



# Scientific Report

## URPP Evolution in Action

Reporting Year 2019

### 1 Management Summary

The URPP Evolution in Action has very successfully completed its seventh year. For the PhD students of the second phase of the URPP, it has been the third year working on their projects. Their progress reports, both during the Site Visit of the Scientific Panel and at the Annual Retreat, showed very promising results. The research groups of the two Assistant Professors and the Academic Fellow of the URPP have been very active and have strongly contributed to the scientific success in 2019. Finally, the progress reports of the 28 Pilot Projects have shown the great diversity of research questions addressed by the URPP Evolution in Action. Some of the Pilot Projects are already completed and have led to interesting results.

The URPP Evolution in Action research community has grown into an active, engaged network of more than 160 scientists of the University of Zurich (UZH), interested in addressing evolutionary questions using molecular approaches. They have met in 2019 at many occasions. The 7<sup>th</sup> Retreat of the URPP Evolution in Action took place in September 2019 in Grindelwald with 60 participants. Progress reports of all current research projects funded by the URPP Evolution in Action provided an overview of our ongoing research activities. A fascinating keynote lecture was held by our new Member and Steering Committee Member Prof. Anna-Liisa Laine. The Seminar Series of the URPP Evolution in Action was well attended, too. The seminars, which are of specific interest to the URPP community, are held as embedded events in the existing seminar series of our affiliated departments. We organized several Informal Get-Togethers and many lively discussions took place at these occasions. At the PhD Committee Meetings, the interdisciplinary PhD Committees of our students lead very engaged and serious scientific discussions among the members from various departments. The PIs state that these interactions are very positive and informative. Finally, the Site Visit of the Scientific Panel provided another opportunity for our entire research community to meet and interact at the one-day symposium. The feedback of the participants at the URPP events was consistently very positive. We are particularly proud that the PhD Students of the URPP Evolution in Action repeatedly stated that they feel very well supported and that the URPP is, for them, the most important network.

The bioinformatics support and tutorials have been continued successfully by the new team of Embedded Bioinformaticians. Six courses took place in 2019 that have been developed by the URPP Evolution in Action over the last years, with topics ranging from Next-Generation Sequencing for Model and Non-Model Species to Human Genetic, Demographic, and Cultural Diversity. The URPP was also very active regarding Public Outreach: we took part in *Scientifica* 2019 with a well-attended booth, and a lot of preparatory work for the planned museum exhibition has taken place.

The URPP Evolution in Action was very positively evaluated by the Scientific Panel during the Site Visit in May 2019. We would like to thank the Panel Members for their time and very helpful recommendations. We also thank the UZH Executive Board for the decision to finance Phase III of the URPP Evolution in Action until 2024. We very much look forward to continuing our work.

## 2 Objectives

### 2.1 Objectives for the reporting year 2019

- Planning and realization of the 7<sup>th</sup> **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.
- **Evaluation 2019**: planning and realization of the Site Visit 2019, where we will welcome the URPP's Scientific Panel; preparing the Development and Financial Plan 2021-2024, including an open call for projects for Phase III of the URPP Evolution in Action.
- **Public Outreach**: preparation of the special exhibition on "Evolution in Action", which will open in December 2019 at the Zoological Museum of the UZH. In addition, participation in the 2019 edition of *Scientifica*, the joint public science festival of ETH Zurich and UZH.
- Continuation of the successful **Seminar Series** of the URPP Evolution in Action, which takes place at various UZH departments.
- Third **Open Call for Research Projects** in Phase II to promote young scientists by supporting innovative and/or high-risk pilot projects, to be issued in spring 2019.
- Planning and realization of **courses for the PhD Program Evolutionary Biology**, covering topics such as Next-Generation Sequencing, Concepts of Evolutionary Biology, Scientific Writing for Evolutionary Biologists, and 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.

### 2.2 Achieved objectives in 2019

- We had a very successful 7<sup>th</sup> **Retreat of the URPP Evolution in Action**. The feedback from the attendees was enthusiastic, regarding both the scientific and the networking parts. The progress reports showed very promising results and many lively discussions took place. The program was complemented with a career workshop for junior scientists.
- For the **Evaluation 2019**, we prepared the Development and Financial Plan 2021-2024. To this aim, we also held an open call for projects for Phase III of the URPP Evolution in Action. The current research and activities of the URPP Evolution in Action were presented to the Scientific Panel Members during their 2-day Site Visit, which ended with the presentation of the very positive evaluation results by the Scientific Panel.
- **Public Outreach**: the URPP Evolution in Action participated in the 2019 edition of *Scientifica* with a well-attended booth. A lot of preparatory work has been achieved for the planned museum exhibition "Evolution in Action". However, the opening of the exhibition had to be postponed for various organizational reasons.

- Seven well-attended seminars took place in 2019 in the framework of the URPP Evolution in Action **Seminar Series**.
- The third **Open Call for Pilot Projects** in Phase 2 was issued in spring 2019. We received a total of 27 applications, whereof ten were granted.
- A number of already existing **courses for the PhD Program Evolutionary Biology**, developed by the URPP Evolution in Action over the last years, were held again in 2019. The topics included topics such as Next-Generation Sequencing, Concepts of Evolutionary Biology, and Scientific Writing for Evolutionary Biologists. Also, a new course on Human Genetic History was held in November 2019.
- **Bioinformatics Support Services** as well as of the **Bioinformatics Tutorial Program** were successfully continued by the new team of Embedded Bioinformaticians, consisting of Carla Bello (joined the URPP in spring 2018) and Gregor Rot (joined the URPP in January 2019).
- Several **Social Events** contributed to further stimulate interactions among students, members, research projects, and departments involved in the URPP Evolution in Action.

### 2.3 Objectives for 2020

- Planning and realization of the 8<sup>th</sup> **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.
- **Public Outreach**: finalization of the museum exhibition “Evolution in Action”, the opening of which is foreseen in 2021.
- Continuation of the successful **Seminar Series** of the URPP Evolution in Action, which takes place at various UZH departments.
- Planning and realization of **courses for the PhD Program Evolutionary Biology**, covering topics such as Next-Generation Sequencing, Concepts of Evolutionary Biology, Genome-Wide Association Studies (GWAS), and Human Genetic History.
- Continuation of the highly successful **Bioinformatics Support Services** as well as of the **Bioinformatics Tutorial Program**.
- Organization of a second **Career Planning Workshop** for the junior scientists within the URPP Evolution in Action.
- **1:1 Meetings for all PhD Students** of the URPP Evolution in Action with the Program Manager, 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.
- **Termination of Phase II and preparation of Phase III** of the URPP Evolution in Action on the scientific, financial, organizational, and administrative levels.

## 3 Research

### 3.1 Research Projects

#### 3.1.1 PhD and Postdoc Projects

##### ADAPTATION

###### Population Epigenomics, Phenotypic Plasticity, and Environmental Adaptation

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

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

Despite the heritability of epigenetic variation (EV), its ecological and evolutionary significance is largely unknown. In plants, epigenetic changes can be heritable and occur more frequently than genetic ones; EV may thus allow rapid responses in the adaptation to environmental change. However, published results are contradictory, possibly because of small sample numbers and insufficient replication. This project aims at analyzing the epigenetic patterns of different populations of *Arabidopsis thaliana* with distinct propagation histories, which are predicted to differ in their level of standing EV. Indeed, a large-scale phenotyping experiment performed in 2019 showed that populations with different levels of EV are phenotypically distinct despite being genetically identical. These data, which are currently being analyzed and prepared for publication, clearly demonstrate that EV contributes to phenotypic diversity. To test the hypothesis that sufficient standing EV is required to show a response to selection, these populations are currently subjected to a highly replicated selection experiment that is in its 4<sup>th</sup> generation. Soon, the response to selection of populations differing in their level of EV can be characterized at the phenotypic and molecular level.

###### 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 (Department of Quantitative Biomedicine, DQBM)

This project aims at studying adaptation during range expansions, focusing 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 with and without abiotic gradients, and for asexual and sexual populations through protist experiments, phenotypic and competition assays, whole genome sequencing and theoretical individual based models. All experimental work has been completed, and only analysis and writing work remains. One project has been accepted for publication, two other projects are either submitted or under revision, and a fourth project is currently being analyzed. The experimental work of the main experiment showed us a first confirmation of the gene swamping hypothesis (the focus of the main experiment), but also that the theory is still incomplete, and may need revising. The genomic analysis of this project is currently underway.

*Molecular Mechanisms of Fast-Evolving Reproductive Barriers in Plants*

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

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

The topic of this project is to evaluate genetic changes underlying mating system evolution from outcrossing to selfing in *Brassica rapa* as a result of selection by hoverflies. We aim to describe the molecular mechanisms underlying the mating system change. We are working on a genome-wide association study (GWAS) and preparing the one before last generation of a back-evolution experiment – then the data will be collected and analyzed. It seems that the GWAS will be a bit more complex on the analysis side, although the quality of the sequencing is good. We had issues with pollinator delivery and diseases, which postponed the back-evolution crosses.

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

PhD student: Alessia Russo (ISEB)

PhD committee: Philipp Schlüter (University of Hohenheim, Germany), Ueli Grossniklaus (IPMB), Thomas Wicker (IPMB), Martin Mascher (IPK Gatersleben, Germany)

The topic of this project is to explore the genetic mechanisms behind sexual deception in *Ophrys* orchids. We aim at producing a genome reference for the genus and build an evolutionary model of species divergence. The genome assembly is ready. We are now annotating the gene space and starting the first analyses. In the previous report (2018), we described the characterization of the Repetitive Elements as a possible new insight. Now, we also included the analysis of the mitochondrial genome of some other *Ophrys* species.

*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 bottlenose dolphin, and to reconstruct the demographic history in the context of adaptation and convergent evolution. The first paper draft for ReSequenceR, a much more realistic simulator for Illumina sequencing data, is almost finished. Minigap, a scaffolding, gap filling, and assembly improvement tool, needs finishing and extensive testing. The bottlenose dolphin assembly and population studies wait for further data. BioNano and Hi-C data creation for the bottlenose dolphin assembly scaffolding turned out to be difficult due to the limitations of skin and blubber tissue.

## LANGUAGE EVOLUTION

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

Postdoc: Chiara Barbieri (EBES)

Supervisors: Kentaro Shimizu (EBES), Balthasar Bickel (Department of Comparative Linguistics);

Collaborators: Hiromi Matsumae (Tokai University, Japan)

We are combining human population genetics and cultural evolution methods to address human dispersal in prehistoric time, in particular linking human history in Eastern North Asia and the

Americas. The ultimate goal is to show patterns of congruence between linguistic, cultural, and biological history and evolution, and to anchor these patterns in time and space. New genetic data was generated and analyzed for key populations of the Pacific Coast and Andes of South America. A systematic review of the matches and mismatches between genetic and linguistic diversity worldwide is being performed. The results on the linguistic and genetic congruences for the Pacific coast will be contextualized against global patterns by a systematic study on a worldwide human genetic database.

## **MICROBIOLOGY AND VIROLOGY**

### *The Evolution of Bacterial Language Diversification*

*PhD student: Alexandre Ribeiro Teles de Figueiredo (DQBM)*

*PhD committee: Rolf Kümmerli (DQBM), Andreas Wagner (EBES), Hanna Kokko (EBES), Gregory Velicer (ETH Zurich)*

The main topic of this project is the evolution of public goods-based cooperation and social interactions in bacterial communities. We aim at understanding how public goods-based cooperation evolves in bacteria and how it differs with varying ecological parameters (i), and community composition (ii). For (i) data collection is complete, analysis is underway, and publication strategy is being discussed. For (ii) experimental phase is in the last stage, analysis is underway, and a publication is to be written up soon. The original project (i) is still underway, but has diversified into interspecific interactions, with a spin-off project (ii). Additionally, a review paper on the overarching topic has been written and submitted.

### *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, France), Roger Kouyos (Institute of Medical Virology, IMV), Silke Stertz (IMV), Weihong Qi (Functional Genomics Center Zurich, FGCZ)*

We investigate rhinovirus uncoating behavior in presence of endosomal acidification inhibitors. We aim to identify the evolutionary consequence of rhinoviruses if forced to evolve endosomal pH-independent uncoating mechanisms. It is in the viral structural proteins, identified as a hotspot, where mutations lowering the capsid stability accumulate. Consequently, a less dramatic destabilization cue – that can be provided by receptor binding or the endosomal ionic environment – is required to trigger the viral uncoating event. The serial passaging procedure that led to the identification of the mutations mediating low endosomal pH-independence was repeated with 10 replicates. Massive parallel sequencing of the resulting populations yielded the same mutations that were observed in the original passaging experiment.

### *Evolution of Microbial Communities Associated with Ancient Human Populations: Molecular Insights from Archaeological and Historical Samples*

*PhD student: Enrique Rayo (Institute of Evolutionary Medicine, IEM)*

*PhD committee: Frank Rühli (IEM), Verena Schünemann (IEM), Christian von Mering (IMLS), Christina Warinner (Max Planck Institute for the Science of Human History, Jena, Germany)*

This project uses innovative metagenomics Next-Generation Sequencing (NGS) methods on diverse archaeological material, as well as medical and pathological collections to study the variation and diversity of both commensal and pathogenic microbial organisms associated with ancient human populations. We aim to establish a valid framework of ancient microbiome studies that allows the comparison of microbial communities from different geographical regions, taphonomical history, and

time periods. Practical laboratory work is basically finished. We are currently analyzing the data we have generated so far and expect to have the last piece of data in the following months. We are having some issues with the integration of certain public datasets into my pipeline.

*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)

For the next stage of the project we are examining how HLA-I type may cause drug resistance mutations to arise in HIV in treatment-naïve patients, or to be maintained when transmitted to patients who are not yet on antiretroviral treatment. Our goal is to better understand how drug resistance mutations arise in conjunction with the selection pressure from HLA. The first set of analyses from this subproject have been preliminary completed - an abstract of which was accepted for presentation at the upcoming International Workshop on HIV and Hepatitis Observational Databases (IWHOD) in March 2020. This project is able to use the extremely extensive data from the Swiss HIV Cohort Study to systematically scan all HLA-I and HIV drug resistance mutations to find significant associations.

## 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 a broad assessment of the 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. More than 100 samples have been sequenced and various analyses on diversity, phylogeny, and the life history of the wheat powdery mildew have been done. We are currently preparing a manuscript to publish these data. Time was spent on a side project on collecting, sequencing, and analyzing various samples of lichen metagenomes to investigate their diversity and evolution. Time was also spent on long-read sequencing and RNA sequencing to create a pan-genomic profile for wheat powdery mildew and more.

*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)

We aim at understanding the basis of host adaptation of Triticale powdery mildew, a pathogen that evolved through hybridization between wheat and rye powdery mildew and emerged on its new host Triticale. The goal of this project is to identify candidate genes responsible for host adaptation of the Triticale powdery mildew using a QTL mapping approach. We generated a chromosome-level genome assembly of the new hybrid pathogen *B.g. triticales* and identified and characterized several loci that control host adaptation on its new host triticale. In addition, we mapped and cloned *AvrPm17* in Triticale and wheat powdery mildew, an avirulence effector that is recognized by the rye resistance gene *Pm17*. Host-adaptation in triticale powdery mildew is a complex trait and is controlled by multiple loci that originated from both the wheat and rye parental *formae speciales*.

## PLANT EVOLUTIONARY ECOLOGY

### 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 this project, we investigate the natural variation of plant microbiomes to understand the factors that shape the microbiome of wild plant populations. Our goal is to investigate how microbiomes form in the wild, and to understand in which aspect (structural or functional) and to what extent such variation might be influenced by host genetics. We characterized the microbiome of the wild strawberry *Fragaria vesca* across two continents, and found an overlap between the most abundant bacteria and fungi in our North American and European samples. Collecting soil and climatic parameters enabled us to identify the environmental factors that shape both the leaf and root microbiome of these two wild populations (for example, the amount of frost-free days and the length of the growing period). Using both Amplicon and metagenomic shotgun sequencing data, we are now testing the hypothesis that the wild strawberry microbiome is heritable and whether hosts influence metabolism in the microbiome rather than taxonomy.

## PLANT EVOLUTIONARY GENOMICS

### Linking Environmental Stress to Transposable Element Activity and Fitness

Postdoc: Michael Thieme (IPMB)

Supervisor: Anne Roulin (IPMB); Collaborators: Todd Blevins (University of Strasbourg, France), Daniel Giddings Vassão (Max Planck Institute for Chemical Ecology, Jena, Germany)

The general topic of this project is elucidation of the diversity of mobile stress-inducible transposons in different accessions of the model plant *Brachypodium distachyon*. We aim at understanding the role of transposable elements (TEs) in genome plasticity and the consequences for local adaptation in the model plant *B. distachyon*. Validation of preliminary results from mobilome-sequencing suggest stress-induced mobility of some retroTE-families in Bd21. We are currently implementing nanopore sequencing to validate active TEs, and CRISPR-CAS9 to knock-out potentially mobile elements and to mutate regulatory genes involved in TE-silencing to increase the activity of TEs. So far there is no indication for a very strong activity of TEs in *B. distachyon* (based on mobilome-seq that can only detect circular TEs). However, it seems that plenty of regions in the genome form circular DNA, which could be an interesting finding. Mutants of epigenetic silencing will be used as a positive control for TE-activity. Additional stresses are being tested.

## 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)

The general topic of this project is workflow development for whole genome DNA methylation data and analysis of DNA rapid methylation changes in a synthetic allotetraploid: *Arabidopsis kamchatica*. Our goal is to improve tools and guidelines for epigenetic research in plants, with a focus on polyploids, and assess the impact and the importance of DNA methylation changes in the rapid evolution of novel

polyploids. We developed an Automated Reproducible Polyploid EpiGenetic workflow (ARPEGgIO), which is being applied on bisulfite sequencing data coming from *A. kamchatica*. A benchmark comparing tools for differential methylation analysis is also being set up. Sequencing data had varying quality and has slowed down the whole analysis. With some new data already acquired and some coming soon, a more confident interpretation is expected.

## THEORETICAL EVOLUTIONARY BIOLOGY

### *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 topic of this project is life history evolution under cancer risk. Our goal is to understand how cancer, as a phenomenon observed across nearly all branches of multicellularity, can affect life history evolution, and in turn, how different traits can change cancer risk across the tree of life. Currently, we have one peer-reviewed scientific communication piece published in 2019, one manuscript under revision (and available as a preprint at bioRxiv), and one manuscript in preparation. The next goal is to work on developing two different models based on the insights from the previous ones.

### 3.1.2 Assistant Professorships, Associate Professor, and Academic Fellow

#### PLANT EVOLUTIONARY GENOMICS – Assistant Professor: Anne Roulin (IPMB)

Our research aims at understanding how transposable elements (TEs) may drive genetic diversity and adaptation in natural populations of the grass *Brachypodium distachyon*. It is articulated around 3 main approaches:

- Population genomics: using sequencing data and computational approaches, we are looking for footprints of selection to identify genes and TEs involved in local adaptation.
- Impact of TEs on gene expression: we are investigating to what extent TEs modify the epigenetic status and the expression of adjacent genes.
- Activation of TEs *in planta*: using a combination of chemicals and stress, we are aiming at activating TEs in planta to directly assess their functional impact.

We identified candidate TE polymorphisms that may directly contribute to gene expression variation across natural populations. However, we showed that these changes in gene expression are not linked to methylation spreading around TEs. We also identified the first ever-reported active TE in *B. distachyon*. TE silencing appears to be extremely efficient in *B. distachyon*, and applying the techniques developed in *Arabidopsis thaliana* has been more challenging than anticipated. We are nonetheless extending our approach to more stress conditions and various genetic backgrounds in order to further identify active TEs.

#### PALEOGENETICS – Assistant Professor: Verena Schünemann (IEM)

Our major goals are to trace back the evolutionary history of pathogens and to obtain new insights into host-microbe interactions in the past. We use state-of-the-art techniques in ancient DNA in combination with Next-Generation Sequencing. With ancient pathogen genomics, we can contribute to the reconstruction of the origin and evolution of major human infectious diseases.

### **STATISTICAL GENOMICS – Associate Professor: Mark Robinson (IMLS)**

High-throughput sequencing technologies are revolutionizing the way genomes, transcriptomes, and epigenomes are studied. Generating, processing, and interpreting this unprecedented magnitude of complex data and integrating multiple dimensions requires considerable research effort, for biologists, statisticians, and computer scientists alike. Our group develops statistical methods for interpreting high-throughput sequencing and other genomics technologies in areas such as genome sequencing, gene expression and regulation, and analysis of epigenomes. Research projects encompass three interlaced themes: contribute to relevant genome-scale experimental design and data analysis challenges in close collaboration with biologists; develop statistical methods and software tools for the interpretation and integration of multiple types of genome-scale data; perform technical investigations to understand the performance of the technologies used to generate and of the algorithms used to process the data.

Our group maintains a firm stance on open and reproducible science. The default policy is that we: i) produce documented open source software for our developed statistical and computational frameworks (typically through the Bioconductor project); ii) create code repositories for manuscript analyses; and, iii) post manuscripts as preprints. In many subfields, modern biologists are transitioning to faster, more transparent modes of scientific dissemination and we fully support these initiatives (e.g., ASAPBio).

### **PLANT EVOLUTIONARY ECOLOGY - Academic Fellow: Matthew Horton (IPMB)**

Our work is focused on understanding how the plant microbiome forms. We use techniques from ecology, molecular genetics, and evolutionary genomics to determine whether and to what extent these communities are shaped by both environmental factors and genetic differences among host plants. We have already shown that microbiome GWAS can be used to understand the genetic architecture of plant-microbial interactions. We are now testing specific candidate genes in functional assays to identify promising candidate genes for follow-up experiments.

#### **3.1.3 Pilot Projects**

To further promote young scientists, the URPP Evolution in Action launched three open calls in Phase II 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 calls was to fund innovative pilot projects setting the stage for subsequent larger grant applications. We received many excellent project proposals that were reviewed and rated by the Steering Committee of the URPP Evolution in Action. In 2017, ten out of 22 submitted projects could be funded. These projects ran until the end of 2018. In 2018, eight out of 25 submitted projects could be funded. These projects ran until the end of 2019. In 2019, ten out of 27 submitted projects could be funded. These projects will run until the end of 2020.

Listed below are the projects from the 2018 and 2019 calls. The research reports of the completed projects of the 2018 call are collected in Appendix A. For the completed projects from the 2017 call, please refer to the Annual Report 2018 of the URPP Evolution in Action.

**Open Call of July 2018**

- Applicant:* Gülfirde Akgül, PhD student (IEM)  
*Title of project:* Analysis of Ancient *Treponema pallidum* in Europe  
*Granted funding:* CHF 19'900
- Applicant:* Nadine Bachmann, PhD student (IMV)  
*Title of project:* The Evolution of HIV-1 Drug Resistance during the 3-month WHO-Recommended Enhanced Adherence Counselling Period  
*Granted funding:* CHF 19'700
- Applicant:* Dr. Shraddha Karve, Postdoc (EBES)  
*Title of project:* Evolution of Latent Traits in Antibiotic Environments  
*Granted funding:* CHF 19'600
- Applicant:* Tiago Meier, PhD student (IPMB)  
*Title of project:* Evolution of a Hermaphroditic Sex Chromosome and Environmentally Induced Sex Reversal in *Carica papaya*.  
*Granted funding:* CHF 10'000
- Applicant:* Anna Neubauer, PhD student (IBES)  
*Title of project:* Hornwort-Cyanobacteria Symbiosis: Genetic Analysis of the Plant Host.  
*Granted funding:* CHF 5'600
- Applicant:* Dr. Özhan Özkaya, Postdoc (EBES)  
*Title of project:* Evolution and Ecology on a Chip  
*Granted funding:* CHF 16'700
- Applicant:* Dr. Coraline Praz, Postdoc (IPMB)  
*Title of project:* Transcriptomic Analysis of the Host and Nonhost Response to Powdery Mildew in the Recent Hybrid Triticale Compared to its Parents Wheat and Rye  
*Granted funding:* CHF 17'500
- Applicant:* Michele Wyler, PhD student (IPMB)  
*Title of project:* Post-transcriptional Transposable Element Silencing in the Grass *Brachypodium distachyon*  
*Granted funding:* CHF 19'400

**Open Call of May 2019**

- Applicant:* Dr. Stefano Bencivenga, Postdoc (IPMB)  
*Title of project:* Understanding Early Events of Speciation Through Cell-Specific Transcriptome Analysis  
*Granted funding:* CHF 20'000
- Applicant:* Thomas Grubinger, PhD student (EBES)  
*Title of project:* Tracing the Genomic Signature of 400 Years of Tomato Domestication in Europe Using Herbarium Specimens  
*Granted funding:* CHF 19'400
- Applicant:* Alexander Kirbis, PhD student (ISEB)  
*Title of project:* The Effect of Mating System on the Strength of Genomic Imprinting in Haploid Plants  
*Granted funding:* CHF 17'800
- Applicant:* Martin Mecchia, Postdoc (IPMB)  
*Title of project:* Evolutionary Basis of Polarized Cell Growth in Land Plants  
*Granted funding:* CHF 20'000

- Applicant:* Enrique Rayo, PhD student (IEM)  
*Title of project:* Reconstructing the Ancient Microbiome of the Appendix  
*Granted funding:* CHF 18'800
- Applicant:* Sebastian Sauppe, Postdoc (Department of Comparative Language Science)  
*Title of project:* The Evolution of Event Cognition in Humans and Hominidae: A Comparative Eye Tracking Study on the Perception of Naturalistic Events  
*Granted funding:* CHF 20'000
- Applicants:* Manuel Poretti and Alexandros Sotiropoulos, PhD students (IPMB)  
*Title of project:* Lichen Symbiosis: Metagenomic Signatures of Adaptation to Different Lifestyles and Environmental Conditions  
*Granted funding:* CHF 20'000
- Applicant:* Xenia Wietlisbach, PhD student (EBES)  
*Title of project:* The Role of Pathogens in Creating Genomic Signatures of Local Adaptation in Alpine Ibex  
*Granted funding:* CHF 20'000
- Applicant:* Narjes Yousefi, Postdoc (ISEB)  
*Title of project:* Testing Recent Theoretical Model of Speciation Using *Sphagnum magellanicum* complex as an Experimental System  
*Granted funding:* CHF 15'100
- Applicant:* Jia Zheng, Postdoc (EBES)  
*Title of project:* Do Fluctuating Temperature Environments Facilitate Evolutionary Adaptation and Innovation?  
*Granted funding:* CHF 19'500

## 3.2 Scientific Activities

### 3.2.1 Scientific Retreat



The 7<sup>th</sup> Retreat of the URPP Evolution in Action took place in Grindelwald on September 11-13, 2019, with 60 participants. All PhD Students and Postdocs funded by the URPP Evolution in Action held oral presentations. 14 Pilot Projects and the research of 4 associated scientists were presented in a lively Poster Session. A fascinating keynote lecture was held by our new member Prof. Anna-Liisa Laine. Another 4 new members (Simon Aeschbacher, Sylvain Bischof, Léa Frachon, Isabelle Mansuy) provided a short introduction into their research areas.

The Retreat also served as an opportunity to discuss general aspects. The scientific and social programme was complemented with faculty and PhD Student meetings as well as a career workshop. As in previous years, the Retreat 2019 was a dynamic and positive event with lots of lively discussions, and the feedback from the attendees was enthusiastic.

### 3.2.2 Site Visit

The two-day Site Visit by the Scientific Panel of the URPP Evolution in Action was part of the evaluation process.

On May 28, 2019, we presented the current research and activities of the URPP in a scientific symposium at Schloss Au. 62 participants attended the symposium. The program included six PhD projects and one Postdoc project presentations, as well as presentations held by the URPP Assistant

Professors Anne Roulin and Verena Schünemann, by the URPP Associate Professor Mark Robinson, and the URPP Academic Fellow Matthew Horton. Progress reports for 25 projects (9 PhD projects, 1 Postdoc project, 15 pilot projects) were presented during the Poster Session. The Directors presented the activities of the URPP Evolution in Action in the areas of Academic Career Development, Public Outreach, and Networking.

On May 29, 2019, the Scientific Panel met the Group Leaders, Directors, PhD Students and Postdocs, Bioinformaticians, Coordination Team, and the University Executive Board for discussion rounds at Irchel Campus. After an internal discussion and the writing of the Evaluation Report, the Scientific Panel presented their very positive results of the evaluation and provided helpful recommendations for the future of the URPP Evolution in Action.

### 3.2.3 Bioinformatics Tutorials and Support

The series of bioinformatics tutorials was continued in 2019, based on the input of the URPP Evolution in Action Members and PhD Students. The tutorials were organized and taught by the Embedded Bioinformaticians of the URPP, Carla Bello (replaced Heidi Lischer in spring 2018), and Gregor Rot (replaced Stefan Wyder in January 2019).

During the Annual Retreat of the URPP Evolution in Action 2019, the Embedded Bioinformaticians gave an overview of their research and support activities. The Embedded Bioinformaticians then walked the audience through a live online questionnaire that was filled on site by all attendees. The results provided valuable input regarding the bioinformatic needs in the URPP Evolution in Action and has been used to develop new topics for the next round of tutorials in 2020.

In 2019, the following 3-hour tutorials were offered:

- Making plots with Python: Learning how to plot with Matplotlib and Seaborn libraries.
- Basic BAM file manipulations using Python+Pysam on iCLIP datasets: Manipulating genome alignment files with Python on dummy datasets.
- Genome annotation formats (GFF, GTF), basic region manipulation, and gene expression quantification: Navigating different genome annotation file formats, and quantifying gene expression.

Each tutorial had a theoretical introduction to the topic and continued with a hands-on part consisting of computer-guided exercises. The tutorials were well attended and, in general, had positive feedback regarding content and format. The students asked that several of the already given tutorials will be repeated. The attendees were mostly PhD students of the URPP Evolution in Action, but also included Postdocs and guests from other departments. The series is being continued in 2020.

Once more, in addition to the other tutorials, the URPP Evolution in Action Embedded Bioinformaticians organized and taught the 2-day course: BIO634 "Next-Generation Sequencing 2 for Model and Non-Model Species: Transcriptomes, Variant Calling and Biological Interpretation", which was given as a follow-up course to a 2-day introduction to Next-Generation Sequencing (BIO610 "Next-Generation Sequencing for Model and Non-Model Species") by Prof. Kentaro Shimizu and others. This course, BIO634, offered students the possibility to extend their knowledge of Next-Generation Sequencing analysis by learning first hand from invited speakers that are experts in the field, together with a hands-on approach by utilizing theoretical and computer-guided exercises given by the Embedded Bioinformaticians of the URPP Evolution in Action. It was attended by 7 individuals (one absent) mostly PhD students in Plant Sciences or Evolutionary Biology from the UZH and ETH Zurich. The student's feedback was very positive and the course will be offered again in 2020. Moreover, the preparatory 1-day course BIO609 "Introduction to UNIX/Linux and Bash Scripting", aiming to increase

computing and scripting skills, was offered once again by the Embedded Bioinformaticians of the URPP Evolution in Action. This course was a pre-requisite to attend BIO610 and BIO634 courses and had 18 participants, mainly PhD and MSc students from the UZH and ETH Zurich. The 5-day course on Next-Generation Sequencing analysis will be continued in 2020.

The quarterly one-to-one meetings between URPP Evolution in Action PhD students and Embedded Bioinformaticians were continued in 2019 and the students were able to discuss their PhD project, including its experimental design, bioinformatic methods, bottlenecks, and challenges. The aim of these meetings is to keep up-to-date with their PhD progress and to help connect the PhD students who are using similar methods. Because most of the PhD students are at an advanced stage of their PhD, the bioinformatic support has gotten more and more hands-on with the particular data and bioinformatic issues, and the bioinformatics team has been helping to solve the arising issues on regular call-on-the-spot meetings.

### 3.2.4 Courses for the PhD Program in Evolutionary Biology

- Concepts in Evolutionary Biology (BIO395); April 1-2, 2019; Lecturers: Barbara König, Marcelo R. Sanchez, Kentaro Shimizu, Michael Krützen, Frédéric F. Guillaume, Wolf Blanckenhorn, Anna K. Lindholm Krützen, Simon Aeschbacher, Macarena Toll Riera
- Scientific Writing for Evolutionary Biologists (BIO555); November 20-21, 2019; Lecturers: Hanna Kokko, Annegret Lesslauer
- Introduction to UNIX/Linux and Bash Scripting (BIO609): Preparatory Course for BIO610 and BIO634; May 20, 2019; Lecturers: Carla L. Bello Cabrera, Gregor Rot
- Next-Generation Sequencing for Model and Non-Model Species (BIO610); May 21-22, 2019; Lecturers: Kentaro Shimizu, Masaomi Hatakeyama, Sun Jianqiang, Jun Sese, Rie Shimizu Inatsugi, Shoji Tatsuma
- Next-Generation Sequencing 2 – Continuation Course: Transcriptomes, Variant Calling and Biological Interpretation (BIO634); June 3-4, 2019; Lecturers: Carla L. Bello Cabrera, Gregor Rot
- Human Genetic, Demographic and Cultural Diversity; November 11-12, 2019; Lecturers: Mark Stoneking, Chiara Barbieri

### 3.2.5 URPP Evolution in Action Seminars

The following URPP Evolution in Action Seminars took place in 2019:

- *Title:* Genetic causes and genomic consequences of plant mating system variation  
*Speaker:* Tanja Slotte, Stockholm University, Sweden  
*Date:* February 6, 2019
- *Title:* The secrets of plant sex determination as revealed by strawberries  
*Speaker:* Tia-Lynn Ashman, University of Pittsburgh, USA  
*Date:* March 8, 2019
- *Title:* The wondrous cycles of polyploidy in plants  
*Speaker:* Jonathan Wendel, Iowa State University, USA  
*Date:* March 28, 2019

- Title: *Prospects of pan-genomics in barley*  
Speaker: *Martin Mascher, IPK Gatersleben, Germany*  
Date: *May 3, 2019*
- Title: *Genes, culture, and human evolution*  
Speaker: *Mark Stoneking, MPI for Evolutionary Anthropology, Leipzig*  
Date: *November 12, 2019*
- Title: *Transposable elements as both causes and consequences of subgenome differentiation in polyploids*  
Speaker: *Damon Lisch, Purdue University, USA*  
Date: *November 15, 2019*
- Title: *The bio-cultural and evolutionary history of domesticated animals*  
Speaker: *Greger Larson, University of Oxford, UK*  
Date: *December 9, 2019*

### 3.2.6 Conferences and Symposia sponsored by the URPP Evolution in Action

The URPP Evolution in Action sponsored the following events that were organized in 2019 by members or students of the URPP and that thematically were of interest for at least parts of the URPP research community. We sponsored either the travel costs of one of the international keynote speakers or a travel grant for an international PhD Student visiting the conference. In return, the members and students of the URPP were invited to the symposia and conferences, including networking events.

- Title: *Biology19 – The Swiss annual meeting of biologists*  
Date: *February 7-8, 2019*
- Title: *TNAM 11 – The 11<sup>th</sup> Tri-National Arabidopsis Meeting*  
Date: *April 10-12, 2019*
- Title: *Perspectives on Human Body Height*  
Date: *June 5, 2019*
- Title: *Modelling Ecology & Evolution Zurich (MEEZ)*  
Date: *June 27-28, 2019*
- Title: *5<sup>th</sup> Annual Meeting of the International Society of Evolution, Medicine and Public Health (ISEMPH 2019)*  
Date: *August 13-16, 2019*
- Title: *Evolutionary Ecology and Human Health*  
Date: *October 30, 2019*

## 4 Academic Career Development

### 4.1 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: PhD Students, Postdocs, an Academic Fellow, and Assistant Professors. In 2019, the URPP Evolution in Action funded salaries and research consumables for 14 PhD students and three Postdocs. Furthermore, the URPP Evolution in Action is financing an Academic Fellow and two Assistant Professors. This support contributes substantially to the career development at the financial level. We also foster young academics by awarding grants for short-term research projects, where proposals can be handed in by PhD Students and Postdocs of the research groups participating in the URPP Evolution in Action. Three calls took place in Phase II, and the third of these was held in 2019. The calls have proved to be very successful in enabling young scientists to develop their own research ideas, in forming new collaborations across the borders of research groups and institutes, and in obtaining 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, departments, 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. A successful format of social events is the “Informal Get-Together”, taking place about three times per year on weekday evenings in Zurich. In addition, the PhD Students and Postdocs of the URPP Evolution in Action started a monthly meeting series called “Very Informal Get-Togethers (VIGT)”, which underlines the good atmosphere and integration in this peer group.

The two Embedded Bioinformaticians of the URPP Evolution in Action have supported all PhD projects since the beginning, such that experimental design, probe preparation, and analysis methods are optimally adapted to the questions asked. In doing so, the Embedded 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 Embedded Bioinformaticians regularly work 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 the 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). At the Retreat 2019, we also held a first of several planned Career Workshops, with which we aim to provide information, examples of career paths both in- and outside of academia, and the opportunity to discuss career-related questions.

PhD Students and Postdocs have the possibility to invite keynote speakers from abroad, thereby gaining experience and establishing new contacts with researchers 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 the departmental

seminar series of 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 meeting 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 emphasize our equal opportunity efforts in all job advertisements. The gender ratio in the URPP Evolution in Action is balanced, at the PhD Student level and among the applicants for positions and research grants. We have appointed two outstanding women scientists as Assistant Professors, thereby providing excellent role models. Furthermore, we aim at a balanced gender ratio in the list of our invited speakers for seminars and keynote lectures. 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. We also provide child-care opportunities at all our events to enable parents to attend.

## 5 Publications

### 5.1 Peer-reviewed publications in 2019

Barbieri C, Barquera R, Arias L, Sandoval JR, Acosta O, Zurita C, Aguilar-Campos A, Tito-Álvarez AM, Serrano-Osuna R, Gray R, Mafessoni F, Heggarty P, Shimizu KK, Fujita R, Stoneking M, Pugach I, Fehren-Schmitz L (2019). The current genomic landscape of western South America: Andes, Amazonia and Pacific Coast. *Molecular Biology and Evolution* 36(12): 2698–2713.

Bergelson J, Mittelstrass J, Horton MW (2019). Characterizing both bacteria and fungi improves understanding of the *Arabidopsis* root microbiome. *Scientific Reports* 9:24.

Bourras S, Kunz L, Xue M, Praz CR, Müller MC, Kälin C, Schläfli M, Ackermann P, Flückiger S, Parlange F, Menardo E, Schaefer LK, Ben-David R, Roffler S, Oberhaensli S, Widrig V, Lindner S, Isaksson J, Wicker T, Yu D & Keller B (2019). The *AvrPm3-Pm3* effector-NLR interactions control both race-specific resistance and host-specificity of cereal mildews on wheat. *Nature Communications* 10:2292.

Erten EY, Kokko H (2019). Diverse ways to think about cancer: What can we learn about cancer by studying it across the tree of life? *Mètode Science Studies Journal - Annual Review* 0(10).

Giesen A, Schäfer MA, Blanckenhorn W (2019). Geographic patterns of postzygotic isolation between two closely related widespread dung fly species (*Sepsis cynipsea* and *Sepsis neocynipsea*; Diptera: Sepsidae). *Journal of Zoological Systematics and Evolutionary Research* 57(1):80-90.

Gretzinger J, Molak M, Reiter E, Pfrengle S, Urban C, Neukamm J, Blant M, Conard NJ, Cupillard C, Dimitrijević V, Drucker DG, Hofman-Kamińska E, Kowalczyk R, Krajcarz MT, Krajcarz M, Münzel SC, Peresani M, Romandini M, Rufí I, Soler J, Terlato G, Krause J, Bocherens H, Schuenemann VI (2019). Large-scale mitogenomic analysis of the phylogeography of the Late Pleistocene cave bear. *Scientific Reports* 9:10700.

Grize SA, Wilwert E, Searle JB, Lindholm AK (2019). Measurements of hybrid fertility and a test of mate preference for two house mouse races with massive chromosomal divergence. *BMC Evolutionary Biology* 19:25.

Izuno A, Wicker T, Hatakeyama M, Copetti D, Shimizu KK (2019). Updated genome assembly and annotation for *Metrosideros polymorpha*, an emerging model tree species of ecological divergence. *G3: Genes, Genomes, Genetics* 9(11):3513-3520.

Meccariello A, Salvemini M, Primo P, Hall B, Koskinioti P, Dalíková M, Gravina A, Gucciardino MA, Forlenza F, Gregoriou ME, Ippolito D, Monti SM, Petrella V, Perrotta MM, Schmeing S, Ruggiero A, Scolari F, Giordano E, Tsoumani KT, Marec F, Windbichler N, Arunkumar KP, Bourtzis K, Mathiopoulos KD, Ragoussis J, Vitagliano L, Tu Z, Papatianos PA, Robinson MD, Saccone G (2019). *Maleness-on-the-Y (MoY)* orchestrates male sex determination in major agricultural fruit fly pests. *Science* 365(6460):1457-1460.

Müller MC, Praz CR, Sotiropoulos AG, Menardo F, Kunz L, Schudel S, Oberhänsli S, Poretti M, Wehrli A, Bourras S, Keller B, Wicker T (2019). A chromosome-scale genome assembly reveals a highly dynamic effector repertoire of wheat powdery mildew. *New Phytologist* 221(4):2176-2189.

Nguyen H, Thorball CW, Fellay J, Böni J, Yerly S, Perreau M, Klimkait T, Kusejko K, Bachmann N, Chaudron S, Paioni P, Thurnheer MC, Battegay M, Cavassini M, Vernazza P, Bernasconi E, Günthard HF, Kouyos R (2019). HIV transmission chains exhibit greater HLA-B homogeneity than randomly expected. *Journal of Acquired Immune Deficiency Syndromes*. 81(5):508-515.

Nowicka M, Krieg C, Crowell HL, Weber LM, Hartmann FJ, Guglietta S, Becher B, Levesque MP, Robinson MD (2019). CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. *F1000Research* 6:748.

Oleairo F, Nguyen H, Bonnet F, Yerly S, Wandeler G, Stoeckle M, Cavassini M, Scherrer A, Costagiola D, Schmid P, Günthard HF, Bernasconi E, Boeni J, D'arminio Monforte A, Zazzi M, Rossetti B, Neau D, Bellecave P, Rijnders B, Reiss P, Wit F, Kouyos R, Calmy A (2019). Impact of the M184V/I mutation on the efficacy of Abacavir/Lamivudine/Dolutegravir therapy in human immunodeficiency virus treatment-experienced patients. *Open Forum Infectious Diseases* 6(10):ofz330.

Orjuela S, Huang R, Hembach KM, Robinson MD, Soneson C (2019). ARMOR: An Automated Reproducible MOdular workflow for preprocessing and differential analysis of RNA-seq data. *G3: Genes, Genomes, Genetics* 9(7):2089-2096.

Översti S, Majander K, Salmela E, Salo K, Arppe L, Belskiy S, Etu-Sihvola H, Laakso V, Mikkola E, Pfrengle S, Putkonen M, Taavitsainen JP, Vuoristo K, Wessman A, Sajantila A, Oinonen M, Haak W, Schuenemann VJ, Krause J, Palo JU, Onkamo P. (2019). Human mitochondrial DNA lineages in the Iron-Age Fennoscandia suggest incipient admixture and eastern introduction of farming-related maternal ancestry. *Scientific Reports* 9(1):16883.

Piñeiro Fernández L, Byers KJRP, Cai J, Sedeek KEM, Kellenberger RT, Russo A, Qi W, Fournier CA, Schlüter PM (2019). A phylogenomic analysis of the floral transcriptomes of sexually deceptive and rewarding european orchids, *Ophrys* and *Gymnadenia*. *Frontiers in Plant Science* 10:1553.

Soneson C, Love MI, Patro R, Hussain S, Malhotra D, Robinson MD (2019). A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. *Life Science Alliance* 2(1):e201800175.

Soneson C, Yao Y, Bratus-Neuenschwander A, Patrignani A, Robinson MD & Hussain S (2019). A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. *Nature Communications* 10:3359.

Stritt C, Wyler M, Gimmi EL, Pippel M, Roulin AC (2019). Diversity, dynamics and effects of LTR retrotransposons in the model grass *Brachypodium distachyon*. *New Phytologist*

van Gestel J, Ackermann M, Wagner A (2019). Microbial life cycles link global modularity in regulation to mosaic evolution. *Nature Ecology & Evolution* 3:1184-1196.

Weber LM, Nowicka M, Soneson C, Robinson MD (2019). diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. *Communications Biology* 2:183.

Weber LM, Saelens W, Cannoodt R, Soneson C, Hapfelmeier A, Gardner PP, Boulesteix AL, Saeys Y, Robinson MD (2019). Essential guidelines for computational method benchmarking. *Genome Biology* 20(1):125.

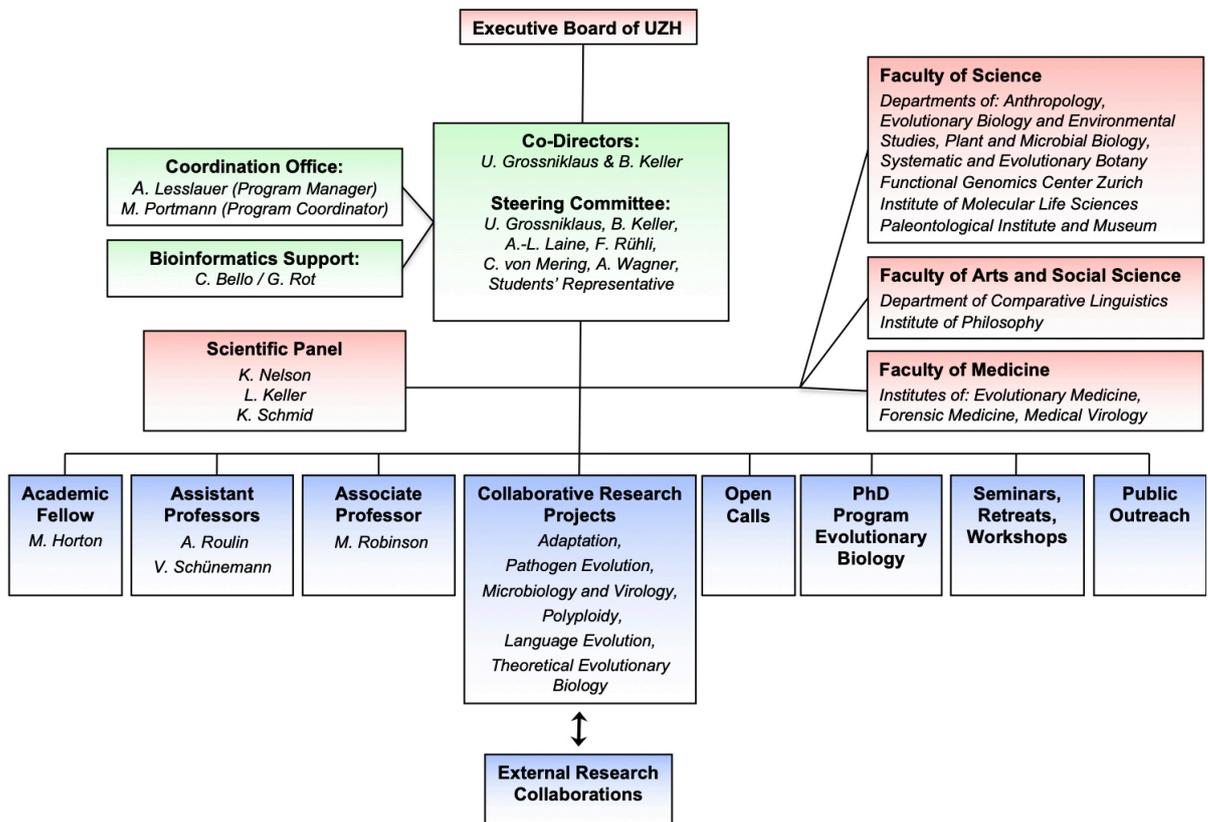
Wyder S, Raissig MT, Grossniklaus U (2019). Consistent reanalysis of genome-wide imprinting studies in plants using generalized linear models increases concordance across datasets. *Scientific Reports* 9:1320.

## 5.2 Selected papers published in previous years

Ferrari G, Lischer HEL, Neukamm J, Rayo E, Borel N, Pospischil A, Rühli F, Bouwman AS, Campana MG (2018). Assessing metagenomic signals recovered from Lyuba, a 42,000-year-old permafrost-preserved woolly mammoth calf. *Genes* 9(9):436.

- Kellenberger RT, Desurmont GA, Schlüter PM & Schiestl FP (2018). Trans-generational inheritance of herbivory-induced phenotypic changes in *Brassica rapa*. *Scientific Reports* 8:3536.
- Leigh DM, Lischer HEL, Grossen C, Keller LF (2018). Batch effects in a multiyear sequencing study: False biological trends due to changes in read lengths. *Molecular Ecology Resources* 18(4):778-788.
- Praz CR, Menardo F, Robinson MD, Müller MC, Wicker T, Bourras S, Keller B (2018). Non-parent of origin expression of numerous effector genes indicates a role of gene regulation in host adaptation of the hybrid *Triticale* powdery mildew pathogen. *Frontiers in Plant Science* 9:49.
- Rezzoagli C, Wilson D, Weigert M, Wyder S, Kümmerli R (2018). Probing the evolutionary robustness of two repurposed drugs targeting iron uptake in *Pseudomonas aeruginosa*. *Evolution, Medicine, and Public Health* 2018(1):246-259.
- Roulin PS, Murer LP, Greber UF (2018). A single point mutation in the rhinovirus 2B protein reduces the requirement for phosphatidylinositol 4-kinase class III beta in viral replication. *Journal of Virology* 92(23):e01462-18.
- Townsend SW, Engesser S, Stoll S, Zuberbühler K, Bickel B (2018). Compositionality in animals and humans. *PLoS Biology* 16(8):e2006425.
- 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.
- 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. *Journal of Evolutionary Biology* 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 A (2016). Evidence of horizontal gene transfer between obligate leaf nodule symbionts. *The ISME Journal* 10:2092-2105.

## 6 Structures



## 7 Third-Party Funds

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

#### Swiss National Science Foundation

Balthasar Bickel / NCCR Evolving Language / 2020-2023

Balthasar Bickel, Kentaro Shimizu (co-applicants) / Out of Asia: Linguistic Diversity and Population History / SNSF Sinergia, 09/2019 – 08/2023

Beat Keller / Molecular analysis of disease resistance specificity in cereals / SNSF Project funding (Div. I-III), 01/2019 – 12/2021

Hanna Kokko / Museum Exhibition "Evolution in Action" / SNSF Agora, 12/2019 – 11/2021

Rolf Kümmerli / An evolutionary ecology approach to disarm bacterial pathogens, control infections, and understand polymicrobial interactions inside hosts / SNSF Project funding (Div. I-III), 12/2018 – 11/2022

Mark Robinson / Beyond the average: computational tools for discovery in high-throughput single cell datasets / SNSF Project funding (Div. I-III), 11/2017 – 10/2021

Mark Robinson (co-applicant) / Defining the identity and differentiation pathways of the immune-stimulating fibroblastic tumor stroma / SNSF Sinergia, 01/2018 – 12/2021

Mark Robinson (project partner) / Road-mapping the serrated pathway of colon tumorigenesis: Step 2: Impact on clinical management of precancerous colorectal lesions. / SNSF Project funding (Div. I-III), 05/2018 – 04/2022

Mark Robinson (project partner) / Stromal Cell Niches at the Nexus of the Innate Lymphoid Cell Interactome / SNSF Project funding (Div. I-III), 01/2019 – 12/2022

Anne Roulin / Impact of transposable elements on plant population evolution: insight from the model grass species *brachypodium distachyon* / SNSF Project funding (Div. I-III), 10/2019 – 09/2023

Verena Schünemann / Towards the origins of syphilis / SNSF Project funding (Div. I-III), 11/2019 – 10/2022

#### Industry

Matthew Horton / Identifying the plant genes that shape the leaf metabolome and microbiome / PSC Syngenta Fellowship, 2019-2022

#### Others

Mark Robinson / This grant supports the development of benchmarks and flexible statistical methods and software tools for discovery in high throughput single cell datasets. / Chan Zuckerberg Initiative, 2018-2019

Alessia Russo / Claraz Schenkung 2018

Verena Schünemann (co-applicant) / Uncovering the genomic signature of tomato domestication in Europe using Caspar Bauhin's (1560–1624) herbarium specimens / Basler Stiftung für biologische Forschung

**UZH internal**

Alexandre Figueiredo / IEU Travel Grant to attend “ESEB 2019” conference in Turku, Finland

Özhan Özkaya / Using single-cell tracking to assess the ecological and evolutionary consequences of cell death on public goods cooperation in bacteria /Forschungskredit Postdoc 2019

Alessia Russo / IPMB Travel Grant 2019