



Scientific Report of the URPP Evolution in Action

Reporting Year 2013

1 Management Summary

2013 was a successful starting year for the University Research Priority Program Evolution in Action. Sixteen research projects have been started in 2013, consistent with the project plan. These research projects were developed as PhD projects and link the areas of classical evolutionary biology, population genetics, ecology, and recent approaches in genomics. The projects thus naturally have an interdisciplinary orientation. This is also reflected in the interdisciplinary PhD committees, by now established for most of the PhD projects. Overall, the research projects of the URPP Evolution in Action bring together scientists from 24 research groups, 8 institutes, and 3 faculties of the University of Zurich.

The first annual retreat of the URPP Evolution in Action took place in July 2013 near Sarnen. It provided an overview of the large variety of research projects and was, at the same time, a lively get-together of UZH-scientists from diverse areas and institutes. A keynote lecture held by Ralf Sommer (MPI Tübingen) highlighted the potential of research at the boundaries of evolutionary and developmental biology, ecology, and population genetics.

The PhD students of the URPP Evolution in Action follow the PhD Program in Evolutionary Biology of the University of Zurich. In collaboration with this PhD program, the URPP Evolution in Action has started to develop new courses and teaching modules in areas that were not represented before in the curriculum. In 2013, we have initiated and supported two courses for the PhD program, both focusing on the use of new genomic technologies to address evolutionary questions.

Our first embedded bioinformatician got the bioinformatics support started from the very beginning of the URPP Evolution in Action. Besides the bioinformatics support of individual projects, a series of bioinformatics tutorials has been initiated, tailored to the needs of the PhD students and postdocs in the program.

We set out to establish activities and formats addressing the public from the very first year onwards. The URPP Evolution in Action was present at the *Scientifica* 2013 exposition with a well-attended booth. This year's main theme of the *Scientifica* was "Risk"; in line with this theme we showed three research projects of the URPP Evolution in Action under the common topic "Evolution of pathogens and immune systems". In 2013 we also established cooperation with the *Volkshochschule Zürich*, the adult learning center of the canton of Zurich. As a result, we will be able to present a series of lectures about evolutionary biology at this institution in 2014.

We have met our main goals for the first year of the URPP Evolution in Action and are very content with this start-up phase. We look forward to the continuation of our work in 2014 and thank the Executive Board of the University for supporting this future-oriented program.

2 Objectives

2.1 Objectives for the reporting year

N/A

2.2 Achieved objectives

N/A

2.3 Objectives for 2014

- Planning and realization of the **Second Retreat of the URPP Evolution in Action**, with a program featuring progress reports from all projects, a brainstorming session to generate new interdisciplinary project ideas, input lectures, and faculty and PhD students meetings.
- Establishment of a series of 1-day **Scientific Symposia** in Zurich
- Advertisement and planning for the **Academic Fellow Position**, foreseen to start in 2015
- Planning and realization of **Courses for the PhD Program** covering topics such as Next Generation Sequencing, Concepts of Evolutionary Biology, and Introduction to Evolutionary Biology
- Strengthening the **Bioinformatics Support** of the URPP Evolution in Action, with a second embedded bioinformatician position starting in 2014
- Continuation and consolidation of the **Bioinformatics Tutorial Program**
- Establishment of regular **PhD Students Meetings** in order to enhance interaction and election of the **PhD Students' Representative** who will join steering committee meetings
- Continuation of **Public Outreach Activities**: a lecture series for the *Volkshochschule Zürich* (the adult learning center of the canton of Zurich) about evolutionary biology is planned in May and June 2014
- Extension of the **Website of the URPP Evolution in Action** with new contents such as a section addressing the public and an internal section providing services to the members of the URPP Evolution in Action (mailing directory, download of documents).

3 Research

3.1 Research Projects

Six collaborative, interdisciplinary research projects – as outlined in the project proposal – started in 2013. By the end of 2013, 16 PhD students had taken up their scientific work within these six research projects. The progress and current status of each project is summarized below.

Project 1: Genomic Correlates of Microbial Co-Evolution

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” aims at the identification and characterization of ecological partnerships of microbes, using modern high-throughput molecular techniques.

Subproject 1.1: Microbial Networks in Lake Zurich

PhD student: Michael Baumgartner (Institute of Plant Biology, IPB); PhD Committee: Jakob Pernthaler (IPB), Leo Eberl (IPB), Rolf Kümmerli (IPB)

The two central aspects of the subproject are the elucidation of seasonal and spatial co-occurrence patterns of microbes in Lake Zurich and the evolutionary adaptation of a model bacterium from this lake to predation. We aim to identify associations of freshwater microbes that succeed in Lake Zurich at particular environmental settings, and to gain insight into evolutionary adaptations of microbes to top-down and bottom-up constraints. Partial 16S rRNA genes of the microbial assemblages from Lake Zurich have been sequenced in >150 samples, spanning a period of 2 years of biweekly sampling. An evolutionary experiment has been conducted in a model predator-prey system, and the genomes of bacterial strains isolated at 3 time points have been sequenced. A first analysis of Lake Zurich data points to unexpected and novel associations between microbes from distant lineages. An evolutionary trade-off between adaptation to predation and optimal substrate utilization was observed in the experimental system. The sequencing of microbial genomes has been more challenging than expected due to DNA quality issues.

Subproject 1.2: Evolutionary Degeneration of an Obligate Symbiont

PhD student: Marta Pinto (IPB); PhD committee: Leo Eberl (IPB), Kentaro Shimizu (Institute of Evolutionary Biology and Environmental Studies, IEBES), Rolf Kümmerli (IPB), Aurelien Carlier (IPB)

This subproject deals with the evolution of partnerships, specifically with the molecular consequences of co-evolution between obligate partners. By analyzing the genomes of bacteria naturally engaged in a closed relationship with their host plant, we seek understanding of the evolutionary determinants of reductive genome evolution, i.e. whether there is a level of determinism to gene loss. We completed the sequencing of the genomes of 8 phylogenetically related bacterial symbionts isolated from leaf nodules of *Rubiaceae* and *Myrsinaceae* species. All the genomes have the hallmarks of reductive genome evolution (small genome size, high proportion of pseudogenes, and insertion sequences) and we are in the process of analyzing the dN/dS ratio of conserved genes.

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

Project lead: Kentaro Shimizu (IEBES)

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” studies 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 (Centre for Evolutionary Medicine, ZEM, Medical Faculty); PhD committee: Kentaro Shimizu (IEBES), Frank Rühli (ZEM, Medical Faculty), Abigail Bouwman (ZEM, Medical Faculty), Christian von Mering (IMLS)

This subproject investigates the molecular evolution of human pathogens using archival and pathological tissue samples of the last two centuries. The ultimate goal of the project is to study the molecular evolution of DNA viruses and bacteria as well as to assess past human health in terms of co-infection patterns and pathogen loads using samples from European historic pathology and archival collections. Seventy-two formalin-fixed and in part paraffin-embedded samples from Austrian and British collections have been acquired and more samples are in the process of being obtained. Optimization of DNA extraction protocols for these samples is in progress, and PCR systems for the detection of different groups of DNA viruses have been designed. PCR inhibition caused by formaldehyde is evident, and DNA quality and concentration are similar to those of ancient samples. Since current methodology is designed for more recent and less damaged material, improvement is needed to better exploit the potential of such archival samples for retrospective molecular studies.

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

PhD student: Kevin Reeh (IEBES); PhD committee: Barbara Tschirren (IEBES), Kentaro Shimizu (IEBES), Beat Keller (IPB), Peter Deplazes (Institute of Parasitology, Vetsuisse Faculty)

We study interactions between wild living-rodents, ticks, and tick-transmitted *Borrelia* pathogens in the Swiss Alps, both at the phenotypic and genetic level. The ultimate goal is to understand how emerging pathogens shape the evolution of their hosts' immune system and how they contribute to the maintenance of genetic variation in natural populations. We performed fieldwork at 12 study sites in the Swiss Alps to collect data on pathogen prevalence, host infection status, and to isolate DNA for immunogenetic analyses. Genetic analyses of host immune genes and *Borrelia* pathogens are currently ongoing. We found that tick vectors occur at higher altitudes than has previously been reported. It indicates that the colonization of higher altitudes by ticks and tick-transmitted pathogens is ongoing, potentially due to climate change.

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

PhD student: Fabrizio Menardo (IPB); PhD committee (under planning): Beat Keller (IPB), Thomas Wicker (IPB), Kentaro Shimizu (IEBES)

This subproject investigates the evolution of new host specificity in *Blumeria graminis* grass powdery mildew. We aim at discovering the genetic modifications and mechanisms that allowed powdery mildew to colonize the new host Triticale. Sequencing of 4 isolates that grow on Triticale has been successfully accomplished, analysis of these sequences is in progress. DNA samples for 24 additional isolates growing on Triticale and rye have been submitted for sequencing. The main challenge will be

to identify a causal gene or a few causal genes mainly with evidence from association data. The number of samples might be a limiting factor.

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

PhD student: Alejandro Morales (IEBES); PhD committee (under planning): John Pannell (University of Lausanne), Thomas Wicker (IPB), Beat Keller (IPB), Kentaro Shimizu (IEBES)

We study the evolution of the coexistence of hermaphrodite and male individuals in a population, the so-called androdioecy. The ultimate goal of this project is to determine the genetic basis and geographical extent of androdioecy of *Cardamine amara* in Switzerland. Genotyping and analysis (with SSR markers) of 1000 individuals collected in 2013 are underway. Around 400 plants are in vernalization for crossing experiments.

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

PhD student: Sofia Grize (IEBES); PhD committee: Barbara König (IEBES), Anna Lindholm (IEBES), Kentaro Shimizu (IEBES)

We investigate how Robertsonian translocations, a kind of chromosomal rearrangement, could lead to reproductive isolation between populations within a mammalian species. The aim of the project is to understand the influence of Robertsonian translocations on hybrid fertility, gene flow, and behavioral reproductive isolation between chromosomally different populations of house mice. We will soon obtain the permissions for animal trapping and experiments, and our laboratory analysis methods have been adjusted for the experiments with wild house mice.

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

PhD student: Athene Giesen (IEBES); PhD committee: Wolf Blanckenhorn (IEBES), Kentaro Shimizu (IEBES), Rie Inatsugi-Shimizu (IEBES), Ernst Hafen (ETH Zürich)

This subproject 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. Preliminary experiments were conducted setting the stage for systematic investigations; flies were prepared and sent for *de novo* sequencing (BGI) in collaboration with groups in Bonn and Singapore, and resequencing of various populations at the Functional Genomics Center Zurich (FGCZ) are currently underway.

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

Project lead: Ueli Grossniklaus (IPB)

The third 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

PhD student: Klara Kropivsek (IPB); PhD committee: Ueli Grossniklaus (IPB), Bernhard Schmid (IEBES), Christian Hardtke (University of Lausanne)

We investigate whether the selection of epigenetic variation contributes to phenotypic responses under selection, specifically whether a change in *Arabidopsis* trichome density caused by aphid herbivory over five generations has an epigenetic basis and is heritable without selection. If we can demonstrate a contribution of epigenetic variation to trichome density, we will identify candidate genes by whole-genome methylome and transcriptome analyses, and try to establish causality by altering the DNA-methylation status of selected candidate genes. Plants from populations that were

subjected to five generations of selection have been genotyped, grown in a randomized block design, phenotypic data has been collected on a daily basis (recordings of the day of bolting; number of rosette leaves, diameter of rosette at day of bolting; scanning and microscopy of leaves for size and trichome numbers), and plant material has been stored for molecular analyses. The phenotypic data is currently being processed to test our hypothesis that phenotypic changes occurred during selection in genetically identical plants, thus having an epigenetic basis. In case our hypothesis about increased trichome density as an epigenetically inherited trait is wrong, we will investigate whether the defense at the chemical level (glucosinolate response) occurred in genetically identical plants and can thus be linked to epigenetic changes.

Subproject 3.2: Epigenetics in Plant Adaptation

PhD student: Roman Kellenberger (Institute of Systematic Botany, ISB); PhD committee: Florian Schiestl (ISB), Phillip Schlueter (ISB), Heather Kirk (ISB), Kentaro Shimizu (IEBES), Ueli Grossniklaus (IPB)

This subproject investigates the link between epigenetic markers and floral signals that mediate plant-pollinator interactions in *Brassica rapa*. We aim at determining whether epigenetic mechanisms can influence plant-pollinator interactions, whether these mechanisms are partly responsible for plastic changes in floral signaling, and whether relevant induced epigenetic changes can be heritable. We have carried out genome-wide demethylation of *Brassica rapa* in order to determine whether methylation states can influence floral signals. We also used methylation-sensitive AFLP markers to determine whether methylation markers and floral signals are influenced by herbivory, and we are currently in the planning stages of a bisulfite-sequencing project that will aim to link specific epimutations to relevant floral signals. We found evidence that the expression of several floral volatile compounds, including breakdown products of glucosinolates, and several nitrogen-containing compounds, are epigenetically regulated. We also showed that genome-wide methylation patterns differ between leaves and flowers, and between herbivore-damaged and undamaged plants.

Subproject 3.3: Epigenetics in Microbial Adaptation

PhD student: hiring in progress, PhD supervisor: Owen Petchey (IEBES)

The subproject concerns how epigenetic mechanisms contribute to the adaption of microbes to changing environments, in particular changes in resource availability and the abundances of competitors and predators. The ultimate goal is enhancing prediction about evolutionary responses to environmental change. The first preparatory experiment is completed and we recently received CHIP- and RNA-Seq data. The hiring of a PhD student for this subproject is in progress.

Project 4: Microevolution of Signaling Pathways relevant for Human Disease

Project lead: Alex Hajnal (IMLS)

Cell growth and differentiation are known to be controlled by a network of conserved signaling pathways that play a key role in the etiology of human disease. This research project addresses the question how small genetic variation in signaling pathways, between related species or between individuals of the same species, generates phenotypic diversity.

Subproject 4.1: Microevolution of the Ras, Wnt, and Notch Signaling Pathways in *C. elegans*

PhD student: Tobias Schmid (IMLS); PhD committee: Ueli Grossniklaus (IPB), Homayoun Bagheri (IEBES), Ralf Sommer (Max Planck Institute Tübingen), Alex Hajnal (IMLS)

We are studying the natural variation in signaling pathways that control cell death and differentiation in *C. elegans*. Our goal is to characterize polymorphic genes and variations in protein

abundance between different *C. elegans* wild isolates to identify new regulators of the Wnt, RAS/MAPK and NOTCH signaling pathways. We have developed a proteomics platform that allows us to simultaneously quantify multiple protein levels in different *C. elegans* isolates. In addition, we are in the process of cloning modifiers of the EGFR/RAS/MAPK pathway identified by QTL mapping of recombinant inbred lines between the *C. elegans* strains Bristol and Hawaii. Molecular cloning of QTLs in *C. elegans* is a time-consuming and labor-intensive project. However, we think it is worthwhile to invest our energy into this approach. For example, we have gained important insights by identifying natural variations in a monoamine oxidase that acts as systemic regulator of the MAP kinase in *C. elegans*.

Subproject 4.2: Systems Genetics of the Wnt Pathway in *Drosophila*

PhD student: Fabian Jenny (IMLS); PhD committee: Konrad Basler (IMLS), Christian von Mering (IMLS), Mark Robinson (IMLS)

We intend to learn more about the diversity of the Wnt signaling cascade in natural populations, by using a systems genetics approach in *Drosophila melanogaster*. To this aim, we assess the diversity of Wnt signaling in a natural *Drosophila melanogaster* population and deduce insights into the evolution of such signaling cascades. A pilot study with 30 lines from the *Drosophila* Genetic Reference Panel (DGRP) was started, where we tried to measure differences in Wnt target gene abundance by qRT-PCR. Reproducibility is an issue in the pilot study. The main problem might be environmental factors that influence Wnt signaling output.

Subproject 4.3: Systems Genetics of Growth and Size Regulation

PhD student: Sibylle Vonesch (ETH Zürich); PhD committee: Trudy MacKay (University North Carolina), Sven Bergman (University of Lausanne), Ernst Hafen (ETH Zürich)

To identify how the genome determines body size in natural populations we perform genome wide association (GWA) studies for wing size on 150 inbred *Drosophila* lines that are derived from a natural population. We want to understand how phenotypic variability is generated in spite of the fact the signaling networks are highly conserved throughout evolution, and how genetic variability between individuals generates phenotypic diversity. The GWA study on the 150 lines is completed and the manuscript is in preparation. We are currently conducting artificial selection experiments on the same population of *Drosophila* lines to investigate how the genome produces phenotypic traits under selection. We are amazed how some phenotypic traits (e.g. wing size) are sensitive to the slightest variations in environmental conditions (e.g. same food cooked on different days) in spite of almost perfect control. This is an important warning to the inferences in human GWA studies.

Project 5: The Evolution of Language: an Integrative Approach

Project lead: Marta Manser (IEBES)

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 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: The evolutionary origins and selective conditions promoting the evolution of human language

PhD student: Katie Collier (IEBES); PhD committee: Marta Manser (IEBES), Carel van Schaik (Anthropological Institute and Museum, AIM), Balthasar Bickel (Dept. of General Linguistics, Faculty of Arts), Simon Townsend (IEBES)

With an integrative and empirical approach, we aim to better understand how language, as one of the key stand-out features of human biology, may have evolved. This project is a highly collaborative effort among research groups from different faculties (MNF/Phil). We submitted a review article (in revision) proposing a new hypothesis regarding the evolution of combinatoriality in language, and conducted 3 months of fieldwork in South Africa on two highly vocal mongoose species in search of proto-combinatorial capacities in non-primate animals. This collaboration, including anthropologists, linguists, and animal communication biologists has been highly stimulating and, through regular meetings over the last year, generated new 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, and this is currently under revision in a biological sciences journal.

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

Project lead: Lukas Keller (IEBES)

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 (IEBES); PhD committee: Lukas Keller (IEBES), Andreas Wagner (IEBES), Arpat Ozgul (IEBES), Simon Aeschbacher (University of California Davis)

PhD student, subproject 6.2: Kasia Sluzek (IEBES); PhD committee (under planning): Lukas Keller (IEBES), Andreas Wagner (IEBES), remainder to be decided

The aim of these two subprojects is to characterize genomic and transcriptomic signatures of past population bottlenecks in this species that may be associated with inbreeding depression and loss of adaptive potential. One of the PhD projects is focusing on the genomic aspects, the second on the transcriptomic aspects of conservation biology questions in the Alpine Ibex. Both PhD students have conducted preparatory work and the sampling of populations will start in 2014.

3.2 Scientific Activities

Scientific Retreat

In July 2013, the first URPP Evolution in Action Retreat took place in Sarnen, with 41 participants. All research projects of the URPP Evolution in Action were presented, mostly by senior scientists but also by some of the newly recruited students, with a special focus on the scientific background of the projects. The aim was to make the scientific questions of the diverse fields understandable to all, and to enable discussion across different disciplines. The presentations were excellent and followed by lively discussions. The keynote speaker, Ralf Sommer (Max Planck Institute Tübingen), gave an inspiring talk about his interdisciplinary research at the boundaries of evolutionary and developmental biology, ecology and population genetics. Being the first get-together of all members of the URPP Evolution in Action, the retreat was also the opportunity to discuss general aspects. We discussed issues such as focus and topics of seminars and symposia series in the URPP Evolution in Action, how to support the PhD students such that they can benefit fully from the networking possibilities within the URPP, organization of the bioinformatics support, etc. Various meetings and

workshops were held during the retreat to gather inputs regarding these questions; the outcome of these meetings proved to be an excellent basis for the further planning of the activities of the URPP Evolution in Action.

Bioinformatics tutorials

Based on the inputs from the URPP Evolution in Action members and PhD students, several bioinformatics tutorials took place from October onwards. These tutorials were organized and taught by Stefan Wyder, embedded bioinformatician of the URPP Evolution in Action. In detail, the following 3-hour-tutorials were offered:

- Linux Bash shell Part 1: Linux basics, command line, filter philosophy, working with files and directories, working with text files, piping, redirection.
- Linux Bash shell Part 2: Connecting to server, installing and running scripts, permissions, automating tasks (scripting)
- Next Generation Sequencing Part 1
 - Introduction, simple workflow, possible biases, sequencing errors, main file formats, samtools, quality control, IGV genome browser
 - Exercises: analyzing a bacterial RNA-seq experiment: quality control of the reads, mapping, visualizing

Each of the tutorials was held twice such that all interested persons could participate. Every tutorial consisted of a theoretical introduction to the topic, followed by two hours of guided exercises. The tutorials were very well attended, with 6 to 13 participants in every class, and a feedback survey with questions regarding class size, content, difficulty and pace of the tutorials was very positive. The participants were mostly PhD students of the URPP Evolution in Action, but also more senior scientists and guests from neighboring institutes attended the tutorials. The series is being continued in 2014.

Courses for the PhD Program in Evolutionary Biology

Two 2-days-courses within the PhD Program in Evolutionary Biology were initiated and/or supported in 2013 by the URPP Evolution in Action.

- “Next-Generation Sequencing (NGS): assembly, annotation and transcriptomes (BIO610)”: This 2-days-course was organized in the spring term 2013 by Kentaro Shimizu and taught together with Jun Sese (Tokyo Institute of Technology), Satoru Akama (Tokyo Institute of Technology), Masaomi Hatakeyama (IEBES, UZH and FGCZ, UZH/ETHZ) and Rie Shimizu-Inatsugi (IEBES, UZH). Eight PhD students of the URPP Evolution in Action attended this course, which is the majority of the URPP PhD students who were already hired at this time. The course was open to all students of the PhD program in Evolutionary Biology, as well as to the Plant Science PhD program. In total, 18 PhD students attended the course. The URPP Evolution in Action supported this course financially by taking over the teaching assignment for the external speakers.
- “Introduction to genome-wide association studies (BIO683)”: this 2-days-course was organized in the fall term 2013 by Ueli Grossniklaus and taught together with Nuno Pires (IPB, UZH), Arthur Korte (Gregor Mendel Institute Vienna), Timothy Paape (IEBES, UZH) and Kentaro Shimizu (IEBES, UZH). Nine of the URPP Evolution in Action PhD students attended this course. In total, 17 participants attended the course, among them guests from ETHZ, Agroscope, and the University of Lausanne. This course was initiated by the URPP Evolution in Action and supported financially as well as on the planning and organizational level.

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: at this time, the URPP Evolution in Action funds salaries and research consumables for 16 PhD students, thereby contributing substantially to their career development on the financial level.

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.

The embedded bioinformatician of the URPP Evolution in Action supported several PhD projects of the URPP already in this first year of the program. In doing so, the bioinformatician himself is expanding his research experience, and the wealth of data available from several projects allows for a productive own research activity. We have taken care to enable a close contact between the embedded bioinformatician of the URPP Evolution in Action and the bioinformatics community at the UZH. E.g., the URPP Evolution in Action bioinformatician regularly works one day per week in the von Mering group (IMLS, UZH), a renowned bioinformatics research group, and also takes part in the weekly meeting of this group. 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 answer the needs of the PhD students in our community and that allow them to become researchers with a comprehensive understanding of the fields of evolutionary biology, genomics, population genetics, and ecology (see also chapter 3.2). We are in the process of setting up a series of Minisymposia, where the PhD students within the URPP Evolution in Action will have the possibility to invite keynote speakers from abroad, thereby gaining experience and new contacts who may well become mentors for their further career.

The PhD students in the URPP Evolution in Action have the possibility to bring in their view in various ways. At the first retreat, they were invited to formulate their needs in a workshop specifically dedicated to this aim. Furthermore, the PhD students have the possibility to delegate a representative to the steering committee meetings of the URPP Evolution in Action.

4.2 Gender Equality Development

Hiring of personnel is on an equal opportunity basis and according to the UZH's hiring guidelines. The observance of the "Gender Equality Action Plan UZH" is a matter of course. Wherever possible, we support efforts to create a family-friendly work environment, for instance by enabling part-time work for young fathers and mothers.

5 Publications

None so far.

6 Third-Party Funds

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

SNSF

- SNSF project funding, Div. I-III (details: <http://www.research-projects.uzh.ch/p17854.htm>)
 - Project leader: Kentaro Shimizu
 - URPP Evolution in Action project name: Hybrid Speciation and Male Invasion in Action in Switzerland
 - Project type: Subproject 2.4

Industry

- PSC Syngenta Fellowship “Causes and consequences of epigenetic variation in plant interactions with pollinators and herbivores” (CHF 50'000)
 - Project leaders: Florian Schiestl, Ueli Grossniklaus, Heather Kirk
 - URPP Evolution in Action project name: Epigenetics in Plant Adaptation
 - Project type: Subproject 3.2
- PSC Syngenta Fellowship “Epigenetic Contributions to Hybrid Vigor in Apomictic Offspring” (CHF 150'000)
 - Project leaders: Ueli Grossniklaus, Bernhard Schmid
 - URPP Evolution in Action project name: Epigenetic Variation and Selection
 - Project type: Subproject 3.1

Others

- Research grant by the Baugarten Stiftung (CHF 26'766)
 - Project leader: Barbara Tschirren
 - URPP Evolution in Action project name: Understanding Variation in *Borrelia* Resistance in Swiss Natural Host Populations
 - Project type: Subproject 2.2
- Young Investigator Award of Human Frontier Science Program (details: <http://www.research-projects.uzh.ch/p15728.htm>)
 - Project leader: Kentaro Shimizu
 - URPP Evolution in Action project name: Hybrid Speciation and Male Invasion in Action in Switzerland
 - Project type: Subproject 2.4
- Promotor-Stiftung (CHF 3'660)
 - Project leader: Barbara König
 - URPP Evolution in Action project name: Speciation through Chromosomal Rearrangements in Wild House Mice in Switzerland
 - Project type: Subproject 2.5

6.2 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 62'500
- Subproject 1.2: Evolutionary Degeneration of an Obligate Symbiont
 - Project leader: Leo Eberl
 - Funding: CHF 62'500
- Subproject 2.1: Virulence evolution in past human pathogens
 - Project leader: Frank Rühli
 - Funding: CHF 62'500
- Subproject 2.2: Understanding Variation in *Borrelia* Resistance in Swiss Natural Host Populations
 - Project leader: Barbara Tschirren
 - Funding: CHF 31'250
- Subproject 2.3: Adaptation of a Fungal Pathogen to New Host Species
 - Project leader: Beat Keller
 - Funding: CHF 31'250
- Subproject 2.4: Hybrid Speciation and Male Invasion in Action in Switzerland
 - Project leader: Kentaro Shimizu
 - Funding: CHF 62'500
- Subproject 2.5: Speciation through Chromosomal Rearrangements in Wild House Mice in Switzerland
 - Project leader: Barbara König
 - Funding: CHF 31'250
- Subproject 2.6: Incipient Speciation Due to Thermal Adaptation or Sexual Selection in Sepsid Flies
 - Project leader: Wolf Blanckenhorn
 - Funding: CHF 31'250
- Subproject 3.1: Epigenetic Variation and Selection
 - Project leader: Ueli Grossniklaus
 - Funding: CHF 62'500
- Subproject 3.2: Epigenetics in Plant Adaptation
 - Project leader: Florian Schiestl
 - Funding: CHF 31'250
- Subproject 3.3: Epigenetics in Microbial Adaptation
 - Project leader: Owen Petchey
 - Funding: CHF 31'250
- Subproject 4.1: Microevolution of the Ras, Wnt and Notch Signaling Pathways in *C. elegans*
 - Project leaders: Alex Hajnal, Michael Hengartner
 - Funding: CHF 62'500
- Subproject 5.1: The evolutionary origins and selective conditions promoting the evolution of human language
 - Project leader: Marta Manser
 - Funding: CHF 62'500

- Subproject 6.1: Conservation Biology of the Alpine Ibex (Genomic Aspects)
 - Project leader: Lukas Keller
 - Funding: CHF 62'500
- Subproject 6.2: Conservation Biology of the Alpine Ibex (Transcriptomic Aspects)
 - Project leader: Andreas Wagner
 - Funding: CHF 62'500

7 Structures

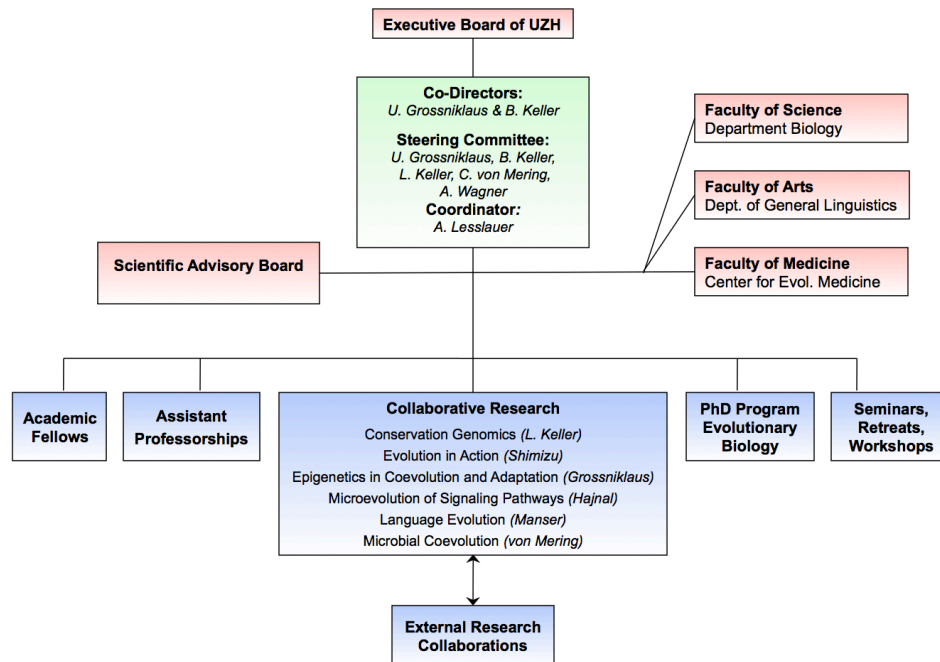


Figure 1: Organizational chart of the URPP Evolution in Action