease. Understanding how microbiomes form, function, and interact is critical for both advancing fundamental science and applying that knowledge to practical challenges in health and ecosystem management.

The NCCR Microbiomes aspires to advance a causal understanding of microbiome formation and functioning across scales and systems, from human and animal microbiomes to plant leaves and roots, soils, and engineered microbiomes. This knowledge will drive the ability to predict, control, and manipulate microbiomes, whether to restore a system's health and performance or to engineer new functionalities within a system.

A central strategy in the project's first phase was the use of the N+1/N-1 methodology, an experimental approach that involves adding or removing individual microbial species from a community to observe how it affects the overall microbiome. This technique allows researchers to pinpoint the specific roles certain microbes play in shaping how communities form and how stable they become over time.

By applying this method across different hosts and environments, researchers not only gained valuable insights into the inner workings of microbiome dynamics, but also helped advance the development of new tools, predictive models, and diagnostic methods for microbiome research and engineering. In this way, a common experimental framework led to both scientific discovery and practical innovation.

Understanding how microbiomes form, function, and interact is critical to applying that knowledge to practical challenges in health and ecosystem management.

Research Aim 1

Microbiome Formation

Understanding how microbiomes form, function and change dynamically as a result of their composition, their metabolic capacities and evolutionary potential

A great diversity of microbiota, the components of microbiomes, can be detected everywhere. However, in order to understand how microbiomes form and evolve, researchers first need a way to rebuild them.

One of the earliest goals of the NCCR Microbiomes was to develop reliable methods to culture complex microbiota within each of its environments - ranging from soil, plant leaves, and roots, to insect and mammalian guts - under highly controlled conditions. This would enable a systematic study of microbial community assembly: discovering which species grow first and fastest, understanding who follows and why, and comparing developmental trajectories. Are the patterns of microbiota development the same across different habitats, or do they diverge?

The solution came in the form of gnotobiotic systems: 'microbiota-depleted' habitats, whether host-associated or environmental, where microbes usually live but are absent at the outset. The consortium established gnotobiotic systems for all the environments and hosts (except human) it had chosen to work with: soil [2, 3], plant [4], fruit fly, honeybee [5], and mouse [6]. The systems provide a blank canvas that can then be selectively inoculated with defined microbial communities or undefined but diverse groups of microbes that originate from a natural habitat or host.

"We can now recompose the earliest stages of a microbiome's life and watch it develop from the ground up," says co-director Julia Vorholt. "For instance, we've taken microbial cells from their natural environment, purified them, and then reintroduced the entire community into either its original gnotobiotic habitat or a completely different

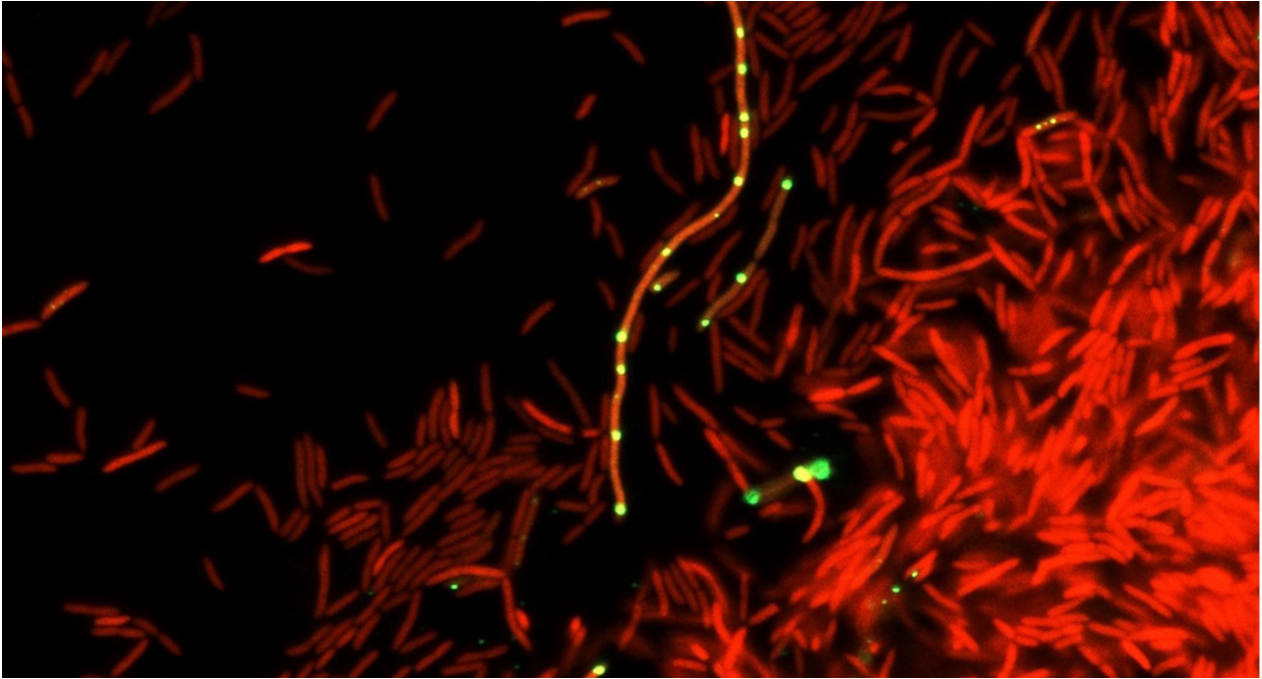
one. This lets us observe how the microbes grow and interact: who arrives first, who follows, and why. It also allows us to test how specific environmental conditions shape the development of the community".

One of the surprising findings from these studies was that even when starting with complex and diverse mixtures of microbes, microbiomes consistently developed into stable, "mature" communities within their gnotobiotic environments. This was evident in the predictable order in which species appeared over time, as well as in the final composition of the community.

The consortium also explored whether microbes could establish themselves in environments outside their original habitat. Remarkably, they found that human gut bacteria could successfully colonise a mouse's gut, some soil and plant microbes could grow in bees, and bacteria from lake water could form communities in soil that closely resembled natural soil microbiomes.

These results suggest that microbiome development is not random; in fact, both the initial mix of microbial species and the environmental conditions play a strong, deterministic role in shaping how the community forms [7].

Importantly, many of these patterns were also observed when using simplified synthetic communities (SynComs), which are made up of a smaller number of well-characterised microbes from the same original environment. This approach allowed researchers to test hypotheses about microbiome behaviour in a more controlled and reproducible way.



To better understand how different microbial species contribute to the behaviour and function of microbiomes, the NCCR built and tested a wide range of SynComs. Research groups focusing on the leaf microbiome were able to systematically vary the composition of these SynComs to study how different combinations of species performed [8].

By analysing the predicted metabolic traits of each microbe, researchers could identify which combinations gave certain species a competitive edge, and which community structures were more stable or efficient [9]. This helped not only understand the ecological dynamics of microbiomes but also begin to predict how microbial communities behave based on their composition.

To support these insights, the consortium also developed mathematical models that simulate how SynComs grow and interact within their environments, using data from the growth characteristics of individual species [10]. These efforts contributed to broader ecological theories about microbiomes, for example, the concept of "community function sharing." This idea explores how key metabolic functions are distributed among microbes: are they carried out by a few versatile generalists, or shared among many specialised species? [11, 12].

Addressing all the scientific questions required developing a suite of advanced tools and techniques to track how microbes colonise and interact within gnotobiotic systems. These included:

- Tags to identify how many and which species grow from an introduced mixture [13]
- Fluorescent reporter constructs to visualise bacterial behaviour in real host or environmental settings [14]
- Real time-resolved imaging to observe how individual bacterial cells divide and form micro-communities over time [15]
- New culturing techniques to isolate single microbial cells from complex communities under conditions that mimic natural habitats, such as the gut [16].

Together, these innovations have enabled the NCCR Microbiomes to open a path into the world of microbiome assembly, revealing not just who's there, but how they work together to build functioning communities.

Research Aim 2

Microbiome and its Host/Environment

Understanding microbiome interactions within the community, the host, and the physical environment

Microorganisms within a community do not live in isolation; different species interact with one another and with their hosts and surrounding environments in ways that evolve over time and can reshape their habitats. However, understanding these microbial interactions, especially at the species level, is a major challenge.

To tackle this, the consortium first developed new tools and methods to experimentally measure species interactions, from simple two-species tests to full community-scale systems. These methods spanned a wide range of environments and scales: from studies in plants [8, 17], to suspended cultures [18], within microfluidic devices [19], and in spatially resolved microdroplet platforms [20, 21]. This required various associated developments in experimental tools as well as image and metabolite analysis.

Then, researchers turned to genome-scale metabolic models (GEMs) to predict how species behave alone or in mixtures, based on their genome. These models, which simulate the metabolic capabilities of bacteria from their DNA sequence, are becoming increasingly vital since genome information is relatively easy to obtain for individual bacterial strains. The NCCR invested heavily in computational innovation, including models that can track metabolite exchange where metabolites from one species influences the other and vice-versa, and models that take into account the effects of cell crowding [22].

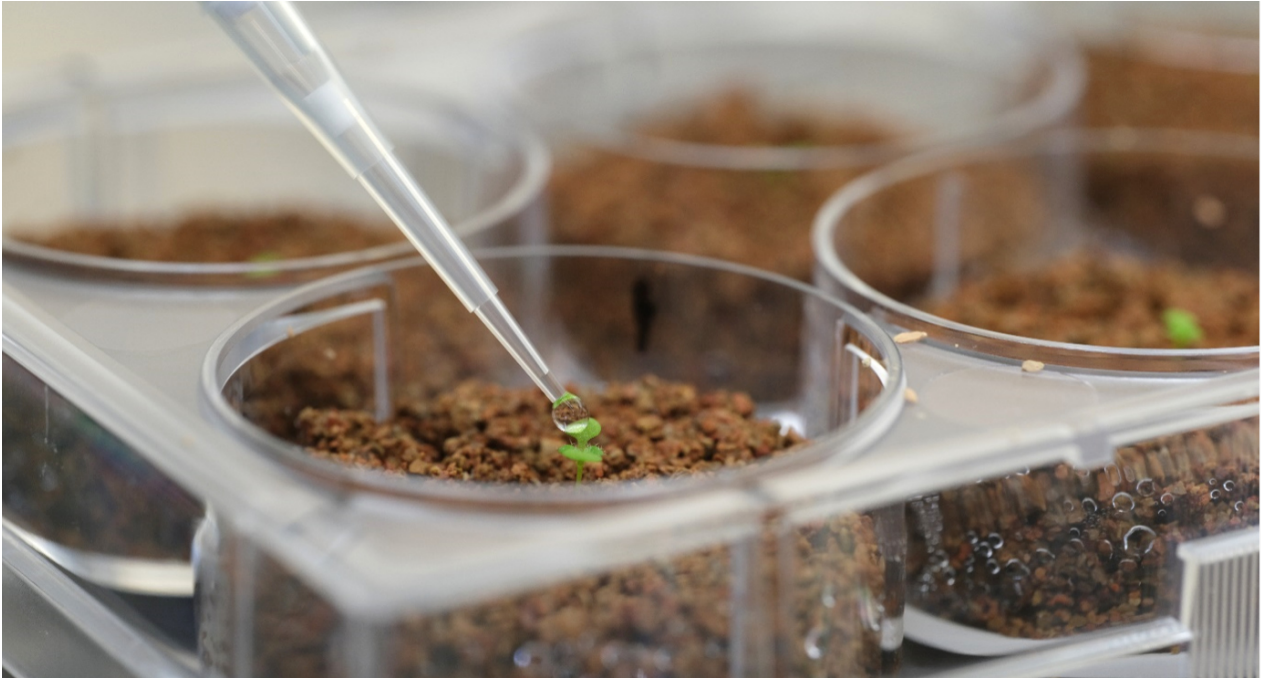
Experiments revealed that metabolic exchanges dominate many microbial interactions [23], shaping both coexistence and competition [24]. Some metabolites were found to support niche expansion, while others actively suppressed pathogen

invasion [25]. In spatially structured habitats, microdroplet experiments showed how ecological fragmentation can flip the sign of interactions thereby allowing species that would otherwise be outcompeted to persist [20, 21].

To group, describe and search species interactions and their effects, the NCCR is developing an open access interaction database [26].

Flow dynamics also emerged as a powerful influence on microbial behaviour. Using microfluidics, researchers showed how fluid movement affects the distance at which metabolic interactions take place as well as spatial organisation [27]. Meanwhile, chemotaxis (the ability of cells to move in response to the concentration of specific chemical compounds) and physicochemical gradients reshaped interspecies dynamics over comparatively large (micrometer) scales [28, 29]. In some cases, microbial competition turned aggressive, with strains deploying toxin systems against closely related competitors and potentially blocking N+1 inoculations [30-32].

These phenomena were not just observed in abstract settings; they were validated in real host-microbiome systems. In honeybees, microbial species were found to rely on host-derived short-chain fatty acids (SCFAs) to coexist [33, 34], in the mouse gut, SCFAs shaped the virulence and phenotypic behaviour of the *Salmonella* Typhimurium bacteria [25]. A newly developed non-invasive technique allowed the detection of volatile metabolites directly on whole bees or mice, enabling real-time mapping of host-microbiota interactions [35]. Additionally, gut microbiota effects on social behaviour were dissected using the honeybee model [36],



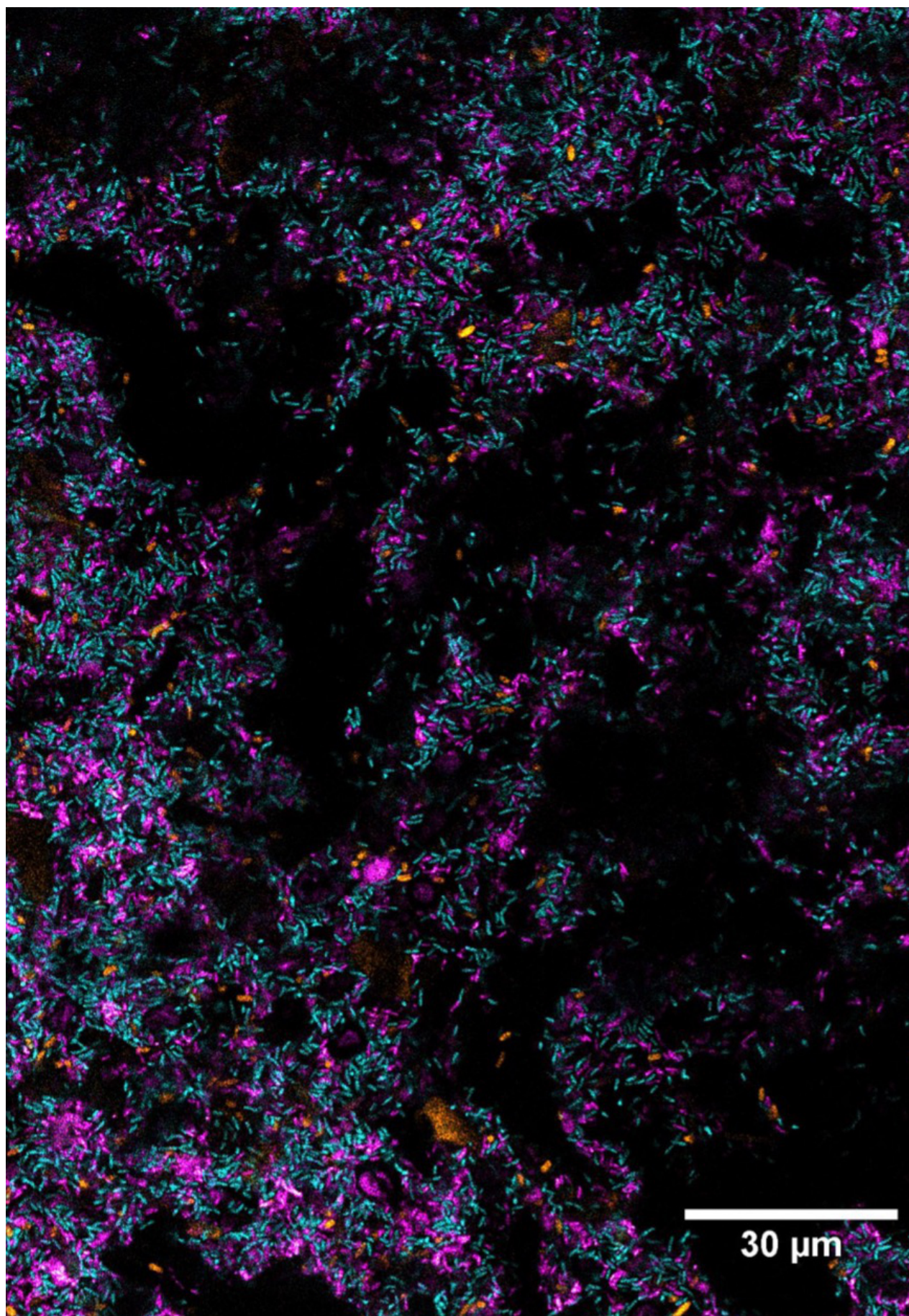
and mechanisms of bee gut colonisation were characterised [37].

In plants, microbiota induced a broad-spectrum immune reaction termed “the general non-self response” [38], while leaf microbiota composition was shown to depend on specific plant regulatory pathways [39]. Microbial strategies to block pathogen establishment, were studied across multiple systems, including the surface of plant leaves [4], mammalian gut [40-42], respiratory tissues [43], and soil [44].

Meanwhile, the metabolic modelling effort scaled up dramatically. Researchers built curated GEMs for more than 200 microbial species [9], achieving high predictive accuracy in identifying metabolic interactions between species pairs. The team’s goal is now to expand these models across all NCCR Microbiomes systems, from human gut pathogens like *S. Typhimurium* and *Clostridioides difficile*, to the bee and mouse gut, synthetic soil communities, and even engineered systems like wastewater reactors.

“We’re not just cataloguing interactions anymore,” says principal investigator Vassily Hatzimanikatis. “We’re building models that can predict them, and even guide microbiome design.”

“We’re not just cataloguing interactions anymore. We’re building models that can predict them, and even guide microbiome design.”



Three-species bacterial biofilm from a SynCom-colonised mouse gut. Fluorescent colours show the different species. Giorgia Greter, Slack Lab, ETHZ

Research Aim 3

Health and Dysbiosis

Understanding dysbiosis and microbiome stability

When does a microbiome go wrong? One of the key challenges in microbiome research is distinguishing between “healthy” and “dysbiotic” states, that is, community configurations that predispose a system to instability, illness, or loss of function.

While this concept is widely used in clinical contexts, the NCCR Microbiomes examined dysbiosis across systems, from humans and animals to soils and plants, and searched for general rules that may underlie its onset and progression.

Researchers launched several studies focused on identifying the microbial and host-related factors that drive resilience or breakdown in microbiome structure. In the clinical sphere, the team examined the gut microbiota of patients suffering from *C. difficile* or *S. Typhimurium* infections, a typical case of N+1 dysbiosis due to pathogen presence. Comparing stool samples from infected patients and healthy donors revealed clear differences in microbiota composition, and pathogen isolates were sequenced to assess genetic diversity linked to disease recurrence. These patterns were successfully replicated in mouse models, shedding light on diverse mechanisms by which pathogens can establish themselves in an already compromised microbiome [45, 46].

Beyond acute infections, the project expanded into chronic conditions. Studies began to define factors involved in lung microbiome stability [47] and early-life nutritional influences on gut dysbiosis [48]. Disruption of the small intestine microbiome, potentially caused by invading oral streptococci, has been linked to stunted growth in children [49]. Crucially, the ability to culture human-derived microbiota in mouse models now allows researchers to

experimentally test clinical hypotheses under controlled conditions.

Similar patterns of dysbiosis have been observed in non-human systems. In plants, disruptions to microbiota homeostasis were linked to specific genes in the host and shifts in microbial function, highlighting how genetic and environmental factors can interact to destabilise microbial community structure [50].

The team also experimentally induced dysbiosis using targeted environmental stressors. In bees, sublethal exposure to herbicides altered gut microbiota composition [51], while aromatic pollutants disrupted reconstructed soil microbial communities. SynCom-based experiments demonstrated that these dysbiotic states were reproducible, providing a robust framework to investigate the mechanisms behind microbial community breakdown, and potential pathways for restoration [52].

These findings lay the foundation for a predictive understanding of dysbiosis, one that moves beyond cataloguing microbial species toward mapping the conditions under which communities thrive or fail.



Beekeeping for honeybee gut microbiome studies, Engel Lab, UNIL

Research Aim 4

Microbiome Engineering

Achieving, maintaining, or restoring functional and resilient microbiomes

Once insights into the principles of formation and failure have been acquired, the next step is to intervene: to restore health, maintain balance, or even construct entirely new microbial functionalities. With Aim 4, the NCCR Microbiomes turned its focus toward the active engineering of microbiomes guided by principles learned in the earlier phases of the project.

At the core of this work is a return to the N+1/N-1 design strategy, which involves adding or removing a single microbial species to understand its impact on community behaviour. This combinatorial approach allowed researchers to identify key players in microbiome assembly and function. In plant systems, this revealed strains that strongly triggered the non-self immune response [4, 38], while in bee gut models, two potentially invasive strains out of 33 tested were identified, providing insight into mechanisms of colonisation resistance and microbial invasion.

A simplified SynCom for the mouse gut helped pinpoint how specific taxa, like *Bacteroides*, gain a fitness advantage, providing a model to test interventions for gut health and pathogen exclusion [16].

In soil and root studies, efforts focused on creating specially designed standardised systems filled with a full set of soil microbes to mimic natural conditions. These allowed plant seedlings to grow in controlled yet ecologically rich environments, making it possible to track the success of added bacteria (N+1). Plant-growth-promoting *Pseudomonas* strains not only colonised their expected niches but also outcompeted naturally occurring relatives, demonstrating the feasibility of engineering soil-root microbiomes [2, 3, 53].

Other experiments revealed the importance of community context. Inoculants designed to degrade pollutants performed well when introduced into an establishing microbiome, but failed to establish in more stable, mature ones except when they had direct access to their preferred carbon source (the pollutant). Moreover, some inoculants lost competitive fitness due to cross-feeding by surrounding soil microbes, which consumed the metabolic by-products the inoculants themselves produced [44].

To advance microbiome engineering, future strategies will need to identify organisms with precise functional traits. This can be achieved through meta-omics approaches [54], as well as by constructing SynComs optimised for target activities. Computational frameworks are emerging to support these goals, such as predictive models that integrate ecological theory, metabolic interaction data, and environmental variables to simulate system-wide outcomes [55].

With this integrated toolkit, microbiome engineering is moving from trial-and-error toward rational design, paving the way for interventions that are not only effective but ecologically informed and resilient.

Research Aim 5

Microbiome Diagnostic and Intervention Tools

Developing precision tools for microbiome assessment, restoration, and management

As our understanding of microbiome structure and dynamics deepens, the ability to accurately measure, monitor, and intervene becomes essential. With Aim 5, the NCCR Microbiomes focused on creating and refining the next generation of diagnostic and therapeutic tools, enabling precise, timely, and effective microbiome interventions in both clinical and environmental contexts.

At the heart of this effort is the challenge of identifying who is present in a microbiome and what they are doing. Traditional approaches relied on sequencing marker genes shared across microbial species, offering a broad-strokes view of microbial composition. However, the field is rapidly shifting toward full metagenomic sequencing, which captures the complete genetic information of all microbes in a sample, offering insight into not only taxonomy but also metabolic function, microdiversity, and evolutionary relationships.

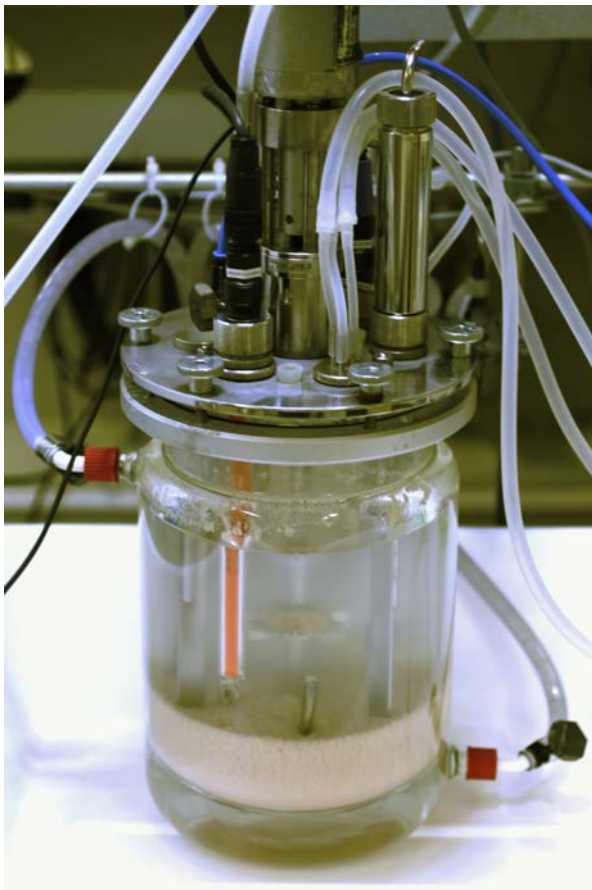
To meet this demand, researchers developed and optimised deep-sequencing workflows for both full metagenomes and targeted gene regions. These cutting-edge methods now provide high-resolution data on microbiome function [56, 57], metabolic pathways [58], and strain-level diversity [59, 60]. Computational tools, such as mOTUs, link metagenomic data to taxonomic units with greater precision, improving our ability to track microbiome changes across systems and time [61-65].

These advances were also applied to viral components of the microbiome, with expanded metagenomic analyses assessing phage diversity [66]. To support broader access and comparability, all publicly available microbiome data and metadata were standardised and made searchable

through the MicrobeAtlas Project, providing a global reference resource.

Importantly, these tools are not limited to research settings. A clinical metagenomics pipeline was established and accredited, providing a benchmark for real-world applications. This is now being compared to research-focused pipelines to optimise diagnostic workflows for patient care [67]. Additional methods under development include MALDI-TOF workflows for rapid strain identification [68] and flow cytometry-based classifiers that use multi-dimensional cell signatures to distinguish microbial populations in complex samples [69-72].

Beyond diagnostics, Aim 5 also advanced innovative microbiome-based interventions. NCCR researchers achieved key breakthroughs in understanding how mucosal immunity, the immune defence at surfaces like the gut lining, can eliminate harmful pathogens. They also investigated the potential of *Salmonella* strains, modified to be immunogenic but unable to cause disease, as candidates for oral vaccines. Building on these findings, the NCCR Microbiomes spin-off Santella is now developing oral vaccination strategies targeting enteropathogens, the bacteria responsible for intestinal infections. Another milestone was the successful clinical production and deployment of bacteriophages targeting *Pseudomonas aeruginosa*, offering a new tool to combat antibiotic-resistant lung infections [73].



*Stirred-tank sequence batch reactor operated to enrich for *Candidatus Accumulibacter*, Laëtitia Cardona, Holliger Lab, EPFL*

Finally, the consortium tested N+1 inoculation strategies, where specific microbial strains were added to existing communities to introduce new functions such as promoting plant growth bacteria [2], breaking down pollutants [74, 75], or accumulating nutrients [76]. These experiments highlighted the critical role of nutrient niches: introduced strains thrived only when they had access to their preferred resources and could outcompete the resident microbiota. The findings also showed that strategically managing nutrient availability can support beneficial inoculants while helping suppress pathogens (N-1) by enabling competition from non-harmful microbes.

Taken together, these diagnostic and intervention tools form a comprehensive platform for microbiome management. By combining omics technologies, computational models, and real-world applications, Aim 5 has laid the groundwork for precision microbiome medicine and ecology, enabling interventions that are targeted, informed, and resilient.

Community

Shaping the Future of Microbiome Science in Switzerland



SymbNET summer school on host-microbe symbioses, 2023

With over 100 researchers and 24 research teams across Switzerland, the NCCR Microbiomes consortium is building a vibrant network of scientists, from students to seasoned professors, working together to uncover the hidden world of microbial communities. This initiative is rooted in a strong commitment to supporting and training the next generation of microbiome researchers.

Young scientists, from undergraduate students to postdoctoral fellows, gain more than academic knowledge. They participate in structured programmes that combine advanced scientific training with practical, hands-on experience. Through lab exchanges, co-mentoring, and access to cutting-edge workshops in areas like bioinformatics, microfluidics, and data science, they develop the skills needed to succeed in today's complex research landscape. A strong emphasis on open science and research transparency prepares early-career scientists for a future built on collaboration and integrity.

Training at the NCCR goes beyond technical expertise. Researchers become part of an active, interdisciplinary community that fosters collaboration, creativity, and leadership. Regular events, such as seminars, annual conferences, and peer-led

discussion groups, encourage the exchange of ideas across disciplines and institutions. PhD students and postdocs are empowered to lead initiatives, build professional networks, and explore diverse career paths in both academia and industry.



NCCR Microbiomes annual meeting, 2022

NCCR Microbiomes also connects science with society. The consortium supports technology transfer and entrepreneurship, helping researchers identify commercial opportunities, collaborate with startups and industry partners, and gain experience in intellectual property, communication, and leadership. These efforts are designed to ensure that scientific



Spring school “Bioinformatics and Computational Approaches in Microbiology”, 2022

discoveries translate into real-world innovations in healthcare, biotechnology, and environmental sustainability.



Summer school, 2023

Public engagement is another central pillar. Researchers take part in science festivals, exhibitions, and interactive outreach events (Les Mystères de l'UNIL, Scientifica, Ma thèse en 180 secondes, etc.) learning to share their work in accessible, engaging ways. These activities not only raise public awareness about the importance of microbiomes but also help scientists build essential communication skills.



Mystères de l'UNIL, 2022

Through its combined focus on education, collaboration, innovation, and outreach, NCCR Microbiomes offers a rich and supportive environment for early-career researchers. It is not just about advancing microbiome science, it is about preparing the next generation of leaders to shape the future of this crucial field.

NCCR Women Campaign

On the 50th anniversary of women obtaining the right to vote in Switzerland, all NCCRs have joined forces in the #NCCRWomen campaign, which highlights the importance of women in the Swiss research landscape.

From International Women's Day on 8 March 2021 until 31 October, the date of the first federal vote in which women were able to participate in 1971, each NCCR presented a series of videos portraying the work of some of its women scientists. These short films illustrate the key roles that women play in all fields of research in Switzerland.

The NCCR Microbiomes, co-organiser of this initiative together with the NCCRs Digital Fabrication, Quantum Science and Technology, and Automation, opened the campaign on Monday 8 March. Between then and Friday 12 March 2021, five short films showed NCCR Microbiomes women scientists working on *Salmonella*, soil microbiomes or food immunology; using computational and experimental approaches; carrying out PhDs or postdocs or leading their labs.

Although there is still much work to be done, in the past 50 years many things have changed and improved. Almost half of the NCCR Microbiomes PhD students, and a third of its principal investigators, are women: the researchers portrayed in the #NCCRWomen campaign are only a very small subset of the many women that make our project possible. The NCCR Microbiomes strives to create working conditions that reduce the hurdles faced by women in science, and to promote equal opportunities among our collaborators, independently of their gender, identity, age, sexual orientation, ethnicity, religion or disability. We are grateful

for our diverse community and look forward to seeing it grow over the next years!

Discover some of the women of the NCCR Microbiomes presented in this campaign.

To see their full profiles and learn more about the #NCCRWomen from all NCCRs in Switzerland, visit our YouTube channelⁱ and the dedicated Instagram account.ⁱⁱ



In 2021, Senka Causevic is a microbiologist and PhD student at the Department of Fundamental Microbiology at the University of Lausanne. She studies how microbial communities interact in the soil.

Senka successfully defended her thesis in 2024.

ⁱ See <https://www.youtube.com/@NCCR-Microbiomes>

ⁱⁱ <https://www.instagram.com/nccrwomen/>



Emma Slack
ETH Zürich

Emma Slack is an immunologist and professor of mucosal immunology at the Department of Health Sciences and Technology at ETH Zurich. Her research focuses on the influence that microbial communities in the gut have on our immune system.



Alyson Hockenberry
ETH Zurich / Eawag

In 2021, Alyson Hockenberry is a microbiologist and postdoc at the Laboratory of Microbial Systems Ecology at Eawag and ETH Zurich. She studies host-microbiome dynamics to identify mechanisms of disease resistance.

Since 2024, Alyson is an assistant professor at the Loyola University Chicago Stritch School of Medicine.



Evangelia Vayena
EPFL

In 2021, Evangelia Vayena is a chemical engineer and PhD student at the Laboratory for Computational Systems Biotechnology at EPFL. She develops computational methods to study cellular metabolism.

Evangelia successfully defended her thesis in 2024.



Sara Mitri
Université de Lausanne

Sara Mitri is a systems biologist and professor of microbiology at the Department of Fundamental Microbiology at the University of Lausanne. Her research focuses on how microbial ecosystems evolve over time, and how they are shaped by the interactions taking place between individual microbial cells.

Scientific Conferences

The Swiss Microbiomes Forum and other significant meetings

The Swiss Microbiomes Forum (SMF) is a biennial event that brings together academic researchers, students, industry professionals, entrepreneurs, and investors for an engaging exchange around microbiome science and its wide-ranging applications.

First held in May 2022 at the EPFL Rolex Learning Center in Lausanne, and followed by a second edition in January 2024 at ETH Zurich, the SMF has quickly established itself as a leading platform for microbiome innovation and collaboration in Switzerland.

Organised by the NCCR Microbiomes, in partnership with student-led associations such as the Innovation Forum Lausanne and the Society for Women in Natural Sciences (WiNS) at ETH Zurich, the SMF is designed to foster meaningful dialogue across disciplines and sectors. With over 250 participants at its latest edition, the event continues to grow in reach and relevance.

The Forum highlights pioneering research and breakthrough technologies that explore the role of microbiomes in healthcare, nutrition, agriculture, and environmental sustainability. The 2022 edition emphasised applications in infection control, gut health, food systems, and soil fertility. In 2024, the scope expanded to include advances in diagnostics, therapeutic interventions, and strategies to conserve microbial diversity which is vital for ecosystem health.

Key features of the Forum include short scientific talks, roundtable discussions, and a start-up pitching competition that provides visibility for early-stage ventures emerging from Swiss universities and research labs. Past editions have welcomed speakers from established companies and innovative start-ups such as Ferring Pharmaceuticals, Nestlé Research, Syngenta, Pharmabiome,

Gnubiotics, REM Analytics, onCyt Microbiology, and Resistell.

Attendees consistently praise the Forum as a much-needed space for cross-sector collaboration in a fast-moving field. As one guest speaker noted, the speed of discovery in microbiome science makes events like SMF essential for aligning academic research with industrial application. It enables researchers to pose relevant questions while helping companies base their innovations on solid scientific foundations.

Following the success of its first two editions, the third Swiss Microbiomes Forum is scheduled for February 2026, returning to the EPFL Rolex Learning Center in Lausanne. As microbiome research continues to expand both in Switzerland and globally, SMF is well-positioned to remain a driving force for interdisciplinary exchange, innovation, and real-world impact.

18th International Symposium on Microbial Ecology - ISME 18

The ISME non-profit symposium is the leading conference in the field of microbial ecology. Held every other year, ISME 18 took place in Lausanne from 14–19 August 2022.

The PIs from the NCCR Microbiomes were closely involved: 14 served on the local organising committee, 7 were members of the Swiss Organising Committee, and 2 were keynote speakers.

The conference was attended by more than 2,000 delegates with several concurrent sessions each day. The programme featured 8 keynote addresses, more than 100 invited talks, over 200 oral presentations, and nearly 1,500 posters.



Swiss Society for Microbiology Annual Meeting - SSM 2022

In honour of its 80th anniversary, the SSM returned to Lausanne - the site of its first meeting - for the 2022 edition of its annual conference at the end of August.

SSM 2022 was co-organised by two NCCR Microbiomes PIs.

Five dedicated sessions were organised by the NCCR Microbiomes, including one in partnership with the NCCR AntiResist.

MEEhubs2024: A hub-based conference on microbial ecology and evolution fostering sustainability

Scientific conferences play a vital role in academic exchange, but their environmental and financial costs can be significant. Air travel contributes to greenhouse gas emissions, and travel expenses often limit participation - particularly for early-career researchers and those from low-income countries.

To address these challenges, we took part in organising MEEhubs2024, a hybrid multi-hub conference on microbial ecology and evolution. This format combined regionally based in-person meetings - held at six hubs across Europe and North America - with virtual participation, aiming to balance

sustainability, accessibility, and the benefits of face-to-face interaction.

Over three days in January 2024, nearly 900 participants joined the event, either virtually or at one of the hubs, demonstrating a promising model for more inclusive and environmentally conscious scientific collaboration.

We analysed feedback from participants and organisers to evaluate the success of the hybrid format. The organisers shared their experience to provide an example to others.ⁱ

ⁱ See <https://academic.oup.com/femsle/article/doi/10.1093/femsle/fnaf022/8003766>

Sharing Knowledge, Data, and Tools

The NCCR Microbiomes is committed to the DORA principles and Open Science.

DORA (San Francisco Declaration on Research Assessment) advocates a focus on the quality of the research output and its wider context and discourages an over-reliance on journal impact factors. Open science is about making research accessible, transparent, and collaborative. It means sharing data, methods, and results freely so others can learn from, use, or build on them. The goal is to make science more trustworthy, inclusive, and useful for everyone, not just scientists.

All datasets and publications generated by the NCCR Microbiomes are deposited in open access repositories. The project proactively organises trainings and workshops, both for its members and for the larger research community, on principles and best practices in open research.

The NCCR has several ongoing Open Science initiatives to increase the interoperability and reusability of microbiomes research.

Enabling interoperability of microbial interaction data

Mapping the interactions that occur among microbial species is key to understanding and engineering microbiomes. Synthesising microbial interaction data from the large volumes that are produced could enable ecological insights that are not achievable from individual studies. However, data on these interactions are collected by diverse methods and are stored in innumerable locations. Many datasets are not accessible, and still more are not comparable with other datasets. To make microbial interaction data more findable, accessible, interoperable, and reusable (FAIR), we have begun to design a Microbial Interactions Database.

The project has drawn participation from NCCR members across projects who use a variety of methods to observe and characterise microbial interactions.

The prototype database is under development. We hope to refine and expand it over time with contributions from researchers outside the NCCR.

Encouraging secondary analysis of microbiomes data

The goal of Open Research Data is to enable data re-use, but in the past there has not been a methodical programme for microbiomes researchers to learn about relevant methods. To meet this need, we have developed a five-week short course on secondary data analysis, offered during the spring semester through the UNIL Life Sciences doctoral programme. In its first iteration, the course drew on expertise from NCCR postdoctoral researchers with sessions on formulating research questions for secondary analysis, working with multiple raw data sets, and on systematic review and meta-analysis. Students choose their own topic for an individual research project and used methods from the course to conduct an analysis.

Although students encountered many challenges with identifying, gaining access to, and working with others' data, they saw opportunities for incorporating secondary data analysis in their own work. Moreover, the course kicked off a discussion on what is needed to overcome existing barriers to data re-use.

Name	Description	Link
MicrobeAtlas	Global-scale database for the 16S ribosomal RNA gene	https://microbeatlas.org/
mOTUs	Taxonomic profiling tool for metagenomic and metatranscriptomic samples	https://motu-tool.org/
zDB	Comparative genomics database for the analysis of clinically relevant strains	https://github.com/metagenlab/zDB
mBARq	Quantitative analysis of barcoded sequencing data	https://github.com/MicrobiologyETHZ/mbarq
NICEgame	Characterise missing metabolic capabilities in genome-scale metabolic models	https://github.com/EPFL-LCSB/NICEgame
ATLASx	Predictions of biochemical reactions and pathways for synthetic biologists and metabolic engineers	http://lcsb-databases.epfl.ch/pathways/Atlas2
CROMICS	Agent-based framework with biophysical details	https://github.com/EPFL-LCSB/cromics

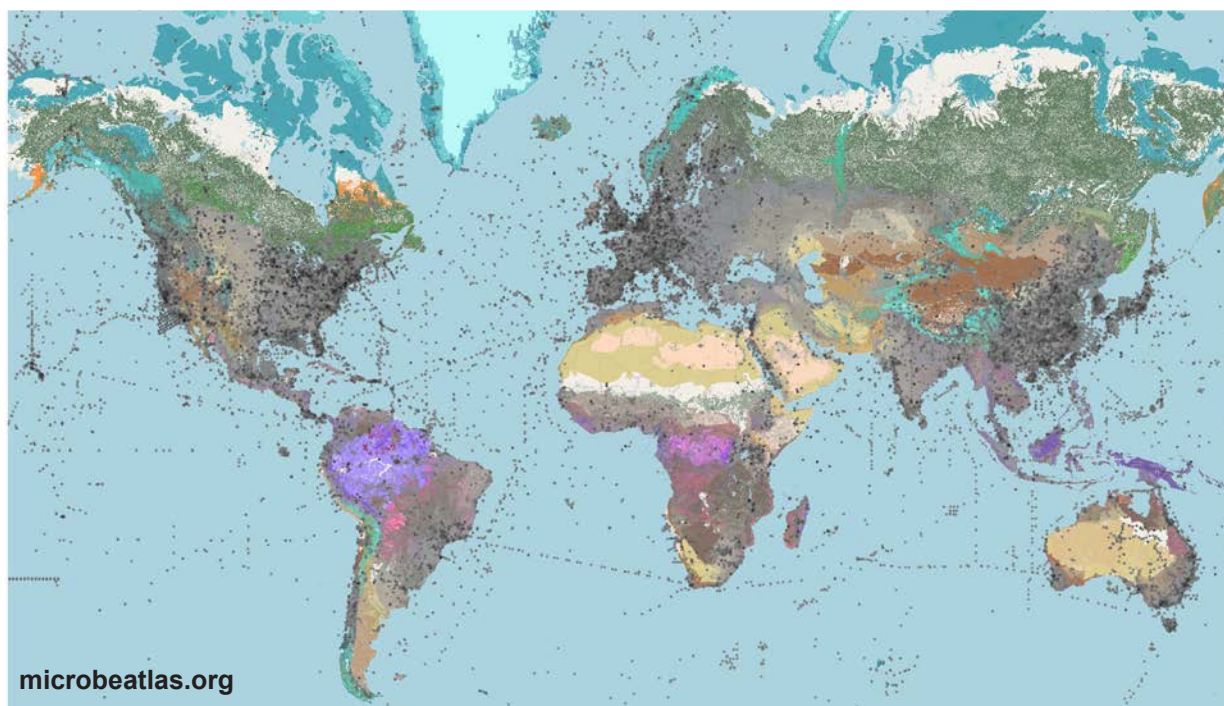
Publicly available NCCR databases and computing tools

Sharing research protocols

Detailed research protocols are essential to enable reproducibility of results. The NCCR supports researchers in developing protocols of their methods to first share internally and eventually publish publicly. Internally, sharing methods helps with training and collaboration. Publishing protocols provides a necessary link between published data and results.

Dataset indices

During Phase I, 133 dataset indices were shared publicly.ⁱ To support data findability and long-term access, 91% of major NCCR journal articles had their underlying data published in public repositories with permanent identifiers, such as DOIs. This ensures that the datasets can be reliably cited, indexed, and accessed for future research.



ⁱ www.nccr-microbiomes.ch/open-science-2/dataset-index/

Clinical Applications and Startups

Microbiome-informed strategies for treating infections

The growing understanding of microbiomes is transforming clinical approaches to infectious disease, leading to treatments that are both highly targeted and microbiome-friendly. Research within the NCCR Microbiomes consortium is driving innovation across several promising strategies now entering clinical use.

Faecal Microbiota Transplantation (FMT) has emerged as a powerful tool to treat recurring *Clostridioides difficile* infections, which often arise after antibiotic use depletes gut microbial diversity. At Lausanne University Hospital (CHUV) - the only centre in Switzerland authorised to perform FMT - patients receive capsules containing screened stool extracts from healthy donors. This therapy restores a healthy microbial balance and leads to long-term recovery in 95% of cases, far outperforming antibiotics. Once considered experimental, FMT is now a standardised treatment and a potential model for other microbiome-based therapies thanks to the work of Benoît Guery and Tatiana Galperine.

Phage Therapy is another precision approach being advanced at CHUV by G. Resch's Bacteriophage Laboratory. By using bacteriophages, viruses that infect and kill specific bacteria, or phage-derived enzymes (phage lysins), the therapy targets multi-drug resistant pathogens without disturbing the rest of the microbiota. This work earned Dr. Resch and collaborators the 2024 Leenaards Foundation Prize for translational research and continues to build clinical capacity for next-generation antimicrobials.

Oral Vaccines that Direct Pathogen Evolution offer a novel strategy for controlling infections without relying on antibiotics. NCCR PIs Emma Slack and Wolf-

Dietrich Hardt (ETH Zurich) have developed a vaccine that induces gut-specific IgA antibodies against *Salmonella* Typhimurium. The immune pressure blocks typical escape routes, forcing the pathogen to evolve into weaker, less virulent forms. This "evolutionary trap" exemplifies how rational vaccine design can guide pathogen evolution toward less harmful outcomes, ushering in a new class of mucosal vaccines applicable to both animals and humans that preserve microbiome health.

Together, these clinical approaches highlight the power of microbiome research to reshape infectious disease treatment, offering solutions that are more targeted, more sustainable, and better aligned with the body's natural microbial ecosystem.

Supporting Microbiome-Based Ventures

Alongside pioneering clinical solutions, the NCCR Microbiomes actively promotes the translation of research into practical applications through entrepreneurship. To support this, the consortium co-organises the annual Bench2Biz (B2B) workshop with its NCCR partners. Since 2019, B2B has provided a platform for young researchers to develop their technology ideas into viable business concepts, supported by expert feedback from technology transfer professionals, academics, and industry specialists. Funded by the Swiss National Science Foundation and supported by the Federal Institute for Intellectual Property, this initiative nurtures a culture of innovation and accelerates technology transfer in the microbiome field.

In this entrepreneurial spirit, two recent NCCR Microbiomes spin-offs are translating cutting-edge research into impactful solutions for animal and human health:



Santella, led by Sabrina Stöckli, Olivier Schären, and Siegfried Hapfelmeier at the University of Bern, is developing a novel live probiotic vaccine for the poultry industry. Originating from research on *Salmonella* and mucosal immunity, Santella targets avian pathogenic *E. coli*, a major threat identified by animal healthcare professionals and poultry breeders. By providing an alternative to antibiotics, Santella's vaccine aims to reduce antibiotic use in livestock and combat antibiotic resistance. In 2023, the spin-off was awarded a BRIDGE Proof of Concept grant from SNSF-Innosuisse, securing up to 130,000 Swiss francs to advance their project.

CellCognize, founded by Birge Özel-Duygan in June 2023, develops machine-learning-based approaches for rapid, simple, and affordable profiling of the human gut microbiome. Using flow cytometry data, CellCognize offers a quantitative analysis capable of distinguishing healthy from dysbiotic microbiota. This technology has been successfully validated against standard 16S rRNA gene sequencing of stool samples, positioning CellCognize as a promising and rapid tool for clinical microbiome diagnostics.

These spin-offs highlight the NCCR Microbiomes' commitment to bridging cutting-edge research and entrepreneurship, driving innovations that benefit animal health and human medicine alike.

Microbiome research reshapes infectious disease treatment - more targeted, sustainable, and aligned with the body's natural microbial balance.

Public Health Engagement

NCCR Microbiomes researchers mobilised against COVID-19

When the COVID-19 pandemic struck, it presented not only a global health emergency but also a call to arms for scientists across disciplines.

In Switzerland, several research groups from the NCCR Microbiomes rapidly redirected their expertise to help slow the spread of the virus, support public health systems, and prepare for future outbreaks. Thanks to rapid funding support from the Swiss National Science Foundation (SNSF), ETH Zurich (ETHZ), and the Lausanne University Hospital (CHUV), researchers pivoted their projects toward pandemic solutions almost overnight.

Different approaches to help contain the COVID-19 pandemic

Martin Ackermann, a professor of molecular microbial biology at ETH Zurich and now Director of Eawag, played a central role on the Swiss National COVID-19 Science Task Force. Initially vice-chair, he became chair in August 2020, helping bridge the gap between fast-moving research and government action.

Under his leadership, the Task Force intensified its collaboration with the Federal Office of Public Health, offering real-time scientific input to guide national measures. One purpose of the Task Force is to develop strategies that keep infection rates low: “It is much easier and less expensive to keep the epidemic under control when infection rates are lower than if they are high” Ackermann said in an ETH Zurich interviewⁱ. “Key for me is the belief that we can successfully beat this crisis by working together.”

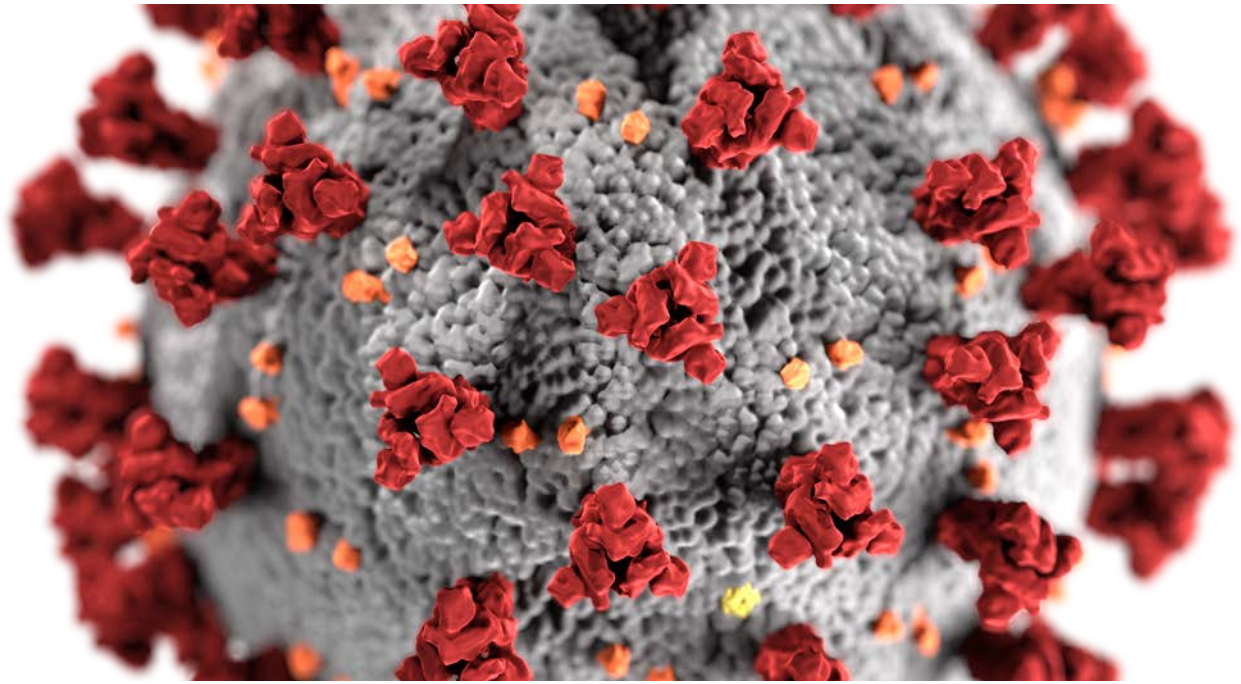
At ETH Zurich, Emma Slack and her team redirected their immunology expertise toward developing a new type of vaccine. Designed as a nasal spray rather than an injection, their candidate is intended to be simple to produce, distribute, and administer, an approach that could significantly broaden access. Beyond targeting COVID-19, the vaccine is being engineered to offer protection against a range of related coronaviruses. The team’s broader vision is to create a versatile vaccine platform that strengthens our preparedness for future outbreaks.

At the Institute of Microbiology at CHUV, led by Gilbert Greub, operations were reorganised within weeks to drastically expand COVID-19 testing. Testing capacity was quadrupled in less than a month, helping health authorities detect and isolate cases more effectively. The team also developed serological tests to detect antibodies, offering critical insights into how the virus was spreading through the population.

In parallel, Greub and infectious disease expert Benoît Guery launched a study into how the microbes in our throat, the pharynx microbiome, may influence the course of a COVID-19 infection. This research could open new avenues for personalised treatments or preventive strategies.

Behind the scenes, efforts were also underway to coordinate scientific resources across Switzerland. NCCR Microbiomes member Roman Stocker chaired the “Academic Resources for COVID” platform, which enabled universities to share lab equipment, consumables and specialised staff with the medical sector.

ⁱ <https://ethz.ch/en/news-and-events/eth-news/news/2020/07/new-head-of-the-science-task-force.html>



The impact: a stronger, more prepared society

These combined efforts spanning vaccine development, diagnostics, microbiome research, resource coordination, and science-policy integration have had a lasting impact beyond the immediate crisis. They reflect a broader lesson: in the face of global threats, scientific agility and collaboration are as vital as any medical treatment.

By investing in scalable solutions and interdisciplinary teamwork, Switzerland's scientific community has not only contributed to managing COVID-19 but also laid a foundation for responding more effectively to future health emergencies.

In the words of Martin Ackermann, "By finding solutions for the current crisis, we can also be better prepared for the next one." This spirit of preparedness, driven by evidence and united effort, is the legacy of science under pressure, and a reason for cautious optimism.

"We can successfully beat this crisis by working together... By finding solutions for the current crisis, we can also be better prepared for the next one."



Microbiology Literacy

Microbiomes, the video game and learning modules

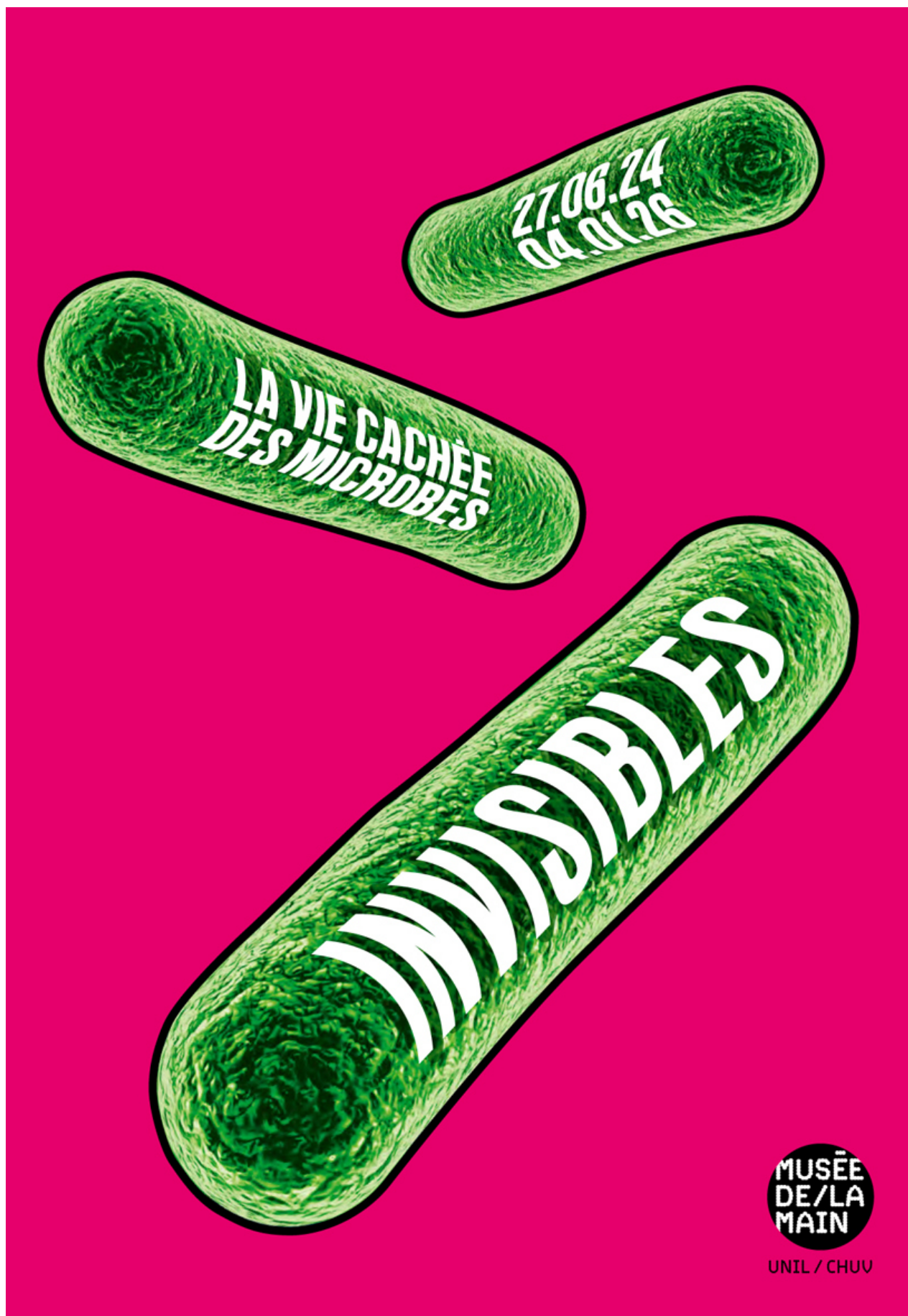
To explain microbiology and microbiome concepts in a playful manner, the NCCR Microbiomes developed the video game 'Microbiomes' in collaboration with Kobold Games GmbH.

The game was published online in 2022 and went on to become a finalist of the Swiss Game Awards that same year. Through 36 different levels and using seven different microbial characters, the players solve puzzle-like questions that illustrate how different microbes reproduce, interact with each other and respond to their environment. The video game can be downloaded, free of charge, to computers, tablets or mobile devices using any operating system.¹

A collaboration was then initiated with middle-school teacher Roxane Moritz, who holds a PhD in microbiology, to develop an educational package. Designed for use alongside the video game, this resource helps teachers introduce core concepts in biology and microbiology. The teaching modules cover several of the learning objectives defined by the educational authorities in Switzerland. In the learning modules, the video game characters guide pupils through basic biology and microbiology concepts. Teachers can use the modules in their class to introduce these concepts, which are then reinforced by carrying out the exercises presented in the modules and by playing the game. After completing two rounds of testing in the classroom, the modules in English, French, and German are now available for download for all interested teachers.¹

A finalist in the Swiss Game Awards, 'Microbiomes' brings microbiology to life through playful puzzle-solving.

¹ Game and modules available via <https://nccr-microbiomes.ch/outreach/microbiomes-the-video-game/>



Museum Exhibition: INVISIBLES. La vie cachée des microbes

An exhibition co-organised by the NCCR Microbiomes and the Musée de la main in Lausanne

Making the invisible world of microbes and microbiomes visible to everyone is the aim that has brought the NCCR Microbiomes and the Musée de la main UNIL-CHUV together. Through an interdisciplinary exhibition combining science and art, we invite the public to discover the essential role that microbial communities play in health and in the environment, from the very beginning of life on Earth.

The exhibition takes the visitors on a journey through several microbial habitats: from soils to oceans, the atmosphere or the human body. What are microbes? How do they live? How do they interact with each other and with their environment? What functions do they perform? Microbiomes are at the heart of many biological processes that are essential to the development, maintenance and even repair of the environments they have helped to shape. Their actions can be involved in decontamination, in food processing and preservation, or even in the production of biodegradable materials.

Through interactive displays, visitors can discover the complexity and dynamism of microbial life, as well as the challenges and achievements of fundamental research. Artistic installations question our relationship with the microorganisms that make up our environment and colonise our bodies. Diverse historical and contemporary creations show how the perception of microbes in society has evolved across history.

“INVISIBLES. La vie cachée des microbes” opened to the public on 27 June 2024, World Microbiome Day, and will remain open until summer 2026. A rich programme of parallel activities, including public

conferences, film screenings, experimental workshops and guided tours, further develop many topics addressed in the exhibition.

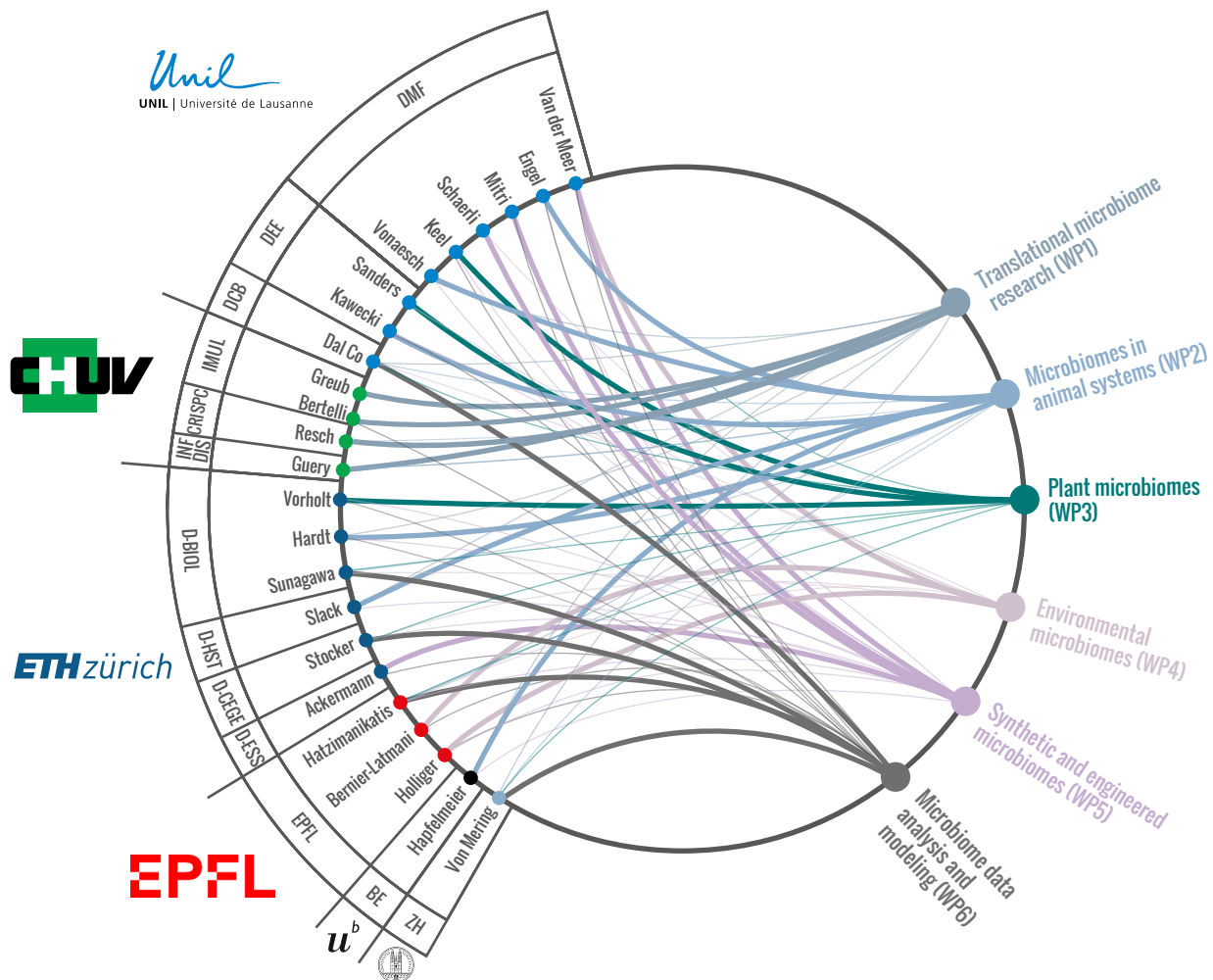
We are extremely grateful to the Musée de la main for embarking on this adventure with us, to the many scientists and artists who have made it possible, and to the institutions and foundations who have generously supported the project.

Conference cycle “Bien vivre avec les microbes ?”

A cycle of moderated conferences highlight certain topics addressed in the exhibition. During the course of an evening, invited experts help visitors dive deeper into the roles of microbial communities in the origin of life on Earth, in human health, agriculture, or in building technologies, to name but a few. The conferences are in French and open to everybody. So far, over 200 attendees have been welcomed during the course of the cycle.

Organisation

Directors, Management, and Principal Investigators



Board of Directors

- **Prof. Jan Roelof van der Meer** (UNIL), Director
- **Prof. Julia Vorholt** (ETHZ), Co-Director
- **Prof. Philipp Engel** (UNIL), Deputy Director
- **Prof. Emma Wetter Slack** (ETHZ), Deputy Co-Director

Management team

- **Dr. Robin Tecon**, Scientific and Technology Programme Manager
- **Dr. Eavan Dorcey**, Phase I Operational Manager
- **Dr. Kendra Brown**, Data Manager & Operational Manager
- **Dr. Sandra Susler**, Phase I Technology Transfer Advisor
- **Dr. Evelynne Schmid Osborne**, Communication Specialist (from Phase II)

Principal Investigators

- **Prof. Martin Ackermann / Dr. Olga Schubert** (Microbial Systems Ecology, ETHZ)
- **Prof. Rizlan Bernier-Latmani** (Environmental Microbiology, EPFL)
- **Prof. Claire Bertelli** (Clinical Metagenomics, CHUV)
- **Prof. Gilbert Greub** (Clinical Microbiology, CHUV)
- **Prof. Benoît Guery** (Bacterial and Fungal Infections, CHUV)
- **Prof. Siegfried Hapfelmeier** (Gut Microbiology, UniBe)
- **Prof. Wolf-Dietrich Hardt** (Salmonella Pathogenesis, ETHZ)
- **Prof. Vassily Hatzimanikatis** (Computational Systems Biotechnology, EPFL)
- **Prof. Christof Holliger** (Phase I - Environmental Biotechnology, EPFL)
- **Prof. Tadeusz J. Kawecki** (Experimental Evolutionary Biology, UNIL)
- **Prof. Christoph Keel** (Pseudomonas Plant and Insect Interaction, UNIL)
- **Prof. Sara Mitri** (Evolutionary Ecology of Microbial Communities, UNIL)
- **Prof. Grégory Resch** (Phage and Phage-Lysin Therapy, CHUV)
- **Prof. Ian Sanders** (Ecology and Evolution of Symbiotic Organisms, UNIL)
- **Prof. Yolanda Schaerli** (Bacterial Synthetic Biology, UNIL)
- **Prof. Roman Stocker** (Environmental Microfluidics, ETHZ)
- **Prof. Shinichi Sunagawa** (Microbiome Diversity and Functions, ETHZ)
- **Prof. Christian von Mering** (Bioinformatics and Systems Biology, UniZh)
- **Prof. Pascale Vonaesch** (Microbiota-targeted Interventions, UNIL)

Members of the Scientific Advisory Board

- **Prof. Willem de Vos**, Wageningen University, the Netherlands
- **Prof. Janet Jansson**, Pacific Northwest National Laboratory, US
- **Prof. em. Dani Or**, ETH Zurich, Switzerland
- **Prof. Kiran Patil**, University of Cambridge, UK
- **Dr. Olga Sakwinska**, Nestlé Research Center, Switzerland
- **Prof. Stefanie Widder**, University of Vienna, Austria
- **Prof. Paul Wilmes**, University of Luxembourg, Luxembourg

Associated Partners

- **Dr. Leyla Davis** (Curator Head of Research, Zoo Zürich)
- **Prof. Adrian Egli** (Applied Microbiology Research, UniZh)
- **Prof. Wenyu Gu** (Microbial Physiology and Resource Biorecovery, EPFL)
- **Dr. Milos Stojanov** (Materno-foetal and Obstetrics Research Unit, CHUV)
- **Dr. Simon Van Vliet** (Systems Ecology of Bacterial Biofilms, UniBas)

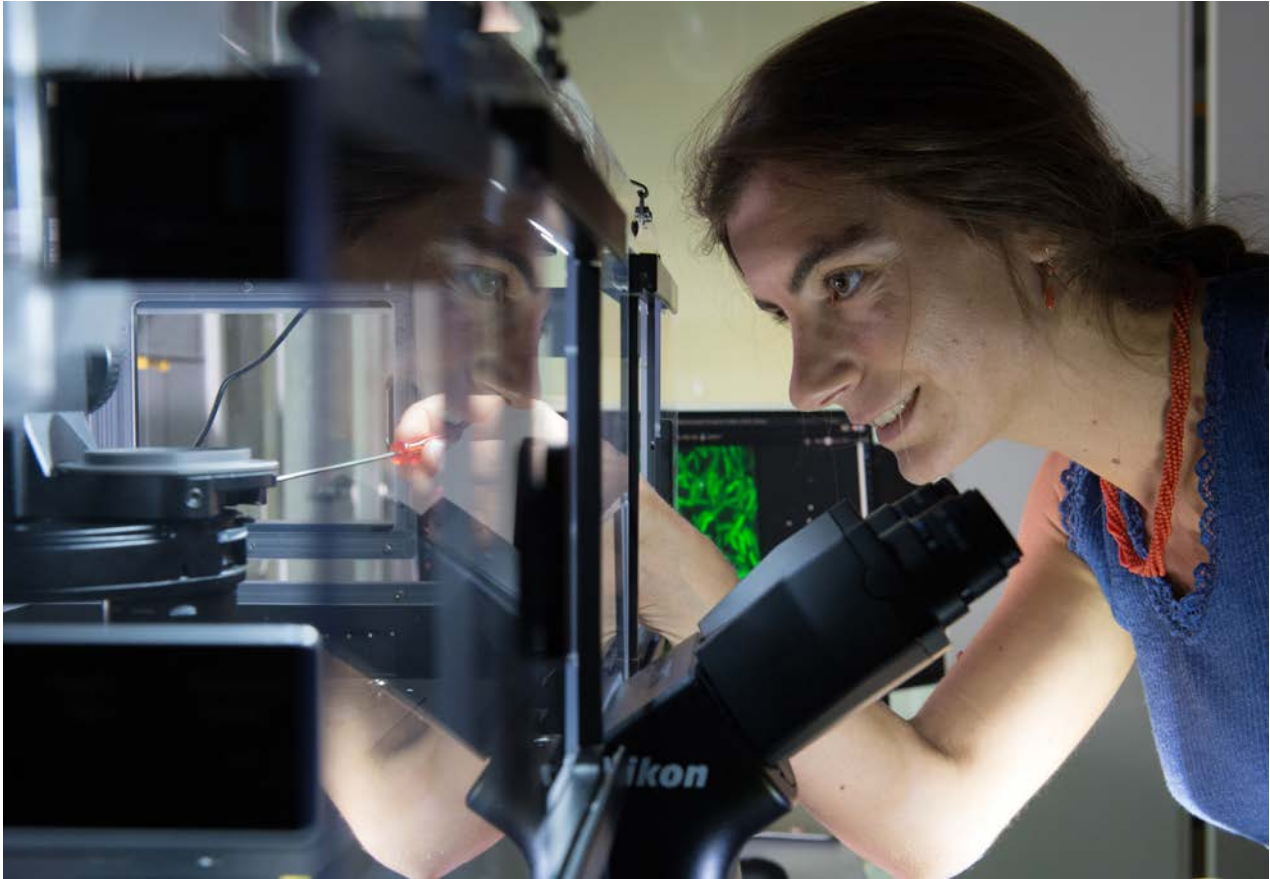


Image © felix imhof

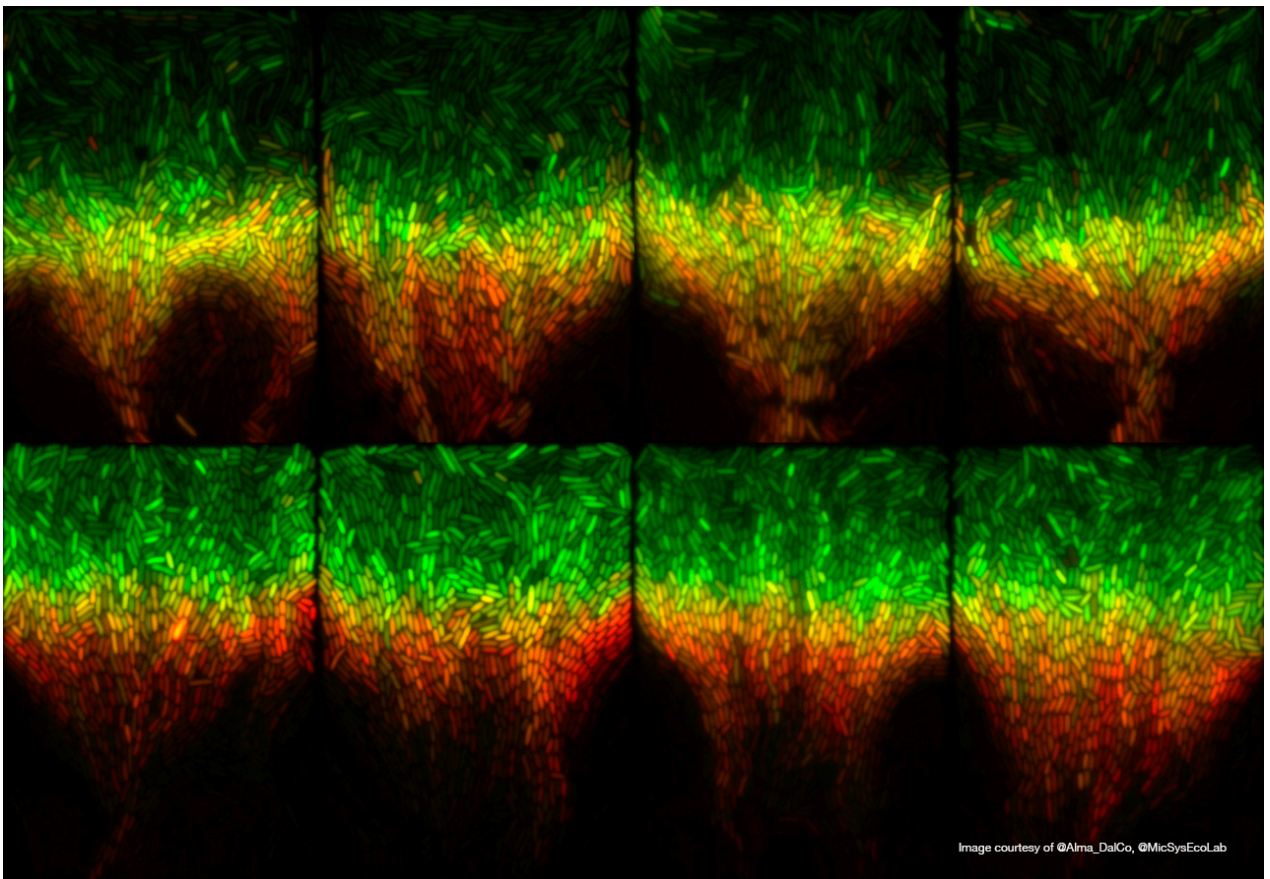


Image courtesy of @Alma_DalCo, @MicSysEcoLab

Image Dal Co, van Vliet & Ackermann, ETHZ & UNIL

Organisation

In Memoriam

Alma Dal Co

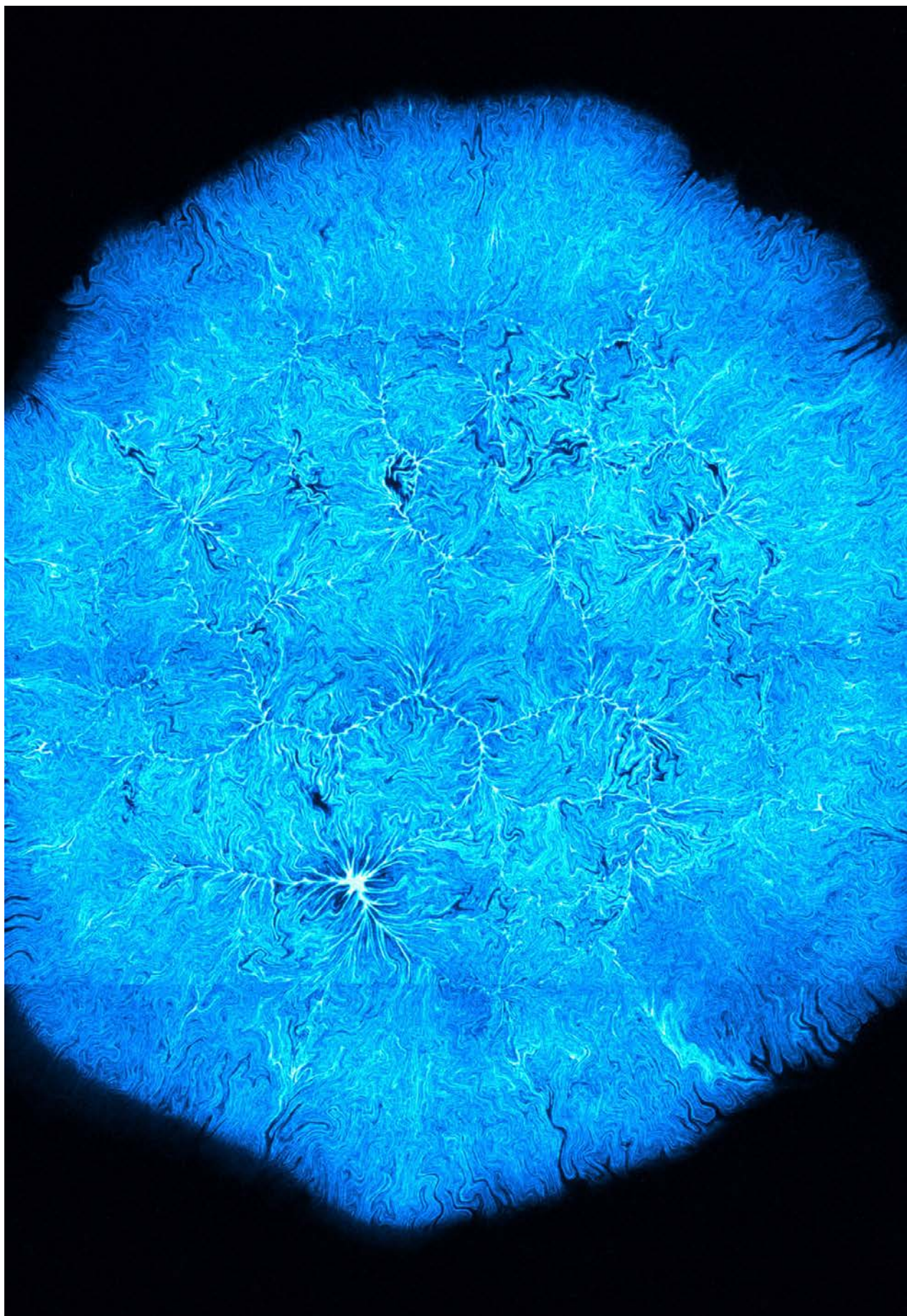
The Dal Co Lab at the University of Lausanne was founded by Dr. Alma Dal Co, a brilliant and deeply curious scientist whose interdisciplinary work elegantly bridged the worlds of physics and biology. Alma had a rare ability to see connections across disciplines, and her creativity shaped not only the questions she asked, but the way she inspired others to think.

In 2021, Alma was appointed to a newly created professorship at the University of Lausanne, established specifically for the NCCR Microbiomes. Through this role, she expanded the consortium's research and became a central part of its mission.

Alma's research focused on understanding how complex behaviours in microbial and multicellular systems emerge from simple, local interactions between individual cells. Using tools like microfluidics, single-cell imaging, and computational modelling, she demonstrated that microbial cells interact mostly with immediate neighbours, shaping spatial structure and limiting metabolic specialisation. Her systems-level approach extended to contexts like pancreatic islets, always with the broader goal of uncovering general principles of biological organisation.

Alma built a dynamic, collaborative lab and left a lasting impact on the scientific community through her intellect, generosity, and passion for team-driven science. Tragically, she passed away in November 2022.

In her memory, the Alma Dal Co Foundation was established to preserve her legacy in both science and music. It supports early-career scientists working on multidisciplinary approaches to complex biological systems, rewards outstanding young musicians, and promotes inclusion and diversity in both fields, reflecting Alma's enduring passion for knowledge, creativity, and collaboration.



Visualisation of a single member of an *E. coli* co-culture exchanging amino acids. Estelle Pignon, Schaefer Lab, UNIL

References

Featured Publications

Discover additional studies at nccr-microbiomes.ch/publications

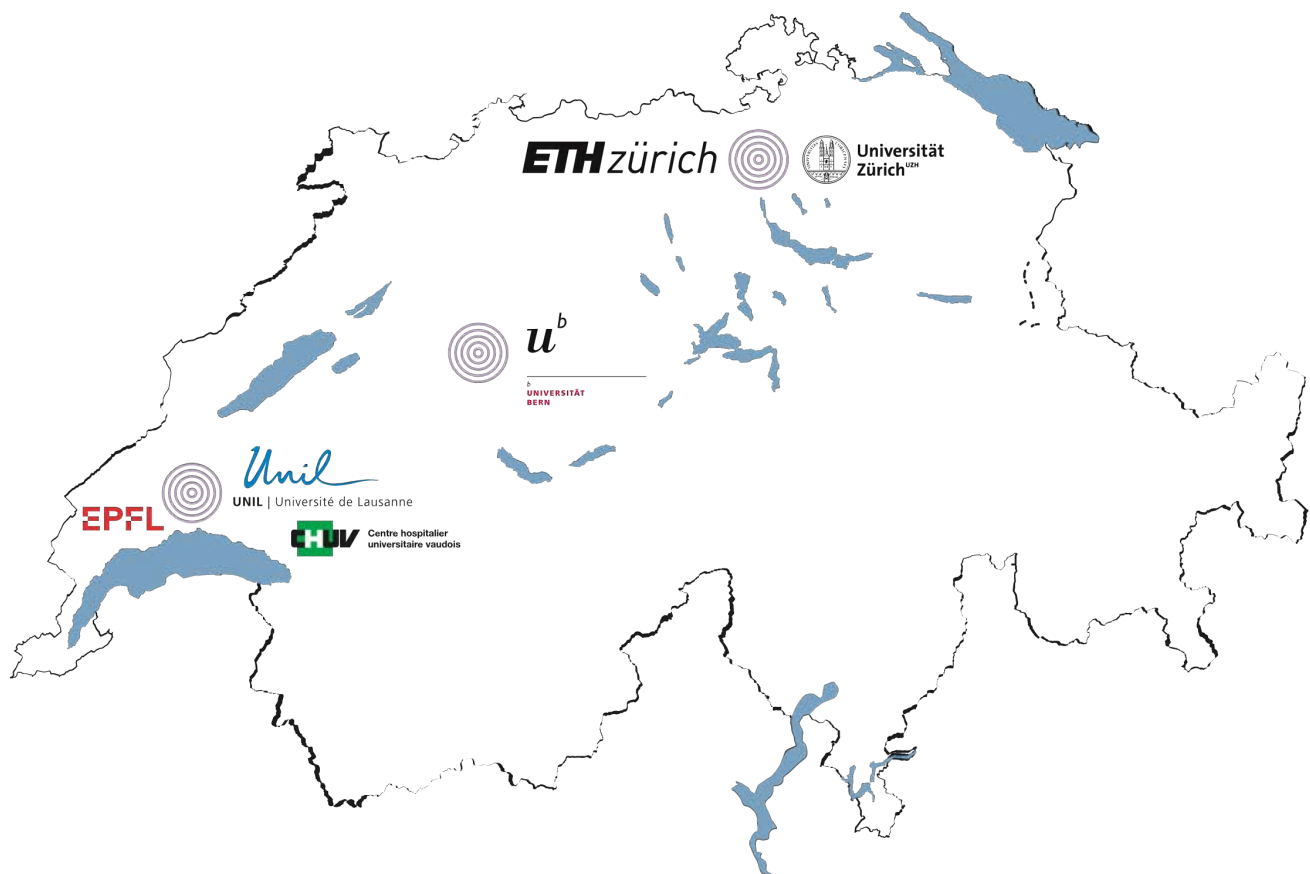
1. Burz, S.D., et al., From microbiome composition to functional engineering, one step at a time. *Microbiology and Molecular Biology Reviews*, 2023. 87(4): p. e00063-23.
2. Garrido-Sanz, D., et al., Changes in structure and assembly of a species-rich soil natural community with contrasting nutrient availability upon establishment of a plant-beneficial *Pseudomonas* in the wheat rhizosphere. *Microbiome*, 2023. 11(214).
3. Čaušević, S., et al., Reproducible Propagation of Species-Rich Soil Bacterial Communities Suggests Robust Underlying Deterministic Principles of Community Formation. *mSystems*, 2022. 7(2): p. e00160-22.
4. Vogel, C.M., et al., Protective role of the *Arabidopsis* leaf microbiota against a bacterial pathogen. *Nature Microbiology*, 2021. 6(12): p. 1537–1548.
5. Cabirol, A., et al., Fecal transplant allows transmission of the gut microbiota in honey bees. *Msphere*, 2024. 9(9): p. e00262-24.
6. Hoces, D., et al., Metabolic reconstitution of germ-free mice by a gnotobiotic microbiota varies over the circadian cycle. *PLoS Biology*, 2022. 20(9): p. e3001743.
7. Dmitrijeva, M., et al., Strain-Resolved Dynamics of the Lung Microbiome in Patients with Cystic Fibrosis. *mBio*, 2021. 12(2): p. e02863-20.
8. Schäfer, M., et al., Mapping phyllosphere microbiota interactions in planta to establish genotype-phenotype relationships. *Nature Microbiology*, 2022. 7(6): p. 856–867.
9. Schäfer, M., Pacheco A. R., et al., Metabolic interaction models recapitulate leaf microbiota ecology. *Science*, 2023. 381(6653).
10. van den Berg, N.I., et al., Ecological modelling approaches for predicting emergent properties in microbial communities. *Nature Ecology & Evolution*, 2022. 6: p. 855–865.
11. Hemmerle, L., et al., Dynamic character displacement among a pair of bacterial phyllosphere commensals in situ. *Nature Communications*, 2022. 13(1): p. 2836.
12. Huelsmann, M. and M. Ackermann, Community instability in the microbial world. *Science*, 2022. 378(6615): p. 29–30.
13. Hausmann, A. and W.D. Hardt, Elucidating host–microbe interactions in vivo by studying population dynamics using neutral genetic tags. *Immunology*, 2021. 162(4): p. 341–356.
14. Chhun, A., et al., An engineered bacterial symbiont allows noninvasive biosensing of the honey bee gut environment. *PLOS Biology*, 2024. 22(3): p. e3002523.
15. Miguel Trabajo, T., et al., Inferring Bacterial Interspecific Interactions from Microcolony Growth Expansion. *microLife*, 2024. 5.
16. Hoces, D., et al., Fitness advantage of *Bacteroides thetaiotaomicron* capsular polysaccharide in the mouse gut depends on the resident microbiota. *Elife*, 2023. 12: p. e81212.
17. Pacheco, A.R. and J.A. Vorholt, Resolving metabolic interaction mechanisms in plant microbiomes. *Current Opinion in Microbiology*, 2023. 74: p. 102317.
18. Dos Santos, A.R., et al., Classifying interactions in a synthetic bacterial community is hindered by inhibitory growth medium. *mSystems*, 2022. 7(5): p. e00239-22.
19. Dal Co, A., et al., Short-range interactions govern the dynamics and functions of microbial communities. *Nature ecology & evolution*, 2020. 4(3): p. 366-375.
20. Dubey, M., et al., Environmental connectivity controls diversity in soil microbial communities. *Communications Biology*, 2021. 4(1): p. 492.
21. Batsch, M., et al., Fragmented micro-growth habitats present opportunities for alternative competitive outcomes. *Nature Communications*, 2024. 15(1): p. 7591.
22. Angeles-Martinez, L. and V. Hatzimanikatis, Spatio-temporal modeling of the crowding conditions and metabolic variability in microbial communities. *PLoS Comput Biol*, 2021. 17(7): p. e1009140.
23. Angeles-Martinez, L. and V. Hatzimanikatis, The influence of the crowding assumptions in biofilm simulations. *PLoS Comput Biol*, 2021. 17(7): p. e1009158.

24. Guex, I., et al., Regulated bacterial interaction networks: A mathematical framework to describe competitive growth under inclusion of metabolite cross-feeding. *PLOS Computational Biology*, 2023. 19(8): p. e1011402.
25. Hockenberry, A.M., et al., Microbiota-derived metabolites inhibit *Salmonella* virulent subpopulation development by acting on single-cell behaviors. *PNAS*, 2021. 118(31): p. e2103027118.
26. Pacheco, A.R., et al., Toward FAIR Representations of Microbial Interactions. *mSystems*, 2022. 7(5): p. e00659-22.
27. Alcolombri, U., et al., Sinking enhances the degradation of organic particles by marine bacteria. *Nature Geoscience*, 2021. 14(10): p. 775–780.
28. Keegstra, J.M., F. Carrara, and R. Stocker, The ecological roles of bacterial chemotaxis. *Nature Reviews Microbiology*, 2022. 20: p. 491–504.
29. Pfreundt, U., et al., Controlled motility in the cyanobacterium *Trichodesmium* regulates aggregate architecture. *Science*, 2023. 380(6647): p. 830–835.
30. Durán, D., et al., *Pseudomonas fluorescens* F113 type VI secretion systems mediate bacterial killing and adaption to the rhizosphere microbiome. *Scientific Reports*, 2021. 11(1): p. 5772.
31. Vacheron, J., C.M. Heiman, and C. Keel, Live cell dynamics of production, explosive release and killing activity of phage tail-like weapons for *Pseudomonas* kin exclusion. *Communications biology*, 2021. 4(1): p. 87.
32. Heiman, C.M., et al., Pivotal role of O-antigenic polysaccharide display in the sensitivity against phage tail-like particles in environmental *Pseudomonas* kin competition. *The ISME Journal*, 2022. 16(7): p. 1683–1693.
33. Brochet, S., et al., Niche partitioning facilitates coexistence of closely related honey bee gut bacteria. *eLife*, 2021. 10: p. e68583.
34. Quinn, A., et al., Host-derived organic acids enable gut colonization of the honey bee symbiont *Snodgrassella alvi*. *Nature Microbiology*, 2024. 9(2): p. 477–489.
35. Lan, J., et al., Non-invasive monitoring of microbiota and host metabolism using Secondary electrospray ionization-Mass spectrometry. *Cell Reports Methods*, 2022. 3(8).
36. Liberti, J., et al., The gut microbiota affects the social network of honeybees. *Nature Ecology & Evolution*, 2022. 6: p. 1471–1479.
37. Schmidt, K., et al., Integration host factor regulates colonization factors in the bee gut symbiont *Frischella perrara*. *Elife*, 2023. 12: p. e76182.
38. Maier, B.A., et al., A general non-self response as part of plant immunity. *Nature Plants*, 2021. 7(5): p. 696–705.
39. Pfeilmeier, S., et al., The plant NADPH oxidase RBOHD is required for microbiota homeostasis in leaves. *Nature Microbiology*, 2021. 6(7): p. 852–864.
40. Kreuzer, M. and W.-D. Hardt, How Food Affects Colonization Resistance Against Enteropathogenic Bacteria. *Annual Review of Microbiology*, 2020. 74(1): p. 787–813.
41. Schären, O.P. and S. Hapfelmeier, Robust microbe immune recognition in the intestinal mucosa. *Genes & Immunity*, 2021. 22: p. 268–275.
42. Herzog, M.K.-M., et al., Mouse models for bacterial enteropathogen infections: insights into the role of colonization resistance. *Gut microbes*, 2023. 15(1): p. 2172667.
43. Yildiz, S., et al., Respiratory tissue-associated commensal bacteria offer therapeutic potential against pneumococcal colonization. *eLife*, 2020. 9: p. e53581.
44. Čaušević, S., et al., Niche availability and competitive loss by facilitation control proliferation of bacterial strains intended for soil microbiome interventions. *Nature Communications*, 2024. 15(1): p. 2557.
45. Fattinger, S.A., M.E. Sellin, and W.-D. Hardt, *Salmonella* effector driven invasion of the gut epithelium: breaking in and setting the house on fire. *Current Opinion in Microbiology*, 2021. 64: p. 9–18.
46. Bakkeren, E., et al., Impact of horizontal gene transfer on emergence and stability of cooperative virulence in *Salmonella* Typhimurium. *Nature Communications*, 2022. 13: p. 1939.
47. Das, S., et al., A prevalent and culturable microbiota links ecological balance to clinical stability of the human lung after transplantation. *Nature Communications*, 2021. 12(1): p. 2126.
48. Tamarelle, J.C., Margaux M, et al., Dynamics and consequences of nutrition-related microbial dysbiosis in early life: study protocol of the VITERBI GUT project. *Frontiers in Nutrition*, 2023. 10.
49. Vonaesch, P., et al., Stunted children display ectopic small intestinal colonization by oral bacteria, which cause lipid malabsorption in experimental models. *Proceedings of the National Academy of Sciences*, 2022. 119(41): p. e2209589119.
50. Pfeilmeier, S., et al., Leaf microbiome dysbiosis triggered by T2SS-dependent enzyme secretion from opportunistic *Xanthomonas* pathogens. *Nature Microbiology*, 2024. 9(1): p. 136–149.
51. Castelli, L., et al., Impact of Chronic Exposure to Sublethal Doses of Glyphosate on Honey Bee Immunity, Gut Microbiota and Infection by Pathogens. *Microorganisms*, 2021. 9(4): p. 845.
52. Piccardi, P., et al., Microbial invasion of a toxic medium is facilitated by a resident community but inhibited as the community co-evolves. *ISME J*, 2022. 16: p. 2644–2652.
53. Garrido-Sanz, D., et al., Relation of pest insect-killing and soilborne pathogen-inhibition abilities to species diversification in environmental *Pseudomonas* protegens. *ISME J*, 2023. 17(9).
54. Viacava, K., et al., Meta-omics-aided isolation of an elusive anaerobic arsenic-methylating soil bacterium. *ISME J*, 2022. 16: p. 1740–1749.

55. Vessman, B., et al. Novel artificial selection method improves function of simulated microbial communities. *bioRxiv*, 2023. 2023.01.08.523165 DOI: 10.1101/2023.01.08.523165.
56. Fullam, A., et al., proGenomes3: approaching one million accurately and consistently annotated high-quality prokaryotic genomes. *Nucleic Acids Research*, 2023. 51(D1): p. D760–D766.
57. Marquis, B., et al., zDB: bacterial comparative genomics made easy. *Msystems*, 2024. 9(7): p. e00473–24.
58. Sveshnikova, A., H. Mohammadi Peyhani, and V. Hatzimanikatis, ARBRE: Computational resource to predict pathways towards industrially important aromatic compounds. *Metabolic Engineering*, 2022. 72: p. 259–274.
59. Ellegaard, K. and P. Engel, The honey bee gut microbiota genomic database, P. Engel, Editor. 2021, Zenodo: UNIL.
60. Paoli, L. and S. Sunagawa, Space, time and microdiversity: towards a resolution revolution in microbiomics. *Environmental microbiology reports*, 2021. 13(1): p. 31.
61. Robinson, S.L., J. Piel, and S. Sunagawa, A roadmap for metagenomic enzyme discovery. *Natural Product Reports*, 2021. 38(11): p. 1994–2023.
62. Ruscheweyh, H.-J., et al., mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. *Current Protocols*, 2021. 1(8): p. e218.
63. Ruscheweyh, H.-J., et al., mOTUs3 - genome metadata, S. Sunagawa, Editor. 2022, Zenodo: ETHZ.
64. Ruscheweyh, H.-J., et al. Reference genome-independent taxonomic profiling of microbiomes with mOTUs3. *bioRxiv*, 2022. 2021.04.20.440600 DOI: 10.1101/2021.04.20.440600.
65. Ruscheweyh, H.-J., et al., Cultivation-independent genomes greatly expand taxonomic-profiling capabilities of mOTUs across various environments. *Microbiome*, 2022. 10: p. 212.
66. Zünd, M., et al., High throughput sequencing provides exact genomic locations of inducible prophages and accurate phage-to-host ratios in gut microbial strains. *Microbiome*, 2021. 9(77): p. 1–18.
67. Scherz, V., G. Greub, and C. Bertelli, Building up a clinical microbiota profiling: a quality framework proposal. *Critical Reviews in Microbiology*, 2022. 48(3): p. 356–375.
68. Asare, P.T., et al., A MALDI-TOF MS library for rapid identification of human commensal gut bacteria from the class Clostridia. *Frontiers in Microbiology*, 2023. 14(1104707).
69. Özel Duygan, B.D., et al., Rapid detection of microbiota cell type diversity using machine-learned classification of flow cytometry data. *Communications Biology*, 2020. 3(1): p. 379.
70. Özel Duygan, B.D., et al., Assessing Antibiotics Biodegradation and Effects at Sub-inhibitory Concentrations by Quantitative Microbial Community Deconvolution. *Frontiers in Environmental Science*, 2021. 9.
71. Özel Duygan, B.D., et al., Assessing Biodegradability of Chemical Compounds from Microbial Community Growth Using Flow Cytometry. *mSystems*, 2021. 6(1).
72. Özel Duygan, B.D. and J.R. van der Meer, Recent advances in microbial community analysis from machine learning of multiparametric flow cytometry data. *Current Opinion in Biotechnology*, 2022. 75: p. 102688.
73. Köhler, T., et al., Personalized aerosolised bacteriophage treatment of a chronic lung infection due to multidrug-resistant *Pseudomonas aeruginosa*. *Nat Commun*, 2023. 14(1): p. 3629.
74. Morales, M., et al., Genome-wide gene expression changes of *Pseudomonas veronii* 1YdBTEX2 during bioaugmentation in polluted soils. *Environmental Microbiome*, 2021. 16(1): p. 1–22.
75. Morales, M., et al., Fitness-Conditional Genes for Soil Adaptation in the Bioaugmentation Agent *Pseudomonas veronii* 1YdBTEX2. *mSystems*, 2023. 8(2): p. e01174–22.
76. Adler, A., et al., Disentangle genus microdiversity within a complex microbial community by using a multi-distance long-read binning method: example of *Candidatus Accumulibacter*. *Environmental Microbiology*, 2022. 24(4): p. 2136–2156.

A Swiss Microbiome Competence Centre

The NCCR Microbiomes creates an expanding network of scientists. It develops durable competences for Switzerland in a new field at the intersection of microbiology, medicine, engineering and environment. It promotes technology transfer, training, career promotion, gender equality and education.



The NCCR Microbiomes integrates research groups from the University of Lausanne, ETH Zurich, EPF Lausanne, CHUV Lausanne University Hospital, University of Bern, and University of Zurich.



NCCR Microbiomes

Management Office
c/o University of Lausanne
Bâtiment Biophore
1015 Lausanne
Switzerland

E-mail: contact@nccr-microbiomes.ch
nccr-microbiomes.ch

Cover image: Pair-wise interactions of bacteria in droplets, Maxime Batsch, van der Meer Lab, UNIL

Copyright: NCCR Microbiomes, 2025

