

Progress Report 2022

1 Management Summary

With 2022, the first half of Phase III of the URPP *Evolution in Action* ended. After 2 years of restrictions provoked by the Covid-19 pandemic, the research program could regain most of its former undertakings, making the 10th year of the URPP *Evolution in Action* one full of activities.

All nine independent research projects are well underway, as is the work in the group of Assistant Professor Anne Roulin. In 2022, fieldwork and work on-site, e.g., in the laboratories and greenhouses, was again possible without restrictions. Travelling became easier, too, leading to the presentation of the projects of the URPP *Evolution in Action* at several conferences. Also, five pilot projects, all approved in 2021, were successfully conducted in 2022.

The URPP *Evolution in Action* offered its community several possibilities for exchange throughout the year. During the Annual Retreat in Grindelwald, progress reports of all current research projects funded by the URPP *Evolution in Action* provided an overview of ongoing scientific activities within the research program. Several informal get-togethers further ensured an exchange within the network of the URPP *Evolution in Action*.

Teaching efforts of the URPP *Evolution in Action* comprised both established and new courses. Seminars could again be organized, and several speakers were invited to discuss their work at UZH. The successful bioinformatics support of the URPP *Evolution in Action* could be invigorated as the Embedded Bioinformatician established new tutorials and novel measures with regard to data handling and storage.

The organization of the International Conference *Evolution in Action* progressed significantly. The Conference Committee, consisting of the directors and four members of the URPP *Evolution in Action*, developed a comprehensive program covering topics relevant to the URPP *Evolution in Action*. The community of the URPP *Evolution in Action* identified suitable speakers who could all be won to participate in the event that will take place in June 2023. The preparations went so well that by the end of the year almost all the necessary measures had been taken to open the conference registration.

The URPP *Evolution in Action* successfully continued its public outreach efforts. While the program pursues a digital visibility to continuously increase its level of awareness, we have also put effort into the forthcoming of our museum exhibition *evolution happens!*. It migrated to the Naturmuseum Solothurn in 2022, where it will be on display until spring 2023. Further partners have been identified that will subsequently show the exhibition on their premises.

We look forward to continuing our work in the second half of Phase III of the URPP *Evolution in Action*.

2 Objectives

2.1 Objectives for the Reporting Year 2022

- Planning and realization of the **10th Retreat of the URPP Evolution in Action** with a program featuring progress reports from all PhD and Postdoc projects, a Keynote Lecture, Faculty and PhD Student meetings, as well as a social program to further the integration of old and new members and junior scientists.
- Ensuring the display of the exhibition *evolution happens!* in other museums across Switzerland to make the key **Public Outreach** activity of the URPP *Evolution in Action* available to as many people as possible.
- Continuation of the successful **Seminar Series** of the URPP *Evolution in Action*, either as an online format or physically at various UZH departments.
- Planning and realization of **courses for the PhD Program Evolutionary Biology**, covering topics such as UNIX/Linux and Bash Scripting, Next-Generation Sequencing, Concepts of Evolutionary Biology, Genome-Wide Association Studies (GWAS), and Scientific Writing.
- Continuation of the highly successful **Bioinformatics Support Services**.
- Continuation of the **1:1 Meetings for all PhD Students** of the URPP *Evolution in Action* with a Program Co-Manager as a low-threshold opportunity for the junior scientists to address any questions and issues.
- Organization of **Social Events** to further enhance interactions among students, members, research projects, and departments involved in the URPP *Evolution in Action*.
- Increase the visibility of work published by members of the URPP *Evolution in Action* through communication via **Social Media** and other **Media Releases**.
- Initial preparations for an **International Conference on Evolution in Action** at Monte Verità, to take place in June 2023, including applications for additional funding, inviting keynote and invited speakers, organizing the registration process, and advertising the meeting.

2.2 Achieved Objectives in 2022

- Successful realization of the **10th Retreat of the URPP Evolution in Action** in Grindelwald comprising a program featuring progress reports from all PhD and Postdoc projects, a Keynote Lecture, Faculty and PhD Student meetings, as well as a social program to further the integration of old and new members as well as junior scientists.
- The exhibition *evolution happens!*, key **Public Outreach** activity of the URPP *Evolution in Action*, closed its doors at the Zoological Museum of the University of Zurich after being shown for more than half a year and is now on display at the Naturmuseum Solothurn.
- The **Seminar Series** of the URPP *Evolution in Action* has successfully been continued. A total of five seminars was offered, mostly in hybrid format.
- The URPP *Evolution in Action* planned and organized several **courses for the PhD Program Evolutionary Biology**.
- The highly successful **Bioinformatics Support Services** of the URPP *Evolution in Action* were continued.

- **1:1 Meetings for all PhD Students** of the URPP *Evolution in Action* with a Program Co-Manager were conducted as a low-threshold opportunity for the junior scientists to address any questions and issues.
- A variety of **Social Events** to further enhance interactions among students, members, research projects, and departments involved in the URPP *Evolution in Action* were organized.
- The URPP *Evolution in Action* further increased the use of **Social Media** (mainly Twitter) and the publication of **Media Releases** to strengthen the reach of the program and its members.
- The URPP *Evolution in Action* started with the preparations for the **International Conference on Evolution in Action** at Monte Verità to take place in June 2023.

2.3 Objectives for 2023

- Planning and realization of the **11th Retreat of the URPP Evolution in Action** with a program featuring progress reports from all PhD and Postdoc projects. With the International Conference Evolution in Action taking place in June, the Retreat in 2023 will be a one-day event.
- Planning and realization of the **International Conference on Evolution in Action** at Monte Verità from June 11 – 15, 2023, with a program comprising 2 Keynote Lectures, 5 oral and two poster sessions, a workshop on machine learning in evolution, and an excursion as a social event for networking among members and international experts.
- Two main **Public Outreach** measures to communicate research from the URPP *Evolution in Action*: Ensuring the display of the traveling exhibition *evolution happens!* in other museums across Switzerland and the participation at the science fair *Scientifica 2023*.
- Continuation of the successful **Seminar Series** of the URPP *Evolution in Action*, either as an online format or physically at various UZH departments.
- Planning and realization of **courses for the PhD Program Evolutionary Biology**, covering topics such as UNIX/Linux and Bash Scripting, Next-Generation Sequencing, Concepts of Evolutionary Biology, Quantitative Trait Loci (QTL), Genome-Wide Association Studies (GWAS), and Scientific Writing.
- Continuation of the highly successful **Bioinformatics Support Services**.
- Continuation of the **1:1 Meetings for all PhD Students** of the URPP *Evolution in Action* with a Program Co-Manager as a low-threshold opportunity for the junior scientists to address any questions and issues.
- Organization of **Social Events** to further enhance interactions among students, members, research projects, and departments involved in the URPP *Evolution in Action*.
- Continue the communication about work conducted in the URPP Evolution via **Social Media** and other **Media Releases**.

3 Research

3.1 Research Projects

3.1.1 PhD and Postdoc Projects

The URPP *Evolution in Action* conducts research with a focus on diversification and adaptation in evolution revolving around the three research core areas of (i) pathogen and host co-evolution, (ii) polyploidy and epigenetics, and (iii) experimental evolution and modelling. Supported are a total of 9 individual research projects as well as an Assistant Professor who additionally supervises an associated postdoc project.

(i) Evolution of Pathogens, Parasites, and Pathosystems

*Mining Herbaria to Explore Phylogeography and Coevolution in Plant Pathosystems: the Case of the Irish Potato Famine Pathogen *Phytophthora infestans* and its Solanaceous Hosts*

PhD Student: Donikë Sejdiu

PhD committee: Simon Aeschbacher (Department of Evolutionary Biology and Environmental Studies, DEBES), Verena Schünnemann (Institute of Evolutionary Medicine, IEM), Thomas Wicker (Department of Plant and Microbial Biology, IPMB), Daniel Wegman (University of Fribourg)

The project develops methodological approaches to increase the yield of pathogen DNA extracted from herbarium samples to be leveraged as time-referenced information in phylogenomic and population genomic analyses of the evolutionary past of plant pathogens and their hosts. To that end, it aims to identify the geographic and genetic origins of early 20th-century *Phytophthora infestans* strains and establish links to 19th-century and modern highly pathogenic strains to trace co-evolutionary changes at effector and resistance genes, and to investigate mating type and polyploidy as drivers of pathogen virulence.

To date, an assay showing that plant-leaf tissue inside and adjacent to pathogen-induced lesions is suitable for pathogen DNA sampling on host leaves has been finished. A total of 131 historical *P. infestans* samples from herbaria in Europe and Japan have been collected, on which phylogenetic analyses of mitochondrial DNA have been performed suggesting that close relatives of the *P. infestans* that caused the Irish Potato Famine persisted in Switzerland well into the 20th century. Also, DNA capture approaches to enrich *P. infestans* mitogenome as well as targeted regions of the nuclear genome, including mating-type and effector genes, from historical samples are being developed.

While long-range PCR for template-based DNA capture of the mitogenome did not work with the initial set of primers and keeps being explored using other primers, the extraction of modern *P. infestans* DNA worked well with the help and in the laboratory of Dr. Daniel Rigling at the Swiss Federal Institute for Forest, Snow and Landscape Research WSL.

The project has been presented at the Bauhin Symposium 2022 and at the Congress of the European Society for Evolutionary Biology ESEB 2022.

Molecular Identification of Plant Immunity Genes Involved in Non-Host Resistance of Triticale to the Wheat Powdery Mildew Pathogen

Visiting Collaborator: Harsh Chauhan

Supervisor: Beat Keller (IPMB)

Collaborators: Kentaro Shimizu (DEBES), Thomas Wicker (IPMB), Javier Sánchez-Martín (IPMB)

With Marion Müller, the former postdoc responsible for the project, moving on to a new position, the work is now being continued by Harsh Chauhan, a visiting collaborator of Beat Keller's laboratory. The project examines molecular plant-pathogen interactions with the aim to clone resistance genes against *Triticale* powdery mildew and to further use them in molecular breeding of cereals, especially wheat. Currently, the phenotyping of the F2 population is performed. Furthermore, mutants in resistant *Triticale* genotypes that correspond to chosen *Triticale* powdery mildew isolates are identified and analyzed via mut-iso-sequencing. Being specific to the target resistance genes/loci, these isolates can provide important information with regard to the cloning of these genes.

Does Selection for Disease Resistance Vary along an Elevation Gradient?

PhD Student: Michael Rechsteiner

PhD committee: Anna-Liisa Laine (DEBES), Andreas Wagner (DEBES), Sergio Rasmann (University of Neuchâtel), Joy Bergelson (New York University), Florian Schiestl (Department of Systematic and Evolutionary Botany, ISEB)

The project investigates selection on disease resistance in *Plantago lanceolata* along an elevation gradient to empirically demonstrate heterogeneous selection pressure on disease resistance mechanisms of a perennial plant species along an altitudinal gradient.

The project consists of 3 subprojects, namely a field transplant experiment, a laboratory inoculation study, and *R*-gene enrichment sequencing. While the manuscript of the laboratory inoculation study is in preparation, all data from the field transplant experiment have been obtained. The subproject on *R*-gene enrichment sequencing is being planned with sample collection and subsequent sequencing scheduled in 2023.

The project has been presented at the Congress of the European Society for Evolutionary Biology ESEB 2022 and at the British Ecological Society (BES) Annual Meeting 2022.

Investigating the Evolution of Mycobacterial Infections through the Combination of Biomolecular Methods

Postdoc: Shevan Wilkin

Supervisor: Verena Schünemann (IEM)

Collaborators: Matthew Collins (University of Copenhagen, UCPH), Liam T. Lanigan (UCPH), Nuria Montes (Universitat Autònoma de Barcelona), Mukul Sharma (Indian Council of Medical Research), Charlotte Avanzi (Colorado State University), Donikë Sejdiu (IEM), Kerttu Majander (IEM), Saskia Pfrengle (IEM), Laura Kunz (Functional Genomics Center Zurich, FGCZ), Antje Dittmann (FGCZ), Frank Rühli (IEM), Pushpendra Singh (National Institute of Research in Tribal Health, India), Maria Fontanals-Coll (University of York), Alberto J. Taurozzi (UCPH)

Through an optimization of protein extractions from archaeological human remains, the project aims to identify pathogen and pathogen-related immune proteins from individuals assumed to have suffered from mycobacterial infections. The goal is to identify proteins associated with specific pathogens to detect which individuals were, in fact, suffering from active infections at the time of their death. As protein analysis is far less costly than DNA, these identifications offer a way to triage individuals for successful metagenomic analyses.

A previous methodological optimization has been successful and enabled for a significant reduction of collagen content in samples. The optimized method now allows to compare the immune-related proteome of the skeletal remains of leprosum and non-leprosum individuals. Moreover, metagenomic DNA extractions on the individuals from the non-leprosum context, which confirmed an absence of *Mycobacterium leprae* in any of the samples, were recently completed.

The work has been presented at the 23rd Paleopathology Association European Meeting 2022.

Rapid Evolution of a Pathogen Recapitulates the Hybridization of Host Polyploid Wheat

PhD Student: Naoto-Benjamin Hamaya

PhD committee: Kentaro Shimizu (DEBES), Beat Keller (IPMB), Thomas Wicker (IPMB), Shuhei Nasuda (Kyoto University), Moeko Okada (Kobe University), Hiroyuki Kakui (Niigata University)

The project investigates rapidly evolving traits, namely the co-evolution of *Triticum aestivum* and *Blumeria graminis* f.sp. *tritici*, as well as the evolution of the number of pollen grains in *T. aestivum* and *Arabidopsis thaliana* to identify QTLs/genes involved in resistance to powdery mildew in bread wheat, as well as genes regulating pollen number.

Currently, double mutants of candidate genes are being created to test their effect on pollen number in *A. thaliana*. The consensus map of the NAM population is finished and the multiparental QTL mapping is ongoing. Also, the phenotyping for powdery mildew is ongoing.

The project has been presented at the 26th International Conference on Sexual Plant Reproduction (ICSPR) in Prague, Czech Republic, and the Plant Science Center Symposium 2022, Switzerland.

(ii) Role of Polyploidy and Epigenetic Variation in Diversification and Adaptation

EpiPop - Investigating the Role, Stability, and Distribution of Epigenetic Variation in Populations of *Arabidopsis thaliana*

PhD Student: Alexander Plüss

PhD committee: Ueli Grossniklaus (IPMB), Simon Aeschbacher (DEBES), Hidetoshi Saze (Okinawa Institute of Technology), Kentaro Shimizu (DEBES)

The project investigates whether epigenetic diversity that correlates with gene expression is functionally relevant for plant adaptation. To that end, it focuses on the identification of functional epialleles in the model plant *Arabidopsis thaliana*. In a field approach, several study populations have been successfully identified and sampled over two years. The experimental pipeline to assess various epialleles throughout the genome using a high-throughput approach based on a Fluidigm BioMark chip has been established and the data are being analyzed. While initially unreliable, the qPCR data quality obtained by BioMark could be improved to levels that are sufficient for future analyses. In a next step, the frequency of selected epialleles will be followed over several years in specific populations to assess whether selection acts upon them.

The project has been presented at the Annual Meeting of the COST Action EPI-CATCH (Epigenetic Mechanisms of Crop Adaptation to Climate Change) in Chania, Greece, and the retreat of the PhD Program Evolutionary Biology in Switzerland.

The Relative Contribution of Genetic and Epigenetic Variability to Adaptation

PhD Student: Lucas Waser

PhD committee: Peter Szövényi (ISEB), Ueli Grossniklaus (IPMB), Bernhard Schmid (DEBES)

This project compares genetic and epigenetic adaptation through experimental evolution in order to gain a better understanding of the adaptive potential of transgenerationally inherited epigenetic variation.

The project's initially proposed plant model system *Physcomitrium patens* and the originally planned cultivation method proved unsuitable with the available infrastructure and budget due to contamination issues and space constraints. Therefore, it has been replaced by *Funaria hygrometrica*, of which cultivation and protoplastation have successfully been established, including first trials for both mutagenesis and epi-mutagenesis. The switch to plate-based cultivation will further allow for the work

with more cultures, enabling the project to build in redundancies and more replicates as a safety measure.

The project was presented at the Plant Science Center Symposium 2022, Switzerland.

(iii) Experimental Evolution and Modelling

Tracking Genomic and Phenotypic Changes Induced by Experimental Manipulation of Natural Pollinator Communities

PhD Student: Elisabeth Authier

PhD committee: Léa Frachon (ISEB), Simon Aeschbacher (DEBES), Florian Schiestl (ISEB), Tobias Züst (ISEB), Carolin Kosiol (University of St Andrews), Maxime Bonhomme (Paul Sabatier University - Toulouse III)

The project investigates the phenotypic and genomic adaptations of generalist flowering plants to limited access to their wild pollinator community to determine the potential of generalist plants to adapt to an actual decline of pollinators.

The experimental part of the project is nearly finished with all field approaches terminated and only greenhouse and laboratory analyses owing. The subsequent sequencing is planned to start soon.

The project has been presented at the Congress of the European Society for Evolutionary Biology ESEB 2022 and at the 4th International Symposium in memory of Stefan Vogel 2022.

Is Dolutegravir-Based Combination Antiretroviral Therapy Evolution Proof in Sub-Saharan Africa

PhD Student: Tom Loosli

PhD committee: Roger Kouyos (Institute of Medical Virology, IMV, Department of Infectious Diseases and Hospital Epidemiology, INF-USZ), Huldrych Günthard (IMV, INF-USZ), Matthias Egger (University of Bern), Urs Greber (Department of Molecular Life Sciences, DMLS)

The project addresses the emergence of drug resistance to the newly rolled out antiretroviral drug dolutegravir (DTG) in people living with HIV in South Africa. The ultimate goal is to capture the HIV epidemic in South Africa including resistance genotypes, to identify the mechanisms determining DTG resistance emergence, and ultimately inform targeted, efficient public health interventions such as ongoing drug resistance surveillance.

The resistance-related parameters in the mathematical DTG MARISA model are derived from a multicohort project, which is close to submission. Concurrent projects including a large international study with prospective enrollment, where valuable insights for the model parameterization can be gained, are progressing. While data availability is slowly improving, advanced methods such as conjunctive Bayesian networks can be applied and yield new insights on mutational pathways, which will be included in the model. Evidence that DTG resistance is a question of 'when, not if' is getting stronger, and the model framework with currently available data is planned to be published in 2023.

3.1.2 Assistant Professorship

Plant Evolutionary Genomics – Assistant Professor: Anne Roulin (IPMB)

Local adaptation represents the first step to biological diversification and speciation. Elucidating the genetic mechanisms underlying this process, therefore, constitutes a key question in the field of evolutionary biology. Mutations and chromosome rearrangements have been shown to be involved in this evolutionary process, but other sources of genetic variation influencing the evolution of natural

populations remains poorly understood. The goal of the group is to reveal genetic mechanisms underlying adaptation processes in the grass species *Brachypodium distachyon*.

Close collaborations of the group exist with other members of the URPP *Evolution in Action*, including Beat Keller (IPMB) and Léa Frachon (ISEB). Moreover, Anne Roulin hosts the group of Fabrizio Menardo, a former PhD Student of the URPP *Evolution in Action* and current SNF Ambizione Fellow.

Linking Environmental Stress to Transposable Element Activity and Fitness

Postdoc: Michael Thieme

Supervisor: Anne Roulin (IPMB)

Collaborators: Todd Blevoins (University of Strasbourg), Vitek Latzel (Academy of Sciences of the Czech Republic)

The project investigates causes and consequences of transposable element (E) mobility in the model plants *Brachypodium distachyon* and *Arabidopsis thaliana*. The goal is to identify genetic and environmental factors that lead to transposition, and to harness this knowledge to generate novel TE-insertions that allow for a better understanding of the adaptive consequences of transposition in plants. Research in this project was able to demonstrate that TE mobility in *B. distachyon* wildtype plants is very limited. Nevertheless, the first mobile retroTE in a mutant of *B. distachyon* that disrupts RNA-mediated DNA-methylation could be detected. In *A. thaliana*, the hypothesis that (heat) stress-induced transposition can lead to an increased (drought) stress tolerance was experimentally confirmed. Also, many smaller (<2kb) extrachromosomal DNA circles have been found in the samples using mobilome-seq. It is likely that most of the detected circles are an artifact caused by the method and have no biological relevance.

3.1.3 Finalization of Phase II Research Projects and graduation of PhD Students

Of the 14 PhD Students funded in Phase II (2017 - 2020), 10 graduated 2021, and two more graduated 2022:

May 19, 2022 – Stefan Milosavljevic: Exploring the Role of DNA Methylation in the Early Stages of Polyploidy with a Focus on Computational Reproducibility

July 1, 2022 – Alexandros Sotiropoulos: Global Population Analyses of Wheat Powdery Mildew Using Whole Genome Sequencing Data

3.1.4 Pilot Projects

The URPP *Evolution in Action* released a Pilot Project Call in July 2021 to promote interdisciplinary approaches to evolutionary questions. Proposals could be submitted by young scientists working in UZH research groups that are either members of the URPP *Evolution in Action* or have applied for membership. The funding per proposal was limited to CHF 20'000.

The Steering Committee of the URPP *Evolution in Action* chose the following 5 projects for funding to be conducted in 2022:

Applicant:	Stefano Bencivenga, Postdoc (IPMB)
Title of project:	Identifying Male-Female Signaling Factors Involved Plant Speciation
Granted funding:	CHF 20'000

Applicant: Gözde Çilingir, Postdoc (DEBES)
Title of project: Age Estimation by DNA Methylation in the Aldabra Giant Tortoise
Granted funding: CHF 20'000

Applicant: Javier Sánchez-Martín, Postdoc (IPMB)
Title of project: Interrogating Alien Chromatin Content of Long-Read Sequenced Bread Wheat Chromosomes for Rapid Resistance Gene Cloning
Granted funding: CHF 19'050

Applicant: Abhishek Meena, PhD Student (DEBES)
Title of project: Genes Involved in the Expression of Secondary Sexual Traits in Male *Drosophila prolongata*: A New Model Species for Sexual Selection Studies
Granted funding: CHF 19'910

Applicant: Vera Vollenweider, PhD Student (Department of Quantitative Biomedicine, DQBM)
Title of project: Pyobiotics: Using Pyoverdine to Revert Selection for Antibiotic Resistance
Granted funding: CHF 17'510

Individual reports for each granted pilot project can be found in Appendix A.

4 Scientific Activities and Outreach

4.1 Scientific activities

4.1.1 Scientific Retreat



The 10th **Annual Retreat of the URPP *Evolution in Action*** took place with approx. 40 participants in Grindelwald during September 5 - 7, 2022. The scientific program comprised 3 sessions with progress reports on the research conducted within the URPP *Evolution in Action*. Additionally, a session with poster flash talks was held prior to the poster session, featuring work from pilot projects and projects with relevance to the work of the URPP *Evolution in Action*. Moreover, Sara Mitri, Head of the Synthetic Ecology of Microbial Communities group at the University of Lausanne, presented a Keynote Lecture, and two new members (Chiara Barbieri and Fabrizio Menardo) introduced their research efforts related to the URPP *Evolution in Action*. The introduction of the new Embedded Bioinformatician Deepak Tanwar and an info session from the Functional Genomics Center Zurich (FGCZ) were also part of the program. The retreat closed with Faculty and PhD/Postdoc meetings.

As every year, we offered a variety of social components such as trial group lessons on the nearby golf course or a bowling evening, and provided for many opportunities for informal exchange, e.g., during meals, coffee breaks, and apéros. As previous URPP *Evolution in Action* retreats, the Annual Retreat 2022 was a dynamic and positive event with many lively discussions, and the feedback from the attendees was enthusiastic.

4.1.2 Bioinformatics Tutorials and Support

Research of the URPP *Evolution in Action* was supported by Embedded Bioinformaticians Gregor Rot until June 2022 and Deepak Kumar Tanwar as of July 2022. They provided assistance to the URPP *Evolution in Action* projects in numerous ways.

Courses

Teaching in 2022 was on-site. The software Docker was used to provide a layer of reproducibility to the courses. The bioinformatics team participated in teaching the courses BIO609 (Introduction to UNIX/Linux and Bash Scripting) and BIO610 (Next-Generation Sequencing for Model and Non-Model Species).

Tutorials

A half-day tutorial on Git and GitHub in December 2022 had to be rescheduled to February 10, 2023.

PhD project presentations in the context of bioinformatics

During the months of July and August 2022, Phase III PhD students were asked to provide an introductory presentation regarding their work with a bioinformatics focus. These brief presentations served as a starting point for discussing and guiding future bioinformatics plans and issues, such as the storage, management, and analysis of sequence data with the new Embedded Bioinformatician.

Bioinformatics and IT support

The Embedded Bioinformaticians provide continuing IT infrastructure assistance, including access to a computer cluster, a huge mainframe with 80 cores CPU and 1TB RAM, and over 60 TB of data storage. They also aid with bioinformatics tasks, such as coding in Python, R, and Bash, as well as analyzing sequencing data in the context of DNA methylation, variant calling, RNA analysis, and enrichment analyses. This guidance is delivered in a flexible manner, with quick response times, via communication tools such as Zoom, Slack, email, and in-person meetings.

Bioinformatics server

The bioinformatics components of the projects of the URPP Evolution in Action are tracked individually. Data from research projects is saved, and analysis findings are shared via the front-end server, which is also accessible from outside the UZH network (secure access, for external collaborators). This work paradigm enables PhD students to learn bioinformatics, scripting, and coding with the assistance of the Embedded Bioinformaticians, and to outsource sections of bioinformatics analyses to Embedded Bioinformaticians or other researchers as needed. It also simplifies data access (and sharing), resulting in a centralized location controlled and delivered by the URPP *Evolution in Action*.

Hub of activities

A new GitHub organization has been created to house all of the courses, tutorials, and code written for bioinformatics projects within the URPP *Evolution in Action* in one place. The URL for the organization is <https://github.com/urppeia>.

Collaboration with the Functional Genomics Center Zurich

The goal of this collaboration is to create a SUSHI server for the datasets created in the projects of the URPP *Evolution in Action*. All datasets are planned to be re-analyzed on the same platform in a reproducible manner using the SUSHI server.

4.1.3 Courses for the PhD Program in Evolutionary Biology

- Introduction to UNIX/Linux and Bash Scripting (**BIO609**); October 31, 2022; Lecturer: Deepak Kumar Tanwar
- Next-Generation Sequencing for Model and Non-Model Species (**BIO610**); November 1 & 2, 2022; Lecturers: Kentaro Shimizu, Masaomi Hatakeyama, Moeko Okada, Jun Sese, Rie Shimizu Inatsugi, Deepak Kumar Tanwar
- Human Genetic, Demographic and Cultural Diversity (**BIO624**); November 22 – 24; Lecturers: Mark Stoneking, Chiara Barbieri, Kentaro Shimizu
- Scientific Writing for Evolutionary Biologists (**BIO555**); November 25 & 28, 2022; Lecturers: Hanna Kokko, Annegret Lesslauer

4.1.4 URPP *Evolution in Action* Seminars

In 2022, the URPP *Evolution in Action* offered five seminars to its community:

Susana Coelho (MPI for Biology Tübingen, Germany); April 1, 2022:
Algal Views on the Evolution and Regulation of Sex Determination

Andrés Bendesky (Columbia University, US); October 11, 2022:
Genetic, cellular, and neuroendocrine bases of parental care evolution in monogamous rodents

Sabine Zachgo (University of Osnabrück, Germany); October 14, 2022:
How stressful was plant terrestrialization? Contribution of transcription factors and redox processes to land plant adaptation

Hiroki Oota (University of Tokio, Japan); November 1, 2022
Our ongoing projects based on ancient genome: coprolite, iPS, and transcriptome of Jomon people

Michael Lässig (University of Cologne, Germany); December 15, 2022
Predicting pathogen evolution: From Influenza to SARS-CoV-2
PhD Guest Speaker invited by URPP Evolution in Action PhD Student Tom Loosli

We further continued disseminating information regarding other events of interest to the community of the URPP *Evolution in Action*. To this end, lectures, talks, mini symposia, and workshops covering topics on Evolution in Action were regularly announced to our mailing list.

4.1.5 International Conference on Evolution in Action

The URPP *Evolution in Action* will host an International Conference with the same name (Evolution in Action) on Monte Verità, Ticino, from June 11 – 15, 2023. The conference aims to bring together a diverse, international group of researchers to foster interdisciplinary discussions about aspects of evolutionary biology based on genomic and computational approaches.

In 2022, we took on the organization of the event. To this end, we have established a Conference Committee consisting of the 2 directors and 4 members of the URPP *Evolution in Action* that determined a program covering all topics of relevance to the URPP *Evolution in Action*. In its current state, the program comprises 5 oral and 2 poster sessions, 2 keynote lectures, and a workshop on machine learning in evolution. In an iterative process, which involved all our members, we identified and invited two keynote speakers, two invited speakers for each session, and two workshop tutors.



International Conference Evolution in Action
Congressi Stefano Franscini, Monte Verità, Switzerland
 June 11-15, 2023

Sunday, June 11	Monday, June 12	Tuesday, June 13	Wednesday, June 14	Thursday, June 15
	Session 2 Polyploidy and Epigenetic Variation <i>Speakers:</i> Jeff Chen Yoav Soen	Session 3 Domestication <i>Speakers:</i> Takao Komatsuda Esther v.d. Knaap	Session 4 Emerging Trends In Evolution <i>Speakers:</i> Tal Dagan Tulio de Oliveira	Session 5 Adaptation to Changing Environments <i>Speakers:</i> Hernán Burbano Tábita Hünemeier
	Lunch	Lunch	Lunch	
Session 1 Pathogen Evolution <i>Speakers:</i> Francois Balloux Eva Stukenbrock	Poster Session	Excursion and Conference Dinner	Poster Session	
Dinner	Dinner	Brissago Islands with Botanical Garden	Dinner	
Keynote 1 Anthropological Genetics <i>Speaker:</i> Anne Stone	Workshop Machine Learning in Evolution <i>Speakers:</i> Franz Baumdicker Sara Mathieson	<i>Participation optional</i>	Keynote 2 Evolution of Plant Reproductive Traits <i>Speaker:</i> George Coupland	



Program of the International Conference Evolution in Action

The URPP *Evolution in Action* also applied for additional funds to support the holding of the conference. To enable the attendance of young academics, we successfully raised funds from the Julius Klaus Foundation and the UZH Alumni Fonds. We further applied for an SNSF Scientific Exchanges grant to cover the costs associated with travels, room, and board of the invited speakers. All preparations relevant for the registration to open early 2023 could be successfully accomplished.

4.2 Outreach activities

4.2.1 Museum exhibition *evolution happens!*

The museum exhibition *evolution happens!* is the key public outreach element of the URPP *Evolution in Action*. It opened its doors on June 15, 2021, at UZH's Zoological Museum (ZM). To meet the high public demand, the duration of the exhibition was extended for two months and was eventually on display at ZM until the end of February 2022.

The closing of the exhibition was celebrated with a finissage on February 28, 2022. In his speech, Beat Keller, former co-director of the URPP *Evolution in Action*, recounted the process of creating the exhibition, from the initial idea to the final product. Subsequently, Joelyn de Lima, researcher in the Working Group Informal Education of the COST Action EuroScitizen and leader of the collaboration to quantify knowledge transfer through the exhibition, presented first study results from observations and questionnaires employed in the exhibition. The finissage - and with it the time for *evolution happens!* at the ZM - ended with an apéro.

Since November 2022, the exhibition is shown in the Naturmuseum Solothurn, where it will be on display until April 2023 before moving on to the Umwelt Arena Schweiz in Spreitenbach. The Naturmuseum Solothurn organized a vernissage for the opening of *evolution happens!* on their premises, during which Rolf Kümmerli, Professor for Evolution of Human Microbiomes and Pathogens and member of the URPP *Evolution in Action*, held a well-received public lecture about evolution in action.

4.2.2 Social Media

The URPP *Evolution in Action* tends to a Twitter account (@uzh_evolution), which is used to disseminate information about research conducted by its members and, within the program, events organized for the community, news regarding PhD defenses, latest publications, the International Conference, and other important information from and for our community.

4.2.3 Press releases

Further promotion of the research conducted within the URPP *Evolution in Action* happened via press releases referring to work published in peer-reviewed scientific journals. The press releases were spread through UZH's media relations offices and yielded a potential reach of more than 10 Mio. readers worldwide.

5 Academic Career Development

5.1 Academic Career Development for Young Academics

Most of the budget granted to the URPP *Evolution in Action* is used to fund young academics at several career stages. We currently provide salaries and research consumables for 7 PhD Students and 3 Postdocs as well as one Assistant Professor, hence contributing substantially to their career development at the financial level.

Additionally, the URPP *Evolution in Action* provides an extensive network comprising scientists from all career stages and from various faculties and departments, supporting the exchange within the field of Evolutionary Biology at UZH. To this end, we organize social events as deliberate activities to grant young academics access to a community of experienced researchers. An established format of the URPP *Evolution in Action*, for example, is the “Informal Get-Togethers”, gatherings for all members and their groups to increase exchange across topical borders and all levels of seniority.

The URPP Evolution in Action involves its PhD Students and Postdocs in its development wherever possible. At our yearly retreat, we hold a PhD and Postdoc meeting, at which information relevant to this target group is communicated and which invites young researchers from our network to contribute their suggestions and formulate their needs about the activities of the URPP *Evolution in Action*. Furthermore, the PhD Students have elected a representative who serves on the Steering Committee of the URPP *Evolution in Action*.

As in the previous years, the Coordination Office of the URPP *Evolution in Action* offered a 1:1 meeting to all PhD Students to provide a low-threshold opportunity for the young scientists to address any questions and issues. Being a voluntary format, the 1:1 with one of the program co-managers was well received with most of the students taking the opportunity for an exchange.

Also, the focus of the work of the Embedded Bioinformatician of the URPP *Evolution in Action* lies on the support of our young academics. It comprises bioinformatic assistance to all PhD and Postdoc projects of the URPP Evolution in Action from the very beginning to ensure that experimental design, probe preparation, and analysis methods are optimally adapted to the research questions asked. Next to a well thought-out study design for all our projects, this teamwork also has a positive effect on the career development of the bioinformatician himself, who can expand his research experience and make use of the wealth of data available from several projects to develop productive research activities of his own.

Lastly, the Conference Committee of the International Conference Evolution in Action has decided to provide substantial financial support to young academics that participate in the conference. To this end, it has been decided to match the funds received from UZH Alumni and the Julius Klaus Stiftung with funds from our conference budget to maximize our support options. Consequently, we will waive the registration fees for all current and former PhD Students and Postdocs of the URPP *Evolution in Action* and have additionally released a call for competitive fellowships for young researchers who face financial challenges in paying the cost of attendance.

5.2 Gender Equality Development

Hiring of personnel is on an equal opportunity basis and according to the “Gender Equality Action Plan UZH” guidelines. We emphasize our equal opportunity efforts in all job advertisements and the gender ratio in the URPP *Evolution in Action* is balanced among the applicants for positions and grants. In the past, we have appointed outstanding women scientists as Assistant Professors, thereby providing excellent role models. We also value gender balance in our governance bodies and continually increase the number of women in our Steering Committee. Moreover, we have staffed our Conference Committee, additionally to our two directors, with two female and two male researchers. We aim at a balanced gender ratio in the list of our invited speakers for seminars and keynote lectures, too. The panel of invited speakers for our International Conference, for example, comprises 6 female and 8 male speakers.

Lastly, we support efforts to create a family-friendly work environment, for instance by enabling part-time work.

6 Publications

6.1 Peer-Reviewed Publications in 2022

Aivelo T, Lemoine M, Tschirren B (2022). Elevational Changes in Bacterial Microbiota Structure and Diversity in an Arthropod-Disease Vector. *Microbial Ecology* 84: 868–878. **Open Access**

Akagi T, Jung K, Masuda K, Shimizu KK (2022). Polyploidy before and after domestication of crop species. *Current Opinion in Plant Biology* 69: 102255. **Open Access**

Barbieri C, Blasi DE, Arango-Isaza E, [...] Bickel B, Shimizu KK (2022). A global analysis of matches and mismatches between human genetic and linguistic histories. *PNAS* 119: 47. **Open Access**

Bergström A, Stanton DWG, Taron UH, [...] Schuenemann VJ, [...] Skoglund P (2022). Grey wolf genomic history reveals a dual ancestry of dogs. *Nature* 607(7918): 313–320. **Hybrid Open Access**

Figueiredo ART, Özkaya Ö, Kümmerli R, Kramer J (2022). Siderophores drive invasion dynamics in bacterial communities through their dual role as public good versus public bad. *Ecology Letters* 25(1): 138–150. **Hybrid Open Access**

Hasterok R, Catalan P, Hazen SP, Roulin AC, Vogel JP, Wang K, Mur LAJ (2022). Brachypodium: 20 years as a grass biology model system; the way forward? *Trends in Plant Science* 27(10): 1002–1016. **Hybrid Open Access**

Izuno A, Onoda Y, Amada G, Kobayashi K, Mukai M, Isagi Y, Shimizu KK (2022). Demography and selection analysis of the incipient adaptive radiation of a Hawaiian woody species. *PLoS Genetics* 18(1): e1009987. **Open Access**

Jayakumar P, Figueiredo ART, Kümmerli R (2022). Evolution of Quorum Sensing in *Pseudomonas aeruginosa* Can Occur via Loss of Function and Regulon Modulation. *mSystems* 7(5): 00354–22. **Open Access**

Kakui H, Tsuchimatsu T, Yamazaki M, Hatakeyama M, Shimizu KK (2022). Pollen Number and Ribosome Gene Expression Altered in a Genome-Editing Mutant of *REDUCED POLLEN NUMBER1* Gene. *Frontiers in Plant Science* 12: 768584. **Open Access**

Karve S, Dasmeh P, Zheng J, Wagner A (2022). Low protein expression enhances phenotypic evolvability by intensifying selection on folding stability. *Nature Ecology & Evolution* 6: 1155–1164. **Open Access**

Karve S, Wagner A (2022). Environmental complexity is more important than mutation in driving the evolution of latent novel traits in *E. coli*. *Nature Communications* 13: 5904. **Open Access**

Moerman F, Fronhofer EA, Altermatt F, Wagner A (2022). Selection on growth rate and local adaptation drive genomic adaptation during experimental range expansions in the protist *Tetrahymena thermophila*. *Journal of Animal Ecology* 91(6): 1088–1103. **Hybrid Open Access**

Müller MC, Kunz L, [...] Sotiropoulos AG, Praz CR, Manser B, Wicker T, Bourras S, Keller B (2022). Ancient variation of the *AvrPm17* gene in powdery mildew limits the effectiveness of the introgressed rye *Pm17* resistance gene in wheat. PNAS 119(30): e2108808119. **Hybrid Open Access**

Murer L, Petkidis A, Vallet T, Vignuzzi M, Greber UF (2022). Chemical evolution of Rhinovirus identifies capsid-destabilizing mutations driving low pH-independent genome uncoating. Journal of Virology 96(2). **Hybrid Open Access**

Neubauer A, Ruaud S, Waller M, Frangedakis E, Li FW, Nötzold SI, Wicke S, Bailly A, Szövényi P (2022). Step-by-step protocol for the isolation and transient transformation of hornwort protoplasts. Applications in Plant Sciences 10(2): e11456. **Open Access**

Patrono LV, Vrancken B, Budt Matthias, [...] Schuenemann VJ, [...] Schnalke T, Wolff T, Lemey P, Calvignac-Spencer S (2022). Archival influenza virus genomes from Europe reveal genomic variability during the 1918 pandemic. Nature Communications 13(1): 2314. **Open Access**

Pla-Díaz M, Sánchez-Busó L, Giacani L, [...] Schuenemann VJ, Nieselt K, Arora N, González-Candelas F (2022). Evolutionary Processes in the Emergence and Recent Spread of the Syphilis Agent, *Treponema pallidum*. Molecular Biology and Evolution 39(1). **Open Access**

Potente G, Léveillé-Bourret É, Yousefi N, Choudhury RR, Keller B, Diop SI, [...] Szövényi P, Conti E (2022). Comparative Genomics Elucidates the Origin of a Supergene Controlling Floral Heteromorphism. Molecular Biology and Evolution 39(2). **Hybrid Open Access**

Prummel KD, Crowell HL, Nieuwenhuize S, [...] Robinson MD, Mosimann C (2022). Hand2 delineates mesothelium progenitors and is reactivated in mesothelioma. Nature Communications 13(1):1677. **Open Access**

Rayo E, Ferrari G, Neukamm J, Akgül G, [...] Bouwman AS, Rühli FJ, Schuenemann VJ (2022). Non-destructive extraction of DNA from preserved tissues in medical collections. Future Science 72(2). **Open Access**

Rayo E, Neukamm J, Tomoum N, [...] Bouwman AS, Schuenemann VJ, Rühli FJ (2022). Metagenomic analysis of Ancient Egyptian canopic jars. American Journal of Biological Anthropology 179(2): 307-313. **Open Access**

Robin M, Ferrari G, Akgül G, Münger X, von Seth J, Schuenemann VJ, Dalén L, Grossen C (2022). Ancient mitochondrial and modern whole genomes unravel massive genetic diversity loss during near extinction of Alpine ibex. Molecular Ecology 31(13): 3548-3565. **Hybrid Open Access**

Russo A, Mayjonade B, Frei D, Potente G, Kellenberger RT, Frachon L, Copetti D, Studer B, Frey JE, Grossniklaus U, Schlüter PM (2022). Low-Input High-Molecular-Weight DNA Extraction for Long-Read Sequencing From Plants of Diverse Families. Frontiers in Plant Sciences 13. **Open Access**

Shimizu KK (2022). Robustness and the generalist niche of polyploid species: Genome shock or gradual evolution? Current Opinion in Plant Biology 69: 102292. **Hybrid Open Access**

Sotiropoulos AG, Arango-Isaza E, Ban T, Barbieri C, Bourras S, [...] Müller MC, Shamanin V, Shimizu KK, Yoshihira T, Zbinden H, Keller B, Wicker T (2022). Global genomic analyses of wheat powdery mildew reveal association of pathogen spread with historical human migration and trade. *Nature Communications* 13(1): 4315. **Open Access**

Stritt C, Gimmi EL, Wyler M, Bakali AH, Skalska A, Hasterok R, Mur LAJ, Pecchioni N, Roulin AC (2022). Migration without interbreeding: evolutionary history of a highly selfing Mediterranean grass inferred from whole genomes. *Molecular Ecology* 31(1): 70-85. **Hybrid Open Access**

Thieme M, Brêchet A, Bourgeois Y, Keller B, Bucher E, Roulin AC (2022). Experimentally heat-induced transposition increases drought tolerance in *Arabidopsis thaliana*. *New Phytologist* 236(1): 182-194. **Open Access**

Toll-Riera M, Olombrada M, Castro-Giner F, Wagner A (2022). A limit on the evolutionary rescue of an Antarctic bacterium from rising temperatures. *Science Advances* 8(28). **Open Access**

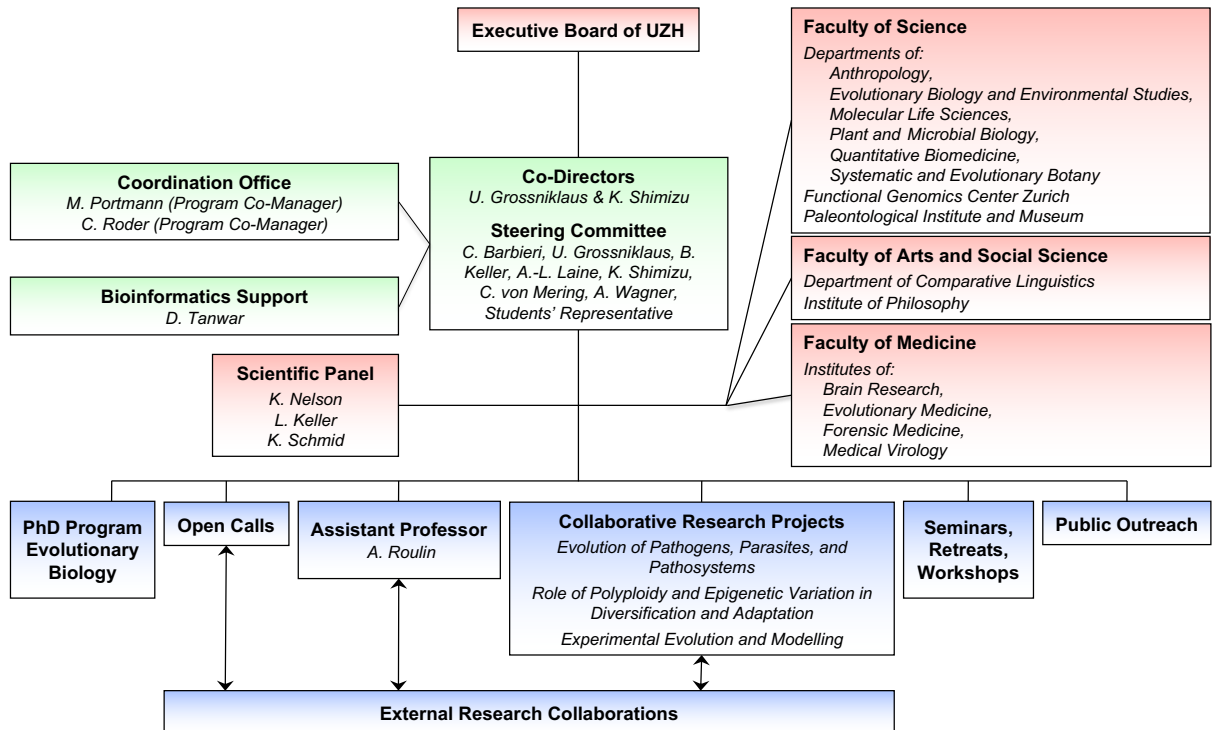
Wicker T, Stritt C, Sotiropoulos AG, Poretti M, Pozniak C, Walkowiak S, Gundlach H, Stein N (2022). Transposable Element Populations Shed Light on the Evolutionary History of Wheat and the Complex Co-Evolution of Autonomous and Non-Autonomous Retrotransposons. *Advanced Genetics* 3(1): 2100022. **Open Access**

6.2 Open Science

The URPP *Evolution in Action* supports Open Science efforts to ensure a consistent and meaningful structure of research data that is stored centrally and accessible as well as usable for others. To this end, we support initiatives that enable scientists to disseminate their findings in a transparent and rapid way.

Firstly, the majority of manuscripts published in the framework of the URPP *Evolution in Action* are Open Access. Additionally, the members of the URPP *Evolution in Action* frequently use the *bioRxiv* platform to provide their manuscripts as open-source preprints to the world-wide scientific community. The URPP *Evolution in Action* moreover ensures that the data and associated analysis tools are open to the public, promoting transparency and reproducibility in the research community. To this end, all high-throughput sequencing (HTS) datasets generated in projects of the URPP *Evolution in Action* will be made publicly available. Currently, the data is being re-analyzed using the SUSHI server of the FGCZ before its publication on our server bioinfo.evolution.uzh.ch. All associated code will also be available through the GitHub account of the URPP *Evolution in Action*, where further material for courses of the URPP *Evolution in Action* can be accessed.

7 Structures



8 Third-party Funds

8.1 Newly approved third-party funding of URPP project leaders

8.1.1 Swiss National Science Foundation – Divisions I to III

Kentaro Shimizu / Evolutionary functional genomics of plant sexual reproduction and polyploid species / SNSF / 12.2022 - 11.2026 / CHF 850'000

Rie Shimizu-Inatsugi / Does environment shape the epigenetic pattern of a newly synthesized *Arabidopsis* polyploid? / SNSF / 12.2022 - 11.2026 / CHF 735'660

8.1.2 Others

Ueli Grossniklaus, Kentaro Shimizu / International Conference Evolution in Action / Congressi Stefano Franscini / 01.2022 – 07.2023 / CHF 13'600

Ueli Grossniklaus / Novel Tools for Plant Gene Discovery / UZH Global / 08.2022 - 07.2025 / CHF 60'000

Donikë Sejdiu / Pilot herbarium-genomics project on the genetic diversity and evolutionary history of the ergot fungus *Claviceps purpurea* / Georges et Antoine Claraz-Foundation / CHF 3'180

Kentaro Shimizu / Key molecular networks in plant reproduction / Grants-in-Aid for Scientific Research / Duration: 7 years / CHF 3'648'642

Kentaro Shimizu / Integrating fundamental and applied plant science: wheat in a changing world / UZH Global / 12.2022 - 01.2025 / CHF 60'000

Lucas Waser / Travel grant to cover expenses for a conference attendance / Georges et Antoine Claraz-Foundation

8.2 Ongoing third-party funding of URPP project leaders

Balthasar Bickel, Kentaro Shimizu (co-applicants) / Out of Asia: Linguistic Diversity and Population History / SNSF Sinergia / 09.2019 – 08.2023

Balthasar Bickel, Kentaro Shimizu (co-applicant) / NCCR Evolving Language / 2020 – 2023

Ueli Grossniklaus / Unlocking epigenetic variation to breed sustainable crops in a changing climate / RESPONSE Doctoral Programme, Marie Skłodowska-Curie Grant / 04.2020 – 09.2025

Rolf Kümmerli / An evolutionary ecology approach to disarm bacterial pathogens, control infections, and understand polymicrobial interactions inside hosts / SNSF / 12.2018 – 11.2022

Mark Robinson / Single cell RNA sequencing of blood and cerebrospinal fluid samples (CSF) from progressive multiple sclerosis patients treated with anti-CD20 (Ocrevus) therapy / F. Hoffmann-La Roche AG / 04.2020 – 03.2022

Mark Robinson (project partner) / Road-mapping the serrated pathway of colon tumorigenesis: Step 2: Impact on clinical management of precancerous colorectal lesions. / SNSF / 05.2018 – 04.2022

Mark Robinson (project partner) / Stromal Cell Niches at the Nexus of the Innate Lymphoid Cell Interactome / SNSF / 01.2019 – 12.2022

Anne Roulin / Impact of transposable elements on plant population evolution: insight from the model grass species brachypodium distachyon / SNSF / 10.2019 – 09.2023

Verena Schünemann / Towards the origins of syphilis / SNSF / 11.2019 – 10.2022

Kentaro Shimizu / Constructing models to confer environmental robustness by developing multiomics technology of polyploid species / Japan Science and Technology Agency / 10.2016 – 03.2022

Kentaro Shimizu / Evolutionary functional genomics of selfing and polyploid speciation / SNSF / 12.2018 – 11.2022

8.3 Newly funded projects within Profit-Center of the URPP

Ueli Grossniklaus, Kentaro Shimizu / International Conference Evolution in Action / Julius-Klaus-Stiftung für Genetik und Sozialanthropologie / 05.2022 – 07.2023 / CHF 2'500

Ueli Grossniklaus, Kentaro Shimizu / International Conference Evolution in Action / UZH Alumni Fonds / 06.2022 – 07.2023 / CHF 2'400

8.4 Ongoing projects within Profit-Center of the URPP

Matthew Horton, Ueli Grossniklaus / Identifying the plant genes that shape the leaf metabolome and microbiome / PSC Syngenta Fellowship / 09.2019 – 08.2022

11 Appendix A

Pilot Projects of the URPP Evolution in Action granted in 2021 and conducted in 2022

Identifying Male-Female Signaling Factors Involved Plant Speciation

Applicant: Stefano Bencivenga, Postdoc (IPMB)

The project investigated the communication between male and female gametophytes of different plant species to identify genes with a relevant role in the interspecific communication, constituting a fertilization barrier. Gene expression analyses of ovules and pollen tubes from different *Arabidopsis thaliana* accessions and *A. lyrata* were conducted. Genes differentially expressed among the *A. thaliana* accessions and between the two species *A. thaliana* and *A. lyrata* were used to identify genes with a role in establishing speciation barriers. A next step will be gene manipulation to affect crossing barriers of two different species in order to generate new hybrids. The prediction of the viability between two different species based on the presence of genes identified in the project will then be possible.

Age Estimation by DNA Methylation in the Aldabra Giant Tortoise

Applicant: Gözde Çilingir, Postdoc (DEBES)

Age constitutes a critically important parameter for population studies; however, it is not always feasible or possible to estimate chronological age in wild animals in a non-invasive way. The ultimate goal in this project was to build a DNA-methylation based age prediction model for Aldabra giant tortoises. First, reduced-representation bisulfite sequencing for five Aldabra giant tortoise individuals with known age was performed. The library preparation and sequencing worked in principle, but a lot of data was lost due to low efficiency in mapping, potentially due to the repetitive content of the Aldabra giant tortoise genome. Given the unsuitability of reduced representation sequencing to Aldabra giant tortoise samples, a production whole genome Nanopore sequencing data was started for 30-40 individuals. The project plans to analyze whole epigenome data and build the epigenetic clock model in 2023.

Interrogating Alien Chromatin Content of Long-Read Sequenced Bread Wheat Chromosomes for Rapid Resistance Gene Cloning

Applicant: Javier Sánchez-Martín, Postdoc (IPMB)

To reduce fungicide use while decreasing yield loss due to pathogen load, molecular cloning of plant resistance genes is of vital importance. This project aimed to establish a rapid and affordable method for disease resistance gene cloning in wheat by flow-sorting chromosomes identified in GWAS analysis of harboring resistance loci to circumvent the need of genetic mapping or mutant population development. As a proof-of-principle, three wheat powdery mildew resistance genes previously identified by GWAS of being embedded in three loci of two chromosomes were molecularly cloned. A small number of candidate genes for each putative resistance gene locus were identified, demonstrating the suitability of the approach to clone genes of interest without the need of genetic mapping or mutant population development. The identified candidate genes are now in the process of being functionally validated using virus-induced gene silencing. In case of successful validation of any of the candidate genes, further experiments to understand the molecular basis of the provided resistance will be conducted.

Genes Involved in the Expression of Secondary Sexual Traits in Male Drosophila prolongata: A New Model Species for Sexual Selection Studies

Applicant: Abhishek Meena, PhD Student (DEBES)

The ubiquitous differences in gene expression observed between species and within sexes lead to unique evolutionary properties of these genes in various species. Exaggerated sexual traits are under incredibly divergent and rapid evolution. However, we still lack a clear understanding of when traits diverge in form and function between the sexes. How can the intricate processes controlling their growth be modified in a sex- and tissue-specific manner without disrupting their function? The project tried to answer the questions on how sexual selection influences sex-biased gene regulation during the development of exaggerated secondary sexual traits and how these changes are reflected in the genomic architecture. Data processing in the project is still ongoing. A comparison between gene expression profiles of different pairs of legs across sexes and species is planned to explore the regulatory cascades that control sex- and segment-specific development in *D. prolongata*, and thus the sexually dimorphic adult structures.

Pyobiotics: Using Pyoverdine to Revert Selection for Antibiotic Resistance

Applicant: Vera Vollenweider, PhD Student (DQBM)

Alternative and more sustainable approaches to treat antibiotic resistant bacteria are urgently needed. The project studied the evolutionary trajectory of β -lactamase carrying *Escherichia coli* under the novel antimicrobial compound pyoverdine. It was found that multicopy plasmids prevented the evolution of resistance against the pyoverdine treatment and against a novel antibiotic, an effect that was not found in *E. coli* without multicopy plasmids. In a next step, a comparison between genes of evolved *E. coli* with and without multicopy plasmids will give some mechanistic insights into resistance evolution.