



## URPP Evolution in Action

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# Scientific Report

## URPP Evolution in Action

Reporting Year 2020

### 1 Management Summary

The 8<sup>th</sup> year of the URPP Evolution in Action was also the last year of the program's Phase II. In 2020, the URPP counted a total of 39 members and supported 15 distinct research projects as well as 1 Academic Fellow, 2 Assistant and 1 Associate Professors. The year was affected by the Covid-19 pandemic, yet the URPP Evolution in Action managed to meet the circumstances with flexibility and inventiveness. As a result, it was a successful year despite the difficult situation. A total of 44 scientific papers were published by members of the URPP in 2020.

For the PhD Students of Phase II, 2020 represented the final year of their projects and most defences are scheduled to take place in the upcoming months. Also, the Academic Fellow is about to complete his work within the URPP and will finalize his projects until July 2021. The Assistant Professor in Plant Evolutionary Genomics is about to enter the second half of her engagement with the URPP in a few months. The program's funding for the Assistant Professor in Paleogenetics as well as for the Statistical Genomics Associate Professor ended with Phase II, yet both will stay committed as members of the URPP in Phase III and will continue their valuable contributions to the URPP Evolution in Action network. Finally, a total of 10 pilot projects selected in 2019 were successfully conducted in 2020.

A key characteristic of the URPP Evolution in Action is its agile network of more than 160 active scientists of the University of Zurich (UZH) that exchange knowledge and collaborate across scientific disciplines addressing evolutionary questions with molecular approaches. Central to this network are the many engagement opportunities provided within the URPP. Their implementations in 2020 had to be modified as a consequence of the Covid-19 pandemic. To ensure a successful maintenance of the URPP's trans- and interdisciplinary efforts, activities were transferred into online formats wherever possible.

To this regard, the 8<sup>th</sup> Retreat of the URPP Evolution in Actions took place as a one-and-a-half day virtual meeting that allowed for its key component – the presentation and discussion of research projects – to be successfully conducted. The online Retreat also comprised several formats for social exchange and a Faculty Meeting with a majority of the URPP members being present. At this late stage of their projects, the Retreat was especially rewarding and useful to the URPP PhD Students. Moreover, most of the URPP's courses, and a seminar were held online and were well attended. The bioinformatics support was continued online and also the career events were conducted virtually. Additionally, in 2020 the 1:1 meetings between the PhD Students and the Coordination Office were timely to address questions and concerns of our junior scientists due to the Covid-19 pandemic.

The contents of the museum exhibition "evolution happens!" could mostly be finalized and the exhibits of this important public outreach activity are currently being manufactured. Its opening, eagerly awaited by the URPP Evolution in Action community and beyond, is scheduled to take place in June 2021 at UZH's Zoological Museum.

We are looking forward to continuing the URPP Evolution in Action in 2021 with Phase III hosting 9 new projects in the areas of 'Evolution of Pathogens, Parasites, and Pathosystems' (3 PhD, 2 postdoc projects), 'Role of Polyploidy and Epigenetic Variation in Diversification and Adaptation' (2 PhD projects), and 'Experimental Evolution and Modelling' (2 PhD projects).

## 2 Objectives

### 2.1 Objectives for the Reporting Year 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 happens!”, 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.

### 2.2 Achieved Objectives in 2020

- The 8<sup>th</sup> **Retreat of the URPP Evolution in Action** took place as a reduced, yet successful and well attended one-and-a-half-day online event. All PhDs and the Academic Fellow were given the opportunity to present their work, a selection of different break formats completed the diversified program that ended with a URPP Faculty Meeting.
- **Public Outreach:** Most of the content for the museum exhibition “evolution happens!” has been finalized, the manufacturing of the exhibits is underway, and the date for the opening was set to June 14, 2021.
- The extent of the **Seminar Series** of the URPP Evolution in Action had to be drastically reduced due to the Covid-19 pandemic; nevertheless, we were able to offer one online seminar.
- 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 2020. The topics included Next-Generation Sequencing, Concepts of Evolutionary Biology, Genome-Wide Association Studies (GWAS), and Human Genetic History.
- The **Bioinformatics Support Services** could successfully be continued despite the Covid-19 pandemic. The **Bioinformatics Tutorial Program** was paused due to the reduced needs of our advanced stage PhD Students.

- The second **Career Planning Workshop** was segmented into a total of 4 well attended career talks that informed about employment opportunities for junior scientists outside academia.
- The **1:1 Meetings** between PhD Students and the Program Manager were very well received. Following the positive feedback, the program intends to establish these interactions in the long-term.
- All **Social Events** planned in 2020 had to be cancelled due to the Covid-19 pandemic. Instead, we organized virtual coffee breaks to offer a platform for regular exchange.
- **Phase II** of the URPP Evolution in Action was successfully terminated. The framework to successfully implement **Phase III** has been established and all necessary preparations for a smooth start have been taken.

### 2.3 Objectives for 2021

- **Launch of Phase III** of the URPP Evolution in Action, with new projects, PhD Students, and Postdocs: ensuring a smooth transition and good integration of all new projects, and promotion of a lively, interactive community life.
- Planning and realization of the **9<sup>th</sup> Retreat of the URPP Evolution in Action**, with a program featuring progress reports from all PhD and Postdoc projects, a keynote lecture, faculty and PhD Student meetings, as well as a social program furthering the integration of old and new members and PhD Students.
- Finalization of the museum exhibition “evolution happens!” and its opening in June 2021 as a key event in the URPP’s **Public Outreach** activities. Acquisition of partnering museums to realize the exhibition’s travel subsequent to its 6 months presentation at the Zoological Museum of the UZH.
- Continuation of the successful **Seminar Series** of the URPP Evolution in Action, either in an online format or physically 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, Quantitative Trait Loci (QTL) Mapping, Genome-Wide Association Studies (GWAS), and Scientific Writing.
- Continuation of the highly successful **Bioinformatics Support Services** as well as resumption of the **Bioinformatics Tutorial Program**.
- **Open Call for Pilot Projects** in Phase III to promote young scientists by supporting innovative and/or high-risk pilot projects, to be conducted in 2022.
- Continuation of the **1:1 Meetings for all PhD Students** of the URPP Evolution in Action with a Program Co-Manager as a low-threshold opportunity for the junior scientists to address any questions and issues.
- Organization of **Social Events** to further enhance interactions among students, members, research projects, and departments involved in the URPP Evolution in Action.
- Increasing **Social Media** use to further strengthen the reach (national and international) of the program and to offer URPP members an additional platform for exchange and dissemination of their research.

## 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 known heritability of epigenetic variation (EV), its ecological and evolutionary significance is largely unexplored. 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. 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. Hence, EV contributes to phenotypic diversity. To demonstrate that sufficient standing EV is required for an adequate response to selection, a subsequent molecular study was initiated. As the Covid-19 pandemic prevented the timely completion of the experiment, the project will be prolonged for a year with the aim to characterize responses to selection at the phenotypic as well as the 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)

The project investigates 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. The aim is to identify range expansion patterns 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. The experimental work of the project has been completed and published, and the genomic results are in preparation for publication (foreseen submission date February 2021). The results show that genetic adaptation during experimental range expansions acted on growth rate and local adaptation. Additionally, a potential genetic mechanism of gene swamping was observed during the experiment.

###### 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)

This project investigates flowering plant adaptation to changing pollinator communities through the evaluation of genetic changes underlying mating system evolution. The aim is to determine traits under

selection of various pollinators and their impact on reproductive strategies on the plant population. The project is in the stage of finalizing data processing and writing thesis chapters. The delay is due to loss of time because of the Covid-19 pandemic in 2020 and some delays with data analysis due to complexity of the data.

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

PhD Student: Alessia Russo (ISEB)

PhD committee: Philipp Schlieter (University of Hohenheim, Germany), Ueli Grossniklaus (IPMB), Thomas Wicker (IPMB), Martin Mascher (Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung, Seeland, Germany)

This project explores the genetic mechanisms behind sexual deception in *Ophrys* orchids and aims to produce a genome reference for the genus as well as to build an evolutionary model of species divergence. A genome reference for *Ophrys sphegodes* was generated and annotated in Gene Space. Furthermore, Repetitive Elements were annotated and gene expression analyses conducted. Currently, the phylogeny of *Ophrys* within plants is being revised.

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

PhD Student: Stephan Schmeing (Department of Molecular Life Sciences, DMLS)

PhD committee: Mark Robinson (DMLS), Michael Krützen (Department of Anthropology, AIM), Lukas Keller (EBES), Christian von Mering (DMLS)

This project develops a new approach to assemble the genome of the Indo-Pacific bottlenose dolphin *Tursiops aduncus*. All data has been collected and a draft-genome was created. To get the most from the collected data, a new software for assembly improvement is currently being written. Due to limitations of the input material, the amount of high-quality BioNano reads is too low for the standard workflow. The new software is employed to make use of this data and to improve the genome assembly.

## MICROBIOLOGY AND VIROLOGY

#### The Evolution of Bacterial Language Diversification

PhD Student: Alexandre Ribeiro Teles de Figueiredo (DQBM)

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

In this project, the ecology and evolution of bacterial social interactions and how they shape microbial communities and interactions with hosts is investigated. The aim is to understand how bacterial public goods-based cooperation evolves under different environments (i), and how it may mediate interspecific cooperation or competition (ii). While results of the first part of the project (i) are already available as a preprint and currently being prepared for submission, the data collection for the second part (ii) is concluded, data analysis is in the final stages, and writing of the manuscript is underway.

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

PhD Student: Luca Murer (DMLS)

PhD committee: Urs Greber (DMLS), Marco Vignuzzi (Institut Pasteur, Paris, France), Roger Kouyos (Institute of Medical Virology, IMV), Silke Stertz (IMV), Weihong Qi (Functional Genomics Center Zurich, FGCZ)

The project investigates rhinovirus uncoating behavior in presence of endosomal acidification inhibitors to identify the evolutionary consequence for rhinoviruses if forced to evolve endosomal pH

independent uncoating mechanisms. A 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. Besides one last set of samples being sequenced and an additional experiment that needs to be conducted, results are currently in preparation for publication.

*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 Rihli (IEM), Verena Schünemann (IEM), Christian von Mering (DMLS), Christina Warinner (Max Planck Institute for the Science of Human History, Jena, Germany)*

The human microbiome is known to play a role in the development of many modern diseases. New technologies increasingly enable the characterization of microbiomes and, therefore, the health states of past human populations. The aim of this project is to explore different types of preserved archaeological and historic soft tissues for ancient microbiome reconstruction using a metagenomic sequencing approach and connect extracted information with current clinical data. The content of ancient Egyptian funerary artifacts associated with internal organs, fixed specimens from anatomical and pathological collections with associated medical diagnoses of infectious diseases, and a set of naturally mummified remains from a 1000-year-old individual were tested. The specificity of these samples required tailoring of the sampling strategy and methods applied, even though an interest in characterizing ancient microbiomes of other body sites existed. Improving the efficiency of DNA recovery and expanding the databases will provide new information about the bacterial communities of ancient human populations and their health state.

*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 (DMLS), Huldrych Günthard (University Hospital Zurich), Jacques Fellay (EPF Lausanne)*

The project examines how human genetic diversity, specifically HLA genes, has a co-evolutionary dynamic relating to HIV. The project aims to have a more holistic, population-level understanding of how HLA, drug resistance mutations, and HIV interact. Currently, the third manuscript, which examines how drug resistance mutations may relate to HLA binding sites, is under preparation. HLA-I may drive the emergence and/or maintenance of viral Drug Resistance Mutations (DRMs), even in patients who are antiretroviral treatment (ART)-naïve. Considering the extremely high geography-dependent HLA-I variation in the human population, these findings may help HIV clinicians and scientists, particularly in low-resource settings, to anticipate certain DRMs arising at varying rates in different ART-naïve populations.

## 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)*

The project investigates the genetic diversity of a global population of *Blumeria graminis forma specialis tritici* to generate a 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. All samples are processed and sequenced, and all population analyses have been finalized.

Transposable elements of *Blumeria graminis* are currently being examined in detail and the species' efficacy is being explored. Currently, these results are processed for publication.

#### 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)

This project investigates host adaption of the triticale powdery mildew, a fungal disease that emerged on its host triticale through hybridization of wheat and rye powdery mildew. The goal is to identify candidate genes responsible for host adaptation of the triticale powdery mildew, using comparative genomics approaches and Quantitative Trait Locus (QTL) mapping in a bi-parental powdery mildew mapping population. Several QTLs controlling host adaptation of triticale powdery mildew on its host triticale could be identified. Based on the two chromosome-level genome assemblies created in this project, we were able to identify candidate genes responsible for host adaption. After focusing on the fungal components involved in host-adaptation of powdery mildew to the cereal crop triticale, the corresponding plant genes will be identified.

### 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)

As plants host diverse microbiota that are involved in their growth, development, and health, understanding the assembly of microbiomes in natural populations is of great interest for agricultural and ecological purposes. This project explores the role of abiotic and edaphic factors and the role of plant-associated factors and host genes in shaping the microbial communities of plants to decipher their relative contribution to microbiome structure. Surveying populations of wild strawberry across a global gradient highlighted the influence of temperature and various soil nutrients on the structure of leaf and root microbial communities. Currently, trajectories of the rhizosphere microbiome and its function to understand the involvement of plant-inherent genetic factors are being studied. Irrespective of the geographic distance between or environmental heterogeneity within the collection sites, similar local factors that were associated with variation in the microbial communities could be identified. This might be interpreted as a plant-mediated effect, with the host plant acting as a vector between environment and microbiome, influencing both directly as well as indirectly.

### 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)

The role of transposable elements in gene regulation, genome plasticity, and the consequences for local adaptation in the model plant *Brachypodium distachyon* are analyzed to elucidate the diversity of mobile stress-inducible transposons (TEs) in different accessions of *B. distachyon*. Therefore, the mobility of TEs in six different accessions of *B. distachyon* in response to seven different stresses were tested. While only limited evidence for the mobility of full-length elements in wild-type plants could be found, the first mobile retroTEs in an RdDM mutant of *B. distachyon* were detected. Furthermore, plenty of smaller (<2kb) circular DNAs were found and are now being studied in more detail. To overcome the limitation

of TE-regulatory mutants that would allow studying the impact of transposition on evolution, the CRISPR-Cas9 system is currently being established.

## 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 (DMLS), Kentaro Shimizu (EBES), Jun Sese (National Institute of Advanced Industrial Science and Technology, Japan), Andreas Wagner (EBES)

Automated and reproducible workflows are being developed, using data from synthetic allotetraploid *Arabidopsis kamchatica* to assess DNA methylation changes in early generations. The aim of the project is to support and guide synthetic polyploid research with new tools to assess the role and importance of DNA methylation changes in the early stages of polyploidization. After the development of an Automated Reproducible PolyPloid EpiGenetic GuIdance Workflow (ARPEGGIO), the workflow is employed to compare: i) *A. kamchatica*'s methylation pattern changes in the 1<sup>st</sup> and 4<sup>th</sup> generation compared to its progenitor species, and ii) methylation pattern changes in the same experimental design, but in different environments. The 1<sup>st</sup> generation of synthetic *A. kamchatica* shows DNA methylation pattern changes of which > 50% are conserved in the 4<sup>th</sup> generation, indicating an increasingly diverging DNA methylation pattern compared to the progenitor species. Also, the environment seems to play an important role, which is currently being analyzed in more detail.

## THEORETICAL EVOLUTIONARY BIOLOGY

### An Integrative Approach to Understanding Cancer Across the Tree of Life

PhD Student: Yagnur 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. The goal is to understand how cancer, as a phenomenon observed across virtually all multicellular organisms, can affect life history evolution and, in turn, how different traits can change cancer risk across the tree of life. Results of the study are included in one peer-reviewed science communication piece published in 2019, one peer-reviewed scientific article published in 2020, and two scientific preprints posted on *bioRxiv*.

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

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

The goal of my group is to decipher how transposable element (TE) activity creates genetic diversity and promotes local adaptation in natural populations. To that mean, we are using both *in silico* and molecular approach in the tractable grass model *Brachypodium distachyon*. In 2020, we have finished the sequencing of 170 genomes of natural accessions originating from France, Italy, and Greece. Combined to the sequencing effort lead by the *Brachypodium* consortium, sequencing data are thus available for 340 genetically diverse genotypes spanning the region from Spain to Iraq. We are using this dataset to investigate how TEs regulate gene expression and physiological traits in the wild. As a major result in 2020, we have activated *in planta* a TE upon cold exposure. Besides of constituting the first ever reported active element in our system (publication in preparation), this opens new avenues of research in my group as identifying active TEs would allow investigating their impact on phenotypic variation.

**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 (DMLS)**

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)**

We recently completed the wet-lab portion of a project in which we sequenced a large mapping panel of diploid wild strawberry accessions (i.e., individual plant samples) to understand the population structure and evolutionary history of the species (*Fragaria vesca*). These data will enable the plant genetics community to conduct genome-wide association studies (GWAS) of ecologically and agriculturally important traits.

For another recently completed project, we have been using Illumina sequencing (e.g. MiSeq) to characterize the leaf and root microbiome of *F. vesca* using samples collected across transects in North America and Europe. The manuscript for this project will be submitted soon. The results from this study indicate that the environmental variables that regulate microbiome assembly are relatively similar over large geographic distances (~8500 km; separate continents).

**3.1.3 Pilot Projects**

To further promote young scientists, in Phase II, the URPP Evolution in Action launched three open calls 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 ran until the end of 2020.

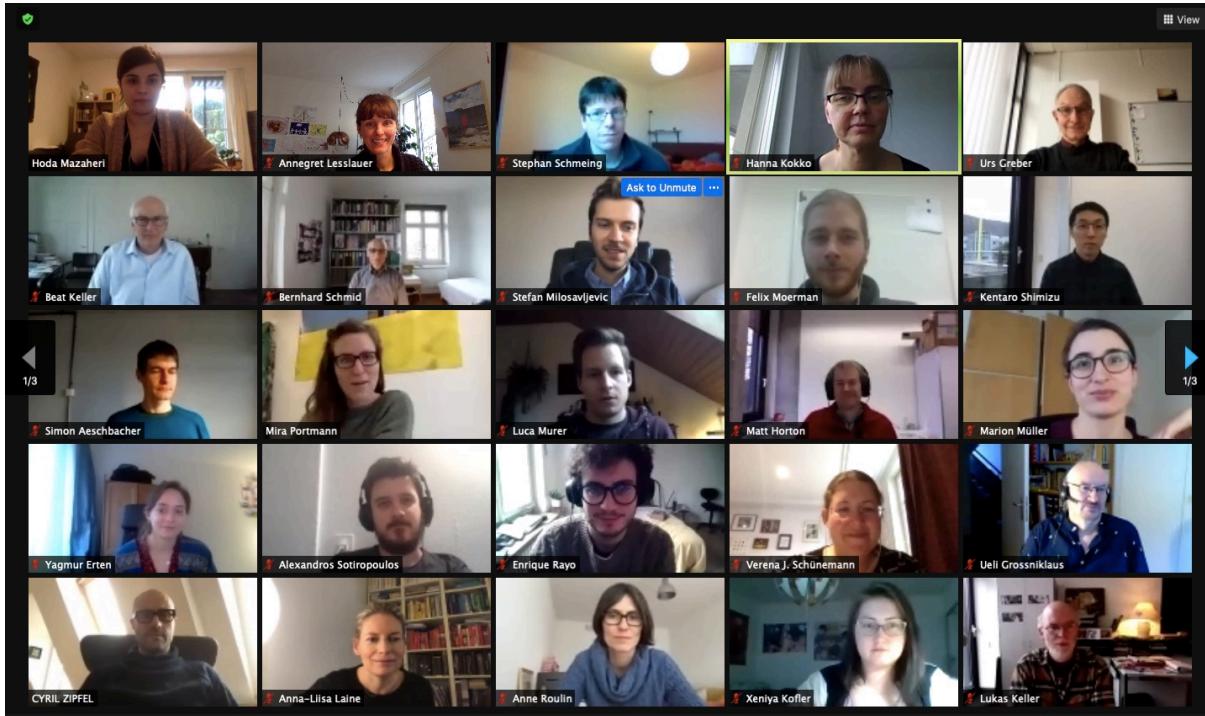
Listed below are the projects from the 2019 call. The research reports of the completed projects are collected in Appendix A. For the completed projects from the 2017 and the 2018 call, please refer to the Annual Reports 2018 and 2019 of the URPP Evolution in Action, respectively.

### Open Call of May 2019

Applicant:	<i>Dr. Stefano Bencivenga, Postdoc (IPMB)</i>
Title of project:	<i>Understanding Early Events of Speciation Through Cell-Specific Transcriptome Analysis</i>
Granted funding:	<i>CHF 20'000</i>
Applicant:	<i>Thomas Grubinger, PhD Student (EBES)</i>
Title of project:	<i>Tracing the Genomic Signature of 400 Years of Tomato Domestication in Europe Using Herbarium Specimens</i>
Granted funding:	<i>CHF 19'400</i>
Applicant:	<i>Alexander Kirbis, PhD Student (ISEB)</i>
Title of project:	<i>The Effect of Mating System on the Strength of Genomic Imprinting in Haploid Plants</i>
Granted funding:	<i>CHF 17'800</i>
Applicant:	<i>Martin Mecchia, Postdoc (IPMB)</i>
Title of project:	<i>Evolutionary Basis of Polarized Cell Growth in Land Plants</i>
Granted funding:	<i>CHF 20'000</i>
Applicant:	<i>Enrique Rayo, PhD Student (IEM)</i>
Title of project:	<i>Reconstructing the Ancient Microbiome of the Appendix</i>
Granted funding:	<i>CHF 18'800</i>
Applicant:	<i>Sebastian Sauppe, Postdoc (Department of Comparative Language Science)</i>
Title of project:	<i>The Evolution of Event Cognition in Humans and Hominidae: A Comparative Eye Tracking Study on the Perception of Naturalistic Events</i>
Granted funding:	<i>CHF 20'000</i>
Applicants:	<i>Manuel Poretti and Alexandros Sotiropoulos, PhD Students (IPMB)</i>
Title of project:	<i>Lichen Symbiosis: Metagenomic Signatures of Adaptation to Different Lifestyles and Environmental Conditions</i>
Granted funding:	<i>CHF 20'000</i>
Applicant:	<i>Xenia Wietlisbach, PhD Student (EBES)</i>
Title of project:	<i>The Role of Pathogens in Creating Genomic Signatures of Local Adaptation in Alpine Ibex</i>
Granted funding:	<i>CHF 20'000</i>
Applicant:	<i>Narjes Yousefi, Postdoc (ISEB)</i>
Title of project:	<i>Testing Recent Theoretical Model of Speciation Using <i>Sphagnum magellanicum</i> complex as an Experimental System</i>
Granted funding:	<i>CHF 15'100</i>
Applicant:	<i>Jia Zheng, Postdoc (EBES)</i>
Title of project:	<i>Do Fluctuating Temperature Environments Facilitate Evolutionary Adaptation and Innovation?</i>
Granted funding:	<i>CHF 19'500</i>

## 3.2 Scientific Activities

### 3.2.1 Scientific Retreat



Because of the Covid-19 pandemic, the 8<sup>th</sup> **Retreat of the URPP Evolution in Action** was initially postponed and finally took place in a reduced online format on November 30<sup>th</sup> and December 01<sup>st</sup>, 2020. In four sessions framing a total of 15 talks, all PhD Students and the Academic Fellow presented their work by means of oral presentations to 58 participants. During the breaks, the attendees had the opportunity to join different break-out rooms to enable discussions in small groups, similar to a real-life coffee-break setting. Next to the interactive coffee breaks, sporty breaks to address the ergonomic challenges of the home office situation were offered. We also provided snacks, drinks, and food for an apéro and a lunch, which was very well received and increased the binding character of this online event.

The retreat finished with a Faculty Meeting which was attended by most members of the URPP. Here, the new members of the URPP, Christine Grossen and Cyril Zipfel, were welcomed and given the opportunity to present their research and motivation to be part of the URPP Evolution in Action.

Despite the Covid-19 pandemic, the retreat 2020 was a dynamic and positive event with much interaction, lots of lively discussions, and a valuable opportunity for scientific exchange.

### 3.2.2 Bioinformatics Tutorials and Support

In 2020, the program's bioinformatic tutorial series was paused due to insufficient demand (PhD Students of Phase II were finishing their theses) and the difficulties caused by the Covid-19 pandemic. The embedded bioinformaticians Carla Bello and Gregor Rot nevertheless taught two online courses.

The 1-day course **BIO609** "Introduction to UNIX/Linux and Bash Scripting" is a prerequisite to attend the courses BIO610 and BIO634 and took place on November 9<sup>th</sup> 2020. In 2020, 20 students attended the course to improve their computing and scripting skills. The 2-day class **BIO634** "Next-Generation

Sequencing 2 for Model and Non-Model Species: Transcriptomes, Variant Calling, and Biological Interpretation" held on December 3<sup>rd</sup> and 4<sup>th</sup>, 2020 was given as a follow-up course to the 2-day introduction to Next-Generation Sequencing (BIO610 "Next-Generation Sequencing for Model and Non-Model Species") by Prof. Kentaro Shimizu and others. In total, 18 students participated in the course.

Both courses were conducted using the online platforms Zoom and Slack, while the employed virtual environment was redesigned using Docker instead of VirtualBox. This combination proved successful, since students could ask questions in Slack channels while following the lecture via Zoom. Especially questions placed in the public Slack channels facilitated an integrative and participative troubleshooting including all participants and tutors. Most technical obstacles associated with the online teaching could be solved and served as valuable experience for future online courses.

The quarterly 1:1 meetings between URPP Evolution in Action PhD Students and embedded bioinformaticians to discuss the individual PhD projects, including experimental design, bioinformatic methods, bottlenecks, and challenges, were continued in 2020. The aim of these meetings is to keep up-to-date with the progress of the PhD theses and to connect PhD Students using similar methods. Because most of the PhD Students are at the finishing stage of their PhD, the bioinformatic support has gotten increasingly dynamic, spontaneous, and hands-on, engaging with distinct data sets rather than theoretical approaches.

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

- Topics in Evolutionary Biology (**BIO554**); HS20; Lecturers: Kentaro Shimizu, Frank J. Rühli, Marcus Clauss, Adrian Jäggi, Marcelo R. Sánchez, Anne C. Roulin, Lukas Keller, Florian P. Schiestl, Martin J. Kapun, Ueli Grossniklaus, Marta Manser, Hugo Bucher, Stefan K. Lüpold, Michael Krützen
- Human Genetic, Demographic and Cultural Diversity (**BIO 624**); October 19-21, 2020; Lecturers: Kentaro Shimizu, Chiara Barbieri, Mark Stoneking
- Concepts in Evolutionary Biology (**BIO395**); October 26-27, 2020; Lecturers: Kentaro Shimizu, Michael Krützen, Anne C. Roulin, Wolf Blanckenhorn, Anna K. Lindholm Krützen, Simon Aeschbacher, Andrei Papkou
- Introduction to UNIX/Linux and Bash Scripting (**BIO609**): Preparatory Course for BIO610 and BIO634; November 9, 2020; Lecturers: Carla L. Bello Cabrera, Gregor Rot
- Next-Generation Sequencing for Model and Non-Model Species (**BIO610**); November 10-11, 2020; Lecturers: Kentaro Shimizu, Carla L. Bello Cabrera, Masaomi Hatakeyama, Sun Jianqiang, Gregor Rot, Jun Sese, Rie Shimizu Inatsugi, Shoji Tatsuma
- Introduction to Genome-Wide Association Studies (GWAS) (**BIO692**); November 18-20, 2020; Lecturers: Matthew W. Horton, Ümit Seren
- Next-Generation Sequencing 2: Transcriptomes, Variant Calling and Biological Interpretation (**BIO634**); December 3-4, 2020; Lecturers: Carla L. Bello Cabrera, Gregor Rot

### 3.2.4 URPP Evolution in Action Seminars

- *Speaker:* Andrés Bendesky, Columbia University, USA  
*Date:* March 19, 2020 – cancelled due to the Covid-19 pandemic
- *How can transferable biology and breeding contribute to improving food systems and climate change?*  
*Speaker:* Ed Buckler, Cornell University, USA  
*Date:* December 11, 2020 - online

## 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. In 2020, the URPP funded salaries and research consumables for 14 PhD Students and one Postdoc. Furthermore, the URPP is financing an Academic Fellow and two Assistant Professors. We also foster young academics by awarding grants for short-term research (pilot) projects, where proposals can be submitted by PhD Students and Postdocs of the research groups participating in the URPP Evolution in Action. Three calls took place in Phase II. They have proven 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 departments, and in obtaining their own funding.

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 organize social events to grant young academics access to a community of experienced researchers. Due to the restrictions caused by the Covid-19 pandemic, all of the URPP's on-site social exchange formats in 2020 had to be cancelled. Yet, we offered a variety of possibilities to engage virtually. We particularly designed the online retreat as a platform offering sufficient room for all young academics not only to present and discuss their work in the plenum, but also to interact with the URPP community, e.g., during virtual coffee breaks and apéros.

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. 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. Fortunately, the PhD cohort of Phase II had mostly entered the final stage of their PhD before the first corona lock-down and was, hence, less severely affected by these circumstances to conduct their work. To ensure their ongoing close support despite the Covid-19 pandemic, we established 1:1-meetings between program manager and students and offered regular online coffee breaks. In 2020, we also held a virtual series of four Career Talks outlining examples of career paths outside academia with the opportunity to discuss career-related questions.

The two Embedded Bioinformaticians of the URPP 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. 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's Embedded Bioinformaticians regularly work in the von Mering (DMLS) 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.

### 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 grants. We have appointed outstanding women scientists as Assistant Professors, thereby providing excellent role models. We aim at a balanced gender ratio in the list of our invited speakers for seminars and keynote lectures. We support efforts to create a family-friendly work environment, e.g. by enabling part-time work. The Covid-19 pandemic demanded increased flexibility, especially for parents working in home office. The URPP supported such flexibility for its members, especially with regard to working hours in order to create best possible conditions to work from home.

## 5 Publications

### 5.1 Peer-Reviewed Publications in 2020

Akiyama R, Milosavljevic S, Leutenegger M, Shimizu-Inatsugi R (2020). Trait-dependent resemblance of the flowering phenology and floral morphology of the allopolyploid *Cardamine flexuosa* to those of the parental diploids in natural habitats. *Journal of Plant Research* 133:147-155.

Aubier TG, Galipaud M, Erten EY, Kokko H (2020). Transmissible cancers and the evolution of sex under the Red Queen hypothesis. *PLoS Biology* 18(11): e3000916.

Barquera R, Lamnidis TC, [...] Barbieri C, [...] Krause J (2020). Origin and Health Status of First-Generation Africans from Early Colonial Mexico. *Current Biology* 30(11): 2078-2091.e11.

Baur J, Giesen A, Rohner PT, Blanckenhorn WU, Schäfer MA (2020). Exaggerated male forelegs are not more differentiated than wing morphology in two widespread sister species of black scavenger flies. *Journal of Zoological Systematics and Evolutionary Research* 58(1):159-173.

Cairns J, Moermann F, Fronhofer EA, Altermatt F, Hiltunen T (2020). Evolution in interacting species alters predator life-history traits, behaviour and morphology in experimental microbial communities. *Proceedings of the Royal Society B* 287(1928):20200652.

Crowell HL, Soneson C, Germain P-L, Calini D, Collin L, Raposo C, Malhotra D, Robinson MD (2020). *muscat* detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. *Nature Communications* 11:6077.

Diop SI, Subotic O, Giraldo-Fonseca A, Waller M, Kirbis A, Neubauer A, Potente G, [...] Grossniklaus U, McDaniel SF, Szövényi P (2020). A pseudomolecule-scale genome assembly of the liverwort *Marchantia polymorpha*. *The Plant Journal* 101(6):1378-1396.

Erten EY, Kokko H (2020). From zygote to a multicellular soma: Body size affects optimal growth strategies under cancer risk. *Evolutionary Applications* 13(7):1593-1604.

Ferrari G, Neukamm J, [...] Rühli F, Bouwman A, Schuenemann VJ (2020). Variola virus genome sequenced from an eighteenth-century museum specimen supports the recent origin of smallpox. *Philosophical Transactions of the Royal Society B* 375(1812):20190572.

Figueiredo ART, Kümmerli R (2020). Microbial Mutualism: Will You Still Need Me, Will You Still Feed Me? *Current Biology* 30(18):R1041-R1043.

Figueiredo ART, Kramer J (2020). Cooperation and Conflict Within the Microbiota and Their Effects On Animal Hosts. *Frontiers in Ecology and Evolution* 8:132.

Furtwängler A, Neukamm J, Böhme L, Reiter E, Vollstedt M, Arora N, Singh P, Cole ST, Knauf S, Calvignac-Spencer S, Krause-Kyora B, Krause J, Schuenemann VJ, Herbig A. Comparison of target enrichment strategies for ancient pathogen DNA. *Biotechniques* 69(6):455-459.

Gerke P, Szövényi P, Neubauer A, Lenz H, Gutmann B, McDowell R, Small I, Schallenberg-Rüdinger M, Knoop V (2020). Towards a plant model for enigmatic U-to-C RNA editing: the organelle genomes, transcriptomes, editomes and candidate RNA editing factors in the hornwort *Anthoceros agrestis*. *New Phytologist* 225(5):1974-1992.

Germain P-L, Sonrel A, Robinson MD (2020). pipeComp, a general framework for the evaluation of computational pipelines, reveals performant single cell RNA-seq preprocessing tools. *Genome Biology* 21(1):227.

- Grossen C, Guillaume F, Keller LF, Croll D (2020). Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex. *Nature Communications* 11:1001.
- Hanya G, Tackmann J, [...] von Mering C, Shimizu-Inatsugi R, Hayakawa T, Shimizu KK & Ushida K (2020). Fermentation Ability of Gut Microbiota of Wild Japanese Macaques in the Highland and Lowland Yakushima: In Vitro Fermentation Assay and Genetic Analyses. *Microbial Ecology* 80:459-474.
- Huang R, Soneson C, Ernst FGM, Rue-Albrecht KC, Yu G, Hicks SC, Robinson MD (2020). TreeSummarizedExperiment: a S4 class for data with hierarchical structure. *F1000Research* 9:1246.
- Kirbis A, Waller M, Ricca M, Bont Z, Neubauer A, Goffinet B, Szövényi P (2020). Transcriptional Landscapes of Divergent Sporophyte Development in Two Mosses, *Physcomitrium* (*Physcomitrella*) *patens* and *Funaria hygrometrica*. *Frontiers in Plant Science* 11:747.
- Kramer J, Özkaya Ö, Kümmel R (2020). Bacterial siderophores in community and host interactions. *Nature Reviews Microbiology* 18:152-163.
- Lähnemann D, Köster J, Szczurek E, McCarthy DJ, Hicks SC, Robinson MD, [...] (2020). Eleven grand challenges in single-cell data science. *Genome Biology* 21:31.
- Li F, Nishiyama T, Waller M, [...] Diop IS, [...] Kirbis A, [...] Neubauer A, [...] Szövényi P (2020). *Anthoceros* genomes illuminate the origin of land plants and the unique biology of hornworts. *Nature Plants* 6:259-272.
- Lindner S, Keller B, Singh SP, Hasenkamp Z, Jung E, Müller MC, Bourras S, Keller B (2020). Single residues in the LRR domain of the wheat PM3A immune receptor can control the strength and the spectrum of the immune response. *The Plant Journal* 104(1):200-214.
- Majander K, Pfrengle S, [...] Arora N, Akgül G, [...] Schuenemann VJ (2020). Ancient Bacterial Genomes Reveal a High Diversity of *Treponema pallidum* Strains in Early Modern Europe. *Current Biology* 30(19): 3788-3803.e10.
- Malan-Müller S, de Souza VBC, Daniels WMU, Seedat S, Robinson MD, Hemmings SMJ (2020). Shedding Light on the Transcriptomic Dark Matter in Biological Psychiatry: Role of Long Noncoding RNAs in D-cycloserine-Induced Fear Extinction in Posttraumatic Stress Disorder. *Oomics: a journal of integrative biology* 24(6):352-369.
- Moerman F, Arquint A, Merkli S, Wagner A, Altermatt F, Fronhofer EA (2020). Evolution under pH stress and high population densities leads to increased density-dependent fitness in the protist *Tetrahymena thermophila*. *Evolution* 74(3): 573-586.
- Moerman F, Fronhofer EA, Wagner A, Altermatt F (2020). Gene swamping alters evolution during range expansions in the protist *Tetrahymena thermophila*. *Biology Letters* 16(6):20200244.
- Morozova I, Kasianov A, Bruskin S, Neukamm J, Molak M, Batieva E, Pudlo A, Rühli FI, Schuenemann VJ (2020). New ancient Eastern European *Yersinia pestis* genomes illuminate the dispersal of plague in Europe. *Philosophical Transactions of the Royal Society B* 375:20190569.
- Nakatsuka N, Lazaridis I, Barbieri C, [...] Fehren-Schmitz L (2020). A Paleogenomic Reconstruction of the Deep Population History of the Andes. *Cell* 181(5): 1131-1145.e21.
- Neukamm J, Pfrengle S, [...] Schuenemann VJ (2020). 2000-year-old pathogen genomes reconstructed from metagenomic analysis of Egyptian mummified individuals. *BMC Biology* 18:108.
- Orjuela S, Machlab D, Menigatti M, Marra G, Robinson MD (2020). DAMEfinder: a method to detect differential allele-specific methylation. *Epigenetics & Chromatin* 13:25.

Orjuela S, Menigatti M, Schraml P, Kambakamba P, Robinson MD, Marra G (2020). The DNA hypermethylation phenotype of colorectal cancer liver metastases resembles that of the primary colorectal cancers. *BMC Cancer* 20:290.

Pick JL, Hatakeyama M, Ihle KE [...] Shimizu-Inatsugi R, Shimizu KK, Tscherren B (2020). Artificial selection reveals the role of transcriptional constraints in the maintenance of life history variation. *Evolution Letters* 4(3):200-211.

Poretti M, Praz CR, Meile L, Kälin C, Schaefer LK, Schläfli M, Widrig V, Sanchez-Vallet A, Wicker T, Bourras S (2020). Domestication of High-Copy Transposons Underlays the Wheat Small RNA Response to an Obligate Pathogen. *Molecular Biology and Evolution* 37(3):839-848.

Shimizu KK, Copetti D, Okada M, Wicker T, Tameshige T, Hatakeyama M, Shimizu-Inatsugi R, [...] Handa H (2020). De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium Resistance Genes in East Asian Genotypes. *Plant and Cell Physiology* pcaa152.

Skalska A, Stritt C, Wyler M, [...] Roulin AC, Hasterok R, Mur LAJ (2020). Genetic and Methylome Variation in Turkish *Brachypodium Distachyon* Accessions Differentiate Two Geographically Distinct Subpopulations. *International Journal of Molecular Sciences* 21(18):6700.

Sun J, Shimizu-Inatsugi R, Hofhuis H, Shimizu K, Hay A, Shimizu KK, Sese J (2020). A Recently Formed Triploid *Cardamine insueta* Inherits Leaf Vivipary and Submergence Tolerance Traits of Parents. *Frontiers in Genetics* 11:567262.

Tabrett A, Horton MW (2020). The influence of host genetics on the microbiome. *F1000Research* 9:84.

Tiberi S, Robinson MD (2020). BANDITS: Bayesian differential splicing accounting for sample-to-sample variability and mapping uncertainty. *Genome Biology* 21:69.

Tsuchimatsu T, Kakui H, [...] Grossniklaus U, Kanaoka MM, Lenhard M, Nordborg M, Shimizu KK (2020). Adaptive reduction of male gamete number in the selfing plant *Arabidopsis thaliana*. *Nature Communications* 11:2885.

Urban M, Barbieri C (2020). North and South in the ancient Central Andes: Contextualizing the archaeological record with evidence from linguistics and molecular anthropology. *Journal of Anthropological Archaeology* 60: 101233.

Walkowiak S, Gao L, [...] Shimizu-Inatsugi R, [...] Shimizu KK, [...] Keller B, [...] Wicker T, Pozniak CJ (2020). Multiple wheat genomes reveal global variation in modern breeding. *Nature* 588:277-283.

Weber de Melo V, Lowe R, Hurd PJ, Petchey O (2020). Phenotypic responses to temperature in the ciliate *Tetrahymena thermophila*. *Ecology and Evolution* 10(14):7616-7626.

Wyder S, Rivera A, Valdés AE, Cañal MJ, Gagliardini V, Fernández H, Grossniklaus U (2020). Differential gene expression profiling of one- and two-dimensional apogamous gametophytes of the fern *Dryopteris affinis* ssp. *affinis*. *Plant Physiology and Biochemistry* 148:302-311.

Wyler M, Stritt C, Walser JC, Baroux C, Roulin AC (2020). Impact of transposable elements on methylation and gene expression across natural accessions of *Brachypodium distachyon*. *Genome Biology and Evolution* 12(11):1994-2001.

## 5.2 Selected Papers Published in Previous Years

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 F, 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.

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.

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.

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

Meccariello A, Salvemini M, Primo P, Hall B, Koskineni 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, Papathanos 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.

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.

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.

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.

Shimizu-Inatsugi R, Terada A, Hirose K, Kudoh H, Sese J, Shimizu KK (2016). Plant adaptive radiation mediated by polyploid plasticity in transcriptomes. *Molecular Ecology* 26(1):193-207.

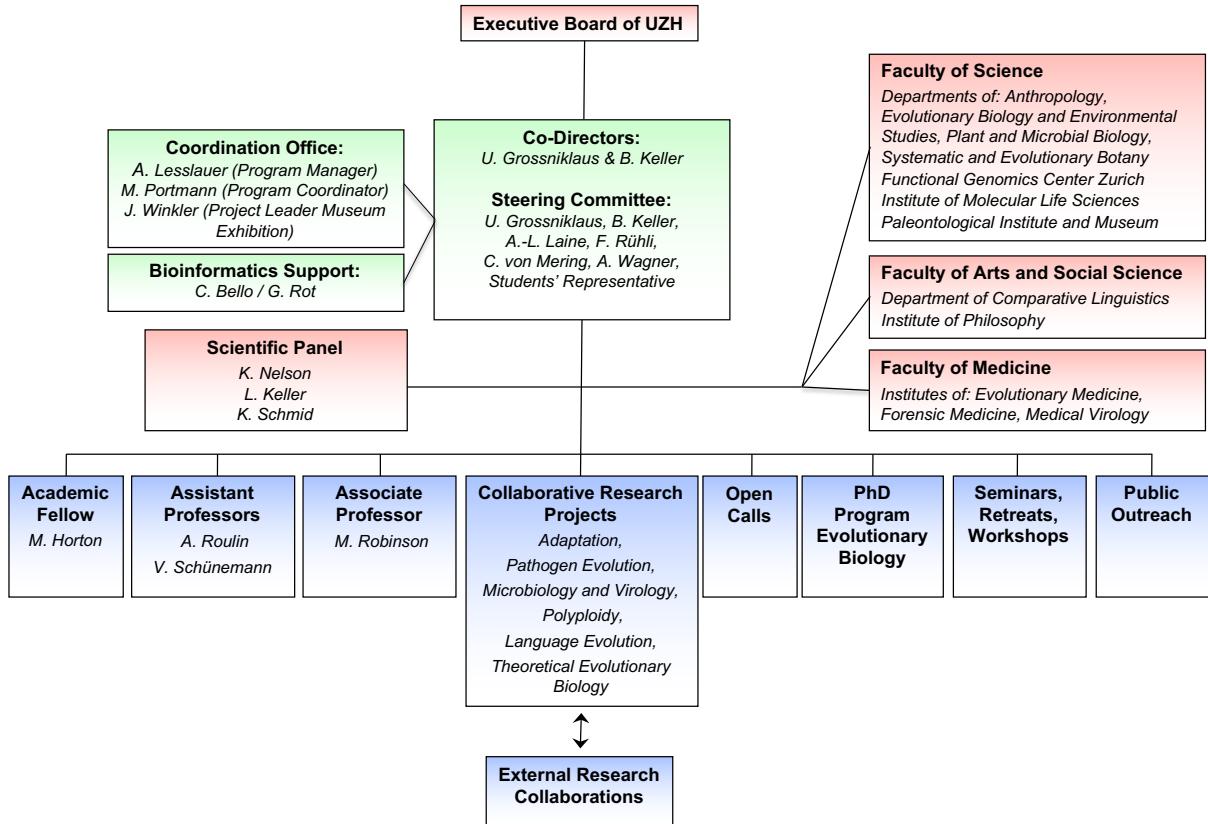
Soneson C, Yao Y, Bratus-Neuenschwander A, Patrignani A, Robinson MD & Hussain S (2019). A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. *Nature Communications* 10:3359.

Townsend SW, Engesser S, Stoll S, Zuberbühler K, Bickel B (2018). Compositionality in animals and humans. *PLoS Biology* 16(8):e2006425.

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.

## 6 Structures



## 7 Third-Party Funds

### 7.1 Third-Party Funding for 2020 Raised in the Context of the URPP Evolution in Action Research Projects during Phase II

#### 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

Kentaro Shimizu / Evolutionary functional genomics of selfing and polyploid speciation / SNSF Project funding (Div. I-III), 12/2018 – 11/2022

#### Others

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

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

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

Rolf Kümmerli / Managing the clinical-environmental resistome bridge in *Pseudomonas aeruginosa* / Novartis Foundation for Medical-Biological Research

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

Kentaro Shimizu / Wheat responses in changing climates studied in Asian varieties as underexploited genetic and genomic resources / RESPONSE Doctoral Programme, Marie Skłodowska-Curie Grant

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

Rie Shimizu-Inatsugi / Modeling of the phenotypes of field-grown allopolyploid plants using gene expression pattern and climate factors / Center for Ecological Research, Kyoto University

#### **UZH Internal**

Balthasar Bickel, Sebastian Sauppe / Ereigniskognition bei Menschenaffen: Einsichten in den Ursprung von Sprache / Stiftung für wissenschaftliche Forschung an der Universität Zürich

Enrique Rayo / GRC Travel Grant 2020

Alessia Russo / GRC Travel Grant 2020