



Scientific Report of the URPP Evolution in Action

Reporting Year 2016

1 Management Summary

2016 was the last year of Phase 1 of the URPP Evolution in Action, and it was both a successful closing year for the projects of Phase 1 and a forward-looking year with many preparative activities for Phase 2. The number of interactions within our program has been steadily growing. This is reflected by the fact that we received a large number of very interesting research proposals in the open call held to define the research plan for Phase 2 of the URPP Evolution in Action. Research proposals were handed in by research groups that participated in the URPP Evolution from the very start, as well as by research groups that have newly joined our program. This demonstrates that the URPP Evolution in Action is of interest both for long-standing partners and for new groups bringing in a variety of new research questions. We are also very happy to see that many new collaborations have been established to formulate the research projects for Phase 2. Overall, the URPP Evolution in Action brings together scientists from 38 research groups, twelve departments, and three faculties of UZH: the Faculty of Sciences, the Medical Faculty, and the Faculty of Arts.

Significant progress has been made in the scientific projects funded by the URPP Evolution in Action. Fourteen research projects were ongoing within the larger framework of five themes, mostly in form of PhD theses projects. First graduations of our PhD students took place in 2016 and the other PhD theses are expected to be completed in 2017. Besides these projects that were defined from the outset in our research plan, a total of 22 pilot projects – granted in an open call procedure – were completed by the end of 2016. These calls were open to PhD students and Postdocs, underlining our effort to foster young scientists, and yielded many interesting and innovative research proposals that were reviewed by the Steering Committee of the URPP Evolution in Action.

The Fourth Retreat of the URPP Evolution in Action took place in September 2016 in Rheinfelden with 65 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 Prof. Johannes Krause (Max Planck Institute for the Science of Human History in Jena, Germany).

The Academic Fellow of the URPP Evolution in Action took up his position in early 2016. His research is independent, but closely linked to the research themes of the URPP Evolution in Action. The Professorial Appointment Process for the non-tenure track Assistant Professor financed through the URPP Evolution in Action was ongoing in 2016.

Our research program is thus evolving on various levels. We look forward to continuing our work in Phase 2 and thank the Executive Board of the University of Zurich for financing the URPP Evolution in Action.

2 Objectives

2.1 Objectives for the reporting year

- Continuation and completion of the **Research Projects** run by the URPP Evolution PhD students and postdocs, publications and first graduations.
- Planning and realization of the **Fourth Retreat of the URPP Evolution in Action**, with a program featuring progress reports from all projects, input lectures, as well as faculty and PhD student meetings.
- Start of the research projects of the **Academic Fellow** of the URPP Evolution in Action.
- Advertisement and filling of the non-tenure track **Assistant Professor Position**, including the organization of a scientific symposium with all short-listed candidates.
- Preparatory works for **Starting Up Phase 2 of the URPP Evolution in Action**, with new members, projects and PhD students. Planning and submission of the Developmental and Financial Plan of the URPP Evolution in Action for the 2nd phase. This will be based on an open call for projects and subsequent selection of the applications by the Steering Committee.
- Presentation of the results from the first two rounds of **Open Calls for Research Projects**, and third Open Call for Research Projects to promote young scientists by supporting innovative and/or high-risk pilot projects.
- Planning and realization of new **Courses for the PhD Program** covering topics such as Next Generation Sequencing, Concepts of Evolutionary Biology, and Scientific Writing for Evolutionary Biologists.
- Continuation of the highly successful **Bioinformatics Support Services** as well as of the **Bioinformatics Tutorial Program**, including the planning for a tutorial curriculum for the new PhD students taking up their positions in Phase 2 of the URPP Evolution in Action.
- Continuation of regular **PhD Students Meetings** to enhance interaction among students, research projects, and departments of the URPP Evolution in Action.
- Organization of **Social Events** to further enhance interaction within the URPP Evolution in Action community.
- Development of **Public Outreach** initiatives for the second phase: further planning of a museum exhibition on topics related to the URPP Evolution in Action, and exploring of potential cooperation with the ZHDK and with the Life Science Learning Center.
- Further extension and development of the **Website** of the URPP Evolution in Action.

2.2 Achieved objectives in 2016

- The **Fourth Retreat of the URPP Evolution in Action** was a highly successful event. It took place in Rheinfelden and was very well attended. Progress reports and poster presentations of all current research projects funded by the URPP Evolution in Action provided an

overview of our ongoing research activities. Further highlights were the keynote lecture held by Johannes Krause (Max Planck Institute, Jena) and the social and cultural program complementing the scientific agenda.

- The **Research Projects** run by the URPP Evolution PhD students were successfully continued, first graduations took place (Michael Baumgartner March 15, 2016; Katie Collier December 20, 2016, Fabrizio Menardo, December 22, 2016), and many papers were published.
- The **Academic Fellow** of the URPP Evolution in Action, Dr. Matthew Horton, successfully started his research activities at the UZH. A first PhD student joined his team in September 2016.
- The **Assistant Professor Position** was advertised and a scientific symposium with all short-listed candidates took place in June 2016. At this occasion, the candidates were also interviewed by the Professorial Appointment Committee. The Berufungsantrag was handed in to the Executive Board of the University in November 2016 and the Professorial Appointment Process is currently running.
- Preparatory works for **Starting Up Phase 2 of the URPP Evolution in Action**, with new members, projects and PhD students. Based on an open call for project proposals, the Developmental and Financial Plan of the URPP Evolution in Action for the 2nd phase was prepared and granted by the Executive Board of the University. Organizational and administrative prearrangements for the 2nd Phase were made.
- The results from the first two rounds of **Open Calls for Research Projects** were presented at the Annual Retreat of the URPP Evolution in Action, as well as the project outlines and preliminary results of the third Open Call for Research Projects issued in spring 2016.
- Several **Courses for the PhD Program** that were established by the URPP Evolution in Action during the first three years of the program were held again in 2016 (such as Next Generation Sequencing, Concepts of Evolutionary Biology). Additionally, a new course on Scientific Writing for Evolutionary Biologists was set up and was a great success among the students.
- Continuation of the highly successful **Bioinformatics Support Services** as well as of the **Bioinformatics Tutorial Program**, including the planning for a tutorial curriculum for the new PhD students taking up their positions in Phase 2 of the URPP Evolution in Action.
- The **Seminar Series** of the URPP Evolution in Action was successfully continued. With the support of the coordination office, PhD students of the URPP Evolution in Action invited speakers for reserved slots in the department seminars of our participating departments. Workshops took place in combination with these seminars, with the speakers teaching in their areas of expertise. The organizing students found this a great opportunity and experience and feedback from the audience was very positive.
- An interdisciplinary two-day **Workshop on Linguistics and Genetics** with more than ten speakers from around the world was organized by members of the URPP Evolution in Action and co-financed by the URPP Evolution in Action and the URPP Language and Space.
- Several **Social Events** (excursions, informal get-togethers) were organized and created opportunities for interactions within the URPP Evolution in Action community and beyond.

- Preparatory works for future **Public Outreach** initiatives, in particular developing a project idea for the participation of the URPP Evolution in Action at the Scientifica 2017. We also continued the planning of a special exhibition in Phase 2 at the Zoological Museum of the UZH on topics related to the URPP Evolution in Action.
- The **Website** of the URPP Evolution in Action has been extended and new content developed.

2.3 Objectives for 2017

- Planning and realization of the **Fifth Retreat of the URPP Evolution in Action**, with a program featuring progress reports from all projects, a keynote lecture, faculty and PhD student meetings, as well as a social program enabling a good integration of old and new members and PhD students.
- **Start of Phase 2 of the URPP Evolution in Action**, with new members, projects and PhD students. We aim at a smooth transition and a good integration of all new projects, and will further promote a lively, interactive community life.
- Finalization of the **Research Projects** run by the URPP Evolution PhD students of the 1st Phase, and graduations.
- Start of the research projects of the non-tenure track **Assistant Professor Position** of the URPP Evolution in Action.
- Presentation of the results from the previous **Open Calls for Research Projects**, and first Open Call for Research Projects in the 2nd Phase to promote young scientists by supporting innovative and/or high-risk pilot projects.
- Planning and realization of **Courses for the PhD Program** covering topics such as Next Generation Sequencing, Concepts of Evolutionary Biology, and Scientific Writing for Evolutionary Biologists.
- Continuation of the highly successful **Bioinformatics Support Services** as well as of the **Bioinformatics Tutorial Program**, including a kick-off event tailored to the needs of the new PhD students starting in the 2nd Phase of the URPP Evolution in Action.
- Set-up of **PhD Students Meetings** for the new PhD students starting in the 2nd Phase of the URPP Evolution in Action, to enhance interaction among students, research projects, and departments of the URPP Evolution in Action.
- Organization of **Social Events** to further enhance interaction within the URPP Evolution in Action community.
- Planning and realization of **Public Outreach** activities, in particular the participation of the URPP Evolution in Action at the Scientifica 2017 and the further planning of a museum exhibition on topics related to the URPP Evolution in Action.
- Further extension and development of the **Website** of the URPP Evolution in Action.

3 Research

3.1 Main Research Projects

In 2016, 14 research subprojects were being conducted in the URPP Evolution in Action, embedded in the framework of our five collaborative and interdisciplinary research projects on different themes in evolutionary biology. In line with the overarching goal of the URPP to educate a next generation of scientists with broad competences for combining molecular and computational approaches with evolutionary questions, all URPP-funded researchers are young scientists, i.e. 11 PhD students and three postdocs. The individual projects, including aims, progress, as well as partners and PhD students involved are described in some detail below.

Project 1: Genomic Correlates of Microbial Coevolution

Project lead: Christian von Mering (Institute of Molecular Life Sciences, IMLS)

Historically, microbes have been viewed as mostly independent organisms. Currently, this view is being challenged as new data hint at intricate ecological interdependencies of microbes. The research project “Genomic Correlates of Microbial Co-Evolution” has made significant progress in identifying and characterizing ecological partnerships of microbes, using modern high-throughput molecular techniques.

Subproject 1.1: Microbial Networks in Lake Zurich

PhD student: Michael Baumgartner (Department of Plant and Microbial Biology, IPMB); PhD Committee: Jakob Pernthaler (IPMB), Christian von Mering (IMLS), Leo Eberl (IPMB), Rolf Kümmerli (IPMB)

This project investigates the experimental evolution of a model predator-prey system with focus on the variability of defense traits and phenotypic plasticity. It aims at understanding the eco-evolutionary trajectories of predator-prey interactions in environmental conditions that select for or against plastic phenotypes. The project has been completed, the graduate student has defended his PhD in mid-March 2016. A short follow-up postdoctoral project has been granted by URPP Evolution, which was concluded in December 2016. We found that bacteria can circumvent evolutionary trade-offs between growth and defense by genome reduction and that phenotypic plasticity was selected over genotypic trait displacement at unstable environmental conditions. Quorum sensing was found to play a role in predation defence.

Subproject 1.2: Evolutionary Degeneration of an Obligate Symbiont

PhD student: Marta Pinto (IPMB); PhD committee: Leo Eberl (IPMB), Kentaro Shimizu (Department of Evolutionary Biology and Environmental Studies, EBES), Rolf Kümmerli (IPMB), Aurelien Carlier (University of Gent, Belgium)

We are investigating the genome evolution of *Burkholderia* obligate symbionts. The goal is to unveil the evolutionary causes and consequences of genome reduction in *Burkholderia* obligate symbionts. We are analyzing the background mutational pattern in *Burkholderia* leaf nodule symbionts and quantifying the bacterial population size in different plant tissues. Genome analysis of the *Burkholderia* symbiont of *Ardesia crenata* identified genes encoding a non-ribosomal peptide synthetase with a predicted role in secondary metabolism. Specifically, we show that the bacterial symbionts are responsible for the synthesis of compound FR900359, a cyclic depsipeptide with biomedical properties previously isolated from leaves of *A. crenata*.

Project 2: Evolution in Action: Environment, Agriculture, and Human Disease

Project lead: Kentaro Shimizu (EBES)

Traditionally, evolutionary biology has been based on phenotypic observations, with genetic change being deduced from statistical patterns. Today, studying complete genomes makes it possible to directly observe evolutionary processes on the genetic level. The project "Evolution in Action: Environment, Agriculture, and Human Disease" focuses on investigating evolution in action using next-generation sequencing (NGS) and detecting the frequencies of sequence changes. It focuses on recent rapid changes in host-pathogen interactions and in the formation of new species.

Subproject 2.1: Virulence Evolution in Past Human Pathogens

PhD student: Giada Ferrari (Institute of Evolutionary Medicine, IEM, Medical Faculty); PhD committee: Kentaro Shimizu (EBES), Frank Rühli (IEM, Medical Faculty), Abigail Bouwman (IEM, Medical Faculty), Christian von Mering (IMLS)

We are investigating pathogen evolution using preserved soft tissue remains. The aim of the study is to gain pathogen genetic data from historic remains. Data acquisition is completed, data analysis is currently on-going. The extraction optimization took much longer than expected, as formalin inhibits DNA amplification.

Subproject 2.2: Understanding Variation in *Borrelia* Resistance in Swiss Natural Host Populations

Postdoc: Luca Cornetti (EBES); supervised by Barbara Tschirren (EBES), mentors: Kentaro Shimizu (EBES), Beat Keller (IPMB), Peter Deplazes (Vetsuisse Faculty)

The aim of the project was to investigate the evolution of resistance mechanisms against emerging *Borrelia* pathogens in natural host populations. Goal of the project was to identify genetic variants that confer resistance against *Borrelia* in natural hosts. Using a genotyping-by-sequencing (GBS) approach we have identified several new candidate regions involved in host-*Borrelia* interactions. Targeted sequencing of these regions confirmed that they are positively selected in response to emerging *Borrelia*. In a next step, we plan to confirm these associations in other host populations. Postdoc Luca Cornetti has been working on this project, thus no PhD committee.

Subproject 2.3: Adaptation of a Fungal Pathogen to New Host Species

PhD student: Fabrizio Menardo (IPMB); PhD committee: Beat Keller (IPMB), Thomas Wicker (IPMB), Kentaro Shimizu (EBES)

We investigate the evolutionary genomics of *Blumeria graminis* grass powdery mildew. The ultimate goal of the subproject is to discover the evolutionary processes that acted on the evolution of *B. graminis*, in particular regarding the recent emergence of powdery mildew on the crop Triticale. The project is completed, we found that triticale powdery mildew originated through a hybridization of wheat and rye powdery mildew. The current URPP project is a continuation of this work and focuses on the identification of the genetic and molecular determinants of the host specificity of triticale powdery mildew. The PhD thesis of Fabrizio Menardo was successfully defended on 22nd December 2016.

Subproject 2.4: Hybrid Speciation and Male Invasion in Action in Switzerland

Postdoc: Hiromi Matsumae (EBES); supervised by Kentaro Shimizu (EBES), mentors: Beat Keller (IPMB), John Pannell (University of Lausanne)

We study evolution in action in polyploid speciation and breeding systems in *Arabidopsis* relatives. We aim at understanding the genomic basis of polyploid speciation as well as of the evolution of breeding systems. We reported genome assembly of parental diploid species (Briskine et al., Gan et al.) as well as reconstructed polyploid genomes (Paape et al.). Using these genome resources, we

established a new molecular pattern stating that hybrid (allopolyploid) species became generalists by combining parental transcriptomes (Paape et al., Shimizu-Inatsugi et al.). The postdoc expanded the study to population genetics of human beings in collaboration with linguistics, which resulted in a project of the second phase. Related to the genome resources above, a few manuscripts also supported by URPP bioinformaticians are in preparation.

Subproject 2.5: Speciation through Chromosomal Rearrangements in Wild House Mice in Switzerland

PhD student: Sofia Grize (EBES); PhD committee: Barbara König (EBES), Anna Lindholm (EBES), Ueli Grossniklaus (IPMB), Kentaro Shimizu (EBES), Aldona Pieńkowska-Schelling (University of Bern), Jeremy Searle (Cornell University, US)

This project investigates the influence of chromosomal variation and hybrid sterility on genetic isolation between house mouse populations. The goal is to understand the maintenance of distinct house mouse populations that vary in number and structure of their chromosomes, despite hybrid dysfunction and gene flow between them. Lab work is complete. Data analyses are mostly complete, and manuscript preparation is the current activity. The genomic data from lab crosses indicate that recombination is likely the key process that prevents genetic isolation of house mice populations of divergent chromosome structures. Health problems of the student lead to a partial sick leave during most of the year.

Subproject 2.6: Incipient Speciation Due to Thermal Adaptation or Sexual Selection in Sepsid Flies

PhD student: Athene Giesen (EBES); PhD committee: Wolf Blanckenhorn (EBES), Kentaro Shimizu (EBES), Rie Inatsugi-Shimizu (EBES), Heidi Lischer (EBES)

This project investigates the evolution of reproductive isolation between the two hybridizing dung flies *Sepsis cynipsea* and *S. neocynipsea*. We aim at understanding the speciation process in this group of flies in general and for these two species in particular, in terms of gene-phenotype relationships. All pre- and postzygotic isolating hybridizations documenting barriers between the species, as well as empirical assessment of genetic differentiation with a combined data analysis of morphological measurements of European and North American *S. cynipsea* and *S. neocynipsea* are analysed and the manuscripts almost finished. Overall, the PhD student is on track. Planned QTL analyses of the mating behavior have been canceled to be performed by another student.

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

Project lead: Ueli Grossniklaus (IPMB)

Traditionally, epigenetic variation has not been given much importance in ecological and evolutionary processes despite its potential for rapid change, which could play an important role in adaptation. This research project aims at assessing the significance of epigenetic variation and inheritance for ecological questions and evolutionary processes.

Subproject 3.1: Epigenetic Variation and Selection

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

We investigate whether the selection of epigenetic variation contributes to phenotypic responses under selection, specifically whether a change in trichome density observed after several generations of aphid herbivory is due to epigenetic variation, providing the basis for adaptation to biotic stress. Plants from populations that were subjected to five generations of selection have been genotyped, grown in a randomized block design, and phenotypic data has been collected. Analysis of this phenotypic data showed that there are heritable differences in how the same plant genotype responds to selection by two different aphid species. Based on this data showing inheritance of selected phenotypes in the absence of any genetic variation, we went ahead and sequenced the methylome of

a large number of individuals from ancestral and independently selected populations. Dr. Vimal Rawat, a postdoc trained in bioinformatics, has taken over this project in 2016 from the PhD student who started it. He is analyzing the methylome data with the goal to identify cytosines that are differentially methylated between ancestrals and treatments, and to identify candidate genes whose expression may have changed due to methylation in response to the selection treatments.

Subproject 3.2: Epigenetics in Plant Adaptation

PhD student: Roman Kellenberger (Institute of Systematic Botany, ISB); PhD committee: Florian Schiestl (ISB), Phillip Schlueter (ISB), Kentaro Shimizu (EBES), Ueli Grossniklaus (IPMB)

We study the induction of trans-generational epigenetic effects in plant-insect interactions. Our aim is to determine the role of DNA methylation in phenotypic responses of plants to pollinators and herbivores. The experimental part of this project is completed and the manuscript is close to submission. It has been decided to not follow up the ecological experimental work on trans-generational effects of herbivory by detailed molecular investigations. The reasons were lack of time and no clearly molecularly targetable phenotype.

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

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

We investigate the importance of epigenetic variation in adaptive processes using *Tetrahymena thermophila* as a model system. The project aims at better understanding the importance of histone modifications in gene expression changes that occur when *T. thermophila* adapts to different conditions, such as increasing population densities and temperature variation. A pilot of the temperature adaptation experiment was performed in August 2016. Nuclei isolation methods have been optimized and tests on the ChIP method are being performed in preparation for the population density experiment. Transcriptomes from a previous population density experiment were sequenced in collaboration with Paul Hurd and Robert Lowe; the resulting data is currently being analyzed.

Project 5: The Evolution of Language: an Integrative Approach

Project lead: Marta Manser (EBES)

Language is widely seen as one of human's defining features, yet there is considerable disagreement concerning what features of language are unique to humans and which one we share with animals. The aim of this project is to unpack the features thought to be unique to human language by employing synergistic theoretical and empirical techniques, and ultimately to better understand the evolutionary preconditions that promote the emergence of complex vocal communication systems.

Subproject 5.1: Vocal complexity in cooperatively breeding mammals

PhD student: Katie Collier (EBES); PhD committee: Marta Manser (EBES), Carel van Schaik (Department of Anthropology, AIM), Balthasar Bickel (Dept. of Comparative Linguistics, IVS, Faculty of Arts), Simon Townsend (EBES), Hans-Johann Glock (Institute of Philosophy)

This project is about the evolutionary origins and selective conditions promoting the evolution of human language. We took a highly collaborative, integrative and empirical approach to better understand how language, one of the key stand-out features of human biology, may have evolved. The PhD student has published a conceptual paper outlining the overall approach we are taking

throughout this project (Collier et al. 2014, Proc. Roy. Soc. B). She spent 6 months conducting observational and experimental research in the field on a second mongoose species (Dwarf mongoose) in South Africa. She later returned for a brief 2 month period to finalize and complete her experiments, followed by data analysis and the preparation of other manuscripts. This collaboration, including anthropologists, linguists, philosophers and animal communication biologists, has been highly stimulating and through regular meetings we have continued to generate new and exciting avenues of research in the field of language evolution. These discussions have led to the formulation of a new hypothesis explaining how combinatorial systems in humans may have evolved (Collier et al. 2014) which has in turn helped guide our own empirical research into the topic of animal vocal combinations. The PhD student has successfully defended her thesis in December 2016.

Project 6: Conservation Genomics: the Role of Functional Genetic Variation in Conservation

Project lead: Lukas Keller (EBES)

Evolutionary adaptation is essential for endangered species to survive global change, yet the role of functionally important genetic variation in the small, isolated populations typical for endangered species is virtually unknown. This research project addresses this gap by applying conservation genomics to an ideal study organism, the Alpine Ibex.

Subproject 6.1 and 6.2: Conservation Biology of the Alpine Ibex

PhD student, subproject 6.1: Deborah Leigh (EBES); PhD committee: Lukas Keller (EBES), Andreas Wagner (EBES), Frédéric Guillaume (EBES), Ueli Grossniklaus (IPMB)

We are characterizing the transcriptomic patterns underlying inbreeding depression in the Alpine Ibex. The aim of the study is to better understand the mechanistic of the physiological disruption occurring in inbred animals with lower phenotypic values at fitness-related traits, and link this to their genetic background. We found 63 genes to be differentially expressed (DE) in response to increasing heterozygosity levels. Candidate genes that were downregulated included MTIL, which is involved in binding reactive oxygen species, thereby mitigating oxidative stress, and CATSPERG, which affects fertility by regulating sperm motility. As we sequenced mRNA from skin tissue, we found a large proportion of reads to be xenobiotic in origin, although this proportion differed in magnitude across libraries. Additionally, due to our reasonably low sample size of 18 individuals we lacked the power to detect significantly enriched gene ontology categories in our gene list of DE genes; we hope to boost our statistical power by sequencing additional samples from the population.

PhD student, subproject 6.2: Kasia Sluzek (EBES); PhD committee: Lukas Keller (EBES), Andreas Wagner (EBES), Thomas Wicker (IPMB), Arpat Ozgul (EBES), Simon Aeschbacher (University of California Davis, US)

This study is about conservation genomics of the Alpine ibex. We are examining the effects population bottlenecks and conservation management exert on evolutionary processes and genetic variation. Currently we are investigating the effects bottlenecks have on regions of the genome with different functions. This is to explore if drift driven variation loss has acted equally on neutral and functional genetic variation. Recent work has signaled an error with earlier analyses due to false SNP loci arising from alignment to a reference genome of a closely related species. This has caused a minor set back but has lead to some exciting further simulation work including simulated selection.

Pilot Projects

To further promote young scientists, the URPP Evolution in Action called three times during Phase 1 for research proposals in the wider field of evolutionary biology. We particularly encouraged applicants to hand in proposals involving an interdisciplinary approach to evolutionary questions. Proposals could be submitted by PhD students and postdocs working in UZH research groups that either are 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 these calls was to fund innovative pilot projects necessary for subsequent larger grant applications. We received many highly interesting project proposals that were reviewed and rated by the Steering Committee of the URPP Evolution in Action. About 40% of the submitted projects could be granted in the three calls.

Open Call of March 2016 (Projects started in April 2016)

Applicant: *Dr. Reiko Akiyama*

Title of project: The genomic basis of potentially ongoing evolution of selfing syndrome in *Cardamine amara*, an emerging model species for plant mating system evolution

Granted funding: CHF 19'335

Applicant: *Dr. Natasha Arora*

Title of project: Exploring the trajectories and genomic consequences of the Walser expansion

Granted funding: CHF 20'000

Applicant: *Dr. Michael Baumgartner*

Title of project: Cooperation or competition: Interactions of bacterial strains with different evolutionary background

Granted funding: CHF 18'300

Applicant: *Dr. Ana Marcela Florez-Rueda*

Title of project: Testing the role of siRNAs in hybrid incompatibility, are they responsible for the drastic shift in allele-specific expression in hybrid seeds?

Granted funding: CHF 18'700

Applicant: *Dr. Kate Ihle*

Title of project: The transcriptional basis of inbreeding depression and fitness rescue by prenatal maternal investment

Granted funding: CHF 18'775

Applicant: *Dr. Ayako Izuno*

Title of project: Genetic bases of the adaptive radiation within a species revealed by the genome-wide polymorphism

Granted funding: CHF 19'780

Applicant: *Dr. Kartal Önder*

Title of project: Probing the epigenetic response to transposable elements

Granted funding: CHF 19'732

Applicant: *Anne Leinweber, PhD Student*

Title of project: Is competition between bacteria based on fixed or phenotypically plastic responses? - answers from a transcriptome study

Granted funding: CHF 15'300

Applicant: *Marion Müller, PhD Student*

Title of project: Genetics of host adaptation of *Blumeria graminis* (powdery mildew)

Granted funding: CHF 20'000

Applicant: *Dr. Timothy Paape*

Title of project: Genome wide association study of heavy metal tolerance in *Medicago truncatula* and evolutionary genomics of metal tolerant nitrogen fixing rhizobia

Granted funding: CHF 20'000

Applicant: *Dr. Yvonne Möller-Steinbach*

Title of project: Distinct changes of floral morphology in *Mimulus aurantiacus* - Discovering underlying epigenetic regulatory DNA marks.

Granted funding: CHF 20'000

For reports of all pilot projects see Appendix A, attached to this document.

3.2 Scientific Activities

Scientific Retreat



On September 6-8, 2016, the fourth URPP Evolution in Action Retreat took place in Rheinfelden, with 65 participants. Progress reports of all current research projects funded by the URPP Evolution in Action provided an overview of our ongoing research activities. The PhD students conducting the main projects held the presentations. The aim was to make the scientific questions of the diverse fields understandable to all, and to enable discussion across different disciplines. All pilot projects selected in the three open calls were presented in a stimulating poster session. Additionally, many of our new members gave a brief 5-minutes insight into their research areas, which led to lively discussions that proved to be a good starting point for new collaborations already at the previous retreat. The keynote lecture, by now an established tradition at each annual retreat, was held by Prof. Johannes Krause (Max Planck Institute for the Science of Human History in Jena, Germany). He provided absolutely fascinating insights into his interdisciplinary research on human evolution.

Similar to the previous annual meetings, the retreat 2016 was also the opportunity to meet all other members and PhD students of the URPP Evolution in Action and to discuss general aspects; as in previous years, faculty and PhD student meetings were held during the retreat. The scientific sessions and meetings were complemented by a social program, during which lots of informal discussions and interactions took place.

Bioinformatics tutorials

The successful series of bioinformatics tutorials was continued in 2016, based on the inputs from the URPP Evolution in Action members and PhD students. These tutorials were organized and taught by Stefan Wyder and Heidi Tschanz-Lischer and are listed in the university calendar (Vorlesungsverzeichnis) as "BIO396 Tutorials in Practical Bioinformatics". At the retreat 2016, a

feedback poll on teaching was held with the PhD students and topics were chosen according to students' feedback. In detail, the following 3-hour-tutorials were offered:

- Phylogenetics and phylogenomics: introduction to phylogenomic tree construction algorithms, assumptions, interpretation, formats, viewing, manipulation and potential pitfalls
- Genomic data visualization: Ensembl and UCSC genome browsers, genome viewers, circular visualization
- Principles of data visualization: basics of graphic design and visual communication; use of saliency, colors, consistency and layout; different chart/graphic types; presentation and discussion of "good" and "bad" graphics
- Reproducible research: problems, forensic bioinformatics, dynamic reports, 10 simple rules

In addition, the following 3-hours tutorial repetitions were offered:

- R Intro/Refresher Course Part 1: loading data, making plots (ggplot2), summarizing groups, writing functions, data types in R
- R Intro/Refresher Course Part 2: automating repetitive tasks (loops and apply functions), plotting (R base graphics), coding habits to avoid

Every tutorial consisted of a theoretical introduction to the topic, and most time was spent on guided exercises. The tutorials were very well attended, with ten to 16 participants for each topic. The students generally gave a very positive feedback about content and format, and for all past tutorials there were requests to repeat the tutorial. The participants were mostly PhD students of the URPP Evolution in Action, but also more senior scientists and guests from neighboring departments attended the tutorials. The series is being continued in 2017.

In addition to the tutorial series, the URPP Evolution in Action bioinformaticians organized and taught a 2-day course: BIO 634 "Next-Generation Sequencing 2 for Model and Non-Model Species: Transcriptomes, Variant Calling and Biological Interpretation" that was organized as a follow-up course to a 2-day introduction to Next-Generation Sequencing (BIO 610 "Next-Generation Sequencing 1 - Introductory Course: Assembly, Mapping, and Variant Calling") organized by Prof. Kentaro Shimizu and others. BIO 634 aimed to extend the knowledge of NGS analysis taking a hands-on approach. The course was attended by 14 persons, mostly PhD students in Plant Sciences or Evolutionary Biology from the University of Zurich and ETH. Students' evaluations were very favorable and the course will be offered again in 2017. In 2016, a new preparatory 1-day course BIO 609 "Introduction to UNIX/Linux and Bash Scripting" aiming to increase computing and scripting skills was offered by the URPP Evolution in Action bioinformaticians that was a prerequisite for the attendance of BIO610 and BIO634. Due to the very large interest the same course was taught twice with a total of 48 participants, primarily PhD and Masters students from the University of Zurich and ETH. The extended format of a 5-day course on Next Generation Sequencing Analysis was considered a success by both participants and teachers and will be continued in 2017.

The quarterly one-to-one meetings between each PhD student and an embedded bioinformatician were continued in 2016 to discuss project designs, methods and challenges. The aim is to keep up-to-date with the progress and to help connecting the PhD students using similar methods.

Courses for the PhD Program in Evolutionary Biology

- Next-Generation Sequencing for Model and Non-Model Species (BIO610); May 18-19, 2016; Lecturers: Kentaro Shimizu, Roman Vladimir Briskine, Masaomi Hatakeyama, Hiromi Matsumae Nogami, Jun Sese, Rie Shimizu Inatsugi, Heidi Tschanz-Lischer
- Next-Generation Sequencing 2 – Advanced Course: Transcriptomes, Variant Calling and Biological Interpretation (BIO634); May 23-24, 2016; Lecturers: Masaomi Hatakeyama, Heidi Tschanz-Lischer, Stefan Wyder
- Concepts in Evolutionary Biology (BIO395); March 8-9, 2016; Lecturers: Barbara König, Andreas Wagner, Lukas Keller, Marcelo R. Sanchez, Kentaro Shimizu, Barbara Tschirren, Wolf Blanckenhorn, Anna K. Lindholm Krützen, Michael Krützen, Erik Postma, Kathleen Marie Sprouffske.
- Scientific Writing for Evolutionary Biologists (BIO555) NEW; November 21-22, 2016; Lecturers: Hanna Kokko, Annegret Lesslauer

Recruitment for the Assistant Professor Position

As part of the Professorial Appointment Process, we held a symposium on the topic of Plant Evolutionary Biology, where all short-listed candidates presented their research projects and plans. The symposium took place on June 21-22, 2016, and comprised the following talks:

Title: Evolution of Parental Conflicts in Plants
Speaker: Dr. Nuno Pires, University of Zurich

Title: The Genomics of Adaptation: generating phenotypic, genetic, and species diversity
Speaker: Dr. Danièle Filiault, Gregor Mendel Institute for Plant Molecular Biology, Austria

Title: The genes and traits that underlie adaptation to drought
Speaker: Dr. John Lovell, University of Texas, Austin, USA

Title: Genomic reconfigurations en route to a fully parasitic lifestyle in flowering plants
Speaker: Dr. Susann Wicke, University of Münster, Germany

Title: Genetic approaches to understanding eco-evolutionary patterns
Speaker: Dr. Samuel Wuest, University of Zurich

Title: Dynamic Genomes: The importance of transposable elements in the evolution of natural populations
Speaker: Dr. Anne Roulin, University of Zurich

Title: A population-genomic approach to understanding adaptation and speciation in the face of gene flow
Speaker: Dr. Simon Aeschbacher, University of California, Davis, USA

PhD Student Organized Seminars

The new seminar series of the URPP Evolution in Action was successfully continued in 2016. With the support of the coordination office, PhD students of the URPP Evolution in Action can invite speakers for reserved slots in the department seminars of our participating departments. Workshops take place in combination with these seminars, with the speakers teaching in their areas of expertise. The organizing students found this a great opportunity and experience and feedback from the audience was very positive.

The following seminar took place in 2016:

- September 20, 2016
Title: Ancient DNA and computational approaches to conservation
Speaker: Dr. Michael Campana, Smithsonian Conservation Biology Institute, Washington DC, USA

4 Academic Career Development

4.1 Academic Career Development for Young Academics

Most of the budget granted to the URPP Evolution in Action is currently used to fund PhD studies: in 2016, the URPP Evolution in Action funded salaries and research consumables for 12 PhD students and three postdocs, thereby contributing substantially to their career development on the financial level. Additionally, we have by now held three calls for pilot projects that were open to PhD students and postdocs of our participating research groups. These calls enable young scientists to develop their own research ideas, to form new collaborations across the borders of research groups and institutes, and to obtain their own funding for pilot projects.

Beyond direct financial support, we are dedicated to providing a network supporting young academics in the field of evolutionary biology, and to creating an atmosphere of lively interaction across the borders of faculties, institutes, and seniority. Besides scientific meetings, we also organize social events and see such activities deliberately as a means to grant young academics access to a community of experienced researchers. PhD students, postdocs, and junior professors who do not receive funding from the URPP Evolution in Action, but work in research areas close to ours, are equally invited to attend events and courses organized by the URPP Evolution in Action. A successful format of social events are the “Informal Get-Togethers”, taking place about 3 times per year on weekday evenings in Zurich. These events are generally attended by many of our members and students. Notably, we linked one of these events in 2016 with a guided tour of the museum exhibition “Das Krokodil im Baum” at the Zoological Museum of the UZH, combining thus a scientific, cultural and social event.

The two embedded bioinformaticians of the URPP Evolution in Action have supported all PhD projects from the beginning, such that experimental design, probe preparation, analysis methods etc. are optimally adapted to the questions asked. In doing so, the bioinformaticians themselves expand their research experience, and the wealth of data available from several projects allows them to develop productive research activities on 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 the UZH. The URPP Evolution in Action bioinformaticians regularly work one day per week in the von Mering (IMLS) and Wagner (EBES) groups, respectively, where they are in touch with the newest developments in bioinformatics research, and take part in 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).

PhD students and postdocs have the possibility to invite keynote speakers from abroad, thereby gaining experience and new contacts who may well become mentors for their further career. To invite speakers, PhD students and postdocs can organize minisymposia with several speakers. In addition, PhD students have the possibility to invite speakers for reserved slots in the department seminars of

our participating departments. In both cases, they receive organizational support from the URPP coordination office and the necessary funding.

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

4.2 Gender Equality Development

Hiring of personnel is on an equal opportunity basis and according to the “Gender Equality Action Plan UZH” guidelines. We mention our equal opportunity efforts in all job advertisements. Already now, the gender ratio in the URPP Evolution in Action is very balanced. At the PhD student level and among the applicants for positions and research grants, there is a majority of women. This is reflected by the fact that more than 80% of our open call research grants were awarded to women scientists.

Wherever possible, we support efforts to create a family-friendly work environment, for instance by enabling part-time work. Our experience with providing such opportunities is highly positive. Furthermore all our social events are, if convenient for children, open to the families of our co-workers. As planned, we have provided child-care opportunities at the Annual Retreat 2016 to enable parents to attend, and we will continue to do so at the annual retreats of Phase 2.

5 Publications

5.1 Peer-reviewed publications

Papers published in previous years

Akama S, Shimizu-Inatsugi R, Shimizu KK, Sese J (2014) Genome-wide quantification of homeolog expression ratio revealed nonstochastic gene regulation in synthetic allopolyploid Arabidopsis. *Nucleic Acids Research* 42: e46.

Collier K, Bickel B, van Schaik C, Manser MB, Townsend SW (2014). Language evolution: Syntax before phonology? *Proceedings of the Royal Society B: Biological Sciences* 281: 20140263.

Morger J, Banjok J, Craig PS, Rogan MT, Lun ZR, Hide G, Tschirren B. (2014) Naturally occurring Toll-like receptor 11 (TLR11) and Toll-like receptor 12 (TLR12) polymorphisms are not associated with *Toxoplasma gondii* infection in wild wood mice. *Infection, Genetics and Evolution*, 26, 180-184.

Morger J, Råberg L, Hille SM, Helsen S, Štefka J, Al-Sabi MM, Kapel CMO, Mappes T, Essbauer S, Ulrich RG, Bartolommei P, Mortelliti A, Balciauskas L, van den Brink NW, Rémy A, Bajer A, Cheprakov M, Korva M, García-Pérez AL, Biek R, Withenshaw S, Tschirren B. (2015) Distinct haplotype structure at the innate immune receptor Toll-like receptor 2 (TLR2) across bank vole populations and lineages in Europe. *Biological Journal of the Linnean Society*. doi: 10.1111/bij.12593

Tedder A, Helling M, Pannell JR, Shimizu-Inatsugi R, Kawagoe T, van Campen J, Sese J, Shimizu KK (2015) Female sterility associated with increased clonal propagation suggests a unique combination of androdioecy and asexual reproduction in populations of *Cardamine amara* (Brassicaceae). *Annals of Botany* 115: 763-776

Tschirren, B. (2015) *Borrelia burgdorferi* sensu lato infection pressure shapes innate immune gene evolution in natural rodent populations across Europe. *Biology Letters*: doi: 10.1098/rsbl.2015.0263

Papers published or submitted in 2016

Baumgartner M, Pernthaler J. Adaptive phenotypic defence is only preserved in a bacterial strain at alternating conditions of predator presence and absence. (Submitted)

Baumgartner M, Roffler S, Wicker T, Pernthaler J. Letting go: genome streamlining allows for simultaneous adaptation to top-down and bottom-up constraints in a phenotypically plastic bacterial strain. *ISMEJ*, under revision

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

Biebach I, Leigh D, Sluzek K, and Keller L. (2016) Genetic Issues in Reintroduction. In: *Reintroduction of Fish and Wildlife populations*. USA: UC Press

Briskine R, Paape T, Shimizu-Inatsugi R, Nishiyama T, Akama S, Sese J, Shimizu KK. (2016) Genome assembly and annotation of *Arabidopsis halleri*, a model for heavy metal hyperaccumulation and evolutionary ecology. *Molecular Ecology Resources*, DOI: 10.1111/1755-0998.12604.

Carlier A, Fehr L, Pinto M, Schäberle T, Dessein S, König G, and Eberl L. The cyclic depsipeptide FR900359 from *Ardisia crenata* Sims is produced by the plant's obligate leaf nodule symbiont *Candidatus Burkholderia crenata*. *Environ Microbiol.* 2016 Sep;18(8):2507-22. doi: 10.1111/1462-2920.13184.

Collier K, Townsend SW, Manser MB, in review. Call concatenation in wild meerkats. *Animal Behaviour*.

Cornetti L, Lemoine M, Hilfiker D, Morger J, Reeh K, Tschirren B. (2016) Higher genetic diversity on mountain tops: the role of historical and contemporary processes in shaping genetic variation in the bank vole. *Biological Journal of the Linnean Society* doi: 10.1111/bij.12723

Didion JP, Morgan AP, Yadgary L, Bell TA, McMullan RC, Ortiz de Solorzano L, Britton-Davidian J, Bult CJ, Campbell KJ, Castiglia R, Ching Y-H, Chunco AJ, Crowley JJ, Chesler EJ, French JE, Gabriel SI, Gatti DM, Garland T, Giagia-Athanasopoulou EB, Giménez MD, Grize SA, Gündüz I, Holmes A, Hauffe HC, Herman JS, Holt JM, Hua K, Jolley WJ, Lindholm AK, López-Fuster MJ, Mitsainas G, Mathias M, McMillan L, Ramalhinho MG, Rehmann B, Rosshart SP, Searle JB, Shiao M-S, Solano E, Svenson KL, Thomas-Laemont P, Threadgill DW, Ventura Queija J, Weinstock GM, Pomp D, Churchill GA, and Pardo-Manuel de Villena F. (2016) R2d2 drives selfish sweeps in the house mouse. *Molecular Biology and Evolution* 33:1381-1395.

Gan X, Hay A, Kwantes M, Haberer G, Hallab A, Dello Ioio R, Hofhuis H, Pieper B, Cartolano M, Neumann U, Nikolov L, Song B, Hajheidari M, Briskine R, Kougioumoutzi E, Vlad D, Broholm S, Hein J, Meksem K, Lightfoot D, Shimizu KK, Shimizu-Inatsugi R, Imprialou M, Kudrna D, Wing R, Sato S, Huijser P, Filatov D, Mayer K, Mott R, Tsiantis M. (2016) The *Cardamine hirsuta* genome highlights the pervasive role of transcription factors and tandem gene duplications in morphological diversity. *Nature Plants*, 2: 16167.

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

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):online.

Kellenberger RT, Desurmont GA, Schlüter PM, Schiestl FP (in prep.) Trans-generational inheritance of herbivory-induced changes in *Brassica rapa*.

Leinweber A, Inglis RF, Kümmerli R (2017). Cheating fosters species co-existence in well-mixed bacterial communities. *ISME*

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, 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.

Novikova PY, Hohmann N, Nizhynska V, Tsuchimatsu T, Ali J, Muir G, Guggisberg A, Paape T, Schmid K, Fedorenko OM, Holm S, Säll T, Schlötterer C, Marhold K, Widmer A, Sese J, Shimizu KK, Weigel D, Krämer U, Koch MA, Nordborg M. (2016) Sequencing of the genus *Arabidopsis* reveals a complex history of non-bifurcating speciation and abundant trans-specific polymorphism. *Nature Genetics*, 48: 1077-82.

Paape, T, Hatakeyama M, Shimizu-Inatsugi R, Cereghetti T, Onda Y, Kenta T, Sese J, Shimizu KK. (2016). Conserved but attenuated parental gene expression in allopolyploids: constitutive zinc hyperaccumulation in the allotetraploid *Arabidopsis kamchatica*. *Molecular Biology and Evolution*, 33: 2781-2800.

Pinto-Carbó M, Sieber S, Dessein S, Wicker T, Verstraete B, Gademann K, Eberl L, Carlier AL. Evidence of horizontal gene transfer between obligate leaf nodule symbionts. *ISME J*. 2016 Sep;10(9):2092-105. doi: 10.1038/ismej.2016.27.

Shimizu-Inatsugi R, Terada A, Hirose K, Kudoh H, Sese J, Shimizu KK. (2017, online in 2016) Plant adaptive radiation mediated by polyploid plasticity in transcriptomes (Special Issue: Molecular Mechanisms of Adaptation and Speciation: Integrating Genomic and Molecular Approaches). *Molecular Ecology*, 26: 193-207.

5.2 Poster abstracts and talks

Ferrari G., Talk at 7th International Symposium on Biomolecular Archaeology.

Florez-Rueda AM, oral presentation in the XIX International Botanical Congress, Shenzhen, China, July 13-29, 2017

Giesen A, No publications so far; poster presented at the Evolutionary Biology Meeting in Lausanne August 2015, Ecology and Behaviour Conference in Lyon July 2016, biology15 in Dübendorf and biology17 in Bern.

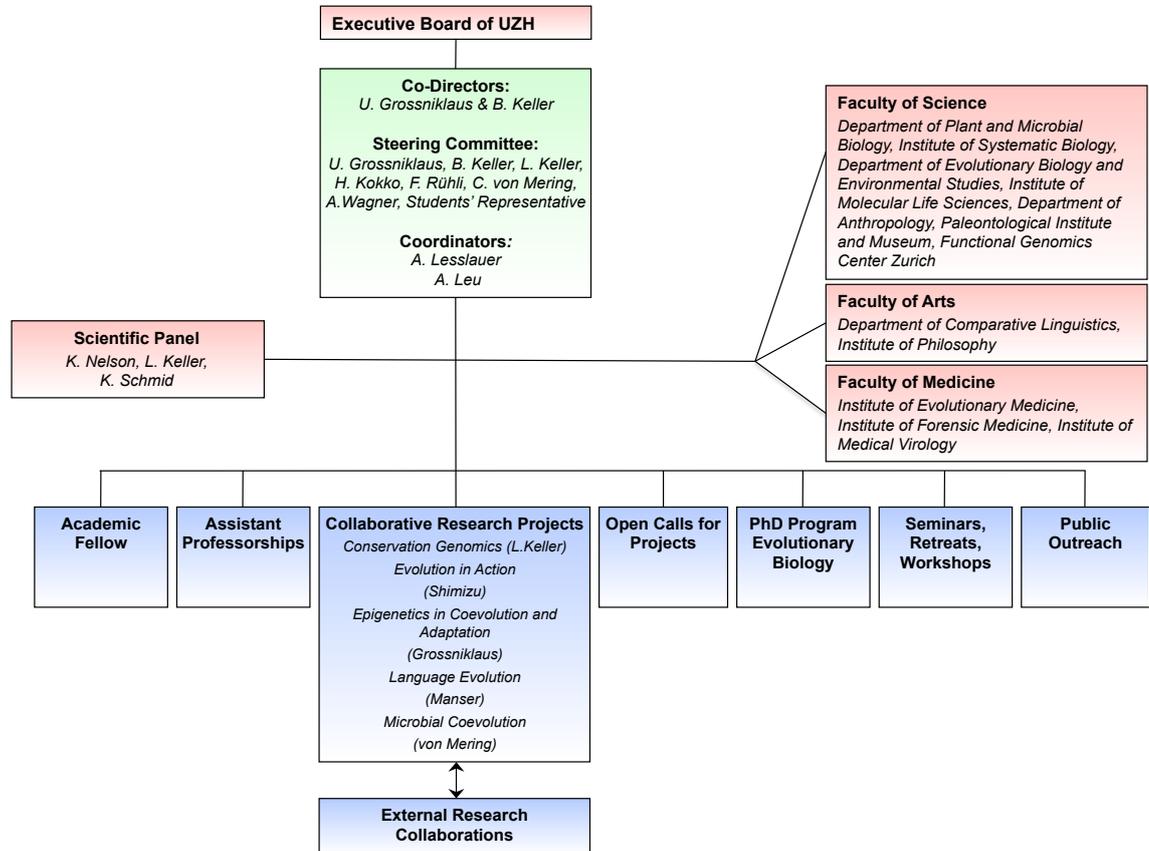
Izuno A, Kitayama K, Onoda Y, Tsujii Y, Shimizu KK, Isagi Y. Population genomic signature of environmental association in an ecologically divergent Hawaiian tree species. LS2 Annual Meeting, Zurich, February 2017. (Selected for a flash talk in the symposium "Plant Genomics" organized by Shimizu KK)

Leinweber A, Talk at ASM Conference on Mechanisms of Interbacterial Cooperation and Competition 2017, Washington, USA and poster presentation at ASM Microbe Conference 2016, Boston, USA

Möller-Steinbach Y, poster presentation at PSC symposium, Zürich.

Sprouffske K, presentation at post-doc day, 2016, Schloss Au and at Novartis Institute for Biomedical Research, 2016, Basel.

6 Structures



7 Third-Party Funds

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

Baumgartner M obtained a University of Zurich Forschungskredit for his Postdoc (6 months) (Suproject 1.1)

Ferrari G obtained a travel grant for PhD students from the Department of Evolutionary Biology and Environmental Science, UZH, CHF 500) (Suproject 2.1)

Aivelo T obtained a Fellowship from the Finish Research Council and Lemoine M obtained a Marie-Heim-Vögtlin Fellowship to work in the project. Grants have been obtained from the Baugarten Foundation and the Claraz Schenkung for fieldwork and consumables. (Subproject 2.2)

Aroras N group has been granted CHF 14'000 from the A.H. Schultz-Stiftung in 2016 to hire a bioinformatician from Jan to Mar 2017 to make genotype calls from raw sequence data and annotate polymorphisms. (Pilot Project 2016)

Shimizu K obtained funding from CREST (Core Research for Evolutionary Science and Technology) by Japan Science and Technology Agency (170,000,000 JPY for Shimizus groups in Zurich and Yokohama, corresponding to about 1'650'000 CHF, 2016-2022). Topic: Constructing models to confer environmental robustness by developing multiomics technology of polyploid species.

Shimizu K further obtained funding from MEXT (Ministry of Education, Culture, Sports, Science and Technology), Japan (38,150,000 JPY corresponding to about 370'000 CHF, 2016-2021). Topic: Determining the principles of the birth of new plant species: molecular elucidation of the lock-and-key systems in sexual reproduction.

(Subproject 2.4)

Giesen A obtained funding for field work from the Claraz Foundation (CHF 2000). De novo sequencing and bioinformatics of 4 *Sepsis* species at Beijing Genomics Institute was conducted and paid for by grants to Bonn University. (Subproject 2.6)

7.2 Funded Projects within the Profit-Center of the URPP Evolution in Action

- Subproject 1.1: Microbial Networks in Lake Zurich
 - Project leader: Jakob Pernthaler
 - Funding: CHF 65'700
- Subproject 1.2: Evolutionary Degeneration of an Obligate Symbiont
 - Project leader: Leo Eberl
 - Funding: CHF 65'700
- Subproject 2.1: Virulence evolution in past human pathogens
 - Project leader: Frank Rühli
 - Funding: CHF 65'700

- Subproject 2.2: Understanding Variation in *Borrelia* Resistance in Swiss Natural Host Populations
 - Project leader: Barbara Tschirren
 - Funding: CHF 65'700
- Subproject 2.3: Adaptation of a Fungal Pathogen to New Host Species
 - Project leader: Beat Keller
 - Funding: CHF 65'700
- Subproject 2.4: Hybrid Speciation and Male Invasion in Action in Switzerland
 - Project leader: Kentaro Shimizu
 - Funding: CHF 32'900
- Subproject 2.5: Speciation through Chromosomal Rearrangements in Wild House Mice in Switzerland
 - Project leader: Barbara König
 - Funding: CHF 65'700
- Subproject 2.6: Incipient Speciation Due to Thermal Adaptation or Sexual Selection in Sepsid Flies
 - Project leader: Wolf Blanckenhorn
 - Funding: CHF 65'700
- Subproject 3.1: Epigenetic Variation and Selection
 - Project leader: Ueli Grossniklaus
 - Funding: CHF 98'600
- Subproject 3.2: Epigenetics in Plant Adaptation
 - Project leader: Florian Schiestl
 - Funding: CHF 32'900
- Subproject 3.3: Epigenetics in Microbial Adaptation
 - Project leader: Owen Petchey
 - Funding: CHF 65'700
- Subproject 5.1: The evolutionary origins and selective conditions promoting the evolution of human language
 - Project leader: Marta Manser
 - Funding: CHF 65'700
- Subproject 6.1: Conservation Biology of the Alpine Ibex (Genomic Aspects)
 - Project leader: Lukas Keller
 - Funding: CHF 65'700
- Subproject 6.2: Conservation Biology of the Alpine Ibex (Transcriptomic Aspects)
 - Project leader: Andreas Wagner
 - Funding: CHF 65'700

Pilot Projects

- Pilot Project: The genomic basis of potentially ongoing evolution of selfing syndrome in *Cardamine amara*, an emerging model species for plant mating system evolution
 - Applicant: *Dr. Reiko Akiyama*
 - Funding: CHF 19'335
- Pilot Project: Exploring the trajectories and genomic consequences of the Walser expansion
 - Applicant: *Dr. Natasha Arora*
 - Funding: CHF 20'000

- Pilot Project: Cooperation or competition: Interactions of bacterial strains with different evolutionary background
 - Applicant: *Dr. Michael Baumgartner*
 - Funding: CHF 18'300
- Pilot Project: Testing the role of siRNAs in hybrid incompatibility, are they responsible for the drastic shift in allele-specific expression in hybrid seeds?
 - Applicant: *Dr. Ana Marcela Florez-Rueda*
 - Funding: CHF 18'700
- Pilot Project: The transcriptional basis of inbreeding depression and fitness rescue by prenatal maternal investment
 - Applicant: *Dr. Kate Ihle*
 - Funding: CHF 18'775
- Pilot Project: Title of project: Genetic bases of the adaptive radiation within a species revealed by the genome-wide polymorphism
 - Applicant: *Dr. Ayako Izuno*
 - Funding: CHF 19'780
- Pilot Project: Probing the epigenetic response to transposable elements
 - Applicant: *Dr. Kartal Önder*
 - Funding: CHF 19'732
- Pilot Project: Is competition between bacteria based on fixed or phenotypically plastic responses? - answers from a transcriptome study
 - Applicant: *Anne Leinweber, PhD Student*
 - Funding: CHF 15'300
- Pilot Project: Genetics of host adaptation of *Blumeria graminis* (powdery mildew)
 - Applicant: *Marion Müller, PhD Student*
 - Funding: CHF 20'000
- Pilot Project: Genome wide association study of heavy metal tolerance in *Medicago truncatula* and evolutionary genomics of metal tolerant nitrogen fixing rhizobia
 - Applicant: *Dr. Timothy Paape*
 - Funding: CHF 20'000
- Pilot Project: Distinct changes of floral morphology in *Mimulus aurantiacus* - Discovering underlying epigenetic regulatory DNA marks.
 - Applicant: *Dr. Yvonne Möller-Steinbach*
 - Funding: CHF 20'000