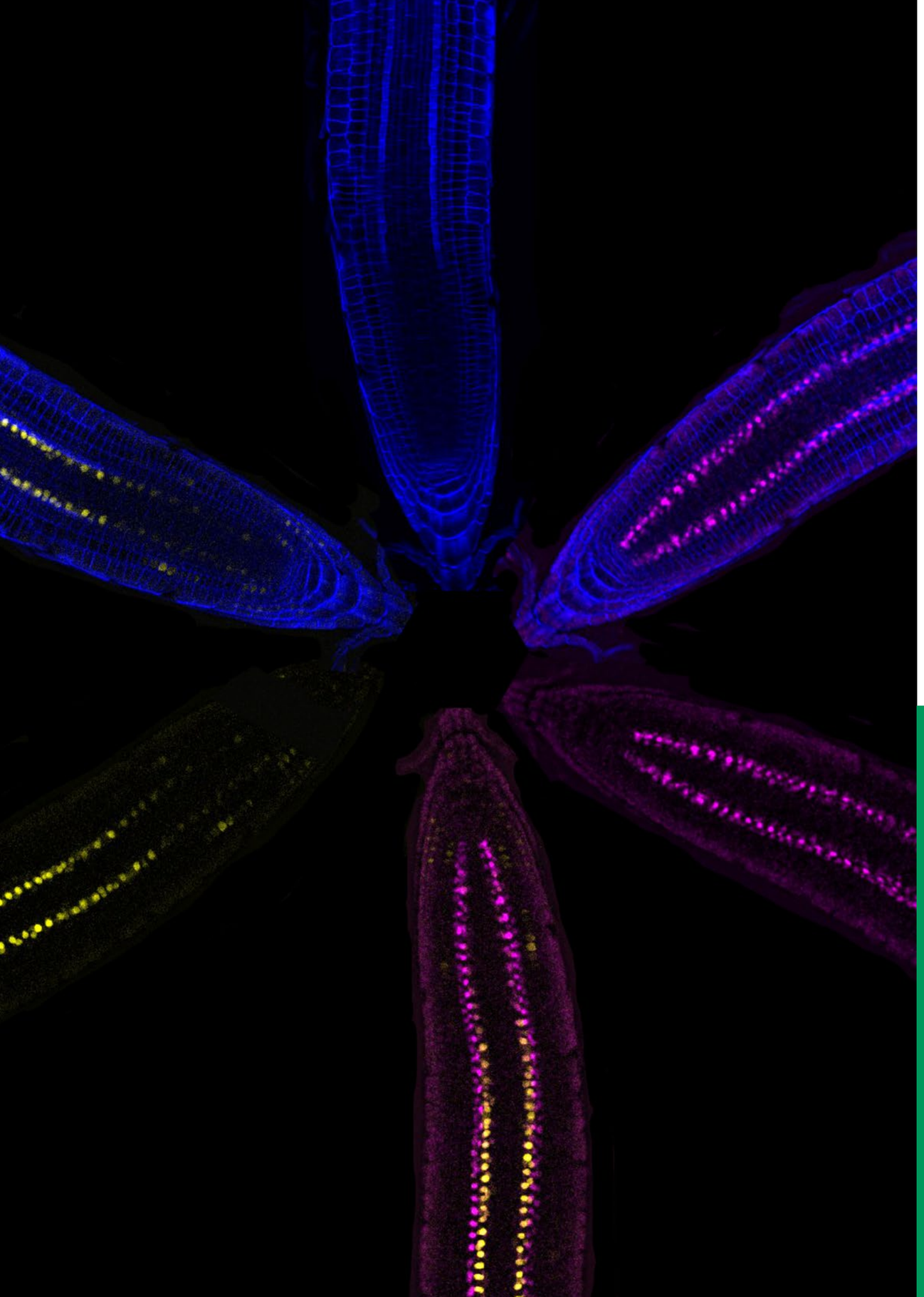
UNIVERSITÉ DE FRIBOURG
UNIVERSITÄT FREIBURG

DEPARTMENT OF BIOLOGY

ACTIVITY REPORT 2021-22

FACULTÉ DES SCIENCES
ET DE MÉDECINE
DEPARTMENT OF BIOLOGY

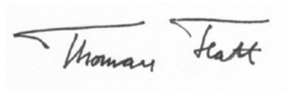
Contents



Welcome from the president

A vote of thanks. A lot of things have happened since the last activity report. A “no-brainer” to mention is the COVID crisis, which has challenged us all. But positive developments have clearly prevailed, as this report bears witness to. It’s a pleasure to see how active, dynamic and successful our department is. But rather than reviewing all (mostly very positive!) that has happened over the past two years (e.g., a new organizational structure, new hires, a new building, new MSc programs, and so forth), I would like to thank all of you for helping to make this department “work” on a daily basis, both in happy times but especially in the face of challenges. I am especially grateful to everyone serving in our working groups, committees and the “collège” – as the word “collège” implies, the well-being of our department is a community effort. But several members of our department deserve our very special gratitude: Philippe Baumann, Evelyn Boll, Boris Egger, Jean-Claude Jaquier, Sabrina Lutz, Jean-Daniel Niederhäuser, Julien Comelli, Eirini Maikanti, Felix Meyenhofer, Laura Morello, Alessandro Puoti, Michael Stumpe, and Alain Werro. Without you, nothing would work. It is because of your dedicated work and because of the collegial collaboration amongst all of us – students, staff and researchers that our department is fit for the future!

Sincerely,
Prof. Thomas Flatt
President of the Department of Biology



Research Support

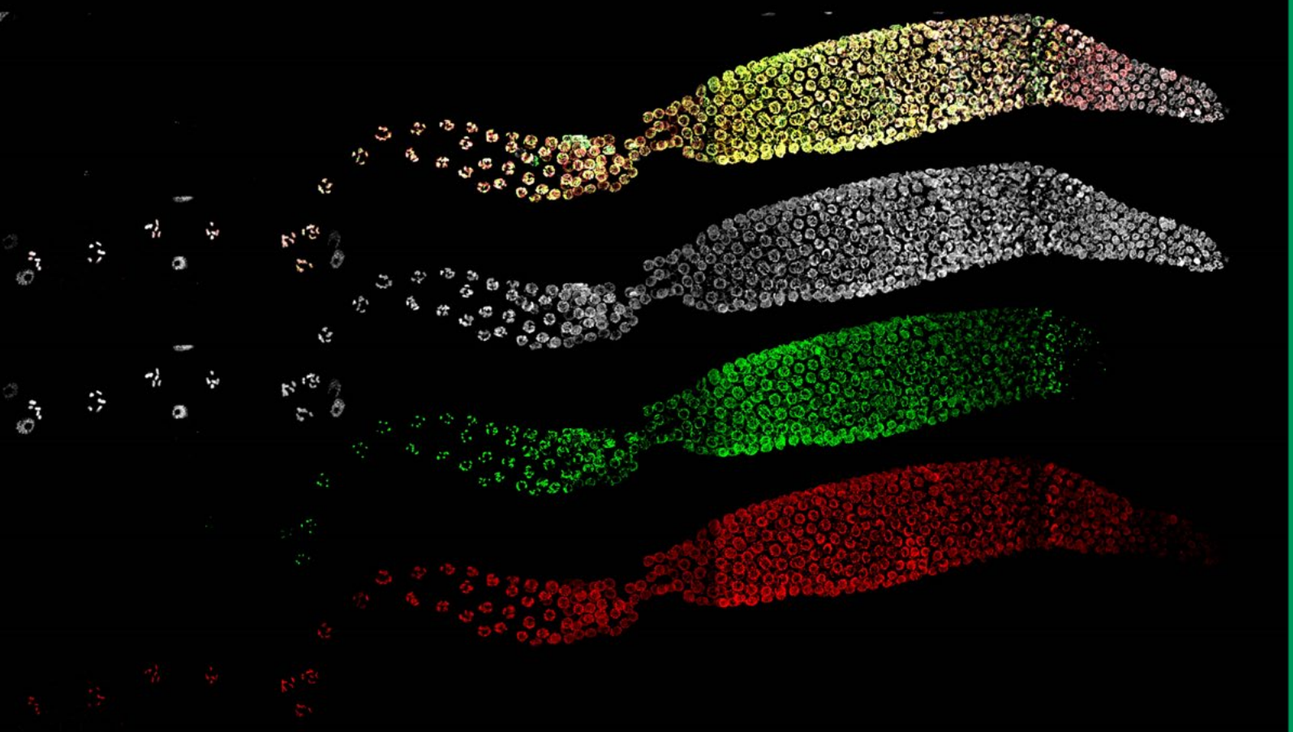
Our research groups benefit from the support of our technical and administrative teams.
They ensure the good working of our Department to allow researchers to focus on what they do best.

Admin Team

Evelyn Boll, Sabrina Lutz
Laura Morello, Eirini Maikanti

Technical and IT Support

Jean-Claude Jaquier, Alain Werro, Jean-Daniel Niederhäuser, Olga Sudan, Felix Meyenhofer, Philippe Baumann, Michael Stumpe



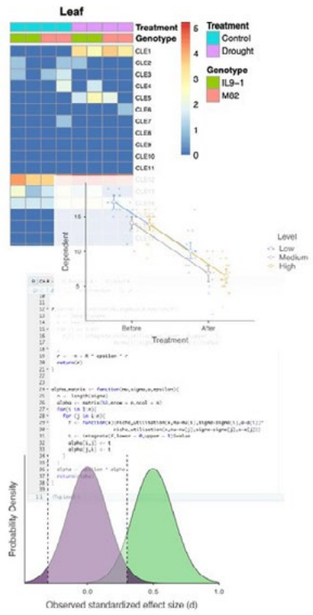
Platforms

BBP

The Bioinformatics & Biostatistics Core Facility (established in 2013) is a joint platform between the Department of Biology and the section of Medicine. It is managed by Dr. Laurent Falquet and Dr. Rudolf Rohr. The expertise of the platform is primarily the analysis of Next Generation Sequencing data and Biostatistics analysis, with emphasis on genome assembly and metagenomics, as well as DNA methylation. We also perform other analyses, such as ANOVA, mixed effect models, RNAseq, ChIPseq, and any large scale data analysis upon request.

For Bioinformatics matter please contact
Dr. Laurent Falquet: bugfri@unifr.ch

For Biostatistics matter please contact
Dr. Rudolf Rohr: rudolf.rohr@unifr.ch



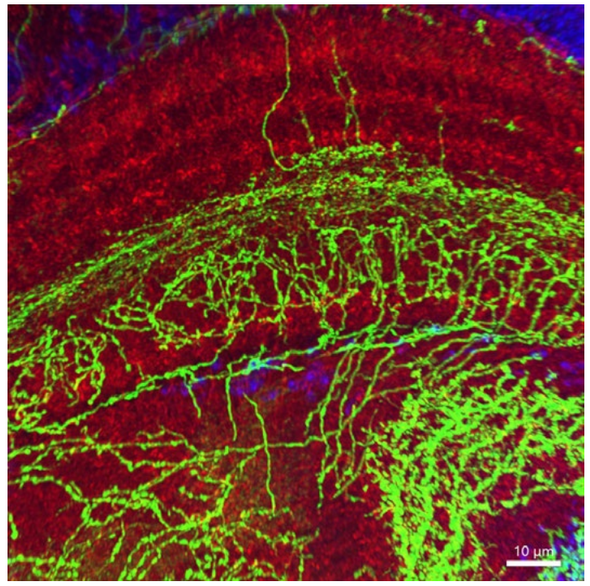
BICORE

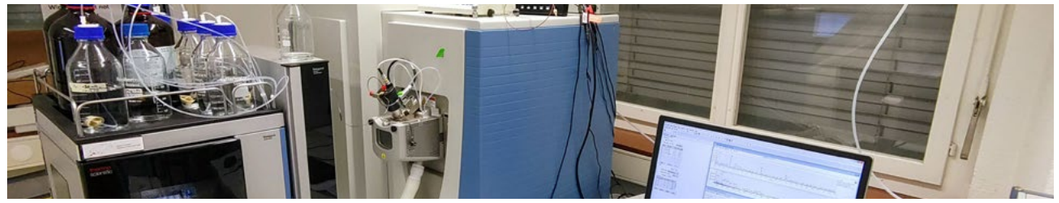
The Bioimage Core Facility (BICORE) of the Department of Biology and the Section of Medicine provides access to state-of-the-art light microscopy.

Currently, about 120 active researchers at the Faculty of Science and Medicine are using the services offered by the facility.

BICORE gives training on high-end microscopes and can be consulted for experimental design, image acquisition and analysis. The facility also organizes Master and Doctoral courses in light and fluorescence microscopy for life sciences.

The facility is managed by Felix Meyenhofer and Boris Egger.





MAPP

The Metabolomics and Proteomics Platform (MAPP) is a service of the Department of Biology of the University of Fribourg. The mission of the platform is to provide expertise, instrumentation, and manpower to enable state-of-the-art implementation of metabolomic and proteomic analyses. To this end, the MAPP offers support in the planning and execution of experiments, including custom-tailored method development, sample preparation, data acquisition and analysis, and researcher training. Since its official start in January 2017, the MAPP has provided its services to many research groups of the Department of Biology as well as to some external customers.

Co-workers
Dr Pierre-Marie Allard (Head of Metabolomics Unit)
Dr Emmanuel Defossez (Platform Manager Metabolomics)
Dr Dieter Kressler (Head of Proteomics Unit)
Dr Michael Stumpe (Platform Manager Proteomics Unit)

Metabolomics Unit

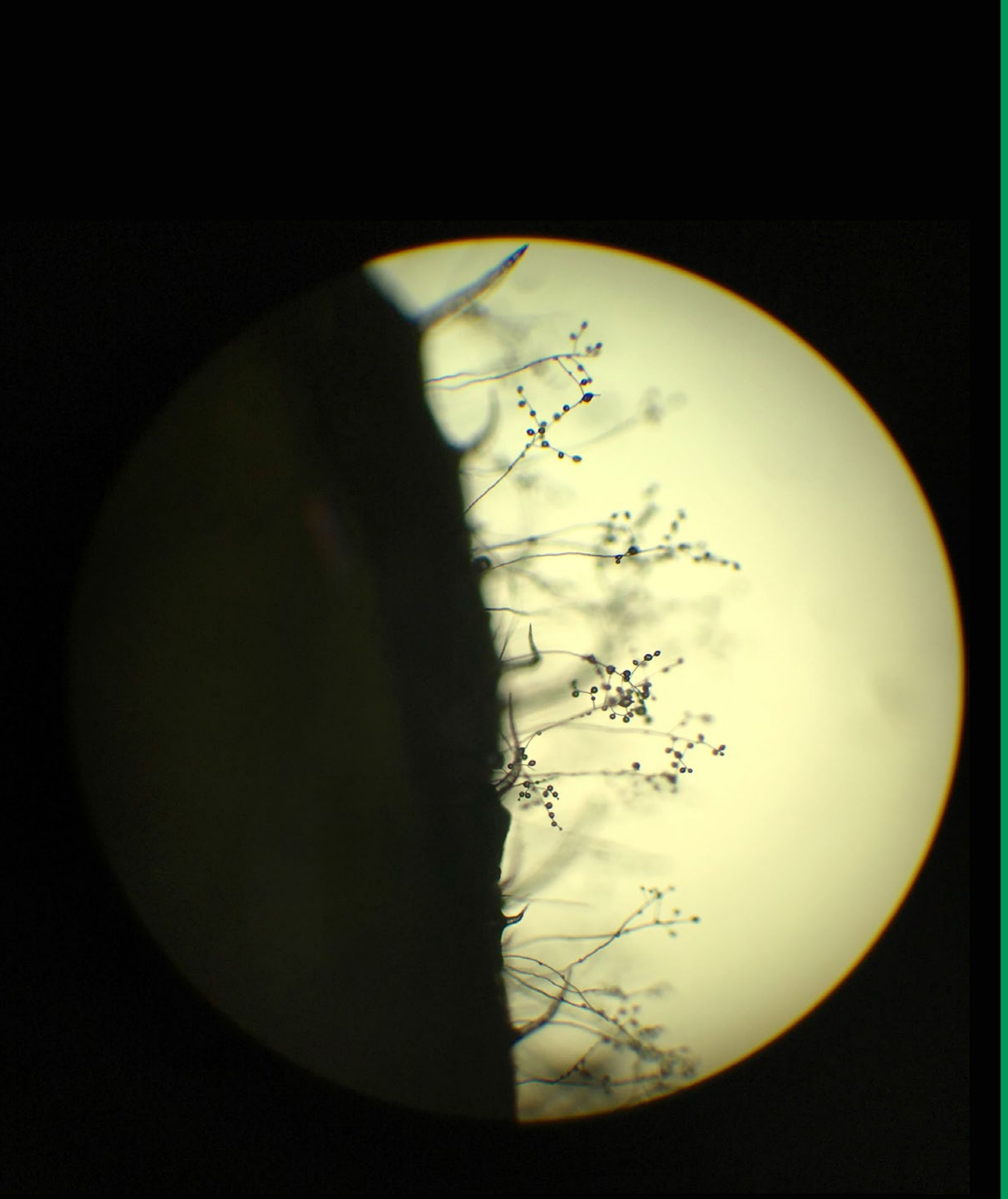
The Metabolomics Unit offers services ranging from sample preparation to data acquisition and data interpretation. The analytical platform allows for Gas Chromatography (GC) based profiling with a GC-FID (Agilent 7890) and a high-resolution Time of Flight mass spectrometer GC-QToF (Agilent 7200) and for Liquid Chromatography (LC) profiling on a UHPLC-HRMS Orbitrap (Vanquish Fusion + Q Exactive Plus). In addition to data acquisition, state-of-the-art computational solutions and biostatistics are proposed for the analysis of untargeted metabolomics datasets.
In the last year, 7 research groups of the Department of Biology, as well as three external customers have utilized the services of the Metabolomics Unit.

Proteomics Unit

The Proteomics Unit mainly offers diverse mass spectrometric (MS) analyses of protein samples. The Proteomics Unit is in the fortunate situation to have access to three high-end nanoLC-ESI-MS/MS instruments, the newly purchased Orbitrap Exploris 480 (2022), a Q Exactive HF-X (2018, financed in part by a R'Equip grant), and a Q Exactive Plus (2016, mainly used by the Metabolomics Unit).
In the last two years, 14 research groups of the Department of Biology, as well as ten external customers (including six research groups of the Section of Medicine), have utilized the services of the Proteomics Unit.

Selected publications

Rutz A. et al. (2022) The LOTUS initiative for open knowledge management in natural products research eLife 11:e70780 / doi: 10.7554/eLife.70780
De Giorgi, J. et al. (2021). The Arabidopsis mature endosperm promotes seedling cuticle formation via release of sulfated peptides. Developmental Cell, 56(22), pp.3066-3081 / doi: 10.1016/j.devcel.2021.10.005
Keppner A, Correia M, Santambrogio S, Koay TW, Maric D, Osterhof C, Winter DV, Clerc A, Stumpe M, Chalmel F, Dewilde S, Odermatt A, Kressler D, Hankeln T, Wenger RH, Hoogewijs D. (2022) Androglobin, a chimeric mammalian globin, is required for male fertility. eLife 11:e72374 / doi: 10.7554/eLife.72374
Hakala SM, Meurville MP, Stumpe M, LeBoeuf AC. (2021) Biomarkers in a socially exchanged fluid reflect colony maturity, behavior, and distributed metabolism. eLife 10:e74005 / doi: 10.7554/eLife.74005



The Department in figures

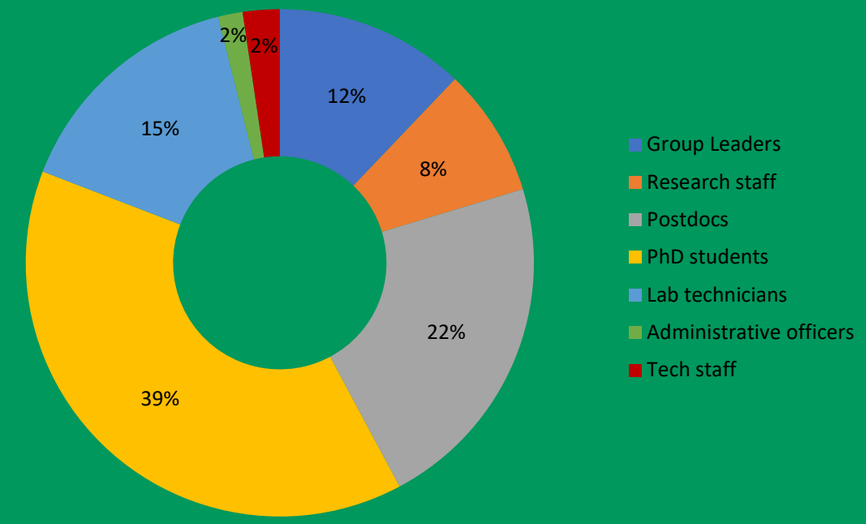
42
Nationalities

268
peer-reviewed publications
in 2021 and 2022

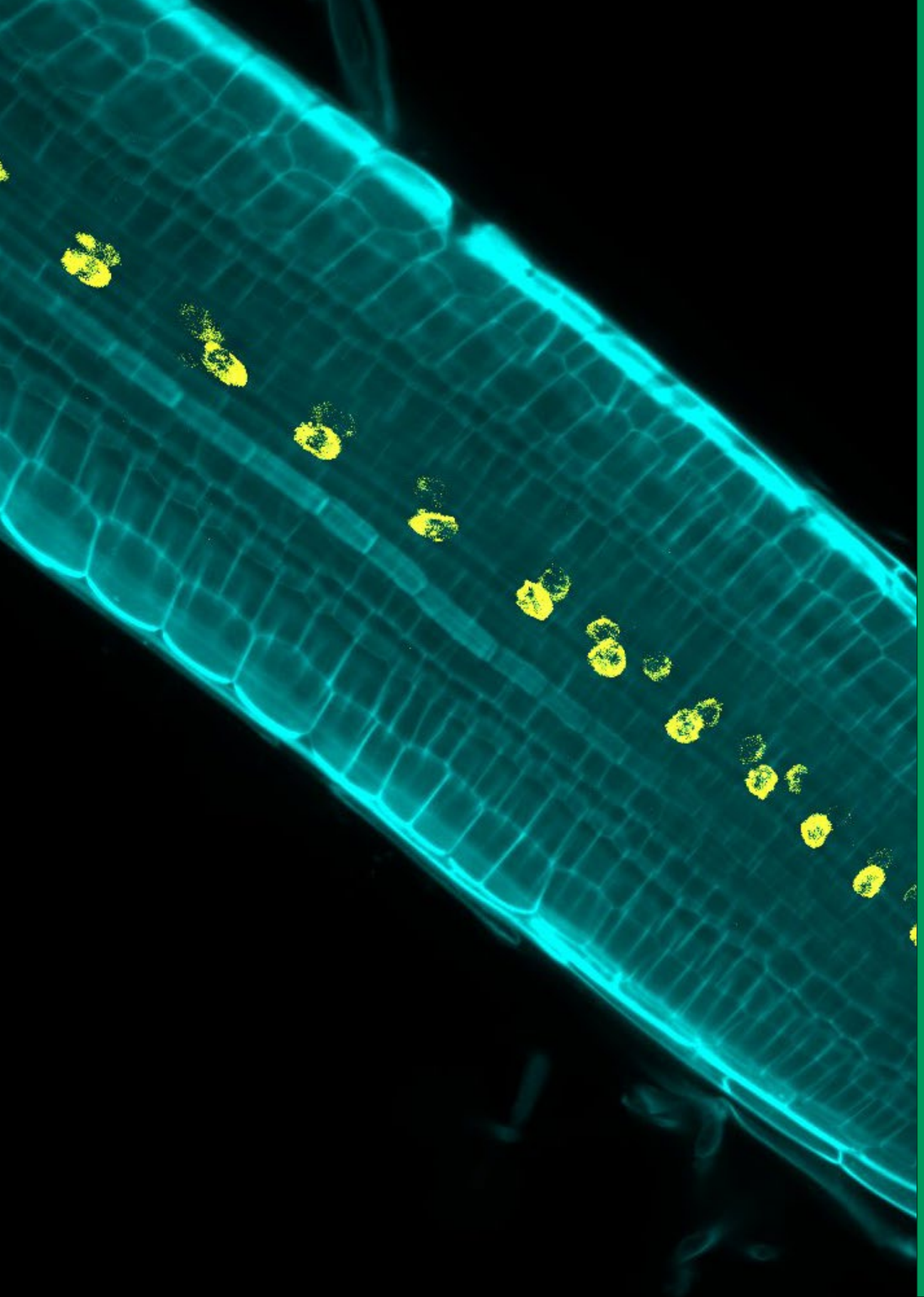
142 courses
188 exams
during the academic year 21/22

61
completed Msc and PhD
theses with graduations

31
research groups



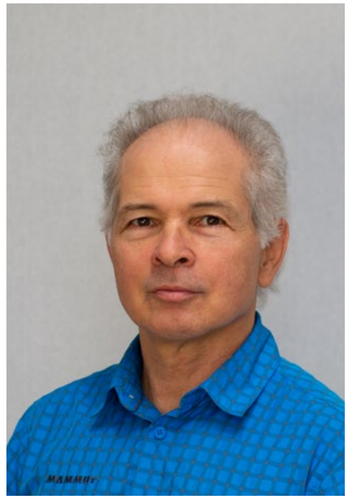
260
people worked at the Department of Biology
in 2021 and 2022



Research

Circadian clock and light

How light affects the clock and mental health



Prof. Urs Albrecht
Analysis of circadian clocks and sleep in mammals

The earth's rotation around its axis causes periodic exposure of half of its surface to sunlight. This daily recurring event has been internalized in most organisms in the form of cellular circadian clock mechanisms. These cellular clocks are synchronized with each other in various ways to establish circadian networks that build the circadian program in tissues and organs, coordinating physiology and behavior in the entire organism. In the mammalian brain, the suprachiasmatic nuclei (SCN) receive light information via the retina and synchronize their own neuronal clocks to the light signal. Subsequently, the SCN transmits this information to the network of clocks in tissues and organs, thereby synchronizing body physiology and behavior. Disruption of cellular clocks and/or destruction of the synchronization between the clocks, as experienced for instance in jet-lag and shift-work conditions, affects normal brain function and can lead to metabolic problems, sleep disturbance, and accelerated neurological decline. We aim to decipher the ways through which light affects the circadian system and thus influences normal brain function. Disturbance of the clock by nocturnal light will lead to sleep problems and age-related cognitive decline, which are on the rise in modern societies. We are using normal and genetically modified mice in order to study causal relationships between light, the circadian clock and neurological disorders. A variety of molecular, biochemical, genomic, proteomic and metabolomic methods are applied towards the understanding of light-clock-mood-sleep relationships.

> "Light and the circadian clock are important factors impinging on health and well-being"

Immunohostochemistry of a section from the suprachiasmatic nucleus (SCN) collected at zeitgeber time 12 from a mouse with deletion of the clock gene Per2 in astrocytes. Per2 is shown in green expressed in neurons, and astrocytes are shown in red. Scale bar: 10 µm

Group members

Stéphanie Aebischer, Lab technician
Antoinette Hayoz, Lab technician
Tomaz Martini, PhD Student
Katrin Wendrich, PhD Student
Yankey Yungdun, PhD Student
Dr. Jürgen Ripperger, Maitre Assistant
Maude Marmy, animal caretaker
Mariana Gutiérrez Pérez, exchange student

Selected publications

Martini T, Ripperger JA, Chavan R, Stumpe M, Netzahualcoyotzi C, Pellerin L, Albrecht U (2021) The hepatic monocarboxylate transporter 1 (*Mct1*) contributes to the regulation of food anticipation in mice. Front. Physiol. 12: 665476.

Olejniczack I, Ripperger JA, Sandrelli F, Schnell A, Mansencal-Strittmatter L, Wendrich K, Hui KY, Brenna A, Ben Fredj N, Albrecht U (2021) Light affects behavioral dispair involving the clock gene *Period1*. PLoS Genet. 17: e1009625.

Martini T, Ripperger JA, Stalin J, Kores A, Stumpe M, Albrecht U (2021) Deletion of the clock gene *Period2* (*Per2*) in glial cells alters mood-related behavior in mice. Sci. Rep. 11: 12242.

Brenna A, Ripperger JA, Saro G, Glauser D, Yang Z, Albrecht U (2021) PER2 mediates CREB-dependent light induction of the clock gene *Per1*. Sci. Rep. 11: 21766.

Molecules in Context

Linked Open Data to explore Life's chemistry

Dr. Pierre-Marie Allard
Natural products chemistry and computational metabolomics

Metabolism embodies the dynamic nature of living processes. The constant interconversion of molecules provides energy and generates the chemical bricks of life. The natural products assembled from these building blocks radiate from a central metabolome, shared by all organisms and consisting of fundamental polymers such as nucleic acids or proteins, to a specialized metabolome consisting of an infinitely more diverse set of molecules shaped by evolutionary processes and which are specific in terms of occurrences in the tree of life, chemical structures and biological functions. Characterization of natural products and elucidation of the roles of specialized metabolites are essential for the fundamental understanding of chemical evolution and ecological interactions, as well as for more applied topics such as drug discovery.

In the COMMONS Lab we explore and develop knowledge management solutions for the study of the chemistry of Life. These solutions are aimed to support the stages of knowledge acquisition, knowledge organization and knowledge dissemination.

> "Chemistry is the common language of Nature"

[Knowledge acquisition] We use mass spectrometry (because of its unrivalled sensitivity and structural determination potential) to profile biological matrices and we develop computational tools to organize, annotate and visualize the obtained spectral data.

[Knowledge organization] We employ Linked Open Data principles to organize and connect mass spectrometry experimental results with publicly available and relevant datasets. The gathered information is organized as hybrid and cross-domain Knowledge Graphs. These graphs allow to better capture the complexity of the ecological, biological, and chemical context in which the analytes are originally found in, but isolated from, when using powerful hyper-reductionist approaches such as untargeted fragmentation mass spectrometry.

[Knowledge dissemination] We finally explore solutions to share the acquired knowledge inside and outside of academia (e.g. the ongoing LOTUS initiative).

Group members

Emmanuel Defossez, Postdoc

Selected publications

Rutz A. et al. (2022) The LOTUS initiative for open knowledge management in natural products research eLife 11:e70780.

Walker, T. W. et al. (2022). Functional Traits 2.0: The power of the metabolome for ecology. Journal of Ecology, 110(1), 4-20.

Gaudry A. et al. (2022) MEMO: Mass Spectrometry-Based Sample Vectorization to Explore Chemodiverse Datasets. Frontiers in Bioinformatics. 2022 ;2:842964.

Defossez, E. et al. (2021). Spatial and evolutionary predictability of phytochemical diversity. Proceedings of the National Academy of Sciences, 118(3), e2013344118.

Metasequoia glyptostroboides pictured in the botanical garden of University of Fribourg. We have recently launched the Digital Botanical Gardens Initiative, an Open Science project aiming to establish robust and scalable workflows for the digitization of chemodiversity at the global scale. More details at: www.dbgi.org

Ecology in the Anthropocene

Alien species: the good, the bad and the ugly

Prof. Sven Bacher
Applied Ecology

Humans change the planet faster than ever before in history. These changes create challenges for science and society, but also opportunities to create better futures. Our research contributes to understanding the mechanisms and consequences of these changes, developing strategies how we can prevent harmful impacts and how we can use this knowledge to enhance ecosystem services we receive from nature. We collaborate with researchers all over the world and advise organizations such as the International Union for Conservation of Nature (IUCN), the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), and the European Commission (EC).

> “Alien species are a major threat to biodiversity and human well-being”

Which are the worst invasive alien species?

The number of alien species is increasing exponentially worldwide and there are many more species than can be managed. There are more than 14000 alien species in Europe, but not all of them cause problems to the environment or human well-being. The seemingly simple and straightforward question «which are the worst invaders?» is difficult to answer because the impacts of alien species can be manifold and comparisons need to work for species as different as for example snails, insects, mammals and plants. We developed methods that allow classifying alien species according to the magnitude of their environmental and socio-economic impacts (S/EICAT), which are now adopted as international standards by the IUCN.

Are all alien species bad?

Not all alien species are harmful, some can even be beneficial for native species or humans. Current research incorporates beneficial impacts into S/EICAT for more comprehensive understanding of how alien species change local ecosystems and human well-being.

Improving biological control

In collaboration with the Swiss Federal Research station Agroscope we are improving biocontrol of important insect pests such as pollen beetles (*Brassicogethes spp.*) and spotted wing fruitfly (*Drosophila suzukii*).

Can we improve wine quality with biodiversity?

In the European project PromESSinG (www.promessing.eu) we investigate how we can use biodiversity-friendly agricultural management techniques to improve grape quality.

The EICAT and EICAT+ frameworks allow classification of negative and positive impacts of alien species.
(from Vimercati et al. 2022 PLoS Biology)

Group members

Mario Coiro, Postdoc
Anna Probert, Postdoc
Lisanna Schmidt, Postdoc
Giovanni Vimercati, Postdoc
Anne-Laure Fragnière, PhD Student
Deborah Kaiser, PhD Student
Lara Reinbacher, PhD Student
Lara Volery, PhD Student
Huiru Li, PhD Student
Marc Diaz, Intern

Selected publications

Vimercati, G. et al. (2022). The EICAT+ framework enables classification of positive impacts of alien taxa on native biodiversity. PLoS Biology, 20(8), e3001729.

Forgione, L. et al. (2022). Are species more harmful in their native, neonative or alien range? Insights from a global analysis of bark beetles. Diversity and Distributions, 28(9), 1832-1849.

Broennimann, O., et al. (2021). Distance to native climatic niche margins explains establishment success of alien mammals. Nature Communications, 12(1), 1-8. (* senior authors)

Volery, L., et al. (2021). Ranking alien species based on their risks of causing environmental impacts: A global assessment of alien ungulates. Global Change Biology, 27(5), 1003-1016.

Community ecology

Community structure and functioning

Prof. Louis-Felix Bersier
Microbial systems and the structure and organisation of natural communities

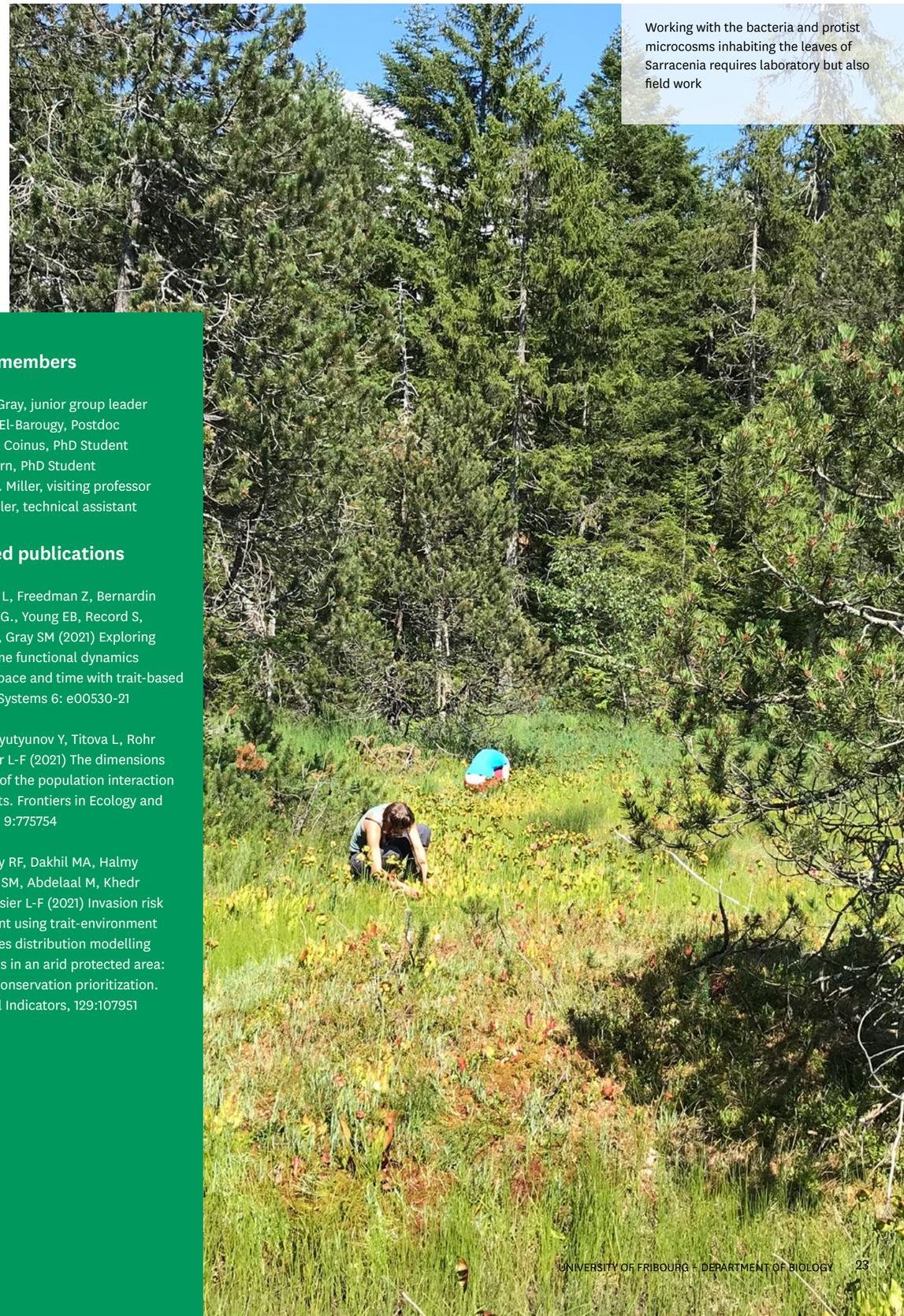
Natural communities are composed of numerous species that interact between themselves and with their environment. Communities deliver essential "services" like food provisioning or carbon sequestration. Understanding how communities are organised and how they function is thus a primary task. The inherent complexity and variability of natural communities makes this undertaking conceptually and methodologically challenging. Microbial systems inhabiting the pitcher-shaped leaves of *Sarracenia purpurea* are a perfect system, being amenable to replicated experiments.

> "Dispersal between communities saves biodiversity"

We conducted an experiment in the field, manipulating the amount of resource, the temperature and the dispersal between local communities. We found that resource and temperature had the strongest impact on diversity. However, by combining all possible treatments, we found a hidden effect of dispersal: it preserves diversity when resource and temperature had negative impacts.

Temperature performance curves (TPCs) describe the response of vital parameters to temperature and are a key tool to understand the effects of global warming. We analysed TPCs for six protist species in our system. This undertaking was much more complex than expected, leading to the development of new TPC models.

Dr. Sarah Gray formed a *Sarracenia purpurea* International Network (SPIN) with scientists to conduct research on this system. It resulted in the hosting of two US PhD Students, Alicia McGrew and Jessica Bernandin. We also hosted a visiting professor, Dr. Thomas Miller, funded through the SNSF. Sarah Gray is also a collaborator on an USA NSF-funded Rules of Life grant, with the overarching objective of using the *Sarracenia* system to define general rules for how microbiome composition and function change during succession.



Working with the bacteria and protist microcosms inhabiting the leaves of Sarracenia requires laboratory but also field work

Group members

Sarah M. Gray, junior group leader
Reham F. El-Barougy, Postdoc
Samantha Coinus, PhD Student
Rachel Korn, PhD Student
Thomas E. Miller, visiting professor
Nilgün Sailer, technical assistant

Selected publications

Bittleston L, Freedman Z, Bernardin J, Jacob JG., Young EB, Record S, Baiser BH, Gray SM (2021) Exploring microbiome functional dynamics through space and time with trait-based theory. mSystems 6: e00530-21

Arditi R, Tyutyunov Y, Titova L, Rohr RP, Bersier L-F (2021) The dimensions and units of the population interaction coefficients. Frontiers in Ecology and Evolution, 9:775754

El-Barougy RF, Dakhil MA, Halmy MW, Gray SM, Abdelaal M, Khedr A-HA, Bersier L-F (2021) Invasion risk assessment using trait-environment and species distribution modelling techniques in an arid protected area: Towards conservation prioritization. Ecological Indicators, 129:107951

Chordate regeneration

Investigating the extreme regenerative capacity of colonial tunicates

Dr. Simon Blanchoud
Whole-body regeneration in *Botrylloides diegensis*

Tunicates are marine invertebrates that belong to the Tunicata subphylum. Together with the more basal Cephalochordata (i.e. the lancelets) and the Vertebrata (i.e. us), they compose the Chordata phylum. Tunicates are estimated to have separated from the vertebrates 500 million years ago, which thus makes them our closest invertebrate relatives! In addition to this unique taxonomic position, tunicates display a variety of physiological and morphological traits that are truly fascinating.

There are currently over 3'000 different species of tunicates identified. Tunicates have a tissue complexity reminiscent of vertebrates, and a morphology organized around a barrel-shaped body with two siphons to filter water. Tunicates are named after the structuring semi-rigid layer of cellulose-based extracellular matrix that encompasses their body.

The diversity of adult forms ranges from from the 15 cm-long Korean delicacy *Halocynthia* to the developmental model organism *Ciona*, from the solitary carnivorous abyssal *Dicopia* to the colonial invasive subtidal *Botrylloides* and from the 1 mm-long dioecious *Oikopleura* that builds extra-corporeal houses for funneling its food to the bioluminescent *Pyrosoma* that assembles into up to 18 m-long tube-shaped pelagic colonies.

> "Imagine if we could do just 1% of what they do"

In our lab, we are particularly interested in the powerful regenerative capacity of *Botrylloides*. Extraordinarily, these animals can regenerate a fully functional adult from a minute fragment of its vascular system in just 10 days. In this species, one tissue has thus the stem-like capacity to recreate all other tissues of an animal! In addition to this dramatic process, we are investigating other fascinating facets of these animals, including asexual reproduction, locomotion, taxonomy and genomics.

Our group works at the interface between engineering and biology, innovating solutions to dissect the unusual scientific questions brought to us by these tunicates.

A top-view picture of a colony of *Botrylloides diegensis* composed of 13 adults.

Group members

Marta Wawrzyniak, lab manager
Nathalie Weber, animal caretaker

Selected publications

Blanchoud S & Galliot B, editors (2022) Whole-body regeneration: methods and protocols. Methods in Molecular Biology 2450: 1-679

Domart-Coulon I & Blanchoud S (2022) From Primary Cell and Tissue Cultures to Aquatic Invertebrate Cell Lines: An Updated Overview. MDPI. Advances in aquatic invertebrate stem cell research: 1-64

Wawrzyniak M, Matas Serrato LA & Blanchoud S (2021) Artificial seawater based long-term culture of colonial ascidians. Developmental Biology 480: 91-104

Dagenais P*, Blanchoud S*, Pury D, Pfefferli C, Aegerter-Wilmsen T, Aegerter C & Jaźwińska A (2021) Hydrodynamic stress and phenotypic plasticity of the zebrafish regenerating fin. Journal of Experimental Biology 224 (15)

Cellular Recycling

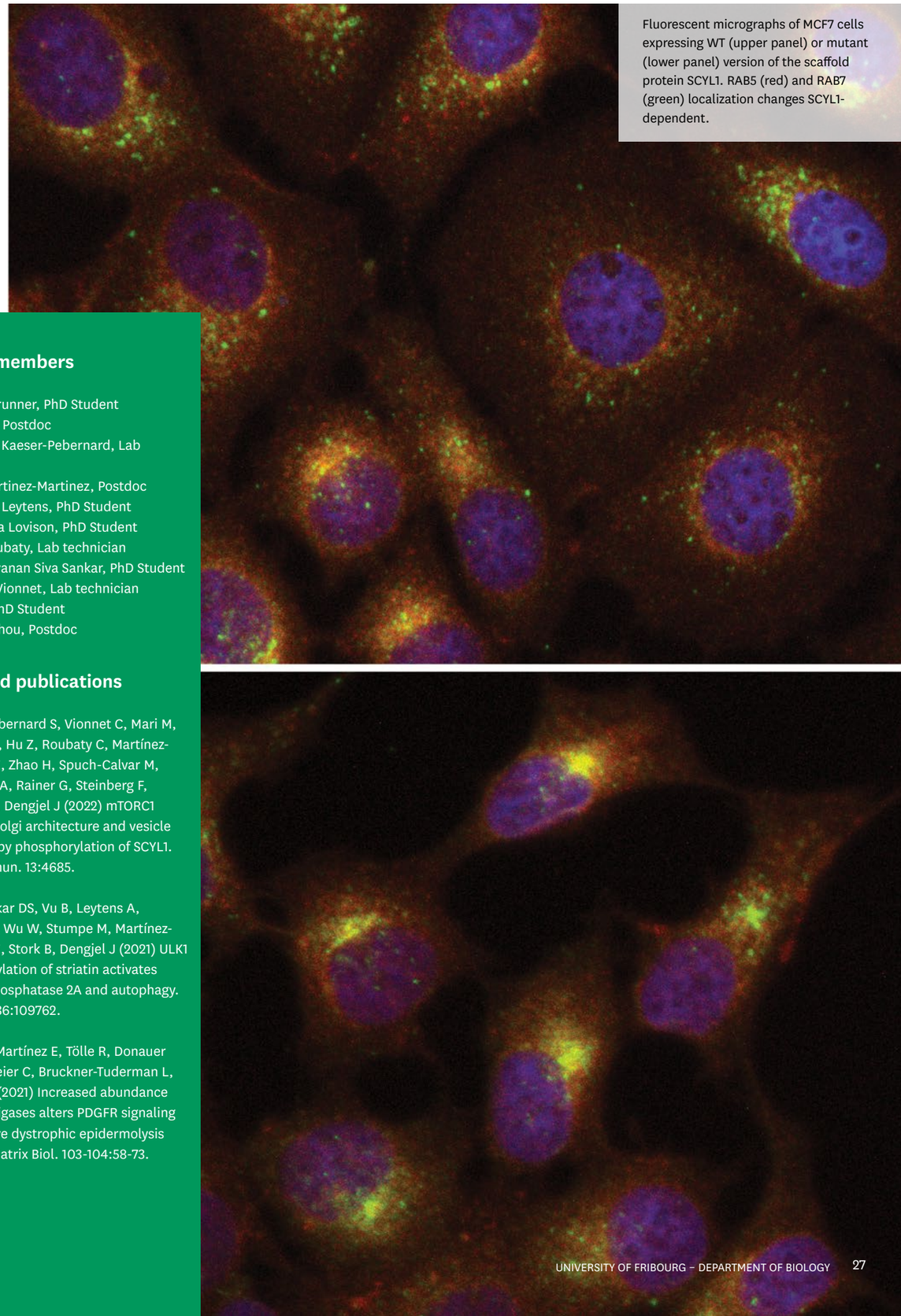
Stay healthy, recycle your proteome

Prof. Jörn Dengjel
Cellular signaling events regulating proteome homeostasis

We study the regulation of protein homeostasis focusing on protein degradation by autophagy, which is an evolutionary conserved, cytoprotective, lysosomal degradation pathway. Autophagy initiation is mainly regulated on a posttranslational level; hence, we study posttranslational protein modifications with the use of quantitative mass spectrometry-based proteomics to characterize mechanisms driving autophagy and regulating protein turnover.

One subtype of autophagy is macroautophagy (hereafter referred to as autophagy), in which new double membrane vesicles are formed, autophagosomes, which enwrap cellular cargo for lysosomal targeting. Initially, autophagy was regarded as non-specific lysosomal degradation pathway; however, it is now clear that autophagy can be very specific leading to the degradation of defined subsets of organelles and/or proteins, especially under stress conditions. Dysregulation of autophagy has been linked to ageing as well as to many human diseases, most notably to neurodegeneration and cancer. We aim to characterize new proteins being crucial for functional autophagy, or being specifically degraded by autophagy, presumably to ensure cell survival under stress conditions. In parallel, we study proteins known to be involved in autophagy regulation, specifically kinases and phosphatases, to better understand their function and to be able to better assess their potential to be used in therapy. A special focus is the crosstalk between the cellular microenvironment, i.e. extracellular matrix and soluble proteins, and autophagy regulators. Here, we use skin as a model system to study the role of autophagy in wound healing employing primary skin fibroblasts and keratinocytes in 3D cell culture systems.

> “Constant turnover is the goal”



Fluorescent micrographs of MCF7 cells expressing WT (upper panel) or mutant (lower panel) version of the scaffold protein SCYL1. RAB5 (red) and RAB7 (green) localization changes SCYL1-dependent.

Group members

Melanie Brunner, PhD Student
Zehan Hu, Postdoc
Stéphanie Kaeser-Pebernard, Lab Manager
Esther Martinez-Martinez, Postdoc
Alexandre Leytens, PhD Student
Alessandra Lovison, PhD Student
Carole Roubaty, Lab technician
Devanarayanan Siva Sankar, PhD Student
Christine Vionnet, Lab technician
Bich Vu, PhD Student
Jianwen Zhou, Postdoc

Selected publications

Kaeser-Pebernard S, Vionnet C, Mari M, Sankar DS, Hu Z, Roubaty C, Martínez-Martínez E, Zhao H, Spuch-Calvar M, Petri-Fink A, Rainer G, Steinberg F, Reggiori F, Dengjel J (2022) mTORC1 controls Golgi architecture and vesicle secretion by phosphorylation of SCYL1. Nat Commun. 13:4685.

Hu Z, Sankar DS, Vu B, Leytens A, Vionnet C, Wu W, Stumpe M, Martínez-Martínez E, Stork B, Dengjel J (2021) ULK1 phosphorylation of striatin activates protein phosphatase 2A and autophagy. Cell Rep. 36:109762.

Martínez-Martínez E, Tölle R, Donauer J, Gretzmeier C, Bruckner-Tuderman L, Dengjel J (2021) Increased abundance of Cbl E3 ligases alters PDGFR signaling in recessive dystrophic epidermolysis bullosa. Matrix Biol. 103-104:58-73.

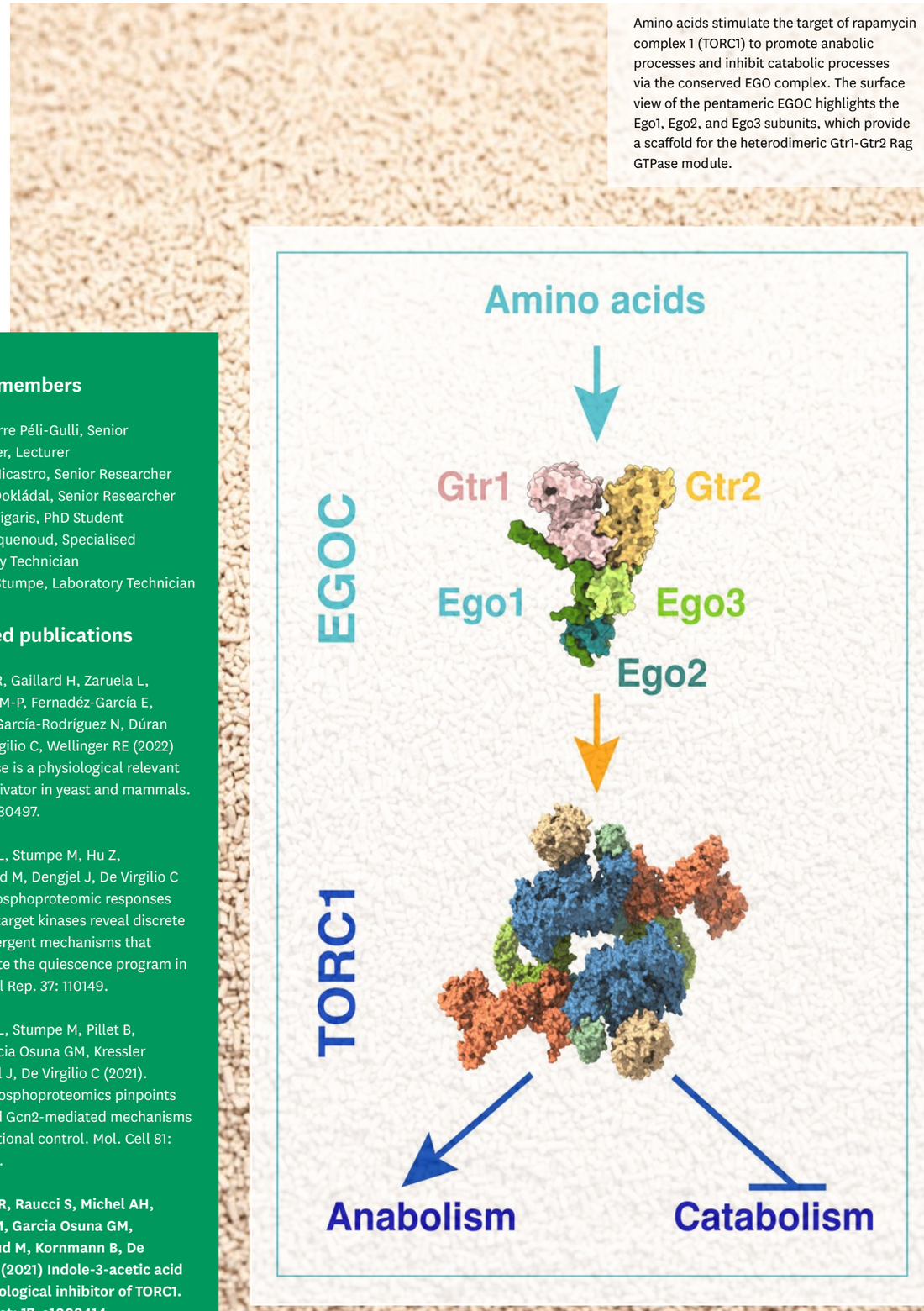
Nutrients and Cell Proliferation

Baker's yeast with an EGO complex

Prof. Claudio De Virgilio
Nutrient signaling and control of quiescence in yeast

All living cells can exit the normal cell cycle and enter into a resting state termed quiescence or G0. Interestingly, most eukaryotic cells, whether they exist as single cells or as part of a multi-cellular organism, spend most of their life time in such a quiescent state. The regulatory mechanisms controlling entry into or exit from quiescence, however, are still largely elusive. Because the disruption of these mechanisms is associated with cellular transformation (in multi-cellular organisms) or dramatically reduced life span (in unicellular organisms), research in this area will likely enhance our basic understanding of diseases such as cancer and be instrumental for the development of diagnostic and therapeutic tools to treat these diseases. To address the basic aspects of quiescence experimentally, we study the unicellular eukaryote baker's yeast as a model system. Our current data indicate that a conserved protein complex, coined target of rapamycin complex 1 (TORC1), plays a central role in yeast in coordinating both entry into and exit from G0 in response to nutrient levels. This fits well with the role of TORC1 in coupling nutrient, energy, and hormonal signals with cell growth, division, and metabolism in higher eukaryotes. Notably, amino acids are important and primeval cues that stimulate TORC1 to promote anabolic processes and inhibit catabolic processes via the conserved Rag GTPases. The latter assemble into heterodimeric complexes consisting of Gtr1 and Gtr2 in yeast, or RagA or RagB and RagC or RagD in mammalian cells, and are integral to larger complexes coined EGO (exit from rapamycin-induced growth arrest) complex (EGOC) in yeast or Rag-Ragulator complex in mammalian cells. In this context, our current research is focused on deciphering the amino-acid sensitive events upstream of the Rag GTPases in yeast. Due to the evolutionary conservation of the EGOC and its regulators, we expect our studies to contribute to the understanding of the molecular mechanisms leading to diseases that are associated with hyperactive mammalian TORC1 including cancer, type 2 diabetes, and neurodegeneration.

> "A little eukaryote makes big contributions to science"



Amino acids stimulate the target of rapamycin complex 1 (TORC1) to promote anabolic processes and inhibit catabolic processes via the conserved EGO complex. The surface view of the pentameric EGOC highlights the Ego1, Ego2, and Ego3 subunits, which provide a scaffold for the heterodimeric Gtr1-Gtr2 Rag GTPase module.

Group members

Marie-Pierre Péli-Gulli, Senior Researcher, Lecturer
Raffaele Nicastro, Senior Researcher
Ladislav Dokládal, Senior Researcher
Marco Caligaris, PhD Student
Malika Jaquenoud, Specialised Laboratory Technician
Susanne Stumpe, Laboratory Technician

Selected publications

Nicastro R, Gaillard H, Zaruela L, Péli-Gulli M-P, Fernadéz-García E, Tomé M, García-Rodríguez N, Dúran RV, De Virgilio C, Wellinger RE (2022) Manganese is a physiological relevant TORC1 activator in yeast and mammals. eLife 11: e80497.

Dokládal L, Stumpe M, Hu Z, Jaquenoud M, Dengjel J, De Virgilio C (2021) Phosphoproteomic responses of TORC1 target kinases reveal discrete and convergent mechanisms that orchestrate the quiescence program in yeast. Cell Rep. 37: 110149.

Dokládal L, Stumpe M, Pillet B, Hu Z, Garcia Osuna GM, Kressler D, Dengjel J, De Virgilio C (2021). Global Phosphoproteomics pinpoints uncharted Gcn2-mediated mechanisms of translational control. Mol. Cell 81: 1879-1889.

Nicastro R, Raucci S, Michel AH, Stumpe M, Garcia Osuna GM, Jaquenoud M, Kornmann B, De Virgilio C (2021) Indole-3-acetic acid is a physiological inhibitor of TORC1. PLoS Genet: 17, e1009414.

Neural development

Neural stem cells, cycling fast and slow

Dr. Boris Egger
Neural stem cell states in the brain of *Drosophila melanogaster*

Stem cells have the remarkable ability to proliferate, self-renew and to give rise to the great variety of different cell types in our body. Tissue specific stem cells, such as neural stem cells generate the neurons and glial cells of the nervous system. During early brain development neural stem cells preferentially proliferate through symmetric divisions and thereby are expanding the progenitor pool. Later during development neural stem cells switch to an asymmetric division mode to self-renew and to generate daughter cells that might lose their mitotic potential and differentiate. The transitions from proliferation to differentiation are tightly regulated by a combination of cell extrinsic or environmental factors and by cell intrinsic factors. Genetic irregularities or failures in these neurodevelopmental programmes can lead to diseases such as microcephaly or brain tumours.

In our current research we focus on cell intrinsic regulators that control the different phases of the cell cycle in neural stem cells. We investigate how cell cycle regulators interact with stem cell state determinants to coordinate the transition from symmetrically to asymmetrically dividing neural stem cells.

We are also interested in how environmental factors interact with cell intrinsic regulators to determine stem cell states. Interestingly, stem cells are often found in niches that are maintained under low oxygen or hypoxia. Increased oxygen supply can be an instructive signal for the switch to genetic programmes initiating neurogenesis and differentiation.

> “Our findings are relevant for the understanding of neurodevelopmental processes in the brain”

To address our research questions, we use genetic methods and immunofluorescent labelling in the fruit fly model system *Drosophila melanogaster*. We monitor cell cycle phases and oxygen availability through genetically encoded biosensors and advanced live cell microscopy in the fly brain.

Many of the genetic element controlling neural stem cell states are highly evolutionary conserved. Therefore, our findings are relevant for the understanding of neurodevelopmental processes in healthy and diseased brains.

Image by Dotun Adeleye Adeyinka shows a developing brain hemisphere with attached eye imaginal disk. Neural stem cell states are labelled by immunofluorescence in blue and green. Mitotic cells are labelled in red while cells that have undergone S-phase are labelled in yellow.

Group members

Dotun Adeleye Adeyinka, PhD Student

Selected publications

Chippalkatti R, Egger B & Suter B (2020) Mms19 promotes spindle microtubule assembly in *Drosophila* neural stem cells. PLoS Genetics 16(11): e1008913 DOI: https://doi.org/10.1371/journal.pgen.1008913

Baccino-Calace M, Prieto D, Cantera R & Egger B (2020) Compartment and cell-type specific hypoxia responses in the developing *Drosophila* brain. Biology Open 9, bio053629 DOI: https://doi.org/10.1242/bio.053629

Miszczak K, & Egger B (2020) Live Cell Imaging of Neural Stem Cells in the *Drosophila* Larval Brain. In: Sprecher S. (eds) Brain Development. Methods in Molecular Biology, vol 2047. Humana, New York, NY DOI: https://doi.org/10.1007/978-1-4939-9732-9_9

Microbial Genomics & Metagenomics

Metagenomics: the living metaverse?

Dr. Laurent Falquet
Microbial Genomics & Metagenomics

We are surrounded and populated by billions of bacteria and other microbial organisms. Any place on Earth can host a bacterial community. Metagenomics allows for the study of these communities by leveraging on next generation sequencing techniques and bioinformatics analysis pipelines, it is like entering into a fantastic metaverse of small living organisms ant trying to understand its functioning.

Our group is involved in several projects focusing on metagenomics data in collaboration with other lab researchers. Here are some examples of questions we are trying to answer.

> “A fantastic metaverse of small organisms”

Can potato rhizospheric microbiome influence the health of the plant? E.g., by protecting the plant against pathogenic fungi. A collaboration with Prof. Weisskopf, UniFr.

Is there a link between the human baby gut microbiome inherited from his/her mother and the appearance of antibiotic resistance or developing asthma later in life? A collaboration with Prof. Zimmermann, UniFr & HFR (Volery et al, 2020).

Can a saliva microbial community help to distinguish human individuals better than genomic fingerprints? E.g., distinguish real twins? A collaboration with Profs. Taroni and Greub, Unil & CHUV. (Bozza et al, 2022)

Can a synthetic microbial community help to compost rice straw? A collaboration with Profs. Uribe and Barreto, Unal, Colombia.

We develop and extend pipelines with which several levels of analysis are performed, from taxonomic distribution, metagenome assembled genomes, antibiotic resistance genes detection, to pathways reconstruction.

We are part of the European COST Action Machine Learning for Microbiome (https://www.ml4microbiome.eu) (Moreno-Indias et al, 2021).

Other projects:
Toxin-Antitoxins in bacteria (Mansour et al, 2022; Hill et al, 2021)

Zooming into the microbiome

Group members

Vivien Pichon, PhD Student
Omer Cetiner, visiting scientist
Jeferyd Yepes Garcia , PhD Student

Selected publications

Bozza et al. Corrigendum to «A probabilistic approach to evaluate salivary microbiome in forensic science when the defense says: ‘It is my twin brother’» [Forensic Sci. Int. Genet. 57, 102638]. Forensic Sci Int Genet. 2022 Mar 31:102701. doi: 10.1016/j.fsigen.2022.102701. Erratum for: Forensic Sci Int Genet. 2022 Mar;57:102638.

Hill et al. Minimalistic mycoplasmas harbor different functional toxin-antitoxin systems. PLoS Genet. 2021 Oct 21;17(10):e1009365. doi: 10.1371/journal.pgen.1009365

Mansour et al. Substrate recognition and cryo-EM structure of the ribosome-bound TAC toxin of *Mycobacterium tuberculosis*. Nat Commun. 2022 May 12;13(1):2641. doi: 10.1038/s41467-022-30373-w

Moreno-Indias et al. Statistical and Machine Learning Techniques in Human Microbiome Studies: Contemporary Challenges and Solutions. Front Microbiol. 2021 Feb 22;12:635781. doi: 10.3389/fmicb.2021.635781.

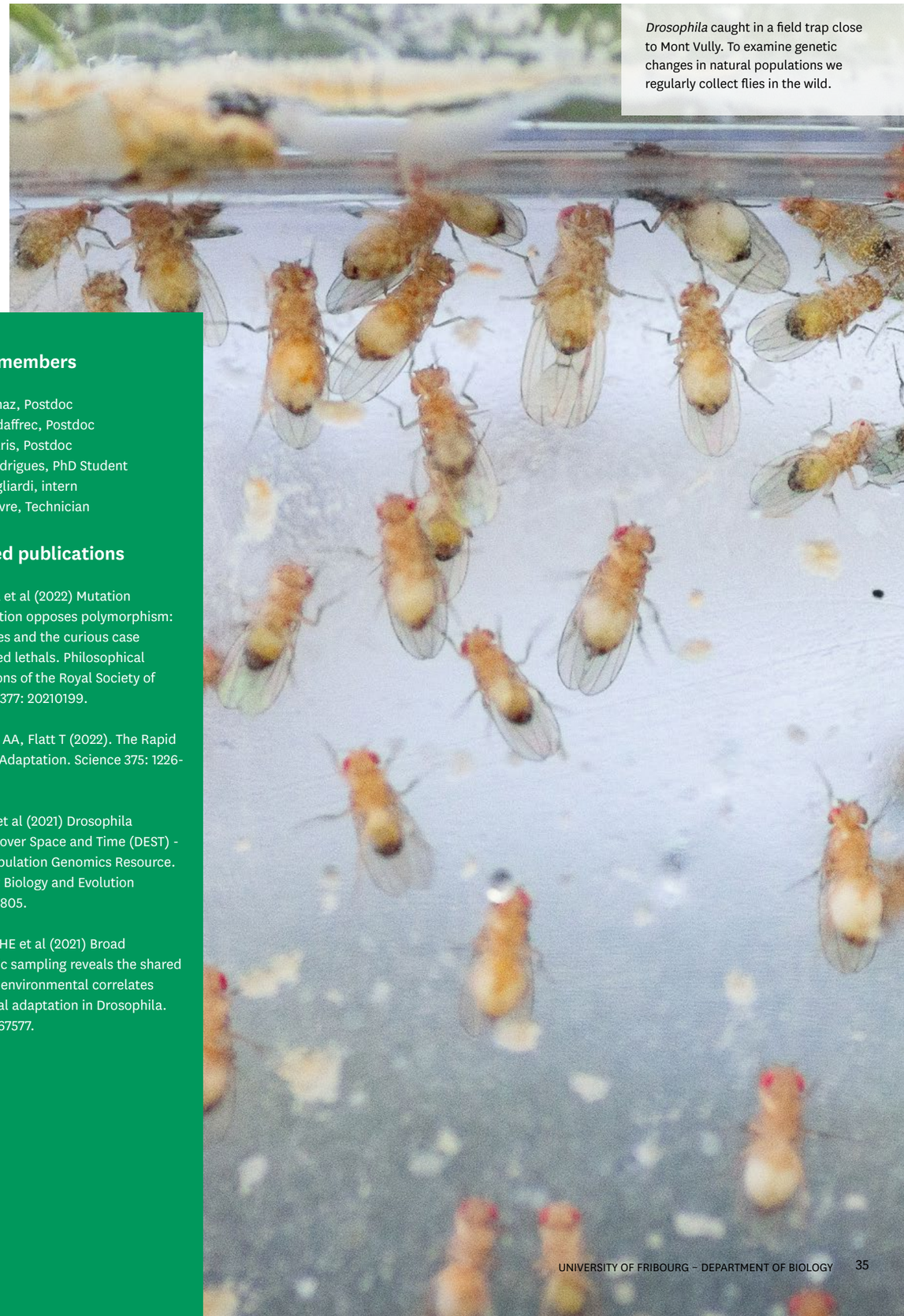
Population Genetics and Evolution

The Genetics of Selection and Adaptation

Prof. Thomas Flatt
Evolutionary Biology, Population Genetics

How do organisms adapt to the environment? Our research seeks to understand the genetic basis of selection and adaptation, using *Drosophila* as an experimental system. Much of our work has focused on the adaptive role of chromosomal inversions. Inversions are structural mutations that reverse a chromosome segment (and thus gene order) relative to the normal noninverted chromosome. The main property of inversions is that they suppress recombination in heterozygous state – this is thought to enable them to "capture" combinations of adaptive loci and protect them from being recombined away. To study the adaptive role of inversions, we have been investigating *In(3R)P*, a 8 Mb-long inversion spanning 1200 genes and exhibiting parallel frequency gradients (clines) on several continents, always at intermediate frequency in subtropical/tropical areas but absent in temperate areas. This compelling pattern led us to hypothesize that *In(3R)P* is a major driver of adaptation along latitudinal clines. Over the past 6 years, we have shown that *In(3R)P* (i) is maintained by spatially varying selection; (ii) undergoes seasonal fluctuations consistent with temporally varying selection; and (iii) affects major fitness traits (viability, size, stress resistance, lifespan). This inversion thus represents a 'supergene', a set of tightly linked loci affecting multiple complex traits. We are currently working towards elucidating its genetic architecture and the form of balancing selection that maintains it. Our research on this adaptive polymorphism contributes to the current 'renaissance' of the classical subject of the role of inversions in adaptation. More generally, our research program promises to yield new insights into the fundamental question of how genetic variation is being maintained.

> "Little is known about the genetic basis of adaptation"



Drosophila caught in a field trap close to Mont Vully. To examine genetic changes in natural populations we regularly collect flies in the wild.

Group members

Esra Durmaz, Postdoc
Envel Kerdaffrec, Postdoc
Margot Paris, Postdoc
Marisa Rodrigues, PhD Student
Fanny Gagliardi, intern
Patrick Favre, Technician

Selected publications

Berdan EL et al (2022) Mutation accumulation opposes polymorphism: Supergenes and the curious case of balanced lethals. Philosophical Transactions of the Royal Society of London B 377: 20210199.

Hoffmann AA, Flatt T (2022). The Rapid Tempo of Adaptation. Science 375: 1226-1227.

Kapun M et al (2021) Drosophila Evolution over Space and Time (DEST) - A New Population Genomics Resource. Molecular Biology and Evolution 38:5782–5805.

Machado HE et al (2021) Broad geographic sampling reveals the shared basis and environmental correlates of seasonal adaptation in Drosophila. eLife 10:e67577.

Plant hormone transport

When the hormones go crazy

Dr. Markus Geisler
Biochemical analysis of hormone transport in plants

My group has a long-lasting interest and expertise in analyzing transmembrane transport processes in plants on a biochemical level. Over the years we were able to assign transporters of different sub-classes to distinct plant hormones by analyzing their impact on plant physiology. However, our main focus still lies on the fascinating cell-to-cell movement of the plant hormone, auxin. This event, called polar auxin transport, represents a unique, plant-specific mechanism that virtually controls all aspects of plant growth and performance and represents a hotspot in plant biology.

> “Exploring the future without forgetting the past”

In 2021/22, we have demonstrated in collaboration with the Jasinski (Poznan) and Shani labs (Tel Aviv) the involvement of ABCG-type ABC transporters in the transport of the plant hormones, abscisic acid (ABA) and cytokinins. While a subset of ABA importers controls redundantly the long-distance translocation and thus ABA homeostasis (Zhang et al. 2021), ABCG56 from Medicago transports cytokinins involved in early stages of legume-rhizobia symbiosis (Jarzyniak et al. 2021).

Together with the Hegedus lab (Budapest) we have provided a quality control for DeepMind’s AlphaFold2 machine learning method allowing for structure prediction of transmembrane proteins by using subsets of ABC transporters (Hegedus et al. 2022). Our results strongly indicate that AlphaFold2 also performs astoundingly well in the case of transmembrane proteins and that the careful application of its structural models will also advance transmembrane protein-associated studies at an unexpected level.

In collaboration with the group of Leah band (Nottingham), we addressed the long-lasting question if polar auxin transport catalyzed by ABCB- and PIN-type exporters functions independently or not. By using a systems biology approach our results revealed that ABCB and PIN proteins mediate co-dependent auxin efflux (Mellor et al. 2022).

Finally, we investigated the role of the immunophilin, TWISTED DWARF1, functioning as a co-chaperone of ABCB-type auxin transporters, during flower development. Our work indicates that TWISTED DWARF1 (green fluorescence in picture) regulates Arabidopsis stamen elongation by differential activation of ABCB-mediated auxin transport (Liu et al 2022).

TWISTED DWARF1 (fused to CFP, green fluorescence) is highly expressed and regulates auxin homeostasis in the distal nectaries of the Arabidopsis flower.

Group members

Laurence Charrier, technician
Jie Liu, PhD Student
Jian Xia, PhD Student
Tashi Tsering, PhD Student
Francesca Iacobini, PhD Student

Selected publications

Liu J, Ghelli R, Cardarelli M, Geisler M (2022) TWISTED DWARF1 regulates Arabidopsis stamen elongation by differential activation of ABCB1, 19-mediated auxin transport. J. Exp. Bot. 73: 4818–4831

Mellor NL, Voß U, Ware A, Janes G, Barrack D, Bishopp A, Bennett MJ, Geisler MM, Wells DM, Band LR (2022) Systems approaches reveal that ABCB and PIN proteins mediate co-dependent auxin efflux. The Plant Cell 34: 2309-2327.

Hegedűs T, Geisler M, Lukács GL, Farkas B. (2022) Ins and outs of AlphaFold2 transmembrane protein structure predictions. Cell Mol Life Sci. 79: 73

Jarzyniak K, Banasiak J, Jamruszka T, Pawela A, Di Donato M, Novák O, Geisler M and Jasiński M (2021) Early stages of legume-rhizobia symbiosis are controlled by ABCG-mediated transport of active cytokinins. Nat. Plant 7: 428-436

Population Genetics

Mutation load during a species range expansion with mating system shift

Dr. Kimberly J. Gilbert
Evolutionary biology – theoretical and applied population genetics

All population exist over geographic space and through time. As environments change with time, this inevitably leads to the movement of populations of species to novel locations, expanding their species range. With climate change, such movements are expected to be more frequent and more drastic. Whether and how these moving populations survive and adapt to new environments is the key motivator to our research. Past studies show that as populations move over geographic space, population bottlenecks that are concurrent with colonizing new habitats lead to a reduction in the efficiency of selection and increased genetic drift. This process, known as gene surfing, can lead to a phenomenon termed expansion load, the reduction in a population's fitness due to the expansion process. This process has been observed in simulations under a wide range of parameter space and also observed in nature for many species, including humans during the out-of-Africa bottleneck in our species' past. There is debate over the prevalence and strength of this expansion load, and in natural populations of plants, there is an additional factor of self-fertilization.

Our most recent research is investigating expansion load through simulations and also with empirical data collected from *Arabis alpina*, an alpine perennial that has expanded its species range from Italy northward into France and Italy since the last glacial maximum. During this expansion, the species also shifted from largely outcrossing to largely self-fertilizing. Selfing is an interesting phenomena, largely considered as an evolutionary dead-end, but still favored evolutionarily under certain situations. We hope to disentangle the effects of range expansion and selfing within our species by comparison to simulations and therefore understand if selfing provided an advantage to purge any expansion load, or if it is simply a consequence of providing faster colonization ability. We have detected load in our samples of *A. alpina*, and through simulations have also found differing impacts of demographic history (range expansion) in combination with a shift to selfing. The expansion largely drives a significant increase in load, and differing degrees of simulated selfing only seem to purge the most lethal and the most recessive deleterious mutations. Whether and how this may have benefitted the range expansion of *A. alpina* and other plant species with shifting mating systems continues to be the focus of our research along with other related projects.

> "We study how populations (mal)adapt over space"

Arabis alpina growing in the Apennine mountain range of central Italy where the species is highly outcrossing, an area of glacial refugia before the species range expansion northward into Switzerland when it also underwent a shift to highly selfing.

Group members

Leo Zeitler, PhD Student

Selected publications

Gilbert KJ, Moinet A, Peischl S (2022) Gene surfing of underdominant alleles promotes formation of hybrid zones. Philosophical Transactions of the Royal Society B 377(1846): 20210006.

Gilbert KJ, Zdraljevic S, Cook DE, Cutter AD, Andersen EC, Baer CF (2022) The distribution of mutational effects on fitness in Caenorhabditis elegans inferred from standing genetic variation. Genetics 220(1): iyab166.

Peischl S, Gilbert KJ (2020) Evolution of dispersal can rescue population from expansion load. The American Naturalist 195(2): 349-360.

Gilbert KJ, Pouyet F, Excoffier L, Peischl S (2020) Transition from background selection to associative overdominance promotes diversity in regions of low recombination. Current Biology 30(1): 191-107.e3.

Nociception and plasticity

Worms telling us how to shut off pain

Prof. Dominique A. Glauser

Analysis of nociception and avoidance behaviours in *Caenorhabditis elegans*

Like most animals, we are able to detect damaging or potentially damaging stimuli, through a process called nociception. Nociception underlies key protective behaviours to avoid injuries and favour healing. However, in pathological situations, pain may become persistent with no actual benefit. Chronic pain affects more than a billion people worldwide. There is an essential need for improved pain management solutions, as available drugs display either detrimental side-effects or limited efficacy. Progress in the field is hindered in mammalian models by ethical concerns, by the complexity of the nervous system, as well as by the difficulty to bridge the gaps in our understanding at the molecular, neuronal, and physiological/behavioural levels.

> “Worm and human pain genes are strikingly similar”

We use the simple *Caenorhabditis elegans* worm as model to elucidate the mechanisms controlling nociception. We focused on recently identified human pain genes, whose functions are poorly understood. Via computer-assisted high-throughput behavioural genetic screens, we identified several dozen conserved worm mutants with impaired nociception and plasticity. Our work highlights the strong genetic conservation of nociceptive processes and provides a collection of new gene-specific models for further analyses. We currently combine cutting-edge *in vivo* imaging techniques, proteomic, transcriptomic, optogenetics and computer-assisted analysis of behaviour to better understand pain regulatory mechanisms at the molecular, cellular and circuit levels. As a whole, our integrative research both deepens our understanding of the mechanisms underlying pain sensation and aversive behaviours and brings insight on new potential drug targets for future pain treatment translational development.

High throughput readout of nociception: computer-assisted quantification of avoidance behaviour in *C. elegans* worm populations

Group members

Laurence Bulliard, lab technician
Georgina Gomez Saldivar, postdoc
Domenica Ippolito, Postdoc
Aurore Jordan, PhD Student
Filipe Marques, Postdoc
Martina Rudgalvyte, Postdoc
Lisa Schild, lab technician
Parvathi Sushama Gopinath, PhD Student
Saurabh Thapliyal, PhD Student

Selected publications

Glauser DA (2022) Temperature sensing and context-dependent thermal behavior in nematodes. Current opinion in neurobiology, 73, 102525.

Ippolito, D, Thapliyal, S, Glauser, DA (2021) Ca2+/CaM binding to CaMKI promotes IMA-3 importin binding and nuclear translocation in sensory neurons to control behavioral adaptation. eLife, 10, e71443.

Marques, F, Falquet, L, Vandewyer, E, Beets, I, Glauser, DA (2021). Signaling via the FLP-14/FRPR-19 neuropeptide pathway sustains nociceptive response to repeated noxious stimuli in C. elegans. PLoS genetics, 17(11), e1009880.

Marques, F, Thapliyal, S, Javer, A, Shrestha, P, Brown, A, Glauser, DA (2020). Tissue-specific isoforms of the single C. elegans Ryanodine receptor gene unc-68 control specific functions. PLoS genetics, 16(10), e1009102.

Plant Signaling

Chasing Peptide Signals in Plant Roots

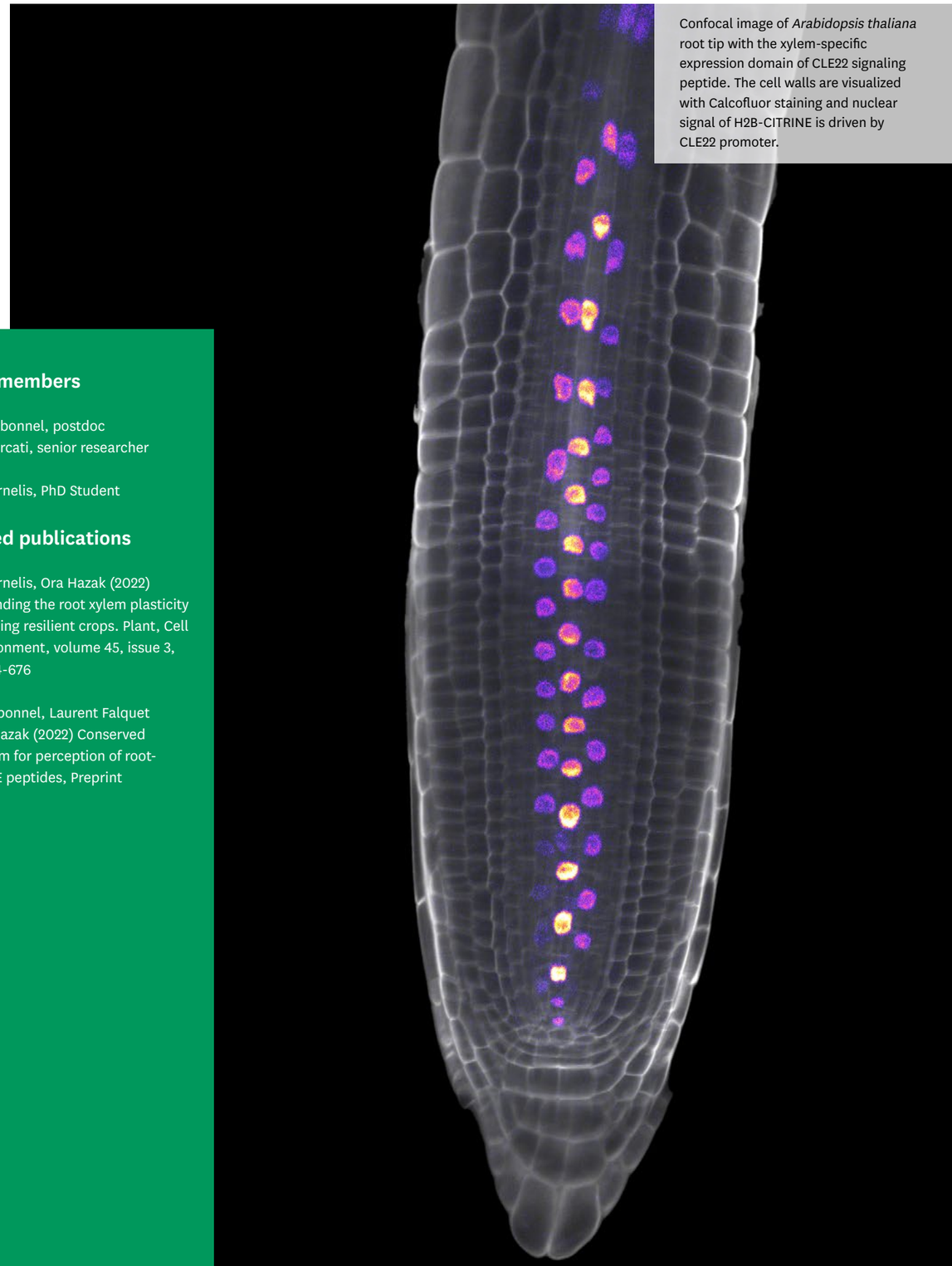
Dr. Ora Hazak
Receptor- peptide mediated pathways shaping vascular tissues

Our planet experiences climate change and associated global warming. With these conditions, plants face a challenge to grow and to produce expected yields. Looking into the future, we need to come up with good solutions how to protect plants and create stress resilient crops. Therefore, there is an urgent need to study how plants sense and respond to environmental stresses to gain insights into plant adaptation mechanisms. For example, plants close stomata (little openings in the leaves) in case of water deficiency; plants grow towards the light to increase the photosynthetic activity; roots avoid high salinity by growing away. But we still miss a deeper understanding of the main players in such adaptation mechanisms and additional circuits need to be described.

> “Cracking the adaptation mechanisms from the very tip of the root”

In plants, the vascular tissues transporting water and minerals (Xylem) and sugars and a myriad of signaling molecules (Phloem) play a central role in long-distance communication, distribution of vital compounds and providing a mechanical support to the plant body. These tissues are constantly produced by special meristematic cells that divide and differentiate. We aim in our research to uncover how water conducting tissue is formed and how environmental stresses affect morphology and functionality of this tissue. The previous work on xylem development uncovered key role of plant hormones like auxin and cytokinin in the early specification of vascular cells and later in differentiation of xylem. In our work, we uncover an additional layer of regulation of xylem formation, that is mediated by small signaling peptides and their cognate receptors. We could identify specific peptides that act fortifying the xylem vessels in Arabidopsis roots and we discovered a new peptide gene, that is essential for root phloem formation.

In addition to Arabidopsis, we use tomato as a plant model and we could recently identify new peptide signals. We now create mutants to be able to study the function of these new genes in tomato development and adaptation mechanisms.



Confocal image of *Arabidopsis thaliana* root tip with the xylem-specific expression domain of CLE22 signaling peptide. The cell walls are visualized with Calcofluor staining and nuclear signal of H2B-CITRINE is driven by CLE22 promoter.

Group members

Samy Carbonnel, postdoc
Sara Vimercati, senior researcher assistant
Salves Cornelis, PhD Student

Selected publications

Salves Cornelis, Ora Hazak (2022) Understanding the root xylem plasticity for designing resilient crops. Plant, Cell and Environment, volume 45, issue 3, pages 664-676

Samy Carbonnel, Laurent Falquet and Ora Hazak (2022) Conserved mechanism for perception of root-active CLE peptides, Preprint

between ecology and genetics

Application of genetic monitoring to the management of endangered species

Dr. Gwenaël Jacob
Conducting research at the interface between ecology and genetics

Early discussions with practitioners in charge of monitoring and managing threatened populations have highlighted several gaps in knowledge on the biology and ecology of Galliformes species, although they are among the most studied species. Brainstorming and workshops between researchers and practitioners allowed to define priorities in terms of conservation and to develop research projects to estimate relevant demographic parameters. Seemingly simple questions, such as estimating the number of individuals is in facts similar to the identification of criminals from partial DNA profiles in forensic science. This problem is non-trivial and remains unsolved. Dialog between research and practice allows to identify relevant research questions and to transfer recent scientific results into practice.

Research conducted since 2010 at University of Fribourg was used to establish strict guidelines for the genetic monitoring of Galliformes populations in the Jura and Vosges mountains, and in the Pre-Alps of the canton of Fribourg. Data collected in the frame of these monitoring programs allowed to estimate the demographic parameters essential for the management of the Capercaillie (*Tetrao urogallus*) and Hazel Grouse (*Tetrastes bonasia*) populations.

> “From species monitoring to research questions, and vice versa…”

The genetic monitoring of Galliformes populations also allows to quantify the risk and the magnitude of inbreeding depression in wild populations. This parameter, long ignored, is critical to define conservation strategies. The work carried out at the University of Fribourg has made it possible to make managers aware of the risk posed by inbreeding and thus, to reorient the National action plan for Capercaillie in France.

Part of the research in the group is carried out by MSc students who have the opportunity to develop and carry out their own research project, from the research question to the collection and analysis of data. Students choose their topics based on personal interest and curiosity, from studying the ecology of wood ants based on intensive field work (project completed) to studying ecology and behaviour of Capercaillie, inferred from data collected in the framework of the monitoring of the species in the Jura mountains (project in progress).

We apply forensic methods to better understand species ecology and identify factors limiting population growth. Management plans designed to promote population expansion lower the risk of species going locally extinct in the short term, and have the potential to restore species census sizes and distribution ranges in the mid- to long term.

Group members

Francesco Foletti, Technician

Selected publications

Cibois A, Beaud M, Foletti F, Gory G, Jacob G, Legrand N, Lepori L, Meier C, Rossi A, Wandeler P & Thibault, J. (2022) Cryptic Hybridization between Common (*Apus apus*) and Pallid (*A. pallidus*) Swifts. Ibis 164 (4), 981–997. https://doi.org/10.1111/ibi.13087.

Cayuela H, Prunier JG, Laporte M, Gippet JMW, Boualit L, Guérold F, Laurent A, Foletti F & Jacob G (2021) Demography, genetics, and decline of a spatially structured population of lekking bird. Oecologia 195 (1), 117–129. https://doi.org/10.1007/s00442-020-04808-4.

Cayuela H, Boualit L, Laporte M, Prunier JG, Preiss F, Laurent A, Foletti F, Clobert J & Jacob G 2019. Kin-dependent dispersal influences relatedness and genetic structuring in a lek system. Oecologia 191:97–112. DOI : 10.1007/s00442-019-04484-z

Regeneration in fish

How do fish regrow their injured body parts?

Prof. Anna Jazwinska
Exploring tissue plasticity in zebrafish and platies

A regrown limb, a renewed retina, or a functionally recovered heart would be a dream for people who have experienced severe injury due to accidents or disease. By contrast, some aquatic vertebrates have the natural power to regenerate their lost body parts nearly perfectly. In our research, we investigate how zebrafish and platyfish perform self-repair of various damaged organs.

We use small tropical fish as model organisms that can be maintained in suitably equipped lab aquaria. Although they are water dwellers, they share genetic and cellular similarities to terrestrial vertebrates, including humans, due to evolutionary conservation. We analyze biological processes in their organs using microscopy, histology, multi-color fluorescence imaging and detection of gene transcription. The results can be compared between species and the findings are of biomedical relevance.

> “Secrets of self-repair are swimming in aquaria”

From our recent progress, we would like to highlight three publications. First, we aimed to understand the embryonic origin of the zebrafish heart, which comprises one ventricle, as opposed to the mammalian heart with two ventricles. We found a cell-based compartmentalization of the zebrafish ventricle, despite the absence of a morphological separation in this chamber. This finding hints at the existence of a cellular scaffold for evolving a cardiac septum in terrestrial vertebrates. Our second study focused on platyfish. Closer examination of their tail skeleton revealed an unconventional contribution of dorsal tissue in the caudal fin, which is normally considered a ventral appendage. This reveals evolutionary innovations of the locomotory appendages among fishes. Thirdly, we addressed a question about the impact of mechanical forces on fin regeneration in zebrafish. In collaboration with the Department of Physics in Zürich, we found that viscous shear stress modulates the regrowing rays. This suggests that mechanical forces are involved in the fine-tuning of fin shape. Altogether, our research provides new biological perspectives by integration of knowledge across disciplines to understand the mystery of organ regeneration in fish.

Caudal skeleton of platyfish. Histological staining detects calcified bone (magenta) and non-calcified bone (cyan).

Group members

Catherine Pfefferli, Postdoc
Marta Wawrzyniak, Postdoc
Thomas Bise, PhD Student
Hendrik Oudhoff, PhD Student
Lana Rees, PhD Student
Verena Zimmermann, Technician

Selected publications

Dagenais, P., Blanchoud, S., Pury, D., Pfefferli, C., Aegerter-Wilmsen, T., Aegerter, C.M., and Jaźwińska, A. (2021). Hydrodynamic stress and phenotypic plasticity of the zebrafish regenerating fin. Journal of Experimental Biology 224, jeb242309. 10.1242/jeb.242309.

Pfefferli, C., Moran, H.R., Felker, A., Mosimann, C., and Jaźwińska, A. (2021). Persistent Ventricle Partitioning in the Adult Zebrafish Heart. J Cardiovasc Dev Dis 8. 10.3390/jcdd8040041.

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Conservation biology and biogeography

Biodiversity in peril: understanding the past, present and future of endangered species

Prof. Gregor Kozlowski
Diversity, distribution and genetics of relict, endemic and endangered plants

Natural ecosystems are under threat, species are disappearing at a rapid pace, and with them our livelihoods. The biodiversity crisis and the climate crisis are the two great ecological challenges of our time - and in many ways two sides of the same coin. Our research group aims in exploring various aspects of biology and biogeography of the endangered and rare species in order to then efficiently protect them.

One of the most important research topics of our group are woody species (trees, shrubs and lianas). The major model organisms since nearly 12 years are trees, mainly of the following families: Ulmaceae, Juglandaceae, Fagaceae, Pinaceae, Rosaceae and Fabaceae. More recently, we are investigating the ecology, phylogeny and phylogeography of an atypical woody shrub *Ptilostemon greuteri* (Asteraceae) endemic to Sicily, and the woody liana *Clematis alpina* (Ranunculaceae) across the European continent. Second very important research topic covers the biogeography, ecology and evolution of arctic-alpine and boreo-alpine taxa such as *Calamagrostis* (Poaceae), *Papaver* (Papaveraceae), *Arenaria* (Caryophyllaceae) as well as selected members of monilophytes (fern and allies).

> “Species are disappearing at a rapid pace”

Our group is directly linked with the Botanic Garden of the University of Fribourg (G. Kozlowski is a director of the garden), as well as intensively collaborating with the Adolphe Merkle Institute (AMI), with the Natural History Museum Fribourg (NHMF) and with the Office of Forest and Nature (SFN/WNA) of the State of Fribourg. Internationally, our group is tightly associated with the Shanghai Chenshan Botanic Garden in China (Plant Systematics and Evolutionary Biology Group at the Shanghai Chenshan Plant Science Research Center of the Chinese Academy of Sciences).

Pinus cembra is an extremely rare tree in Canton of Fribourg. Larger populations occur only along the Gastlosen chain.

Group members

Nicolas Küffer, Research Assistant
Laurence Fazan, PhD Student
Yann Fragnière, PhD Student
Sébastien Bétrisey, Research Assistant
Luca Champoud, Research Assistant-
Benoît Clément, Technician/gardener

Selected publications

Silva SV, Andermann T, Zizka A, Kozlowski G, Silvestro D. (2022). Global estimation and mapping of the conservation status of tree species using artificial intelligence. Frontiers in Plant Science 13: 839792.

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Ribosomal protein homeostasis

The life cycle of ribosomal proteins

Dr. Dieter Kressler
Analysis of eukaryotic ribosome biogenesis in *Saccharomyces cerevisiae*

Ribosomes are the molecular machines that carry out the synthesis of all cellular proteins from mRNA templates. Eukaryotic 80S ribosomes are composed of a small 40S and a large 60S subunit, which contain a total of four different ribosomal RNAs (rRNAs) and ~80 ribosomal proteins (r-proteins). Research carried out over the last 50 years, mainly with the yeast *Saccharomyces cerevisiae*, revealed that the biogenesis of eukaryotic ribosomes, i.e., the accurate piecing together of these rRNAs and r-proteins, is an extremely complex process.

> “Ribosomal protein production needs to be tightly regulated ”

My laboratory is interested in understanding how r-proteins, which are synthesized in the cytoplasm, safely reach their assembly site on pre-ribosomal subunits in the nucle(ol)us and how all the different r-proteins are provided in roughly equimolar amounts. Research over the last decade has revealed that several r-proteins require so-called dedicated chaperones to be protected from aggregation and get efficiently incorporated into pre-ribosomal subunits. Expecting that additional r-proteins also rely on such selective binding partners, our current research focuses on the identification, by applying a powerful proximity-labeling approach, and functional characterization of novel dedicated chaperones. In another project, we are exploring how the co-translational binding of dedicated chaperones influences the production of the r-protein client. Interestingly, we could recently show that the abundance of the *RPL3* and *RPL4* mRNAs decreases when the availability of the respective dedicated chaperone is limited and nascent Rpl3 and Rpl4 are instead recognized by a regulatory machinery that subjects the encoding mRNAs to degradation. Notably, deregulated expression of Rpl3 and Rpl4 leads to their massive aggregation and a perturbation of overall proteostasis in cells lacking the E3 ubiquitin ligase Tom1, which marks orphan r-proteins for degradation. We propose that this unprecedented regulatory mechanism adjusts the de novo synthesis of r-proteins to their actual consumption during ribosome assembly and, thereby, protects cells from the detrimental effects of their surplus production.

Deregulated expression of ribosomal proteins leads to their aggregation in the nucleus when they cannot be cleared by the ubiquitin-proteasome system. The image shows a dividing yeast cell (meshed contour) with aggregates of the ribosomal protein Rpl4 (orange) in the nucleus (blue).

Group members

Benjamin Pillet, Postdoc
Alfonso Méndez-Godoy, PhD Student
Sébastien Favre, PhD Student

Selected publications

Pillet B, Méndez-Godoy A, Murat G, Favre S, Stumpe M, Falquet L, Kressler D (2022) Dedicated chaperones coordinate co-translational regulation of ribosomal protein production with ribosome assembly to preserve proteostasis. eLife 11:e74255. doi: 10.7554/eLife.74255.

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Evolution of social behavior

The evolution and impact of socially transferred materials

Asst. Prof. Adria LeBoeuf
Superorganismal development

After just a few minutes of watching ants in your kitchen, you may observe them performing a behavior that looks like kissing. Upon closer inspection, you might even see droplets of fluid pass from one insect to another. This behavior is called trophallaxis.

Trophallaxis is a fluid-exchange behavior observed in ants, bees, wasps, termites, some nonsocial insects, and even in some birds and mammals. Amongst ants, some species engage in this behavior and others do not.

> “Ant colonies are distributed developing systems”

The fluid passed between ants during trophallaxis is rich with information beyond simply the food it contains. There are many components of trophallactic fluid produced by the ants, proteins, miRNA, nestmate recognition cues and growth hormones that enable complex communication and consensus building in ant colonies. Some of these growth-regulating components are under strong positive selection and influence larval development.

Our research harnesses this fluid exchange to study the evolution of behavior, indirect genetic effects, evolutionary economics, manipulation and control. We use proteomics, metabolomics and RNA sequencing to explore these fluids passed between individuals and quantitative behavioral and developmental tracking to see how components of these fluids flow through the colony and impact receivers. We look over the ant phylogeny at how this fluid has evolved. Using big-data, fluorescence microscopy and computer vision, we monitor each individual in the colony, from a tiny larva to the queen, and observe how trophallactic fluid flows over the social network. We also use these tools to assess the function of transmitted molecules and to explore the evolutionary economics of collective investment in care.

What began as food-for-protection mutualism between ants, plants and honeydew-producing insects has evolved into an important social behavior instrumental in ants’ ecological dominance. The derived version of this behavior, seen in Formicine ants for example, creates a social circulatory system that enables within-colony cooperation and long-term collective decision making.

Infrared illuminated ants engaging in trophallaxis (white) and their surrounding nestmates pseudo-colored in red

Group members

Marie-Pierre Meurville, PhD Student
Matteo Negroni, Postdoc
Sanja Hakala, Postdoc
Haruna Fujioka, Postdoc
Guillaume Kuhn, animalier
Amritansh Vats, PhD Student
Jeanne Brülhart, technician

Selected publications

Hakala, S; Meurville, MP; Stumpe, M; LeBoeuf, AC (2021) Biomarkers in a socially exchanged fluid reflect colony maturity, behavior and distributed metabolism. eLife 10.7554/eLife.74005

Meurville, MP; LeBoeuf, AC (2021) Trophallaxis: the functions and evolution of social fluid exchange in ant colonies (Hymenoptera: Formicidae). Myrmecological News 31: 1-30

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To double or not to double...

How do plant genomes evolve across heterogeneous environments?

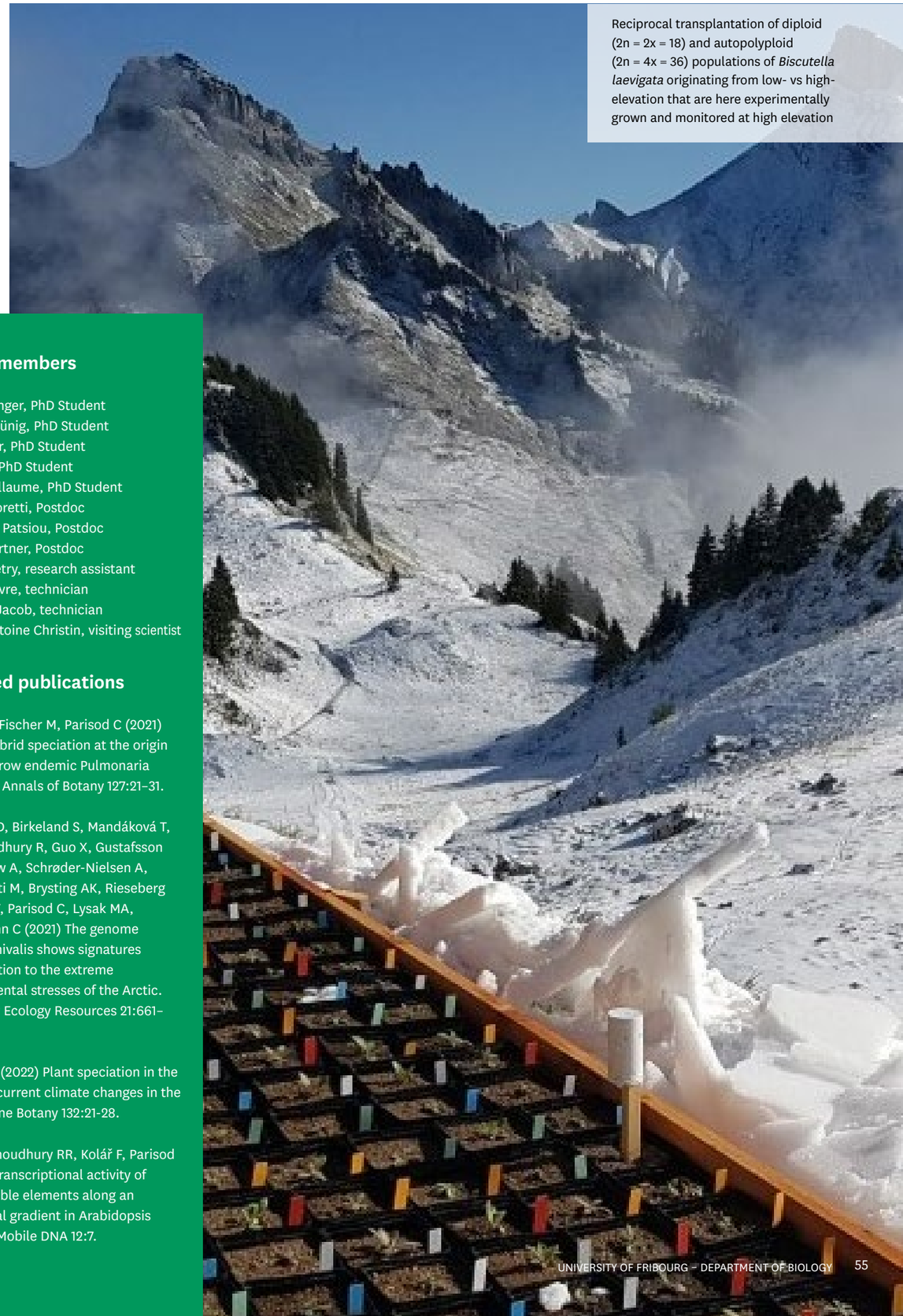
Prof. Christian Parisod
Plant Ecological Genomics

Plants have evolved sophisticated responses to environmental changes in order to survive and reproduce, and are usually adapted to the climate and the other species that they experience across their distribution range. In our lab, we use various plant species to address the genetics of such local adaptation and how it promotes the origin of new species in the face of climate changes.

To do so, we characterize plants from natural and experimental populations using high-throughput approaches and we assess processes having shaped genomic and phenotypic variation. For instance, we have shown that a narrow endemic species, *Pulmonaria helvetica* growing across only 1000 km2 in cantons Vaud and Fribourg, originated recently through the hybridization of two species having recolonized the space left by the retreat of glaciers. In that case, 1 + 1 gave 3 species and the conservation of that new, original species is of great importance for Switzerland.

Our current focus is on the consequences of whole genome duplication (or autopolyploidy) for the evolutionary radiation of plants. It is indeed largely unknown to what extent the doubling of all chromosomes promotes or hinders plant adaptation across environmental gradients. We have thus assembled genomes and transcriptome atlases of arctic-alpine relatives of the model plant *Arabidopsis thaliana* to investigate how duplicated genes as well as transposable elements respond to various environmental stresses. We are now using a textbook example of autopolyploidy under climate changes (*Biscutella laevigata*) to investigate diploid and polyploid populations from low- vs high-elevation and to integrate the genomic and environmental drivers of plant diversification in the Alps. In that case, we still do not understand what 1 x 2 yields.

> “A century that plants are known to abruptly double their genes, but is it good or bad?”



Reciprocal transplantation of diploid (2n = 2x = 18) and autopolyploid (2n = 4x = 36) populations of *Biscutella laevigata* originating from low- vs high-elevation that are here experimentally grown and monitored at high elevation

Group members

Marc Beringer, PhD Student
Sandra Grünig, PhD Student
Leo Zeitler, PhD Student
Vera Ogi, PhD Student
Annie Guillaume, PhD Student
Manuel Poretti, Postdoc
Theofania Patsiou, Postdoc
Martin Certner, Postdoc
Adrian Metry, research assistant
Patrick Favre, technician
Gwenael Jacob, technician
Pascal-Antoine Christin, visiting scientist

Selected publications

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RNA and developmental biology

How do germ cells choose their destiny?

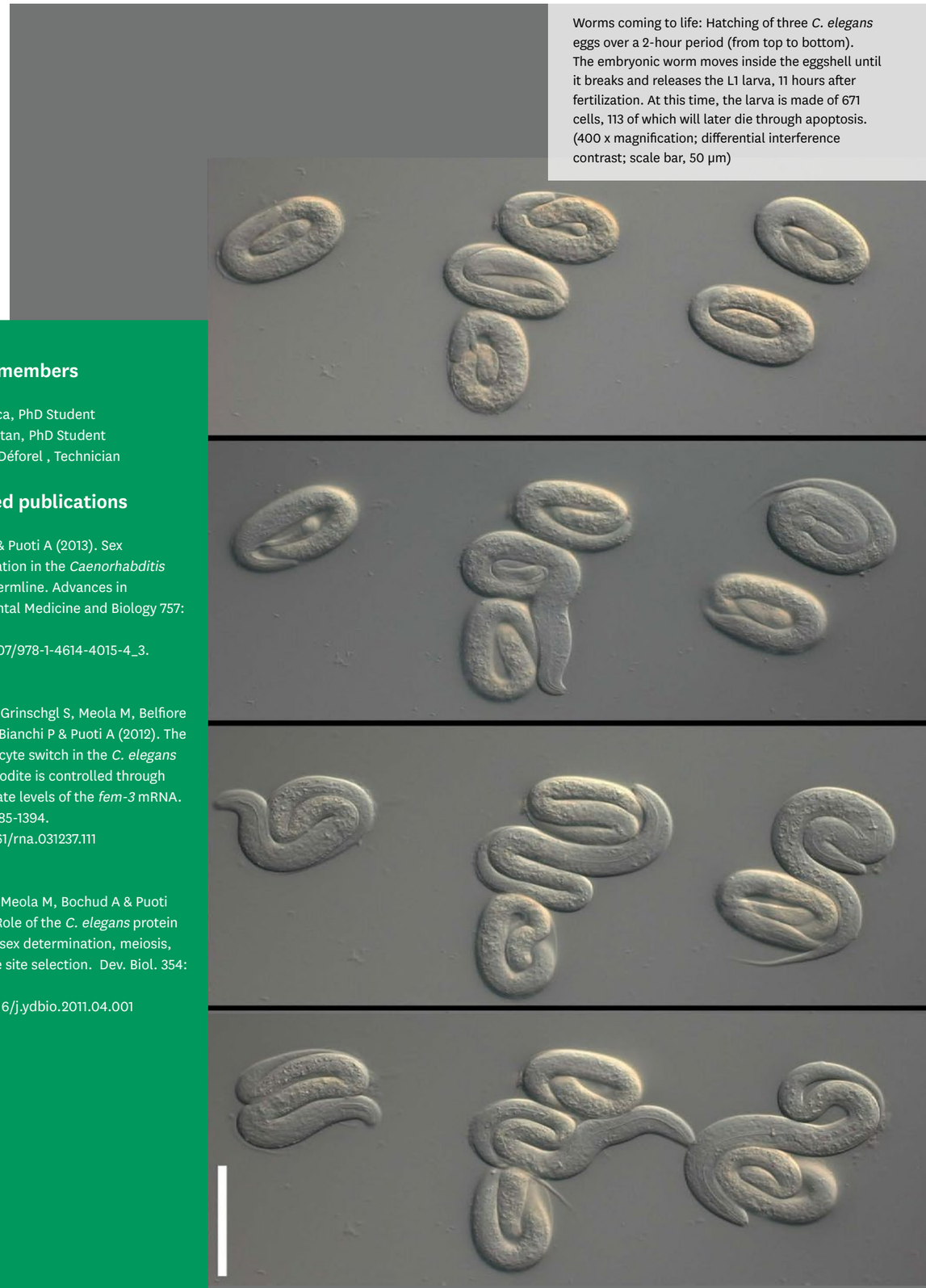
Dr. Alessandro Puoti
Genetic networks regulating gamete sex determination in *Caenorhabditis elegans*

While spermatozoans and oocytes usually originate separately from male and female organisms, the hermaphroditic nematode *Caenorhabditis elegans* produces spermatids during larval development and oocytes as an adult. Consequently, gametes of both sexes are derived from the same pool of precursors. A central question in our laboratory is how this decision is made at the molecular level.

The switch from spermatogenesis to oogenesis in *C. elegans* hermaphrodites is controlled through post-transcriptional mechanisms, comprising the stabilization or decay of specific mRNAs, the processing of pre-mRNAs, and of course the regulation of translation. Our laboratory focuses on the role of genes that have been identified through mutant screens for hermaphrodites that show abnormal gamete sex determination. For example, the *mog* genes are needed for the switch from spermatogenesis to oogenesis in the transition from the L4 larva to the young adult hermaphrodite. *mog* loss-of-function mutants never switch to oogenesis in their otherwise female body, but continue producing spermatids throughout their life. Intriguingly, *C. elegans mog* genes code for proteins that are homologous to vertebrate and yeast pre-mRNA splicing factors. Consequently, some aspects of sex determination in worms may depend on the splicing of specific target mRNAs. Central questions include the identification of such target mRNAs, and their respective molecular roles. In this context, we study mRNAs that are deregulated in *mog* mutants and the role of splicing signals for default versus alternative splicing.

> “Big decisions in a small worm”

With its reproductive cycle of only 3 days, *C. elegans* offers powerful genetic, biochemical, and molecular tools. The availability of numerous mutant alleles, and if needed, the possibility to create mutants by genome editing, allows to investigate genetic pathways and their role in regulating sex determination of germ cells.



Worms coming to life: Hatching of three *C. elegans* eggs over a 2-hour period (from top to bottom). The embryonic worm moves inside the eggshell until it breaks and releases the L1 larva, 11 hours after fertilization. At this time, the larva is made of 671 cells, 113 of which will later die through apoptosis. (400 x magnification; differential interference contrast; scale bar, 50 µm)

Group members

Maria Tarca, PhD Student
Aimen Sultan, PhD Student
Christine Déforel , Technician

Selected publications

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Plant Immunity

How do plants fight microbial threats and how do microbes deal with plant defences?

Prof. Stefanie Ranf
Plant-bacteria interactions

Plants have a multi-layered immune system with extra- and intracellular immune receptors that sense danger signals such as microbe-derived molecules and cellular perturbations caused by the microbes. Receptor activation triggers a variety of immune responses, both locally at the site of infection and systemically throughout the plant, to control microbial colonization. To overcome this robust host immune barrier, pathogens deploy virulence factors such as effectors and toxins that undermine plant immunity and promote their proliferation. In a continuous arms race, plants evolve new immune receptors and microbes develop new virulence factors.

> “ Microbes face a highly effective immune system in plants”

We focus on lipopolysaccharide, the main component of the cell wall of Gram-negative bacteria. Lipopolysaccharide is a complex and heterogenous glycolipid that is fascinating but also challenging to work with. We have identified the immune receptor LORE in crucifers that senses bacterial 3-hydroxy fatty acids, which are released during biosynthesis of lipopolysaccharide in Pseudomonas bacteria and probably via other, yet-unknown microbial pathways. We aim for a detailed understanding of the activation and regulation of the LORE receptor complex at the molecular level. Understanding the molecular mechanisms will provide the basis for future deployment of natural plant immune mechanisms in disease resistance engineering and sustainable plant protection strategies.

Complementarily, we are investigating how bacteria evade and adapt to plant immune responses. Lipopolysaccharide contributes to bacterial virulence by forming a protective barrier. In animal hosts, lipopolysaccharide remodelling is a prominent bacterial virulence strategy to adapt to the hostile host niche, evade host immune sensing, and resist antimicrobial agents. The role of lipopolysaccharide as a virulence factor in plant-bacteria interactions is poorly understood. We explore whether and how bacteria modulate lipopolysaccharide metabolism to evade LORE immune sensing and promote plant colonization and uncover the underlying molecular mechanisms.

Xanthomonas bacteria (yellow) colonizing a leaf of *Arabidopsis thaliana*. Plant cell membranes are stained in red.

Group members

Katia Zbinden, Lab technician
Cheryl Pillonel, Lab technician
Priyanka Raviraj, PhD Student
Bruno K.M. Smet, PhD Student
Fan-Yu Yu, PhD Student
Lin-Jie Shu, senior researcher

Selected publications

Kutschera A, Dawid C, Gisch N, Schmid C, Lars Raasch L, Tim Gerster T, Schäffer M, Smakowska-Luzan E, Belkhadir Y, Vlot A C, Chandler C E, Schellenberger R, Schwudke D, Ernst R K, Dorey S, Hückelhoven R, Hofmann T, Ranf S (2019) Bacterial medium-chain 3-hydroxy fatty acid metabolites trigger immunity in Arabidopsis plants. Science 364: 178-181.

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The multifaceted functions of lipopolysaccharide in plant-bacteria interactions. Biochimie 159: 93-98.

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How Cells invade Cells

Cellular programs required for establishment and maintenance of symbiosis in plants

Prof. Didier Reinhardt
How plants control their fungal and bacterial symbionts

More than a decade ago, we have isolated from *Petunia hybrida* a new component required for symbiotic signaling in the arbuscular mycorrhizal (AM) symbiosis. Based on its two protein domains (VAP domain and ankyrin domain), the protein has been named VAPYRIN. Two other groups in the US independently identified the orthologous gene in another AM host (*Medicago truncatula*), thereby confirming the conserved function of VAPYRIN in AM symbiosis. Ever since, it's molecular function has been explored, however, apart from multiple interacting proteins that highlight a relation to cellular secretion (exocytosis), the molecular function of VAPYRIN remained elusive. We have recently isolated a new *vapyrin* alleles that has a transposon insertion in close proximity to the stop codon (leaving only six codons intact, and therefore causing a complete null allele). In this new allele, we observed a general activation of cellular defense mechanisms such as cell wall reinforcement and accumulation of lignin (Chen et al., 2021). In addition, many molecular markers for defense (Pathogenesis-Related (PR) proteins) are induced in *vapyrin* mutants, suggesting that one of the functions of VAPYRIN is to repress defense during symbiosis.

In an attempt to identify negative regulatory mechanisms that attenuate the extent of symbiosis, we identified the phytohormone gibberellic acid (GA) as a second messenger involved in inhibiting AM symbiosis under conditions of high nutrient supply (Nouri et al., 2021).

A vising student from Tunesia (Takwa Gritli) has performed an interesting study towards protection of an important fodder legume (Lathyrus cicero) by various combinations of beneficial microbes. This work is described in a paper that has recently been accepted for publication (Gritli et al., 2022).

> "Colonization of host cells is under tight control by a dedicated genetic symbiosis program."

An important collaboration with AMI on the protection of plants from microbial pathogens with the use of silica nanoparticles has been published as well (El-Shehety et al., 2021). This paper is highly recognized and is cited 3-4 times every month since its publication in March 2021.

Finally, two developmental topics that have been a focus of my lab were covered in two recent review articles. The first review deals with the developmental role of the phytohormone strigolactone in shoot architecture (Khuvung et al., 2022). This is a rather recent topic that emerged from an international COST project (STREAM, FA1206; https://www.cost.eu/actions/FA1206/). While this COST project has been terminated, a PhD Student (K. Khuvung) is following up on this. Lastly, we wrote a review on phyllotaxis (Reinhardt & Gola, 2022), that marks the end of my research in this domain of plant development. This article has been highlighted by the journal editor with the selection of our proposal for a cover illustration (see image).

Vegetative shoot tip of Norway spruce Picea abies with 8/13 spiral Fibonacci phyllotaxis. Two respective parastichies in the clockwise (red) and counterclockwise (blue) directions are highlighted (photo by R. Rutishauser)

Group members

Nazli Dursun, PhD Student
Min Chen, PhD Student
Khopeno Khuvung, PhD Student
Abdellatif Essahibi, Postdoc
Axelle Raisin, PhD Student
Laura Baude, PhD Student
Maro Widmer, Scientific Collaborator

Selected publications

M. Chen, S. Bruisson, L. Bapaume, G. Darbon, M. Schorderet, and D. Reinhardt. (2021). VAPYRIN attenuates defence by repressing PR gene induction and localized lignin accumulation during arbuscular mycorrhizal symbiosis of *Petunia hybrida*. New Phytologist 229, 3481-3496.

M. El-Shetehy, A. Moradi, M. Maceroni, D. Reinhardt, A. Petri-Fink, B. Rothen-Rutishauser, F. Mauch, and F. Schwab (2021). Silica nanoparticles enhance disease resistance in Arabidopsis plants. Nature Nanotechnology16, 344-353.

E. Nouri, R. Surve, L. Bapaume, M. Stumpe, M. Chen, Y. Zhang, C. Ruyter-Spira, H. Bouwmeester, G. Glauser, S. Bruisson, D. Reinhardt (2021). Phosphate suppression of arbuscular mycorrhizal symbiosis involves gibberellic acid signaling. Plant Cell Physiol. 62(6), 959-970.

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Eco-Evolutionary dynamics

Is eco-evolution an optimizing process?

Dr. Rudolf P. Rohr
Theoretical ecology and evolution

Understanding biodiversity maintenance and how it relates to the ecosystem functioning is a key question in ecology. During the last years, we have been developing new theoretical approaches to understand coexistence in species-rich communities — the structural approach of coexistence — and to the relationship between biodiversity and ecosystem-functioning (BEF). These concepts have paved the way to a new integrative view of biodiversity and ecosystem-functioning.

However, evolution has shown that it can act at short time scale (Gervasi & Schiestl 2017). Moreover, co-evolved communities differ from random experimental assemblages or non-coevolved communities. This pleads that one cannot fully understand biodiversity maintenance and ecosystem functioning without incorporating evolutionary aspects.

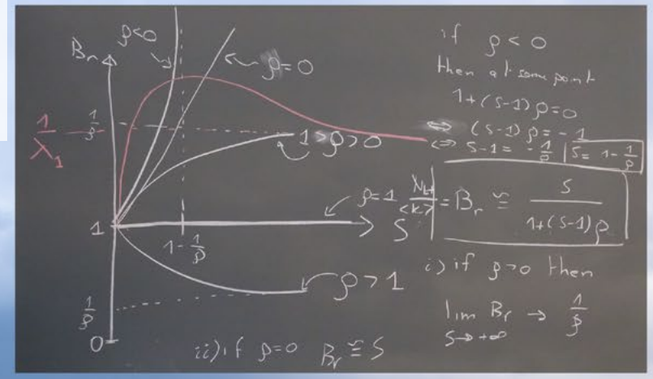
Our group aims at understanding to what extent eco-evolutionary dynamics impacts biodiversity and ecosystem-functioning, and in particular, whether eco-evolution optimizes emergent populations or communities' properties.

In a recent contribution, we study how eco-evolution impacts population properties such as growth rates and biomass production. Contrary to the common belief that evolution climbs the fitness landscape and maximizes growth rate or biomass production — r-selection or K-selection paradigm — we argue that this is a particular case of evolutive selection. Such particular cases arise when niche differentiation does not occur along evolutionary trajectories, and therefore, they are fundamentally incompatible with the emergence of polymorphism and ultimately of biodiversity through disruptive selection.

> "Evolution seldom optimizes emergent properties"

Upper panel: Mathematical models behind the biodiversity ecosystem-functioning relationship (Parin et al. 2018)

Lower panel: Projection of a co-evolutionary trajectory into the coexistence space



Group members

Vasco Lepori, PhD Student
Edgard Djahoui, PhD Student
Phuong Ngyuen, Postdoc

Selected publications

Saavedra S, Bartomeus I, Godoy O, Rohr RP, Zu P (2022) Towards a system-level causative knowledge of pollinator communities. Phil. Trans. R. Soc. B, 377:20210159.

Weinbach A, Loeuille N, Rohr RP (2022) Eco-evolutionary dynamics further weakens mutualsitic intersction and coexsitences under population decline. Evolutionary Ecology, 36: 373–387.

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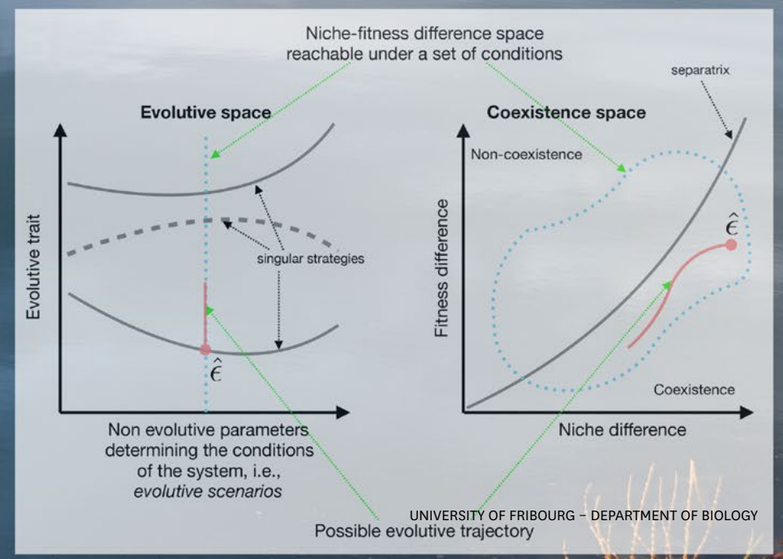

Storing Fat

A Highway Interconnects Lipid Droplets

Prof. Roger Schneiter
Lipid Droplet Biogenesis

Lipid droplets (LDs) are globular intracellular structures dedicated to the storage of fat in form of neutral lipids. LDs are closely associated with the major biosynthetic organelle of the cell, the endoplasmic reticulum (ER), both in yeast and mammalian cells. Unlike other cellular compartments, however, LDs are enclosed by an unusual membrane monolayer, which is continuous with the cytoplasmic leaflet of the ER membrane. LDs contain a specific set of proteins, many of which function in neutral lipid synthesis or degradation. How these proteins are exactly targeted to the LD surface is not fully understood. To address this question, we have devised a yeast mating-based microscopic readout to monitor the transfer of LD proteins upon zygote formation in living cells using three color time-lapse imaging. The results of this analysis indicate that fusion of the ER membrane between mating partners is required for the transfer of proteins between the LDs of the two cells. Interestingly, this transfer of proteins between individual LDs is continuous, bidirectional and affects most LDs simultaneously. In cells where otherwise LD-localized proteins are mis-localized to the ER, we observe that these proteins reach the LDs of the mating partner. These observations suggest that LDs do not fuse upon mating of yeast cells, but that they form a network that is interconnected through the ER membrane. Consistent with this, LD proteins rapidly move onto LDs of a mating partner and this protein transfer is affected by seipin, a protein important for proper LD biogenesis and the functional connection of LDs with the ER membrane.

> “Lipid droplets form an interconnected network”

Group members

Stéphanie Cottier, Postdoc
Aslihan Ekim Kocabey, Postdoc
Ola El Atab, Postdoc
Rasha Khaddaj, Postdoc
Jiri Stribny, Postdoc
Barkha Gupta, PhD Student
Juliette Graff, PhD Student
Zhū Han, PhD Student

Selected publications

Schneiter R, Choudhary V (2022). Seipin collaborates with the ER membrane to control the sites of lipid droplet formation. Curr Opin Cell Biol 75, 102070.

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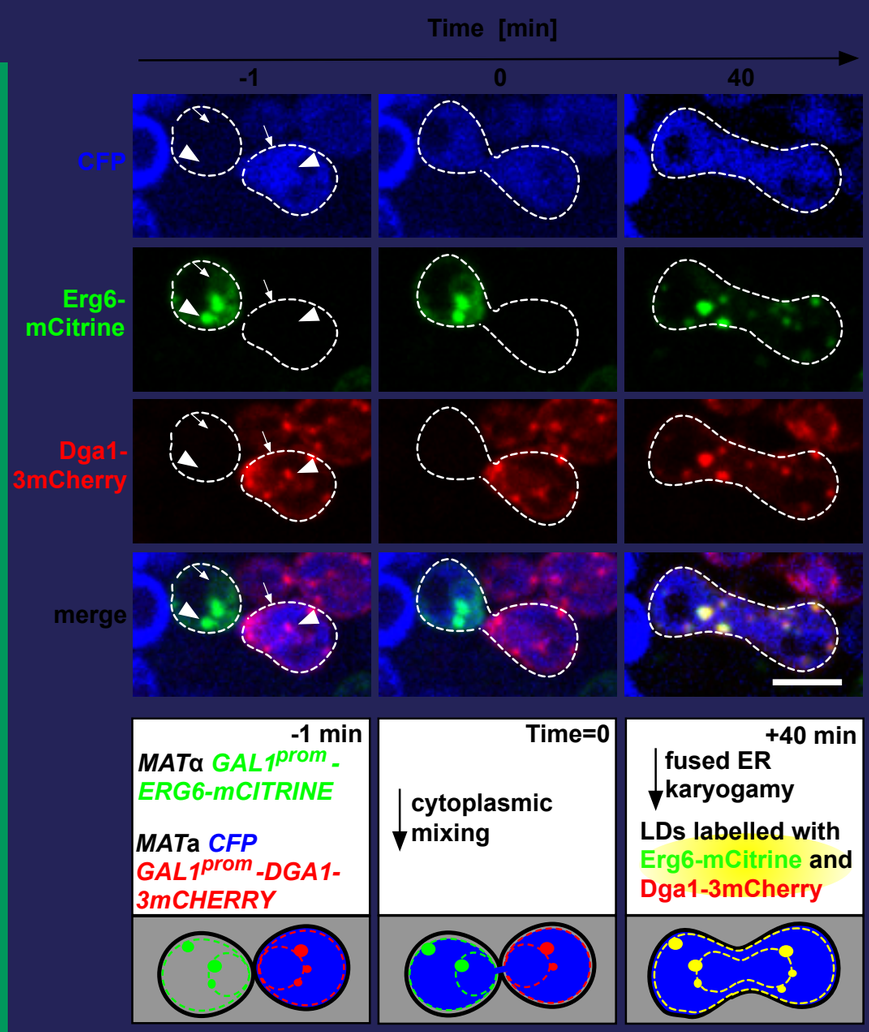
Cottier S, Schneiter R (2022). Lipid droplets form a network interconnected by the endoplasmic reticulum through which they equilibrate their proteins. J. Cell Sci. 135, doi: 10.1242/jcs.258819.

El Atab O, Ekim Kocabey A, Asojo O A, Schneiter R (2022). Prostate secretory protein 94 (PSP94) inhibits sterol-binding and export by the mammalian CAP protein CRISP2 in a calcium-sensitive manner. J. Biol. Chem. 298, 101600.



Experimental design to monitor the exchange of lipid droplet (LD) proteins upon mating and zygote formation. The exchange of LD-localized proteins is monitored by three color time-lapse imaging. MATa cells are co-expressing the red fluorescently labelled LD-protein Dga1–3mCherry with a soluble blue cytosolic CFP and MATα cells express Erg6–mCitrine (green). Time 0 of the mating event is defined as the time point of cytoplasmic mixing, monitored by the dispersion of the blue CFP into the newly formed zygote. Confocal sections for each of the three fluorophores are shown 1 min before (t=-1), at the time of cytoplasmic mixing (t=0), and 40 min after cell fusion had occurred. A schematic illustration of the mating event and transfer of marker proteins is shown to the right. Arrows point to the membrane of the endoplasmic reticulum, arrowheads to LDs. Dashed white lines indicate cell outlines. Scale bar: 5 µm.

Computational Evolutionary Biology

Computational methods to model and protect biodiversity

Asst. Prof. Daniele Silvestro
Computational Evolutionary and Conservation Biology

Biodiversity has been evolving on our planet for billions of years and has faced in the process countless challenges, including dramatic events of climate change, mass extinctions and mass diversification. Today, biodiversity is facing a number of new threats deriving from anthropogenic direct and indirect pressure. In our lab we develop computational tools to model and understand how biodiversity and ecosystems have evolved in the past. We also implement new methods using artificial intelligence to estimate the current status of biodiversity and to optimize conservation action and policies.

> “ We leverage AI to understand evolution and help protecting biodiversity ”

Our research typically involves the development and release of opensource software implementing new models. For instance, we have recently released new programs to infer dispersal and extinction dynamics through time from fossil datasets, an R package to approximate the extinction risk of modern species based on geographic occurrence data using machine learning, and a Python program for conservation planning using reinforcement learning. We also use these tools to carry out empirical studies. For example, we have recently mapped the origination and expansion of grasslands in North America using deep learning and estimated the current extinction risk across 50,000 species of trees.

We develop new software to model the past and future of biodiversity using fossil, phylogenetic and spatial data.

Group members

Bruna Farina, PhD Student
Rebecca Cooper, PhD Student
Ornela de Gasperin, Postdoc
Torsten Hauffe, Postdoc
Juan Carrillo, Postdoc
Tobias Andermann, Postdoc
Zhuo Zhou, Postdoc
Carlos Calderon del Cid, PhD Student
Bernard Koch, PhD Student

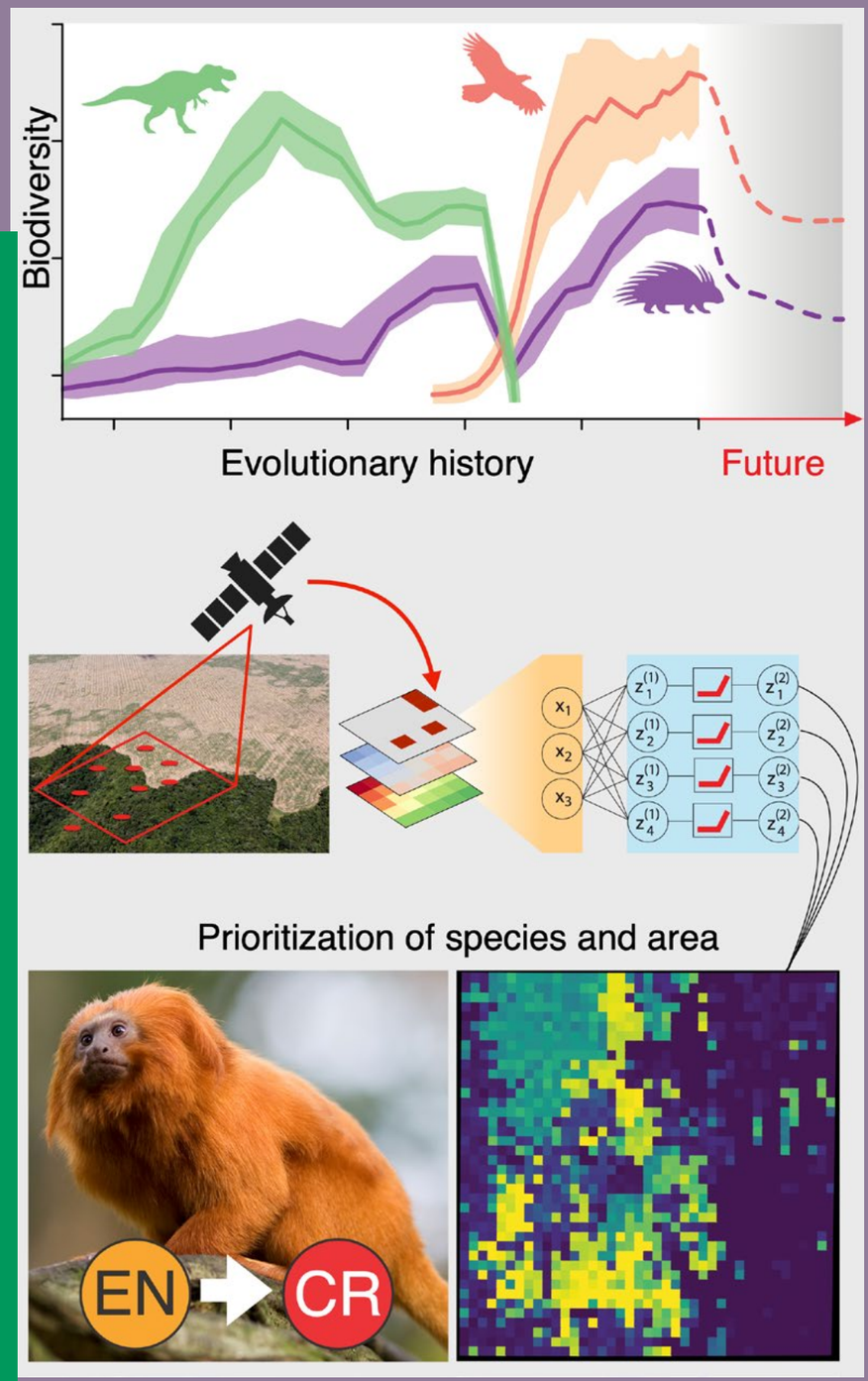
Selected publications

Andermann T, Strömberg C A E, Antonelli A, Silvestro D (2022). The origin and evolution of open habitats in North America inferred by deep learning models; Nature Communications: doi: 1 0. 1 038/s41 467-022-32300-5

Hauffe T, Quental T B, Pires M M, Silvestro D (2022). A quantitative framework to infer the effect of traits, diversity and environment on dispersal and extinction rates from fossils. Methods in Ecology and Evolution doi: 10.1111/2041-210X.13845

Silva S V, Andermann T, Zizka A, Kozlowski G, Silvestro D (2022). Global estimation and mapping of the conservation status of tree species using artificial intelligence. Frontiers in Plant Science, doi: 1 0.3389/ fpls.2022.839792

Silvestro D, Goria S, Sterner T, Antonelli A (2022). Improving biodiversity protection through artificial intelligence, Nature Sustainability, doi : 10.1038/s41 893-022-00851-6



Genetics and neurodegeneration

Deciphering how the brain functions: from sensory coding to neurodegeneration

Prof. Simon Sprecher
Cellular, molecular and functional neurogenetics using Drosophila and other invertebrates

The way our brain functions and what can go wrong during aging and in neurodegenerative diseases, remains still mostly a mystery. In particular with more than hundred billion neurons and a trillions of synaptic connections the human brain will remain unresolvable for decades despite rapid technical advances. Since the molecular and genetics nature of all nervous systems are shared among all animals the only way of understanding how the brain works is studying animal models with less complicated brains. In our laboratory we use diverse, impacting genetic model systems to understand the brain.

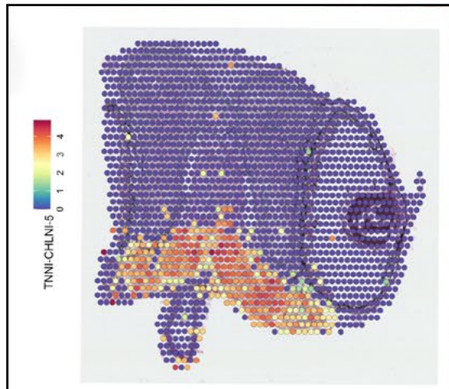
> “How do neurons make and forget memories?”

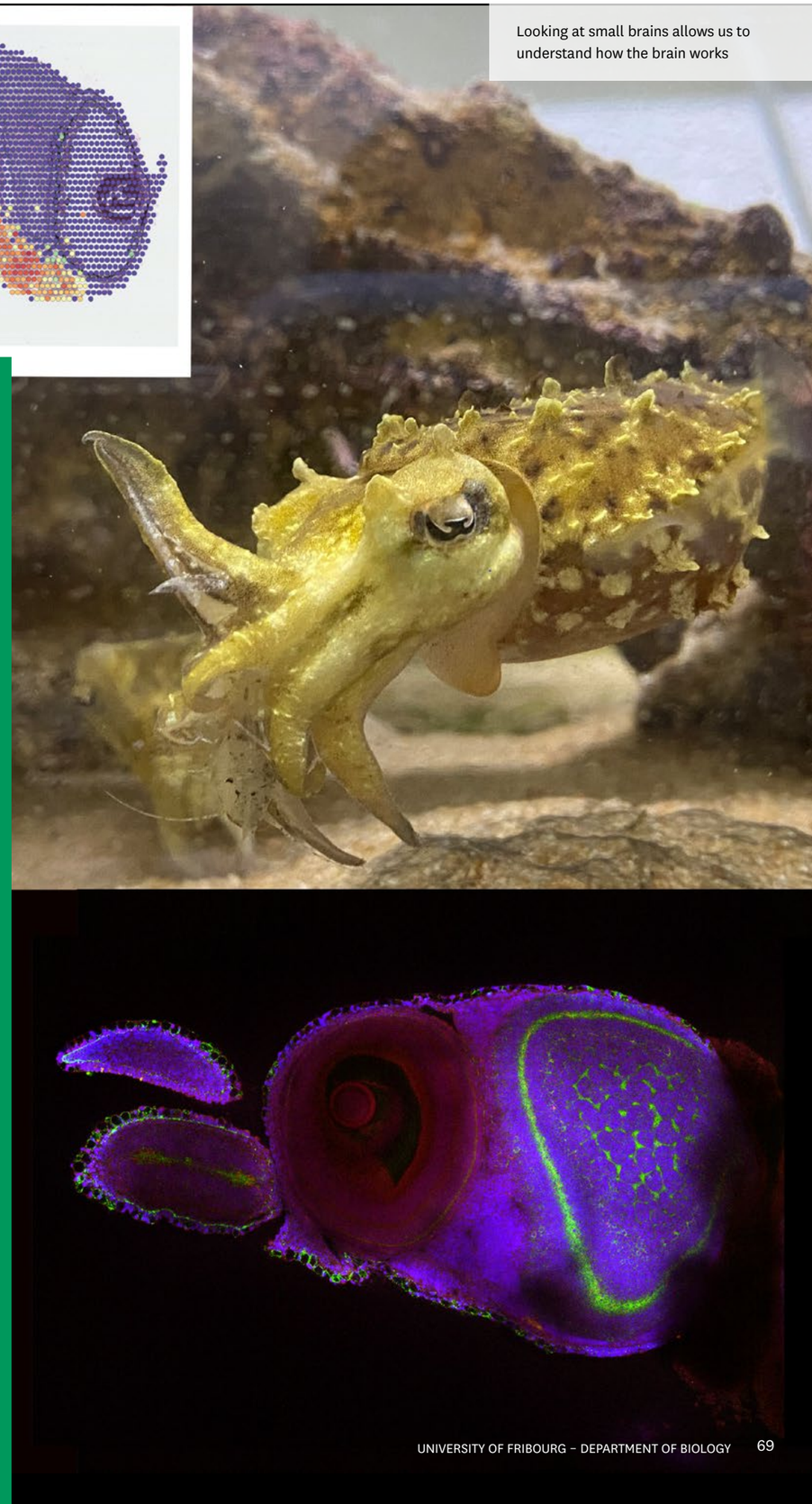
Dissecting the nervous system with single-cell resolution

The brain is without any doubt the most complex organ. How is such a complicated organ with thousands of highly interconnected cell types formed? How do cells know what how they fit into this complex puzzle? We study the genetic and molecular mechanisms that control the fate of neurons. Using single-cell transcriptomics in combination with powerful molecular genetic techniques we decipher the processes that allow neurons to diversify and how neural networks are able to function in the way they do.

Forgetting: humanizing flies to resolve dementia and neurodegeneration

While some memories are kept for years other memories are rapidly forgotten. However forgetting is not a passive, random process but underlies tightly controlled molecular machinery. Neurodegenerative diseases such as Alzheimers disease cause problems with the formation of memories or enhance the forgetting process. Studying the memory center of the fruit fly allows us to unveil these mechanisms. We therefore used CRISPR/Cas9 to convert the flies Alzheimer Precursor Protein gene to the hereditary mutations of human Alzheimer Precursor Proteins, allowing is to study the molecular and genetic processes of this disease.





Looking at small brains allows us to understand how the brain works

Group members

Jules Duruz, Postdoc
Jenifer Kaldun, Postdoc
Lucia de Andres, Postdoc
Marta Sprecher-Trujillo, Scientific collaborator
Ana Humbert, PhD Student
Larisa Maier, Postdoc
Abhishek Mishra, Postdoc
Noemi Sgammeglia, PhD Student
Gaelle Botton-Amiot, PhD Student
Al-Sayed Al-Soudy, Postdoc
Nikita Komarov, PhD Student
Cornelia Fritsch, Lab Technician

Selected publications

Sgammeglia N and Sprecher SG. Interplay between metabolic energy regulation and memory pathways in Drosophila.TRENDS IN NEUROSCIENCE. 2022 Jul;45(7):539-549. doi: 10.1016/j.tins.2022.04.007.

Maier GL, Komarov N, Meyenhofer F, Kwon JY and Sprecher SG. Taste sensing and sugar detection mechanisms in Drosophila larval primary taste center
eLife 8, e 67844

Kaldun JC, Lone SR, Humbert Camps AM, C Fritsch C, Widmer YF, Stein JV, Tomchik SM and Sprecher SG. Dopamine, sleep, and neuronal excitability modulate amyloid-b–mediated forgetting in Drosophila
PLoS Biology 19 (10), e3001412

AK Mishra, C Fritsch, R Voutev, RS Mann, SG Sprecher. Homothorax Controls a Binary Rhodopsin Switch in Drosophila Ocelli PLoS Genetics. 2021 Jul 27;17(7):e1009460.IF: 5.5

Lipid Metabolism

How is fat stored, transported, and utilized in our cells?

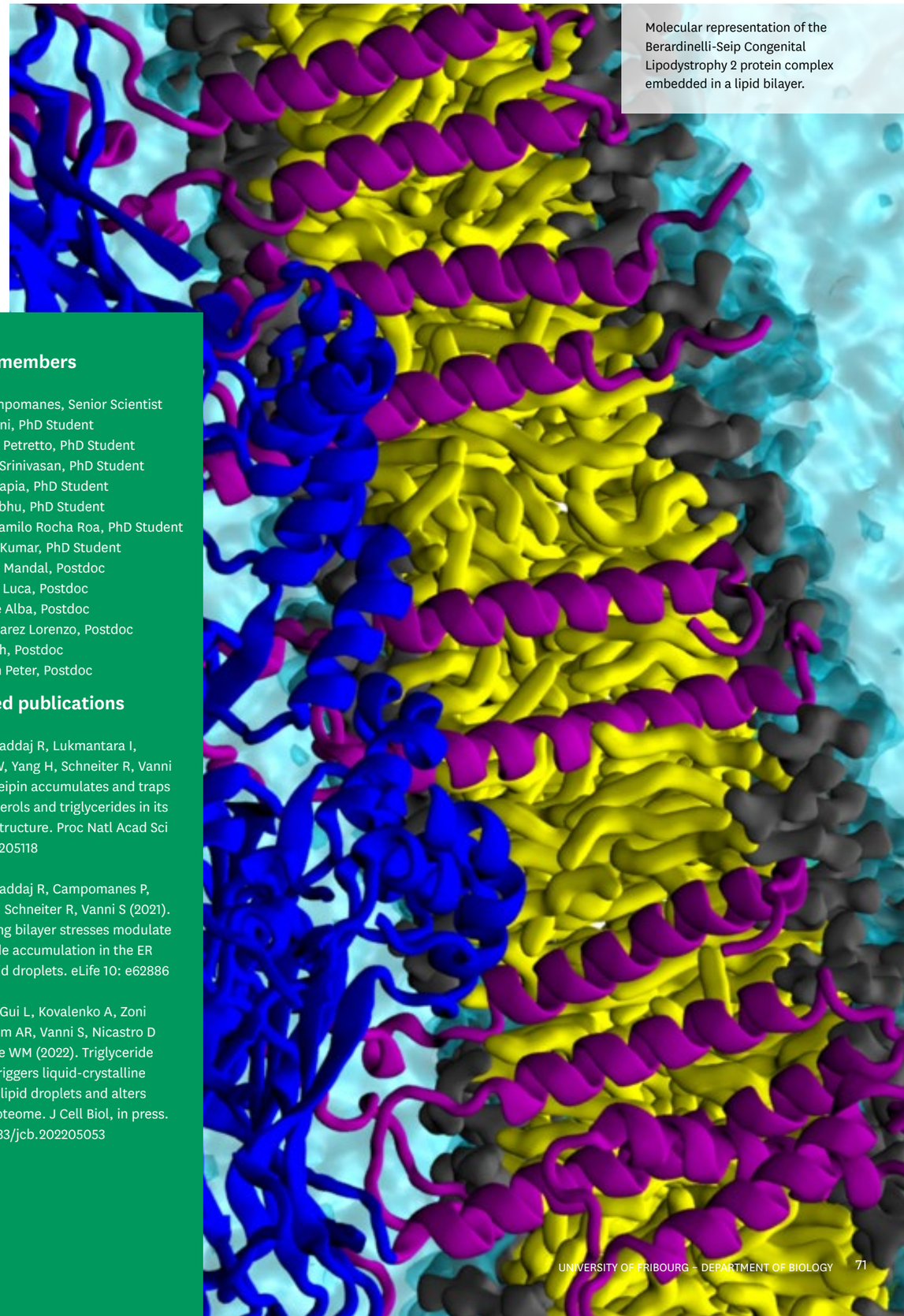
Prof. Stefano Vanni
Molecular Biophysics of cellular membranes

In our lab, we use computer simulations to understand the inner workings of cells down to molecule-by-molecule and atom-by-atom detail. Traditionally, biologists have been studying how cells work and behave in living organisms - in vivo – and in their lab tubes - in vitro – but many features are too complex and too small to understand in this way.

To overcome this limitation and understand complex biological problems with atomistic-level resolution, we develop new computational approaches to study biological systems in silico, and we combine these investigations with biochemical and biophysical approaches. Our main methodology is called molecular dynamics (MD) simulations. Using this approach, we can describe molecular systems in the range of 1-100 nanometers with atom-level accuracy. To use Feynman words, we investigate living matter by studying the "the jiggling and wiggling of atoms".

"There is no life without fat"

Currently, our focus is to understand the mechanisms that determine how lipid homeostasis is maintained in the cell. In particular, we are interested in how lipids are stored, transported or mobilized to produce energy. These lipid remodelling processes are governed by the interplay between specialized proteins and membrane properties, but in most cases, we still lack a detailed molecular explanation of how these processes are controlled. Our goal is to understand these processes in molecular detail, with the ultimate goal to translate our findings to the medical domain.



Molecular representation of the Berardinelli-Seip Congenital Lipodystrophy 2 protein complex embedded in a lipid bilayer.

Group members

Pablo Campomanes, Senior Scientist
Valeria Zoni, PhD Student
Emanuele Petretto, PhD Student
Sriraksha Srinivasan, PhD Student
Jennifer Sapia, PhD Student
Janak Prabhu, PhD Student
Cristian Camilo Rocha Roa, PhD Student
Ashutosh Kumar, PhD Student
Taraknath Mandal, Postdoc
Andrea Di Luca, Postdoc
Josephine Alba, Postdoc
Daniel Alvarez Lorenzo, Postdoc
Akhil Singh, Postdoc
Arun John Peter, Postdoc

Selected publications

Zoni V, Khaddaj R, Lukmantara I, Shinoda W, Yang H, Schneiter R, Vanni S (2021) Seipin accumulates and traps diacylglycerols and triglycerides in its ring-like structure. Proc Natl Acad Sci 118: e2017205118

Zoni V, Khaddaj R, Campomanes P, Thiam AR, Schneiter R, Vanni S (2021). Pre-existing bilayer stresses modulate triglyceride accumulation in the ER versus lipid droplets. eLife 10: e62886

Rogers S, Gui L, Kovalenko A, Zoni V, ..., Thiam AR, Vanni S, Nicastro D and Henne WM (2022). Triglyceride lipolysis triggers liquid-crystalline phases in lipid droplets and alters the LD proteome. J Cell Biol, in press. DOI:10.1083/jcb.202205053

Who we are

Computational methods to infer our past

Prof. Daniel Wegmann
Statistical & Computational Biology

All living organisms have an evolutionary history. What is ours? Our DNA tells a large part of that story, as it does for any other species. Using modern computational and statistical methods, we seek to extract that information.

The basic idea is simple: genetic data is informative about genealogical relationships. We all have two parents, eights grandparents and more than a thousand ancestors 10 generations ago. The more recent ancestors two individuals share, the more genetically similar they are. Siblings, for instance, share half of their DNA, cousins about one eights.

Our goal is to link patterns of relationships to evolutionary histories. Two randomly drawn samples from a large population, for instance, should not be closely related, but they might easily turn out to be cousins if sampled from a small population (picture the locals of your favorite ski resort). But if done right, relationships tell us much more: they are informative about population size changes, migration between and mixing of past populations.

Excitingly, it is now possible to extract DNA also from fossils, which give us an even more detailed glimpse of the past. We pioneer the statistical analysis of such data, which is difficult as fossil DNA is very scarce and heavily damaged. Using our dedicated tools, we could trace back the history of the first farmers of Europe and uncovered a complex pattern of splintering into smaller groups during challenging conditions such as the last ice ages and recurrent interactions and admixure when the climate was more favorable.

> “My ancestry is complicated. Just like yours.”

What does that tell us about ourselves ? That each of us traces their ancestry back to multiple, highly diverged peoples that migrated, met and interacted repeatedly over thousands of years.

Sequencing reads obtained from a 9,500 years old human skull from the Zagros mountains in modern Iran.

Group members

Andreas Füglistaler, Postdoc
Ilektra Schulz, PhD Student
Carlos Reyna, PhD Student
Liam Singer, PhD Student
Madleina Caduff, PhD Student
Xenia Wietlisbach, PhD Student
Raphael Eckel, PhD Student
Ernest Fotsing, PhD Student
Margarida Vaz, PhD Student
Aimée Freiberg, PhD Student

Selected publications

Marchi N, Winkelback L, Schulz I et al. (2022) The genomic origins of the world’s first farmers, Cell 185(11): 1842-1859.

Louis M, Galimberti M, Archer f, et al. (2021) Selection on ancestral genetic variation fuels repeated ecotype formation in bottlenose dolphins, Science advances 7(44).

Ait Kaci Azzou S, Singer L, Aebischer T et al. (2021) A sparse observation model to quantify species distributions and their overlap in space and time, Ecography 44(6): 928–940.

Luqman H, Widmer A, Fior S, Wegmann D (2021) Identifying loci under selection via explicit demographic models, Molecular ecology resources 21(8): 2719–2737.

Mighty Microbes

Bacteria called to plant rescue

Prof. Laure Weisskopf
Exploring how plant-associated bacteria protect the health of their host

Our group is interested in microbes living in close association with plants, either on leaves or on roots. We aim to understand how they live, which chemical language they use to communicate, and how their functions may impact plant health. We typically isolate microbes from the crops we want to protect (e.g. potato or grapevine), characterize their multifaceted abilities and try to use the strains alone or in consortia as potential alternatives to currently used fungicides.

In recent years, we have discovered that *Pseudomonas* associated with potato emit potent volatile organic compounds that block different developmental stages of the oomycete pathogen *Phytophthora infestans*, the causative agent of late blight in potato which was responsible for the Irish Famine in the middle of the 19th Century. Further work led to the discovery that such volatile compounds also have strong impact on the physiology of neighboring organisms and can thus be considered long-distance modulators of microbial behavior, influencing many functions of relevance for plant health.

While our work in the last ten years mainly focused on a particular group of multi-talented bacteria belonging to the *Pseudomonas* genus, we have recently learned that plants select themselves specific helper bacteria when suffering from pathogen attack.

> “Microbial wonders never cease to amaze us”

Among the bacteria responding most strongly to this “cry for help” from infected potato plants, many *Bacillus* strains were identified and isolated (see one example on the picture on the right).

These newly isolated strains, some of which indeed show anti-oomycete activity *in vitro*, represent promising candidates for the sustainable control of plant diseases.

A side view on microbial Everest skillfully built by a Bacillus subtilis strain isolated from potato roots and enriched in both roots and leaves of potato following late blight infection.

Group members

Floriane L’Haridon, Lab manager
Eliane Abou-Mansour, Senior researcher
Sébastien Bruisson, Postdoc
Mout De Vrieze, Postdoc
Alsayed Alfiky, Postdoc
Abhishek Anand, PhD Student
Vivien Pichon, PhD Student
Ola Abdelrahman, PhD Student
Fanny Germanier, PhD Student
Nicolas Rappo, Junior scientist
Elissa El Feghaly, Junior scientist

Selected publications

Abdelrahman O, Yagi S, El Siddig M, El Hussein A, Germanier F, De Vrieze M, L’Haridon F & Weisskopf L (2022). Evaluating the Antagonistic Potential of Actinomycete Strains Isolated From Sudan’ s Soils Against *Phytophthora infestans*. Frontiers in Microbiology 13: 827824.

Alfiky A, L’Haridon F, Abou-Mansour E & Weisskopf L (2022). Disease inhibiting effect of strain *Bacillus subtilis* EG21 and its metabolites against potato pathogens *Phytophthora infestans* and *Rhizoctonia solani*. Phytopathology 112 : 2099-2109

Weisskopf L, Schulz S & Garbeva P (2021). Microbial volatile organic compounds in intra-kingdom and inter-kingdom interactions. Nature Reviews in Microbiology 19: 391–404.

Chromatin function

Understanding cellular reprogramming for better or worse

Dr. Chantal Wicky
Chromatin function in *C. elegans* development

Every cell in a specific tissue of an organism must turn on the appropriate set of genes to function for example as a neuron, as a muscle cell or as a sperm. Defects in the regulation of the adequate gene repertoire leads cells to acquire new identities, proliferate in an uncontrolled manner and disrupt tissue function. Thus, studying this regulation is crucial to understand how cells maintain their identity and do not engage in uncontrolled proliferation and differentiation, which are processes underlying tumorigenesis.

> “A master plan is controlling cell ID”

Our lab is using the nematode *Caenorhabditis elegans* as model organism to study how genes are regulated to ensure proper development of an organism. Using various experimental approaches, we were able to identify several key regulators of the germline gene repertoire. The transcription factor LSL-1 is a master regulator, which is required to activate genes involved in germ cell proliferation, in meiosis and in germ cell fate maintenance. LSL-1 is functioning by antagonizing the activity of repressors, such as the heterochromatin proteins HPL-2/HP1 and LET-418/Mi2, which exert important gene regulatory functions in somatic cells. Without proper LSL-1 activity, germ cells lose their identity and reprogram into neurons. The worms become sterile and exhibit teratomas in their gonads. Altogether, our research demonstrates the importance of tightly regulating gene repertoires and provides an understanding of the underlying mechanisms. Since all these transcriptional regulators, that we examined in *C. elegans* are conserved in human, our research has implications in regenerative medicine and tumorigenesis.

Artificially colored C. elegans embryos, where the two primordial germ cells appear in contrasting different colors.

Group members

David Rodriguez Crespo, PhD Student
Shweta Rajopadhye, PhD Student
Magali Nanchen, PhD Student
Fariba Heydari, PhD Student

Selected publications

Rodriguez Crespo D, Nanchen M, Rajopadhye S, Wicky C. (2022) The zinc-finger transcription factor LSL-1 is a major regulator of the germline transcriptional program in *Caenorhabditis elegans.* Genetics 221, 1. doi.org/10.1093/genetics/iyac039.

Wadji, D. L., Naser, M., Martin-Soelch, C. and Wicky, C. (2022) Methylation of the glucocorticoid receptor gene (NR3C1) in dyads mother-child exposed to intimate partner violence in Cameroon: Association with anxiety symptoms. MedRxiv doi.org/10.1101/2022.08.14.22278760

Saudenova, M and Wicky, C. (2019) The Chromatin Remodeler LET-418/Mi2 is Required Cell Non-Autonomously for the Post-Embryonic Development of *Caenorhabditis elegans* J. Dev. Biol. 7, 1 doi:10.3390/jdb7010001

Apprentices formation

Apprenticeship as Lab Technician in Biology

Every year, the Biochemistry Division of the Department of Biology hires two apprentices, for a period of three years.

Under the supervision of Julien Comelli, the apprentices' main task is to prepare the biochemistry's practical courses for the 2nd-year students from the Faculty of Science (doctors, biologists, biochemists, chemists, BMS).

The practical training enables the apprentices to learn in detail the different aspects of the profession according to the various themes, subjects, and techniques specific to clinical laboratory chemistry, such as blood and its components, glucose, or cholesterol, to name but the most common.

Julien Comelli's lab is also in charge of preparing the practical exams for students who have completed their practical work, as well as developing new analyses, techniques, methods, and several other tasks specific to the department.

Julien Comelli
Chief laboratory technician, responsible for apprentices

Studies

Multidisciplinary Study Programmes

Our students in the Bachelor's programmes in Biology and in Biochemistry enjoy the diversity of courses, the practical training, and the easy and informal access to our research groups. MSc students find the opportunity to apply the knowledge gained during their BSc training, and to focus on more specific aspects in Biology, Biochemistry, or Bioinformatics and computational biology. PhD Students appreciate networking within different fields of research in and outside of our Department, leading them to apply for positions in the academic and private sectors. Our mission is to advance the understanding and appreciation of biology and biochemistry through cutting-edge research in a large range of fields in Life Sciences.

Bachelor studies

From 2022, the Bachelor in Biology has been streamlined and now proposes 120 ECTS of core teaching that can be completed with the two new minors, *Biology-from genes to ecosystems* and/or *Medical and molecular life sciences*, or other minors from our or other Faculties. The BSc in Biology is offered in parallel with the Bachelor in Biochemistry, which is complemented for example with minors in chemistry and/or biology.

Master studies

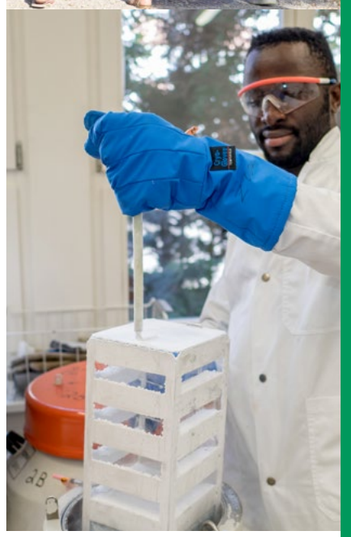
In 2021, the Department of Biology has successfully launched two new Master's programmes aimed at tackling the World's environmental and health challenges. Replacing the previous Master in *Biology*, the Master in *Environmental Biology* and the Master in *Molecular Life and Health Sciences* join the thriving BeFri Master in *Bioinformatics and Computational Biology* of our training offer. With this initiative, the Department aims at extending the study offer and at providing more visibility to its core research areas, and its technical platforms. Both Biology Masters programmes also offer a specific option for future teachers at secondary level II.

Master in Environmental Biology

This Master program centers on plant health and applied and evolutionary ecology. Major environmental problems, in particular global change and its consequences on biodiversity and ecosystem functioning, are intimately interconnected and pose a threat to our future. Solving these problems requires an integrative and synergistic approach in terms of both fundamental and applied research. The program ranges from fundamental concepts in ecology and evolution, to molecular aspects of plant and microbial sciences, and applied solutions for environmental policies and sustainable development. It provides students with state-of-the-art training and background in conceptual, technical, and applied aspects of environmental biology.

Master in Molecular Life and Health Sciences

This Master program focuses on the molecular mechanisms and cellular processes related to human health. The Department of Biology of the Faculty of Science and Medicine offers this multidisciplinary master programme with five different options that address molecular aspects in organisms ranging from yeast to mammals. The Master of Science in *Molecular Life and Health Sciences* provides a solid background including aspects on understanding human disease, neurosciences, marine sciences, biochemistry, cell biology, and animal development. This programme gives to the student the opportunity to acquire advanced theoretical background on molecular topics, hands-on experience in the laboratory, and the ability to communicate science. Master's students are integrated in research teams and thus gain extensive experience in fundamental academic research.



FGLM Events

2022
FGLM General Assembly, Welcome Assembly, FGLM Retreat with Dr. Kaycie Butler, Dr. Raphael Genolet, Dr. Hendrik Nolte, FGLM Autumn Assembly, FGLM Workshop "How to perform in the storm" Dr. Thomas Teichler

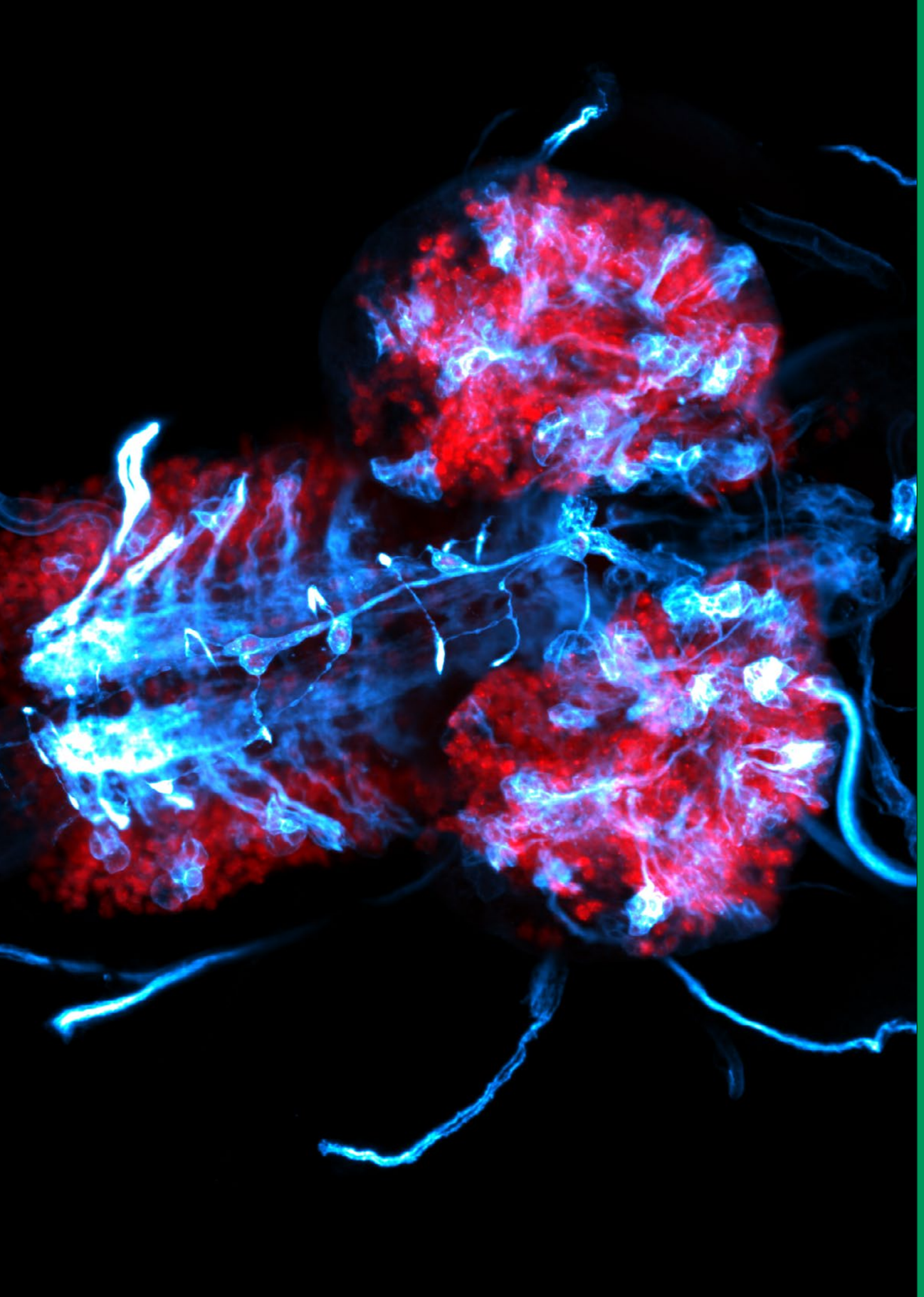
FGLM Seminars: "Sharing Strange Stuff and Funky Things" Dr. Pierre Kerner / "Women Scientists in Switzerland" Dr. Claudia Kasper / "Real-time to Real-life: Sequencing and SARS-CoV-2" Dr. Emma Hodcroft

2021
FGLM General Assembly, FGLM Retreat with Dr. Samuel Lagier and workshops, FGLM Autumn Assembly, FGLM Career Day with Prof. Adria LeBoeuf, Dr. Pierre-Marie Allard, Dr.Daniele Cassatella, Prof. Ana Marques, Dr. Marie-Paul Charnay, Dr. Lucia de Andres
FGLM Seminars: "Imposter syndrome" Dr. Georgia Loukatou / "Graphical abstracts and scientific illustration" Dr. Marzia Munafok / "How to write a research paper" Dr. Kaycie Butler / "From data to statement" Prof. Dr. Dan Cacsire Castillo-Tong / "The long road to scientific publishing" Dr. Markus Geisler / "Classification and regressions using (Bayesian) Neural Networks" Prof. Daniele Silvestro / "PhD management - mental health & project management" Dr. Pauline Fritsch / "In Search for Common Decency: The Case of CRISPR as a Powerful and Frightening Genome Editing Tool" Prof. François Rochat

Fribourg Graduate School of Life Sciences and Medicine FGLM

The Fribourg Graduate School of Life Sciences and Medicine (FGLM) emerged from the Fribourg Graduate School of Life Sciences (FGLS), founded in 2017 by the Department of Biology, and the Doctoral Module in Cell Migration in Cancer and Immunology of the Department of Oncology, Microbiology and Immunology of the Section of Medicine, which started in 2011. Due to a generous support by the University of Fribourg, FGLM was founded in 2021 and offers an interdisciplinary training program covering state-of-the-art methods and developments in life science. Next to an interdisciplinary academic training and to supporting PhD Students during their studies, FGLM aims to convey skills for careers outside the academic sector, enabling students to establish their own network, both for scientific and social exchange. In the last years, FGLM members increased to more than 80 students from up to ten different departments of the university, with an average of ten graduations per year. Thus, FGLM left its infancy and can now be considered as an established and well running graduate school.

Due to the support of several departments and the University of Fribourg, we aim to further consolidate FGLM in the coming years. An increase in academic and administrative personnel should help to further develop the structured training program for the full benefits of PhD Students. Also, FGLM should be the primary contact point for life science-related graduate programs from other Swiss and international universities to establish scientific exchange networks with the University of Fribourg. As we are in a global competition for the brightest minds, the scientific and personnel support of FGLM staff and members should help us to attract the next generation of promising young scientists to Fribourg.



Highlights

Events in 2021

09-17.03.21 Masterweek
26.03.21 CUSO BEFRI Genomics Day, Laurent Falquet
01.06.21 Department Day : Bachelor Symposium, General Assembly
28.07.21 – 30.07.21 CBC CephRes Course FELASA accredited at Sprecher Lab
25.08.21 End of Projet Erasmus +DigitalMarine project, Simon Sprecher
02.09.21 Swiss Chronobiology Meeting, Urs Albrecht
17.09.21 Getting started Journée d'accueil
25.09.21 Explora Journée portes ouvertes
08-09.11.21 CUSO Workshop *Evolution and impact of socially exchanged materials*, Adria LeBoeuf
10-11.11.21 CUSO Workshop *Systems Biology of the Brain*, Simon Sprecher
17.11.21 Infoday 2021 auf Deutsch
24.11.21 Infoday 2021 en français
25.11.21 Bachelor & Master evening
26.11.21 Eccellenza Symposium
21.12.21 Christmas Apéro

Department Seminars in 2021

02.03.21 Marc-André Selosse, CNRS
16.03.21 Henrique Teotonio, ENS Paris
23.03.21 Luc Pellerin, University of Poitiers
20.04.21 : Ilya and Kandice Levental, University of Virginia
27.04.21 Eva Schultner, University of Regensburg
04.05.21 Aurélien Carlier, INRAE Toulouse
11.05.21 Guillermo Velasco, Complutense University, Madrid
18.05.21 Frank Jiggins, University of Cambridge
25.05.21 Christian Münch, Goethe University Frankfurt
21.09.21 Mathias Beller, Heinrich Heine University Duesseldorf
05.10.21 Christian Parisod, Inaugural lecture
19.10.21 Pierre-Marie Allard, Inaugural lecture
26.10.21 Benjamin Towbin, University of Bern
09.11.21 Shaul Yalovsky, Tel Aviv University
16.11.21 Hanna Kokko, University of Zürich
23.11.21 Pascal-Antoine Christin, University of Sheffield
30.11.21 Florian Steiner, University of Geneva
07.12.21 Hui-Chen Lu, Indiana University, Bloomington
14.12.21 Markus Künzler ETHZ
21.12.21 Brigitte Galliot, University of Geneva

Exhibition about aging and lifespan

A major exhibition on the diversity of aging patterns, lifespans and life cycles among organisms, called *"Tic Toc – The Countdown of Life"*, was featured in the Natural History Museum Fribourg (NHMF).

It was conceived by NHMF director Peter Wandeler, Thomas Flatt from our department as scientific consultant, and Pia Viviani from Catta AG. By using graphic design elements, it brought some fundamental questions closer to the public: Why do we age? Why do different organisms have such different lifespans? Are there truly immortal organisms? Can we humans escape aging? The exhibition, in part funded by a SNSF AGORA grant to T. Flatt, has been widely publicized in the local and national media

Biology Image Contest@UniFR 2021

To showcase the artistic side of scientific imaging, the Biology Image Contest@UniFR2021 was organized by our Department in 2021. All the members of the Department of Biology - starting from Master students to Professors - were invited to submit their best images and show the beauty of their research.

In total, 24 authors submitted 56 images that were judged by a panel of jury. All images represent different areas of Biology - from Ecology to Cell Biology and judging was based on originality and artistic and/or visual impact of the images. Among the jury members were: Didier Reinhardt, Ora Hazak, Urs Albrecht, Boris Egger, Rudolf Rohr, and Fanny Germanier. The selection of the best images was done in two steps. First, every jury member could vote for 10 images. In the second round, 14 images that received at least two votes were evaluated by every jury member with points (from 1 to 5). Finally, eight images that received the most points have been selected as WINNERS. Among the winning authors are: Prof. Urs Albrecht, Dr. Samy Carbonnel, Min Chen, Ana Humbert Camps, Dr. Mout de Vrieze, David Rodriguez Crespo, and Salves Cornelis. The images are pictured in this activity report.

Department Seminars in 2022

22.02.22 Stefanie Ranf, Inaugural lecture
15.03.22 Kimberly Gilbert, Inaugural lecture
29.03.22 Sara Mitri, University of Lausanne
05.04.22 Ben Schuler, University of Zurich
12.04.22 Thomas Rey, University Paul Sabatier
26.04.22 Walter Salzburger, University of Basel
10.05.22 Francesco Pomati , EAWAG
17.05.22 Heribert Hirt, INRAE, KAUST (Saudi Arabia), University of Vienna
24.05.22 Alexei Maklakov, University of East Anglia
31.05.22 Pedro Beltrao, ETHZ
20.09.22 Michael Thomas Raissig, University of Bern
27.09.22 Jessica Abbott, Lund University
04.10.22 Ana Claudia Sima, University of Lausanne
25.10.22 Olivier Panaud , University of Perpignan
08.11.22 Enrica Bordignon , University of Geneva
15.11.22 Maja Köhn, University of Freiburg-Breisgau
22.11.22 Marco Trujillo, University of Freiburg-Breisgau
29.11.22 Jürgen Kleine-Vehn, University of Freiburg-Breisgau
06.12.22 Ben Engel, University of Basel
13.12.22 Benjamin Blackman, University of California, Berkeley
20.12.22 Guido Grossmann, Heinrich-Heine-University Düsseldorf

Events in 2022

21-25.03.22 Masterweek
31.05.22 Department Day : Bachelor Symposium, General Assembly, Barbecue
20-21.06.22 CUSO *Workshop Critical transition, early-warning sign, and coexistence theory*, Rudolf Rohr, Louis-Félix Bersier
01.09.2022 Swiss Chronobiology Meeting, Urs Albrecht
05-09.09.21 CUSO course *Introduction to Bayesian Inference in Practice*, Daniele Silvestro
16.09.21 Getting started Journée d'accueil
19.09.2022 Welcome Day and information for Masters students
21-22.11.22 CUSO Workshop *Identifying the fundamental differences between neonative and introduced species to inform research and management*, Bacher group
23.11.2022 Infoday 2021 auf Deutsch
24.11.2022 Bachelor & Master Evening
25.11.2022 SNSF Fellowship Interview Day
30.11.2022 Infoday 2021 en français
15.12.2022 Christmas Party

Ecology & Evolution Groups Move in

Since 2022, the Ecology & Evolution research groups of Sven Bacher, Louis-Félix Bersier, Thomas Flatt, Kimberly Gilbert, Christian Parisod, Rudolf Rohr and Daniel Wegmann groups are working in the former "laboratoire cantonal" building, PER23. E&E administrative officer Eirini Maikanti has also moved to PER23. The other E&E research groups, i.e. the Kozwlowski, LeBoeuf and Silvestro groups, are respectively located in PER04, PER01 and PER17.

The diverse research of the groups in E&E spans the areas of applied ecology, conservation biology and biogeography, community ecology, population genetics and genomics of adaptation, plant ecological genomics, the evolution and mechanisms of social behavior, theoretical ecology and evolution, computational evolutionary (paleo-) biology, and statistical and computational biology

KidsUni at the Biology Department

Every year, kids from 9 to 11 years old are invited to discover various funny scientific activities at UniFr through the program called KidsUni (https://events.unifr.ch/kidsuni/fr/) coordinated by Dr. Sofía Martín Caba. These afternoons are dedicated to "learning by doing" via small experiments, have fun and end with a snack. In our Biology department these activities are centered around two topics: the practical testing of dewormer drugs for cats and the identification of cheese brand with bioinformatics tools. Dr. Chantal Wicky and Dr. Laurent Falquet are responsible of these activities.

How cool it is to look through a microscope at small C.elegans worms wriggling in the chemical bath, but then one must learn to calculate an average! What's that? GAATATCCGAACCTGCTGCCGCGCTTTCTGAAATATGTGAA even more surprising, cheeses are full of bacterias! One can identify the cheese brand and verify the PDO (AOP in French) with the help of DNA sequencing and bioinformatics tools! Computers can be more fun than just a game console!

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Impressum

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