



Scientific Report

URPP Evolution in Action

Reporting Year 2017

1 Management Summary

In the year 2017, the second Phase of the URPP Evolution in Action started. It was characterized by intense preparative activities to welcome and integrate new PhD students for the projects, to realize the start of the non-tenure track Assistant Professorship, and to accommodate personnel changes in the Coordination Office. During Phase 1 of the URPP Evolution in Action, the number of interactions and scientific exchange had been growing. This is reflected in the number of funded PhD thesis projects and their diverse research fields, either from research groups that already participated in the URPP Evolution in Action during Phase 1, or by research groups that joined for Phase 2. Overall, the URPP Evolution in Action brings together scientists from 38 research groups, 12 departments, and three faculties of UZH: The Faculty of Sciences, the Medical Faculty and the Faculty of Arts.

Scientific progress is being made in 15 new research projects, combined into six themes, mostly in the form of PhD thesis projects. All of these projects are interdisciplinary, which is also reflected in the PhD committees that consist of members from different departments of UZH.

Based on the successful experiences from Phase 1 on funding young scientist to work on innovative and high-risk research questions, an open call for pilot projects was issued in autumn of 2017. The call resulted in a total of 22 research proposals that were reviewed by the Steering Committee of the URPP Evolution in Action. Ten of these 22 pilot projects were granted and are supposed to run until the end of 2018.

To present our research to the public, the URPP Evolution in Action contributed to the *Scientifica '17*. In line with the main theme "Was Daten verraten", we presented two research projects of the URPP Evolution in Action under the common topic "Vom DNA-Buchstabensalat zur Erkenntnis". Based on the number of people visiting our booth, our contribution was a great success.

To facilitate scientific exchange between the people participating in the URPP Evolution in Action, the fifth URPP-Retreat took place in September 2017 in Brunnen with 54 participants. All new research projects funded by the URPP Evolution in Action were presented and provided an overview of the diversity of our research activities in Phase 2. An inspiring keynote lecture on plant pathogen evolution was held by Prof. Sophien Kamoun (The Sainsbury Laboratory, Norwich, UK).

The professorial appointment process for the non-tenure track Assistant Professorship financed through the URPP Evolution in Action was completed in 2017, and all preparatory work for the position could be performed. We are very happy that Anne Roulin accepted the offer as an URPP Assistant Professor in Plant Evolutionary Genomics, and she started her position in January 2018. In addition, the URPP Evolution in Action could welcome Mark Robinson as an URPP Associate Professor at the Institute of Molecular Life Sciences.

The Academic Fellow of the URPP Evolution in Action, Matt Horton, continued his research in 2017. His research is independent, but closely linked to the research themes of the URPP Evolution in Action. One PhD thesis project is running under his supervision.

We look forward to continuing our work in the next three years and thank the Executive Board of the University for financing the URPP Evolution in Action to bring together the diverse research community working on evolutionary questions.

2 Objectives

2.1 Objectives for the reporting year 2017

- Planning and realization of the **Fifth Retreat of the URPP Evolution in Action**, with a program featuring progress reports from all projects, a keynote lecture, faculty and PhD student meetings, as well as a social program enabling a good integration of old and new members and PhD students.
- **Start of Phase 2 of the URPP Evolution in Action**, with new members, projects, and PhD students. We aim at a smooth transition and a good integration of all new projects, and will further promote a lively, interactive community life.
- Finalization of the **Research Projects** run by the URPP Evolution PhD students of Phase 1, and graduations.
- Start of the research projects of the non-tenure track **Assistant Professor** position of the URPP Evolution in Action.
- Presentation of the results from the previous **Open Calls for Research Projects**, and first Open Call for Research Projects in the Phase 2 to promote young scientists by supporting innovative and/or high-risk pilot projects.
- Planning and realization of **Courses for the PhD Program** covering topics such as Next Generation Sequencing, Concepts of Evolutionary Biology, and Scientific Writing for Evolutionary Biologists.
- Continuation of the highly successful **Bioinformatics Support Services** as well as of the **Bioinformatics Tutorial Program**, including a kick-off event tailored to the needs of the new PhD students starting in the Phase 2 of the URPP Evolution in Action.
- Set-up of **PhD Students Meetings** for the new PhD students starting in the Phase 2 of the URPP Evolution in Action, to enhance interaction among students, research projects, and departments involved in the URPP Evolution in Action.
- Organization of **Social Events** to further enhance interactions within the URPP Evolution in Action community.
- Planning and realization of **Public Outreach** activities, in particular the participation of the URPP Evolution in Action at the *Scientifica '17*, and the further planning of a museum exhibition on topics related to the URPP Evolution in Action.
- Further extension and development of the **Website** of the URPP Evolution in Action.

2.2 Achieved objectives in 2017

- The **Fifth Retreat of the URPP Evolution in Action** was a very successful event. It took place in Brunnen and was well attended (54 participants). Presentations of all new research projects funded by the URPP Evolution in Action provided an overview of our research activities in Phase 2. A further highlight was the keynote lecture held by Sophien Kamoun (The Sainsbury Laboratory, Norwich, UK). A social and cultural program complemented the scientific agenda.
- Three **Research Projects** run by URPP Evolution PhD students of Phase 1 were successfully completed and graduations took place (Athene Giesen July 6, 2017; Deborah Leigh September 20, 2017; Giada Ferrari September 29, 2017).
- The first **Open Call for Research Projects** of Phase 2 was issued in summer/fall 2017. We received 22 interesting and innovative project proposals. The Steering Committee of the URPP Evolution in Action granted ten projects, which started thereafter and will last until the end of the year 2018.
- Several **Courses for the PhD Program** that were established by the URPP Evolution in Action during Phase 1 were held again in 2017, such as Next Generation Sequencing and Concepts of Evolutionary Biology. A workshop for URPP PhD students in the framework of the Symposium “Polygenic Adaption” was established together with the Swiss Federal Institute for Forest, Snow and Landscape Research (WSL). The course on Scientific Writing for Evolutionary Biologists was postponed to FS2018.
- The highly successful **Bioinformatics Tutorial Program** was continued and the **Bioinformatics Support Services** for PhD students of Phase 2 of the URPP Evolution in Action was set up. The first (“welcome”) PhD meeting occurred in May 2018
- **New PhD students and postdocs** were successfully integrated into the URPP Evolution community through meetings and social events (excursions, informal get-togethers).
- The URPP Evolution in Action was present at the *Scientifica '17* with a well-attended booth and continued with the planning of a museum exhibition at the Zoological Museum on topics related to the URPP Evolution in Action.
- The **Website** of the URPP Evolution in Action has been extended and new content was developed.

2.3 Objectives for 2018

- Planning and realization of the **Sixth Retreat of the URPP Evolution in Action**, with a program featuring progress reports from all PhD projects, a poster presentation of the pilot projects, a keynote lecture, faculty and PhD student meetings, as well as a social program furthering the integration of old and new members and PhD students.
- Start of the research projects of the non-tenure track **Assistant Professorship in Plant Evolutionary Genomics** funded by the URPP Evolution in Action.
- Planning and realization of a **Mini-Symposium** addressing a topic of broad interest in the URPP Evolution in Action community, organized by members, PhD students, and postdocs of the URPP Evolution in Action.

- Continuation and further development of the **Seminar Series** of the URPP Evolution in Action that takes places at various UZH institutes.
- Second **Open Call for Research Projects** in Phase 2 to promote young scientists by supporting innovative and/or high-risk pilot projects, to be issued in fall 2018.
- Planning and realization of **courses for the PhD Program** covering topics such as Next Generation Sequencing, Concepts of Evolutionary Biology, and Scientific Writing for Evolutionary Biologists. A new course covering the topics of Genome-wide Association Studies (GWAS) is planned as well.
- Continuation of the highly successful **Bioinformatics Support Services** as well as of the **Bioinformatics Tutorial Program**.
- Organization of **Social Events** to further enhance interactions among students, members, research projects, and departments involved in the URPP Evolution in Action.
- Planning of **Public Outreach** activities, in particular the planning of a museum exhibition on topics related to the URPP Evolution in Action.
- Further extension and development of the **Website** of the URPP Evolution in Action including upcoming events and news about publications from URPP funded projects.

3 Research

3.1 Main Research Projects

In 2017, fifteen research subprojects were ongoing in the URPP Evolution in Action, embedded in a framework of six main research topics in evolutionary biology: adaptation, pathogen evolution, microbiology and virology, polyploidy, language evolution, and theoretical evolutionary biology. Furthermore, our Academic Fellow continued his research activities and is supervising a PhD project. The individual projects, including aims, progress, as well as partners and PhD students/postdocs involved are described in some detail below.

ADAPTATION

Population Epigenomics, Phenotypic Plasticity, and Environmental Adaptation

PhD student: Hoda Mazaherikalahrud (Department of Plant and Microbial Biology, IPMB)

PhD Committee: Ueli Grossniklaus (IPMB), Bernhard Schmid (Department of Evolutionary Biology and Environmental Studies, EBES), Jose Gutierrez-Marcos (University of Warwick)

This project focusses on standing Epigenetic Variation (EV) in various populations of *Arabidopsis thaliana* that have been propagated in different ways to generate distinct levels of EV. We hypothesize that genetically identical populations with different levels of EV vary in their response to selection. This hypothesis is addressed in (1) a phenotyping experiment to assess whether there are differences in phenotypic variation between populations with different levels of EV, and (2) in a selection experiment using these different populations. The populations have been generated and the selection experiment is running; the phenotyping experiment was planned in parallel and should start in the near future.

Understanding Invasions: from the Genetic Basis to the Ecological Dynamics of Spreading Populations

PhD student: Felix Moerman (EBES); PhD committee: Florian Altermatt (EBES), Andreas Wagner (EBES), Emanuel Fronhofer (EAWAG), Hanna Kokko (EBES), Rolf Kümmerli (IPMB)

We aim to study adaptation during range expansions in landscapes and focus on the role of abiotic gradients during expansion and the role of sex and recombination for adaptive potential of populations undergoing range expansion. Our goal is to study range expansion in landscapes using protist experiments, phenotypic and competition assays, whole genome sequencing, and theoretical individual-based models. In the first year, pilot studies and small experiments have been performed. Work has been done to resolve technical issues associated with the main experiments, and significant progress has been made on model development. In 2018, the main experiments will be performed to allow enough time for data analysis, genomic analyses, and work on the model in the next years. A smaller experiment already gave data/insights on the expected adaptation to an abiotic stressor, and modelling work resulted in some preliminary results on adaptation range expansion in different landscapes.

Molecular Mechanisms of Fast-Evolving Reproductive Barriers in Plants

PhD student: Xeniya Rudolf (Department of Systematic and Evolutionary Botany, ISEB)

PhD committee: Florian Schiestl (ISEB), Ueli Grossniklaus (IPMB), Kentaro Shimizu (EBES), Karl Schmid (University of Hohenheim), John Pannell (University of Lausanne)

Brassica rapa changed its mating type as a result of hoverfly selection for nine generations. This study aims to discover the underlying molecular mechanism leading to this phenotypic change. So far preliminary work on the plants has been performed and genome wide association study (GWAS) is planned to be used to determine candidate genes being involved in changing mating type. To evaluate the strength of selection/possibility of reversal, an experiment for reverse evolution is planned.

Molecular and Genomic Mechanisms of Early-Evolving Reproductive Barriers in Orchids

PhD student: Alessia Russo (ISEB); PhD committee: Philipp Schlüter (ISEB), Ueli Grossniklaus (IPMB), Thomas Wicker (IPMB), Martin Mascher (IPK Gatersleben)

The topic of this project is to explore the genetic mechanisms behind speciation processes in the genus *Ophrys* (Orchidaceae). In the light of a genome reference for this genus, we aim at building an evolutionary model of population/species divergence. By collecting sequencing data, the genome reference will be assembled and gene annotation started. Besides that, population data will be collected and serves as basis for the second part of the project. The challenging part lays on the assembly of the genome reference due to the large genome of *Ophrys*. A good pipeline for the efficient use of the bioinformatic facilities, provided by the URPP, will be established.

Unraveling the Genetic Architecture and Population Diversity of Bottlenose Dolphin Using New Sequence Technologies and Bioinformatics

PhD student: Stephan Schmeing (Department of Molecular Life Sciences, IMLS); PhD committee: Mark Robinson (IMLS), Michael Krützen (Department of Anthropology, AIM), Lukas Keller (EBES), Christian von Mering (IMLS)

In this project, we aim at leveraging long-range information for studying the evolution of the Indo-Pacific bottlenose dolphin (*Tursiops aduncus*). Our goal is to assemble a reference genome for the Indo-Pacific bottlenose dolphin, and to reconstruct the demographic history in the context of adaptation and convergent evolution. Extraction and transport methods are tested to get dolphin DNA of high molecular weight to the sequencing centers in order to receive optimal results needed for high-quality assembly. A much more realistic simulator for Illumina sequencing data is close to being finished. Due to a yet unknown reason, the dolphin DNA of high molecular weight degrades strongly between the extraction and the quality control at the sequencing center. The emulation of the systematic error profile of Illumina data in a realistic way requires several statistics that can only be stored in the memory of normal server systems by a combination of iterative proportional fitting and a logarithmic data transformation.

LANGUAGE EVOLUTION

Out of Asia: Integrating Genomic, Linguistic and Cultural Evidence on Early Human Migration Paths in the North Pacific Coast of Eurasia

Postdocs: Hiromi Matsumae (EBES); Supervisor: Kentaro Shimizu (EBES); Mentors: Balthasar Bickel (Department of Comparative Linguistics), Frank Rühli (IEM), Marcelo Sanchez (Paleontological Institute and Museum, PIM)

Within the project matches and mismatches in genetic and linguistic diversity using linguistic and genomic datasets focusing on the Pacific region will be studied. We hope to understand similarity and dissimilarity in the mechanisms of genomic and linguistic evolution. A manuscript on the language and genetics in circumpolar regions is in preparation. Genome-wide polymorphism of hunter-gatherers are under analysis, and phylogenetic methods are being applied to linguistic data. Due to the maternity leave of Hiromi Matsumae, the progress of the project got delayed, but a substitute was found. The new postdoc (Chiara Barbieri) started in 2018. She will begin to establish the database "GELATO" (GENes and LANGUAGES TOgether) as the first large-scale platform to study the matches and mismatches in genetic and linguistic diversity.

MICROBIOLOGY AND VIROLOGY

The Evolution of Bacterial Language Diversification

PhD student: Alexandre Ribeiro Teles de Figueiredo (IPMB); PhD committee: Rolf Kümmerli (IPMB), Andreas Wagner (EBES), Hanna Kokko (EBES), Gregory Velicer (ETH Zurich)

The main topic of this project is social cheating as a selective force behind the diversification of public goods or cooperative behaviors. We aim at understanding whether signals/public goods diversify when social cheating occurs, through the use of a bacterial model system and theoretical modelling. Long-term experimental evolution analysis is in progress and theoretical modelling will be started soon. Determining the conditions for experimental evolution required many pilot experiments, but the experiment itself is now running according to plan. New insights/results will be evaluated and analyzed during the next months.

Evolutionary Dynamics of Influenza and Rhinovirus by Chemical Pressure on Host Factors

PhD student: Luca Murer (IMLS); PhD committee: Urs Greber (IMLS), Marco Vignuzzi (Institut Pasteur, Paris), Roger Kouyos (Institute of Medical Virology, IMV), Silke Stertz (IMV)

We are using directed evolution to investigate rhinovirus uncoating mechanisms and cues. Our goal is to find and identify uncoating cues different than endosomal H⁺ concentration, and describe the underlying molecular mechanism. The directed evolution process is finished. We are now identifying and reverse engineering the mutations giving rise to the drug-resistant viruses.

Evolution of the Human Microbiome: Molecular Insights from Ancient Egyptian Samples

PhD student: Enrique Rayo (Institute of Evolutionary Medicine, IEM); PhD committee: Frank Rühli (IEM), Abigail Bouwman (IEM), Christian von Mering (IMLS), Christina Warinner (Max Planck Institute, Jena)

Microbiome studies have significantly advanced over the last years, and now the importance of the microbiome for human health is being unraveled. This project addresses the question whether the human microbiome has evolved across time and populations by using innovative techniques in the field of paleo-genetics. Due to the problematic nature of the samples, the main goal is to develop techniques and protocols that allow a proper metagenomic analysis (and microbiome reconstruction) of naturally and artificially preserved soft tissues. After initial preparations and troubleshooting, preliminary Next Generation Sequencing data from Egyptian millennial samples have been generated. Nevertheless, its quality and importance is yet to be determined by bioinformatics analysis. More samples from different eras, populations, and organ sample types are needed.

The Role of HLA Diversity for HIV Transmission and Evolution along Real-World Transmission Chains

PhD student: Huyen Nguyen (IMV); PhD committee: Roger Kouyos (IMV), Urs Greber (IMLS), Huldrych Günthard (University Hospital Zurich), Jacques Fellay (EPF Lausanne)

The project studies the effect of the host's immune system diversity on the evolution of HIV, both, within the individual and transmission chains. The aim is to quantify HLA diversity along HIV transmission chains, and assessing its impact on viral adaptation as well as to identify transmitted versus acquired HLA escape mutations, thus providing new insights into the clinical and epidemiological impact of HLA diversity. HIV transmission clusters were demonstrated to exhibit less HLA-B diversity within the clusters when compared to randomly assorted patients. This serves as the basis for a follow up project where we will examine escape mutations, which the virus develops as it moves from one individual to the next. It is exciting to observe the greater HLA-B homogeneity within HIV transmission clusters, which is supported by results reported in the literature pointing to the importance of HLA-B with regard to HIV pathogenesis. So far, we only have HLA data from a minority of patients in the Swiss HIV Cohort Study. Further intense data collection by colleagues at EPFL is ongoing, the results of which will be used to solidify the findings.

PATHOGEN EVOLUTION

Evolution of Global Diversity and Dynamics of Plant Pathogen Proliferation

PhD student: Alexandros Georgios Sotiropoulos (IPMB); PhD committee: Thomas Wicker (IPMB), Beat Keller (IPMB), Kentaro Shimizu (EBES), Bruce McDonald (ETH Zurich)

In this project, we aim at assessing the genetic diversity of a global population of *Blumeria graminis* forma specialis *tritici*. The ultimate goal of the project is to generate broad assessment of global diversity of a fungal plant pathogen, and to allow conclusions on the evolution of new mildew strains and the dynamics of their proliferation worldwide. So far, 17 samples have been sequenced, more were collected and will be sequenced soon. Initial population analysis has been done on a small scale (fewer samples analysis). A considerable amount of time was also spent on the annotation of centromeres and transposable elements on a new genomic assembly.

Molecular Basis of Recent Host Expansion and Adaptation of the Wheat Powdery Mildew Pathogen

PhD student: Marion Müller (IPMB); PhD committee: Beat Keller (IPMB), Daniel Croll (University of Neuchatel), Kentaro Shimizu (EBES), Thomas Wicker (IPMB)

The general topic of this project is the recent host adaptation of the triticale powdery mildew to its new host triticale. The aim is to understand the genetic basis of host-adaptation of the recently emerged B.g. triticale on its new host triticale. We created a new reference genome for *Blumeria graminis* f. sp. *tritici*, which resulted in a more improved understanding of its genome evolution. A mapping population allowing QTL mapping of host-adaptation traits has been created, phenotyped, and genotyped. Preliminary data from the QTL mapping suggest that host-adaptation to the new host triticale is controlled by several loci.

PLANT EVOLUTIONARY ECOLOGY - Academic Fellow: Matthew Horton

We are broadly interested in ecological and evolutionary questions, especially when those questions pertain to plants. One of our main goals is to understand how environmental variation and genetic differences among host individuals combine to shape the plant microbiome. We spent most of our time in 2017 collecting wild strawberries accessions from different field sites throughout the European Alps, isolating corresponding DNA samples and submitting those DNA samples to the sequencing core facility (Functional Genomics Center Zurich, FGCZ). Hopefully, the results can be analyzed soon.

Identifying Factors that Shape the Microbiome of the Wild Strawberry *Fragaria vesca*

PhD student: Jana Mittelstrass (IPMB); PhD committee: Matt Horton (IPMB), Ueli Grossniklaus (IPMB), Andreas Wagner (EBES), Alex Widmer (ETH Zurich)

In the scope of this project, the wild strawberry *Fragaria vesca* is used as model system to investigate the environmental and genetic cues behind the assembly and function of the host microbiome. The overall aim of this project is to characterize the above- and belowground microbiome of *F. vesca* samples collected in the wild, and to find out how microbial diversity is affected by host genetic and phenotypic variation. The sequencing and analysis of the taxa (bacteria, fungi) that co-occur with *F. vesca* across the European Alps and the Rocky Mountains in Utah, USA, is ongoing. To characterize the metabolic capacity and its changes over time, a longitudinal common garden experiment is planned. Currently, it is being tested whether the primers used during the generation of amplicon libraries can reduce the bias of this PCR-based approach. New protocols have been established for work on *F. vesca* that will help to promote it as a model system to study evolutionary and microbial ecology.

POLYPLOIDY

New Statistical Tools for Allele- or Homeolog-Specific Epigenomics Data, with Applications to Rapid Adaptation of Artificially Synthesized Polyploid Species to Environmental Niches

PhD student: Stefan Milosavljevic (EBES); PhD committee: Rie Inatsugi-Shimizu (EBES), Mark Robinson (IMLS), Kentaro Shimizu (EBES), Jun Sese (National Institute of Advanced Industrial Science and Technology, Japan), Andreas Wagner (EBES)

DNA methylation changes over short timescales in a synthetic allotetraploid of *Arabidopsis kamchatica*. Our goal is to assess the impact and the importance of epigenetic changes in rapid evolution of plants. The project is divided into an experimental part and a data analysis part, where the former is being optimized to have sequencing data with the best quality possible. The experimental part is planned to be completed by end of March 2018 the latest. Three different methylation kits need to be tested for DNA conversion efficiency and DNA recovery, because so far published research did not focus on plant species.

THEORETICAL EVOLUTIONARY BIOLOGY

The Population Genetics of Polygenic Adaptation: from Method Testing to NGS Data Analysis

Postdoc: Champak Beeravolu Reddy (EBES); Supervisors: Fred Guillaume (EBES); Mentors: Peter Szövényi (ISEB), Katalin Csilléry (ETH Zurich)

The aim of this project is to develop tools to understand how species adapt to environmental changes, and to predict species' responses to ongoing climate change. We aim at detecting the genomic signal of polygenic adaptation and, more specifically, at determining the role of epistasis. By using extensive simulations, we are in the process of studying how various forms of epistasis, mutation/recombination rates, and selection influence the rate of adaptation. We have successfully verified our implementation of epistasis in our forward-in-time simulation software (Nemo) by reproducing published results.

An Integrative Approach to Understanding Cancer Across the Tree of Life

PhD student: Yagmur Erten (EBES); PhD committee: Hanna Kokko (EBES), Natasha Arora (Institute of Forensic Medicine, IRM), Wolf Blanckenhorn (EBES), Kathleen Sprouffske (EBES)

The general topic of this project is life history evolution under cancer risk in multicellular organisms. The ultimate goal is to increase our understanding of how cancer risk affects life history evolution across multicellular organisms by combining theoretical and empirical approaches. Currently, two computational models of body size and cancer defense coevolution are underway, addressing organismal and cell-level strategies, respectively. The bioinformatics part will be started in March 2018 and contacts with collaborators for the experimental part have been established in order to design and undertake the experiments. Thus far, we did not have any problems in the modelling part of the project. Our main challenge this year will be designing and arranging the logistics of the experimental part, for which we will get assistance from our collaborators.

ONGOING PROJECTS FROM PHASE 1

Project 3: Investigating the Importance of Epigenetics in Adaptation and Coevolution

Subproject 3.1: Epigenetic Variation and Selection by Aphids in *Arabidopsis thaliana*

Postdoc: Vimal Rawat (IPMB); Supervisors: Ueli Grossniklaus (IPMB), Bernhard Schmid (EBES)

It is currently not clear to what extent epigenetic variation contributes to plant adaptation, so we have performed selection experiments in uniform genotypes to address this issue. Our goal is to determine whether increased trichome density resulting from selection with aphids, compared to control plants of the same genotype, is due to epigenetic variation. Using genome-wide bisulfite-sequencing (BS-Seq), we aim to identify differentially methylated cytosines and investigate whether they contribute to this difference in phenotype within a given genotype. We have analyzed BS-Seq data and identified differentially methylated cytosines/regions in selected *versus* control populations. BS-Seq and data analysis is challenging when a limited amount of DNA is used or the DNA samples were not prepared for this purpose. Nevertheless, using careful analyses, we found some candidate genes with a strong indication for involvement in the observed phenotype.

Subproject 3.3: Effects of Epigenetic Variation in Adaptive Processes in *Tetrahymena thermophila*

PhD student: Vanessa Weber de Melo (EBES); PhD committee: Owen Petchey (EBES), Ueli Grossniklaus (IPMB), Paul Hurd (Queen Mary, University of London, UK), Bernhard Schmid (EBES), Sinead Collins (University of Edinburgh, UK)

This general topic of this project is about the importance of epigenetic variation in ecological and evolutionary processes using *Tetrahymena thermophila* as a model system. The project aims at a better understanding of the importance of histone modifications in gene expression changes that occur when *T. thermophila* adapts to different conditions, such as increasing population densities and temperature variation. A population density experiment has been performed and data from two ChIP-seq samples are being analyzed; the remaining 16 samples are being processed and will be sequenced soon. Temperature adaptation experiment should be performed in the upcoming months. Results from the ChIP-seq data analyses might lead to modifications in the temperature adaptation experiment.

PILOT PROJECTS

To further promote young scientists, the URPP Evolution in Action made a first open call in Phase 2 for pilot projects in the wider field of evolutionary biology. In particular, applicants were encouraged to hand in proposals using an interdisciplinary approach 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 purpose of the call was to fund innovative pilot projects setting the stage for subsequent larger grant applications. We received many highly interesting project proposals that were reviewed and rated by the Steering Committee of the URPP Evolution in Action. Out of 22 submitted projects ten could be funded in 2017. The projects will run until the end of 2018.

Open Call of October 2017

Applicant: Dr. Salim Bourras, Oberassistent (IPMB)

Title of project: An Experimental Evolution Approach to Disease Interactions in Wheat.

Granted funding: CHF 20'000

Applicant: Dr. Glauco Camenisch, Postdoc (EBES)

Title of project: Genetic Basis of Diversity in Immune Phenotypes in Alpine Ibex.

Granted funding: CHF 19'144

Applicant: Seydina Issa Diop, PhD student (ISEB)

Title of project: Linkage Map of the Liverwort *Marchantia polymorpha*.

Granted funding: CHF 17'800

Applicant: *Dr. Ana Marcela Florez-Rueda, Postdoc (IPMB)*

Title of project: Testing siRNA Functions: Methylation Role in Hybrid Seed Failure.

Granted funding: CHF 20'000

Applicant: *Alejandro Giraldo Fonseca, PhD student (IPMB)*

Title of project: Testing the Presence of Genomic Imprinting beyond Angiosperms: Transcriptome Profiling of the Gametes and the Sporophyte of the Liverwort *Marchantia polymorpha*.

Granted funding: CHF 20'000

Applicants: *Enrique Rayo, PhD student; Dr. Giada Ferrari, Postdoc (IEM)*

Title of project: Evaluation of a Non-Destructive DNA Sampling Method for the Analysis of Museum Wet Tissue Specimens

Granted funding: CHF 14'100

Applicant: *Jan-Niklas Runge, PhD student (EBES)*

Title of project: How Has a Selfish Genetic Element Shaped the House Mouse Genome?

Granted funding: CHF 20'000

Applicant: *Dr. Charlotte Soneson, Postdoc (IMLS)*

Title of project: Surveying Male Determining Factors across *Musca domestica* (House Fly) Strains Using Nanopore cDNA Sequencing

Granted funding: CHF 20'000

Applicant: *Dr. Macarena Toll Riera, Ambizione Fellow (EBES)*

Title of project: Integrating Transcriptomics and Proteomics Data to Understand how a Cold-Adapted Bacterium Responds to Temperature Changes.

Granted funding: CHF 8'623

Applicant: *Dr. Jordi van Gestel, EMBO Fellow (EBES)*

Title of project: The Evolution of Bacterial Division of Labor: a Cell Type-Specific Transcriptomic Analysis.

Granted funding: CHF 18'954



3.2 Scientific Activities

Scientific Retreat



The fifth retreat of the URPP Evolution in Action took place in Brunnen on September 5-7, 2017 with 54 participants. Progress reports of all current research projects funded by the URPP Evolution in Action provided an overview of the ongoing research activities. The PhD students and postdocs conducting the main projects held presentations. The aim was to make the scientific questions of the diverse fields understandable to all, and to enable discussion across different disciplines. Additionally, our new member and future Assistant Professor, as well as the Academic Fellow gave a 30-minute insight into their research areas. The keynote lecture, by now an established tradition at each annual retreat, was held by Prof. Sophien Kamoun (The Sainsbury Laboratory, Norwich, UK). He provided absolutely fascinating insights into his research on plant pathogen evolution.

Similar to the previous annual meetings, the Retreat 2017 served as an opportunity to meet all other members and young scientists of the URPP Evolution in Action and to discuss general aspects. Additionally, faculty and PhD student meetings were held during the retreat. The scientific sessions and meetings were complemented by a social program, during which a lot of informal discussions and interactions took place.

Bioinformatics Tutorials

The successful series of bioinformatics tutorials was continued in 2017, based on the inputs from the URPP Evolution in Action members and PhD students. These tutorials were organized and taught by Drs. Stefan Wyder and Heidi Tschanz-Lischer and are listed in the university lecture index (Vorlesungsverzeichnis) as BIO 396 "Tutorials in Practical Bioinformatics". At the PhD Welcome Meeting in May 2017, a feedback poll on teaching was taken with the new cohort of PhD students, and topics were chosen according to students' feedback. In detail, the following 1-day-tutorials were offered:

- Introduction to UNIX/Linux and Bash Scripting: Writing bash scripts, control structures
- R Intro/Refresher Course Part 1: loading data, subsetting, making plots (ggplot2), summarizing groups, writing functions, data types in R, automating repetitive tasks (loops and apply functions), coding habits to avoid

In addition, the following 3-hour tutorials were offered:

- R Intro/Refresher Course Part 2: making plots (R base graphics), programming exercises
- Principles of data visualization: basics of graphic design and visual communication; use of salience, colors, consistency, and layout; different chart types; presentation and discussion of "good" and "bad" graphics
- Reproducible research: problems and challenges, 10 simple rules

Every tutorial consisted of a theoretical introduction to the topic, but most of the time was spent on guided exercises. The tutorials were very well attended, with nine to 15 participants for each topic. The students generally gave a very positive feedback about content and format, and for all past tutorials there were requests to repeat the tutorial. The participants were mostly PhD students of the URPP Evolution in Action, but also more senior scientists and guests from other departments attended the tutorials. The series is being continued in 2018.

In addition, the embedded bioinformaticians of URPP Evolution in Action organized and taught again a 2-day course: BIO 634 "Next-Generation Sequencing 2 for Model and Non-Model Species: Transcriptomes, Variant Calling, and Biological Interpretation", which was organized as a follow-up course to a 2-day introduction to Next-Generation Sequencing (NGS) (BIO 610 "Next-Generation Sequencing 1 - Introductory Course: Assembly, Mapping, and Variant Calling") organized by Prof. Kentaro Shimizu and others. BIO 634 aimed to extend the knowledge of NGS analysis taking a hands-on approach. The course was attended by 17 people, mostly PhD students of the Plant Science or Evolutionary Biology PhD Programs from the University of Zurich and ETHZ. Students' evaluations were very favorable, and the course will be offered again in 2018. The preparatory 1-day course BIO 609 "Introduction to UNIX/Linux and Bash Scripting", aiming to increase computing and scripting skills, was offered again and represents a prerequisite for the attendance of BIO 610 and BIO 634. Due to the high interest, the same course was taught twice with a total of 37 participants, primarily PhD and MSc students from the University of Zurich and ETHZ. These courses on NGS analysis will be continued in 2018.

The quarterly one-to-one meetings between each PhD student and an embedded bioinformatician were continued in 2017 to discuss project designs, methods, and challenges. The aim is to keep up-to-date with progress, and to help connect the PhD students using similar methods. Both embedded bioinformaticians of the URPP Evolution in Action published a methodological advancement as first-author in 2017.

Courses for the PhD Program in Evolutionary Biology

- Concepts in Evolutionary Biology (BIO395); April 10-11, 2017; Lecturers: Barbara König, Lukas Keller, Marcelo R. Sanchez, Kentaro Shimizu, Wolf Blanckenhorn, Anna K Lindholm-Krützen, Michael Krützen, Frédéric F. Guillaume, Madeleine Geiger, Macarena Toll Riera
- Introduction to UNIX/Linux and Bash Scripting (BIO609): preparatory course for BIO610 and BIO634; May 3 + 9, 2017; Lecturers: Stefan Wyder, Heidi Tschanz-Lischer
- Next-Generation Sequencing for Model and Non-Model Species (BIO610); May 10-11, 2017; Lecturers: Kentaro Shimizu, Roman Vladimir Briskine, Masaomi Hatakeyama, Tony Kuo, Jun Sese, Rie Shimizu Inatsugi, Heidi Tschanz-Lischer
- Next-Generation Sequencing 2 – Advanced Course: Transcriptomes, Variant Calling and Biological Interpretation (BIO634); May 16-17, 2017; Lecturers: Masaomi Hatakeyama, Heidi Tschanz-Lischer, Stefan Wyder, Kentaro Shimizu

PhD Student Guest Speaker Seminars

The PhD Student Guest Speaker Seminar Series of the URPP Evolution in Action was successfully continued in 2017. With the support of the coordination office, PhD students of the URPP Evolution in Action can invite speakers for reserved slots in departmental seminar series of the participating departments. The organizing students generally find this a great opportunity and experience.

The following seminar took place in 2017:

- *Title:* Predicting and Altering Viral Evolution
Speaker: Prof. Marco Vignuzzi, Pasteur Institute, Paris, France
Date: October 31, 2017

URPP Evolution Seminars and Symposium

The following seminars took place in 2017:

- *Title:* Building a Bigger Brain: Genetic Bases for the Evolution of the Human Cortex
Speaker: Greg Wray, Duke University, USA
Date: April 26, 2017
- *Title:* Evolution in Darwin's Dreampond: the Adaptive Radiation of Cichlid Fishes in East African Lake Tanganyika
Speaker: Prof. Walter Salzburger, University of Basel, Switzerland
Date: October 9, 2017

The following symposium was co-organized and -financed by the URPP Evolution in Action:

- *Title:* Detecting the Genomic Signal of Polygenic Adaptation and the Role of Epistasis in Evolution
Date: August 31 and September 1, 2017
Speaker: Simon Aeschbacher, University of Bern, Switzerland,
Nick Barton, IST Austria,
Jeremy Berg, Columbia University, USA,
Örjan Carlborg, Uppsala University, Sweden,
Daniel Croll, University of Neuchatel, Switzerland,
Josephine Daub, University Pompeu Fabra, Barcelona, Spain,
Santiago C. González-Martínez, INRA, France,
Thomas Hansen, University of Oslo, Norway,
Joachim Hermisson, University of Vienna, Austria,
Sergey Kryazhimskiy, University of California San Diego, USA

Mato Lagator, IST Austria,
Anna Maria Langmüller, Vetmed University Vienna, Austria
Luke Mackley Noble, New York University, USA
John Mckay, Colorado State University, USA,
Josh Payne, University of Zurich, Switzerland
Martina Rauscher, University of Cologne, Germany
Diana Jessie Rennison, University of Bern, Switzerland
Anna Santure, University of Auckland, New Zealand
Markus Stetter, University of California Davis, USA
Peter Visscher, University of Queensland, Australia
Sam Yeaman, University of Calgary, Canada

4 Academic Career Development

4.1 Academic Career Development for Young Academics

Most of the budget granted to the URPP Evolution in Action is currently used to fund PhD students and postdoctoral fellows. In 2017, the URPP Evolution in Action funded salaries and research consumables for 13 PhD students and two postdocs, thereby contributing substantially to their career development at the financial level. Furthermore, the URPP Evolution in Action is financing an Academic Fellow, who in addition is supervising a PhD student. Following our tradition of funding short-term research projects, we held one call for pilot projects open to members of the research groups participating in the URPP Evolution in Action. These calls enable young scientists to develop their own research ideas, to form new collaborations across the borders of research groups and institutes, and to obtain their own funding for pilot projects.

Beyond direct financial support, we are dedicated to providing a network supporting young academics in the field of evolutionary biology, and to creating an atmosphere of lively interactions across the borders of faculties, institutes, and seniority. We also organize social events and see such activities deliberately as a means to grant young academics access to a community of experienced researchers. PhD students, postdocs, and junior professors who do not receive funding from the URPP Evolution in Action, but work in research areas close to ours, are equally invited to attend events and courses organized by the URPP Evolution in Action. A successful format of social events is the “Informal Get-Together”, taking place about three times per year on weekday evenings in Zurich.

The two embedded bioinformaticians of the URPP Evolution in Action have supported all PhD projects since the beginning, such that experimental design, probe preparation, analysis methods etc. are optimally adapted to the questions asked. In doing so, the bioinformaticians themselves expand their research experience, and the wealth of data available from several projects allows them to develop productive research activities of their own. The embedded bioinformaticians have regular meetings with the PhD students and developed a very well attended tutorial series, which endows the PhD students with the necessary bioinformatics skills. We have taken care to enable a close contact between the embedded bioinformaticians of the URPP Evolution in Action and the bioinformatics community at UZH. The URPP Evolution in Action bioinformaticians regularly work one day per week in the von Mering (IMLS) and Wagner (EBES) groups, respectively, where they are in touch with the newest developments in bioinformatics research, and take part in weekly group meetings. This approach allows for a continued transfer of knowledge at the forefront of current research topics and trends in bioinformatics.

We put a lot of effort into developing courses and tutorials that address the needs of the PhD students in the URPP Evolution in Action community. These teaching efforts should allow them to become researchers with a comprehensive understanding of the fields of evolutionary biology, genomics, bioinformatics, population genetics, and ecology (see also chapter 3.2).

PhD students and postdocs have the possibility to invite keynote speakers from abroad, thereby gaining experience and establish new contacts with researcher who may well become mentors for their further career. To invite speakers, PhD students and postdocs can organize mini-symposia with several speakers or they have the possibility to invite speakers for reserved slots in departmental seminar series of the participating departments. In both cases, they receive organizational support from the URPP Evolution in Action coordination office and the necessary funding.

The PhD students in the URPP Evolution in Action have the possibility to bring in their views in various ways. At our retreats, they are invited to formulate their needs in a workshop specifically dedicated to this aim. Furthermore, the PhD students have elected a representative who serves on the Steering Committee of the URPP Evolution in Action.

4.2 Gender Equality Development

Hiring of personnel is on an equal opportunity basis and according to the “Gender Equality Action Plan UZH” guidelines. We mention our equal opportunity efforts in all job advertisements. Nevertheless, the gender ratio in the URPP Evolution in Action could have been balanced as at the end of Phase 1 (6 female and 8 male PhD students; 2 male postdocs; 4 female and 7 male pilot project holders), and we will keep paying attention to the issue of gender balance in the future. This also applies to the invitation of keynote speakers and we will preferentially approach potential female speakers for the next retreats. ,.

Wherever possible, we support efforts to create a family-friendly work environment, for instance by enabling part-time work. Our experience with providing such opportunities is highly positive. Furthermore, all our social events are, if convenient for children, open to the families of our co-workers.

5 Publications

5.1 Peer-reviewed publications in 2017

Baumgartner M, Roffler S, Wicker T, Pernthaler J (2017) Letting go: genome streamlining allows for simultaneous adaptation to top-down and bottom-up constraints in a phenotypically plastic bacterial strain. *The ISME Journal* 11: 2258–2266.

Briskine R, Paape T, Shimizu-Inatsugi R, Nishiyama T, Akama S, Sese J, Shimizu KK (2017) Genome assembly and annotation of *Arabidopsis halleri*, a model for heavy metal hyperaccumulation and evolutionary ecology. *Molecular Ecology Resources* 17 (5): 1025–1036.

Collier K, Townsend SW, Manser MB (2017) Call concatenation in wild meerkats. *Animal Behaviour* 134: 257-269.

Giesen A, Blanckenhorn WU, Schäfer MA (2017) Behavioural mechanisms of reproductive isolation between two hybridizing dung fly species. *Animal Behaviour* 132: 155-166.

Izuno A, Kitayama K, Onoda Y, Tsujii Y, Hatakeyama M, Nagano AJ, Honjo MN, Shimizu-Inatsugi R, Kudoh H, Shimizu KK, Isagi Y (2017) The population genomic signature of environmental association with gene flow in an ecologically divergent tree species *Metrosideros polymorpha* (Myrtaceae). *Molecular Ecology* 26 (6): 1515–1532.

Lischer HEL, Shimizu KK (2017) Reference-guided *de novo* assembly approach improves genome reconstruction for related species. *BMC Bioinformatics* 18: 474.

Menardo F, Wicker T, Keller B (2017) Reconstructing the evolutionary history of grass powdery mildew lineages (*Blumeria graminis*) at different evolutionary time scales with NGS data. *Genome Biology and Evolution* 9 (2): 446-456.

Menardo F, Praz CR, Wicker T, Keller B (2017) Rapid turnover of effectors in grass powdery mildew (*Blumeria graminis*). *BMC Evolutionary Biology* 17: 223.

Shimizu-Inatsugi R, Terada A, Hirose K, Kudoh H, Sese J, Shimizu KK (2017) Plant adaptive radiation mediated by polyploid plasticity in transcriptomes. *Molecular Ecology* 26 (1): 193-207.

Wyder S, Raissig MT, Grossniklaus U (2017) Consistent Reanalysis of Genome-wide Imprinting Studies in Plants Using Generalized Linear Models Increases Concordance across Datasets. bioRxiv 180745; doi: <https://doi.org/10.1101/180745>

Selected papers published in previous years

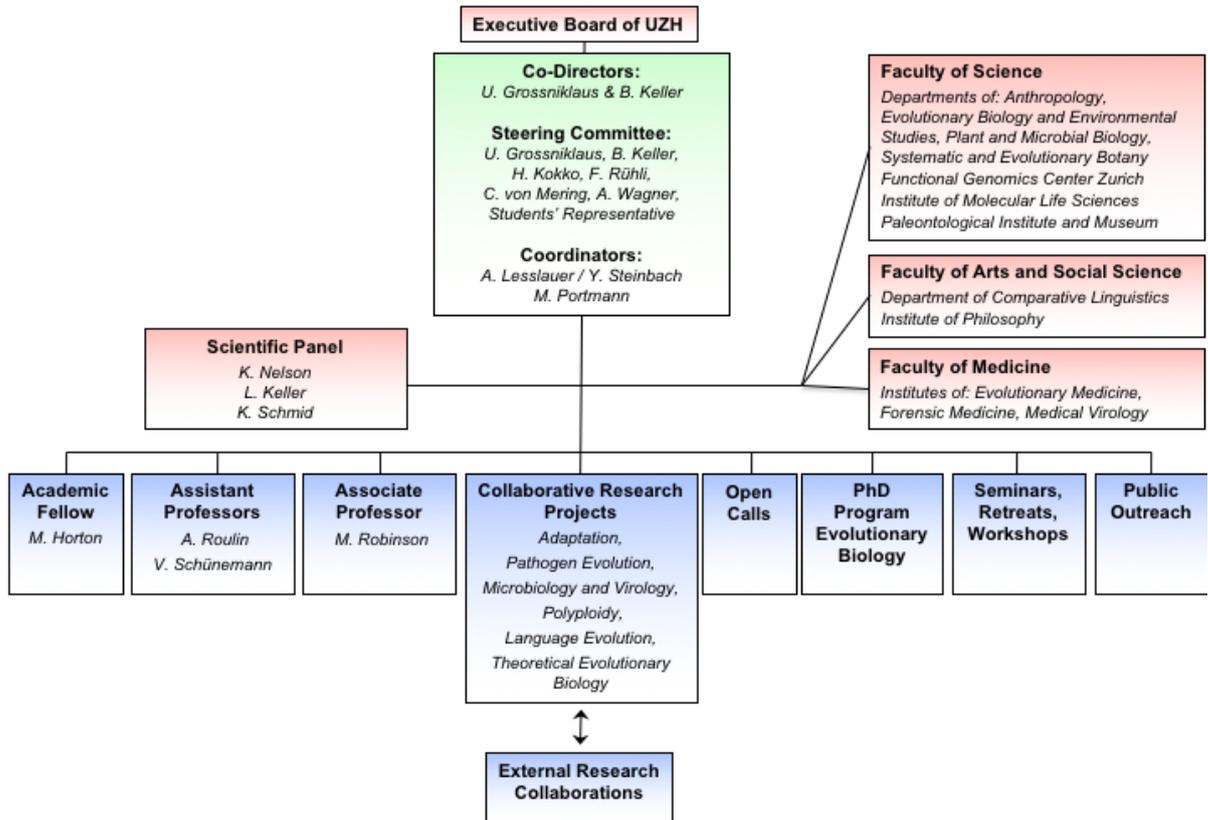
Baumgartner M, Neu TR, Blom JF, Pernthaler J (2016) Protistan predation interferes with bacterial long-term adaptation to substrate restriction by selecting for defence morphotypes. *J Evol Biol.* 29(11):2297-2310.

Kellenberger RT, Schlüter PM, Schiestl FP (2016) Herbivore-induced DNA demethylation changes floral signalling and attractiveness to pollinators in *Brassica rapa*. *PLoS ONE*, 11(11): e0166646.

Menardo F, Praz CR, Wyder S, Ben-David R, Bourras S, Matsumae H, McNally KE, Parlange F, Riba A, Roffler S, Schaefer L, Shimizu KK, Valenti L, Zbinden H, Wicker T, Keller B (2016) Hybridization of powdery mildew strains gives rise to pathogens on novel agricultural crop species. *Nature Genetics* 48 (2), 201-205.

Pinto-Carbó M, Sieber S, Dessein S, Wicker T, Verstraete B, Gademann K, Eberl L, Carlier AL (2016) Evidence of horizontal gene transfer between obligate leaf nodule symbionts. *The ISME Journal* 10: 2092-2105.

6 Structures





7 Third-Party Funds and funded URPP Projects

7.1 Third-party Funding Raised in the Context of the URPP Evolution in Action Research Projects

Mittelstrass J obtained a travel grant from the Department of Plant and Microbial Biology (IPMB) and a UW Biostatistics Summer Institutes Scholarship for visiting two statistical genetics courses and conducting field sampling abroad (July 2017).