Scientific Report of the URPP Evolution in Action: From Genomes to Ecosystems

Reporting Year 2014

1 Management Summary

The second year of the URPP Evolution in Action was characterized by strengthening and improving collaborations in research, increasing teaching activities, and significant progress in the scientific projects funded by the URPP Evolution in Action. Sixteen research projects were ongoing within the larger framework of six themes, mostly in form of PhD theses projects. Most of these projects are interdisciplinary, as reflected by the PhD committees that consist of members from different institutes or even different faculties of UZH. Overall, the research projects bring together scientists from 24 research groups, eight institutes, and three faculties of UZH: the Faculty of Sciences, the Medical Faculty, and the Faculty of Arts. One of the six research themes was terminated at the end of 2014 due to lack of sufficient integration of the projects of this theme into the URPP Evolution in Action. In two research projects the work is being continued by postdocs instead of the PhD students who have left the project. Neither remaining funds nor time were sufficient to start new PhD theses but the funding of postdocs will allow us to reach the goals.

The second annual retreat of the URPP Evolution in Action took place in June 2014 in Diessenhofen am Rhein. All research projects were presented to the 50 participants, and Henrik Kaessman from the Center for Integrative Genomics & the Swiss Bioinformatics Institute gave an inspiring keynote talk on molecular evolution. Furthermore, we had an input talk from URPP member Balthasar Bickel on linguistics and biology.

With regard to education, the emphasis in 2014 was on teaching at the graduate level. In particular, we organized a number of "Bioinformatics Tutorials", mostly for PhD students, to ensure integration of the most up-to-date bioinformatics analysis tools into the different projects. These tutorials were given by the two embedded bioinformaticians of the URPP Evolution in Action, the second of whom was hired at the beginning of 2014. Each tutorial was repeated twice and consisted of a theoretical introduction and guided exercises. In addition, several courses for PhD students were held, and a scientific mini-symposium in conservation biology was organized.

To promote young scientists, an open call for research projects was announced in autumn 2014. In December, the steering committee evaluated 18 applications mostly from PhD students and young postdocs, and awarded six of them with maximally CHF 20'000. High-risk projects as well as pilot studies were preferentially selected.

The position of an Academic Fellow was advertised in November 2014, targeting young postdocs. The research of the Academic Fellow will be completely independent, but has to be linked to the research themes of the URPP Evolution in Action. A successful candidate was chosen from a selection of five invited candidates in March 2015. Furthermore, in 2014 the first steps were taken to hire a non-tenure track Assistant Professor financed through the URPP Evolution in Action.

The URPP Evolution in Action is highly popular at UZH and we received and granted applications for membership in the URPP Evolution in Action from five colleagues.

Several public outreach activities were organized by the URPP Evolution in Action. The most important was a series of lectures in a course on evolution of the "Volkshochschule" with speakers from the URPP.

2 Objectives

2.1 Objectives for the reporting year

Below is the list of objectives for 2014 as provided in last year's report:

- 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 an Academic Fellow Position, foreseen to start in 2015
- Planning and realization of Courses for the PhD Program in Evolutionary Biology 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 Student 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, e.g. public and an
 internal sections providing services to the members of the URPP Evolution in Action (mailing
 directory, download of documents).

2.2 Achieved Objectives in 2014

- The Second Retreat of the URPP Evolution in Action, which took place in June 2014 in Diessenhofen am Rhein, was a great success. Progress reports of all current research projects funded by the URPP Evolution in Action provided an overview of our ongoing research activities. Balthasar Bickel from the Department of Comparative Linguistics gave an input talk about the great potential of interdisciplinary collaborations between linguistics and biology. His presentation led to lively discussions and, in the meantime, gave rise to new research initiatives across the borders of the Faculties of Arts and Science. Henrik Kaessmann from the Institute of Integrative Genomics (University of Lausanne) held a fascinating keynote lecture about his research in evolutionary genomics. Both at a brainstorming session and during the social program, animated discussions and interactions took place between all participants, across the borders of disciplines and seniority.
- A first pilot Scientific Minisymposium was successfully held in March 2014 in Zurich, featuring talks held by Mark Beaument (University of Bristol) and Mike Bruford (Cardiff University), as well as a half-day practical course taught by the speakers.
- The Search Committee for the Academic Fellow Position was elected at the Faculty Meeting during the second retreat, consisting of eight members from various research groups of the URPP Evolution in Action, including representatives of the professors, junior group leaders, and PhD

students. The position was advertised in late fall and we received a large number of very good international applications. The successful candidate was selected in March 2015 and will start the position in summer.

- A Course for the PhD Program Evolutionary Biology covering the topic of Next Generation Sequencing was organized spring term 2014. Moreover, several of the professors who as a result of the URPP Evolution in Action are newly associated with the PhD Program in Evolutionary Biology participated in the course "Topics in Evolutionary Biology" (Bio554).
- The Bioinformatics Support of the URPP Evolution in Action was greatly strengthenedby hiring a second embedded bioinformatician who started in February 2014. Beyond basic bioinformatics support service on request, regular one-to-one meetings of PhD students with the embedded bioinformaticians were held to maximize accessibility to the bioinformatics support of the URPP Evolution in Action. Furthermore, a close contact to the Functional Genomics Center Zurich (FGCZ) was established to create additional synergies.
- The Bioinformatics Tutorial Program was continued and consolidated. These tutorials, tailored to
 the needs of the PhD students and open to all members of the URPP Evolution in Action, were well
 attended and got excellent feedback.
- The PhD Students' Representative was elected in January 2014 and since then serves as a
 member of the Steering Committee and the Faculty Meeting of the URPP Evolution in Action.
 Regular PhD Students Meetings were established and are now being held and organized
 independently by the PhD students peer group, including both scientific and social events.
- A series of regular Social Events (informal get-togethers) was initiated to enhance interactions within the community of the URPP Evolution in Action.
- Public Outreach Activities were successfully continued with a lecture series for the Volkshochschule Zürich (the adult learning center of the canton of Zurich) about evolutionary biology. The lecture series took place in May and June 2014, with an attractive program of lectures about various topics regarding evolution. These presentations were held by five members of the URPP Evolution in Action and two invited experts. The lecture series was well attended, led to lively discussions with the public audience, and received very good feedback.
- The first Open Call for Research Projects was issued in fall 2014. Its aim is to promote young scientists by supporting innovative pilot projects. The steering committee evaluated 18 applications mostly from PhD students and young postdocs, and awarded six of them with maximally CHF 20'000. High-risk projects as well as pilot studies were preferentially selected.
- The Recruiting Process for the non-tenure track Assistant Professor Position of the URPP Evolution in Action was initiated by putting together a search committee.
- We have set up the opportunity for all UZH group leaders to become officially affiliated as Members of the URPP Evolution in Action. Within six months, we have received as many as five applications from both the Faculty of Science and Arts. We could thus integrate seven new groups in our community that provide valuable input and further strengthen our growing network within the URPP Evolution in Action community.

2.3 Objectives for 2015

- Planning and realization of the Third 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. The retreat 2015 will be combined with the site visit of the Scientific Panel of the URPP Evolution in Action. Thereby we would like to provide a comprehensive overview of our research projects to the members of the Scientific Panel as well as to give them the opportunity to directly meet with all our members and PhD students.
- Continuation and further development of the Seminar Series of the URPP Evolution in Action that takes places at various UZH institutes.
- Organization of further Scientific Minisymposia and small Workshops is specific areas of evolutionary biology, primarily organized by PhD students and postdocs.
- Start of the Academic Fellow Position of the URPP Evolution in Action.
- Advertisement and planning for the non-tenure track Assistant Professor Position, foreseen to start in 2016.
- Second Open Call for Research Projects to promote young scientists by supporting innovative and/or high-risk pilot projects, to be issued in fall 2014.
- Planning and realization of new Courses for the PhD Program covering topics such as Next Generation Sequencing, Concepts of Evolutionary Biology, and Introduction to Evolutionary Biology.
- Continuation and consolidation of the highly successful Bioinformatics Tutorial Program and the bioinformatics support services.
- Continuation of regular PhD Students Meetings to enhance interaction among students, research projects, and institutes of the URPP Evolution in Action.
- Organization of Social Events (excursions, informal get-togethers) to further enhance interaction within the URPP Evolution in Action community.
- Continuation of **Public Outreach** initiatives, including the planning of a future 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 Research Projects

In 2014, 16 subproject within the framework of six collaborative and interdisciplinary research projects on different themes in evolutionary biology were being conducted within the URPP Evolution in Action. Owing to the overarching goal of URPPs to educate a next generation of scientists with broad competences for combining molecular and computation approaches with evolutionary questions, the vast majority of the workforce was made up of 13 PhD students, while only two URPP-funded researchers are postdocs. In agreement with the leaders of Project 4, the Steering Committee of the URPP Evolution in Action decided to terminate Project 4 at the end of 2014 because of a failure to recruit new PhD students for the funded subprojects and the limited integration in, and contribution to, the URPP Evolution of Action. 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 Co-Evolution

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

Historically, microbes have been viewed as largely independent organisms. Currently, this view is being challenged because recent evidence hints 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), Christian von Mering (Institute of Molecular Life Sciences, IMLS)

The two aspects of the subproject are the elucidation of spatiotemporal co-occurrence patterns of microbes in Lake Zurich and the evolutionary adaptation of a model bacterium from this lake to protistan predation. We aim to develop a strategy to reconstruct diversity and co-occurrence patterns in environmental samples more accurately than by current approaches, and to gain insight into evolutionary adaptations of microbes to top-down and bottom-up constraints. We have developed a novel strategy for the analysis of microbial diversity from high throughput tag sequencing data that has the potential to replace the traditional distance-based clustering. Experiments on bacterial strains evolved with and without predators revealed distinct fitness differences that can in part be related to genomic modifications. The weaknesses of current methodological approaches for microbial diversity analysis have forced us to focus more strongly on method development. In our experimental system, the exposure of bacterial strains to predation has repeatedly induced massive genome streamlining.

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 coevolution between obligate partners. By analyzing the genomes of bacteria naturally engaged in a closed relationship with their host plant, we seek to understand the evolutionary determinants of reductive genome evolution, i.e. whether there is a level of determinism to gene loss. Marta Pinto started her PhD project in Jan. 2013 and has now completed the sequencing of the genomes of eight 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). Surprisingly, we find signatures of recent horizontal gene transfer events within the core genomes of the symbiotic bacteria, suggesting that genome reduction and gene flow are not mutually exclusive.

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 evolution of human pathogens using historical and ancient soft tissues. The ultimate goal is to establish a workflow for the use of fixed specimens for reconstructing and investigating historical pathogen genomes. Sampling has been concluded and methodologies for obtaining DNA from fixed tissues are being developed. Shot-gun sequencing of mummified tissues is ongoing. Currently, the major problems in this subproject are delays due to changes in the laws governing the handling of human tissues and long waiting times for NGS services at the FGCZ.

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

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

The project investigates how resistance mechanisms evolve in a natural rodent-*Borrelia* system. We aim to identify molecular mechanisms underlying adaptive processes in host-parasite interactions. We have performed large-scale field sampling in 12 rodent populations along altitudinal gradients in Graubünden, determined the prevalence of *Borrelia* infection, and sequenced candidate immune genes in hosts. In a next step, we plan to complement the bottom-up candidate gene approach with a top-down NGS approach. The PhD student Kevin Reeh discontinued working on this project after 1.5 years. He was replaced by postdoc Luca Cornetti to continue the project.

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

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

The general goal of the project is to investigate the evolution of the different forms of grass powdery mildew (*Blumeria graminis*), a fungal pathogen of cereals. In particular, we are investigating the adaptation of *B. graminis* to the new host triticale, a human-made cereal crop species originally immune to this disease when triticale was first commercially grown in the 1960ies. Based on the genome sequences of strains with different host ranges, we could show that the new pathogen originated through hybridization of two other pre-existing forms specialized on different hosts. A publication will be soon submitted. This finding

represents a major progress in our understanding of evolution of new host specificities in powdery mildew and is one of the best-documented reports of the emergence of a new fungal pathogen through hybridization. To elucidate the genetic mechanisms of the evolution of the new disease, additional experiments have to be done. As a first step, we crossed two isolates with different host range. Based on the segregation of host specificity in the progeny we want to analyze and identify the genetic determinants of the host specificity.

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

Postdoc Hiromi Matsumae (starting April 2015);, supervised by Kentaro Shimizu (IEBES), mentors: Beat Keller (IPB), John Pannell (University of Lausanne)

We study recent speciation by genome duplication and evolution of breeding systems. The ultimate goal is to reveal the molecular basis of rapid adaptive evolution in polyploid speciation and the evolution of breeding systems using interdisciplinary methods encompassing genome assembly, re-sequencing, field and lab experiments. An efficient bioinformatics workflow to study polyploid species is established (Akama et al. 2014). Sequencing and data analysis of the genome assembly and the re-sequencing of 25 individuals of the diploid *Cardamine amara* is ongoing. Because the PhD student discontinued his thesis, the project was conducted *ad interim* by a several lab members (Tedder et al. 2015; Kubo et al. 2015; Bachmann, MSc Thesis). Postdoc Hiromi Matsumae will take over the re-sequencing project in April 2015 and expand the scope to start a collaboration with Prof. Balthasar Bickel (project 5) and Prof. Frank Rühli (project 2) for the integrated study of language evolution, population demography, and ancient DNA.

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), Ueli Grossniklaus (IPB)

We aim to better understand the causes and consequences of variation in chromosomal arrangements for reproductive isolation between populations of house mice. We investigate in the field and with experimental lab work whether new species of house mice are in the process of forming as a result of the extraordinary variation in chromosomal arrangements found in wild house mouse populations in Switzerland. Data collection for a long-term laboratory experiment to investigate reproductive isolation has nearly been completed. SNP analyses of field-caught wild mice are underway. We have found that male hybrids of adjacent populations (10km apart) of house mice are completely sterile, while female hybrids have very low fertility or are sterile. Surprisingly, back-crossing of female hybrids to a parental population fully restores fertility, and we are currently investigating the mechanism underlying this phenomenon.

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 (IMLS & 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 genotype-phenotype relationships. Flies of four *Sepsis* spp. Were prepared and sent for *de novo* sequencing to the Beijing Genomics Institute in collaboration with groups in Bonn and Singapore. Furthermore, the main hybridization experiment of continental populations and the main population genetic F_{st} assessment are almost completed. In the near future, we will re-sequence the flies in collaboration with the FGCZ, and the sample collection for this has already been completed. Overall, good progress was made, despite some delays related to sequencing delays and personal issues. The PhD student accrued all required credit points and is involved in teaching ReproBio361 and EvoBio351.

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

Project lead: Ueli Grossniklaus (IPB)

Traditionally, epigenetic variation has not been given much importance in ecological and evolutionary processes despite their 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

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

We are investigating whether the selection of epigenetic variation contributes to phenotypic responses under selection. Specifically, we ask whether a change in trichome density observed after several generations of aphid herbivory is due to epigenetic variation, which could serve as a basis for epigenetic 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 differences in how one genotype can respond to selection by different aphid species. As we could indeed demonstrate a contribution of epigenetic variation to trichome density, we now aim at identifying candidate genes by whole-genome methylome and transcriptome analyses. We are currently preparing the libraries for methylome analyses of individual plants from the aphid-treatment groups. Should the signatures of selecting epigenetic variation for trichome density be weak or absent, we will investigate whether epigenetic variation contributed to their glucosinolate response, which was also shown to change during the selection regime

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)

The aim of this project is to decipher the role of epigenetic mechanisms in plant adaptation to environmental changes, using a plant-herbivore interaction model. We are assessing the induction, function, and transmission of epigenetic changes in short-term adaptation of *Brassica rapa* to different herbivore species. Currently, the herbivore treatments are ongoing and the molecular work is expected to start in the course of 2015. Interestingly, herbivore-specific phenotypic changes have been recorded during the course of the experiment. Refinement of the study design has created a moderate delay of the experimental phase.

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

PhD student: Vanessa Weber de Melo (IEBES); PhD committee: Owen Petchey (IEBES), Bernhard Schmid (IEBES), Ueli Grossniklaus (IPB), Paul Hurd (Queen Mary University of London), Sinéad Collins (Edinburg University)

The aim of the project is to better characterize the influence of epigenetics in gene expression changes that occur when *Tetrahymena thermophila* adapts to different conditions, such as increasing population densities and temperature variation. The project started with a delay only in January 2015. Currently the PhD research proposal is being written and the main experiments of the project are being designed. Moreover, RNA-Seq and ChIP-Seq data from previous experiments are already available and are currently being analyzed, helping to improve the design of future experiments.

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: Alex Hajnal (IMLS), Ueli Grossniklaus (IPB), Homayoun Bagheri (IEBES), Ralf Sommer (Max Planck Institute Tübingen)

The goal of this project is determine how the genetic background affects complex disease signaling pathways. The PhD student completed this quantitative genetic analysis and defended his thesis in 2014. Currently, we focus on the SRM proteomic analysis of natural genetic variation on protein abundances in *C. elegans* signaling pathways. To achieve this goal, we quantified core proteins from the Apoptosis, Notch, Ras, and Wnt signaling pathways in recombinant inbred lines (RILs) generated from wild-isolates of *C. elegans*, N2 and CB4856, by targeted mass-spectrometry. To date, we finished quantitative trait locus (QTL) analysis for 7 selected proteins, based on protein abundance differences in RILs. One protein (PSR-1) shows a significant trans-QTL we plan to verify this analysis using near-isogenic lines generated from same parental strains using validated antibodies against PSR-1 by Western-blotting.

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)

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 (IMLS & ETH Zürich)

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 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 (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), Hans-Johann Glock (Philosophisches Seminar, Faculty of Arts)

In this subproject we intend to learn more about the evolutionary origins and selective conditions promoting the evolution of human language. With an integrative and empirical approach, we aim to better understand how language, one of the key stand-out features of humans, may have evolved. Our PhD student, Katie Collier returned from field work in April 2014, published a review article, and has since returned to South Africa to collect more observational and experimental data on a second cooperatively breeding mongoose

species. Using comparative data we have presented an alternative theory within the field of language evolution and development. This theory states that certain forms of sound combinatoriality (syntax) might be more likely to emerge first in communication systems. We have also continued to have thoroughly stimulating discussions amongst the Language Evolution URPP PhD committee, and this has given rise to further collaborative projects.

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), Thomas Wicker (IPB), Simon Aeschbacher (University of California Davis)

PhD student, subproject 6.2: Kasia Sluzek (IEBES); PhD committee: Lukas Keller (IEBES), Andreas Wagner (IEBES), Ueli Grossniklaus (IPB), Armando Caballero (Universidad de Vigo)

We aim to advance the mechanistic understanding of inbreeding depression by studying the molecular level (gene expression) changes in inbred Alpine ibex. Specifically, we want to characterize genomic and transcriptomic signatures of past population bottlenecks in this species that may be associated with loss of adaptive potential and inbreeding depression, respectively. Tissue samples were collected in the field in mid-2014 and RNA and DNA extraction trials are currently ongoing, with the view to send samples for Illumina HiSeq sequencing by May 2015. In parallel, a method of quantifying individual-level inbreeding depression is being developed. Targeted sampling of individuals proved a challenge, due to the uncertainty of them being in the study area during the brief fieldwork window; nonetheless, samples from 18 individuals of varying inbreeding coefficients were obtained. Simultaneous extraction of RNA and high molecular weight DNA were initially unsuccessful due to the tough nature of skin tissue, but the protocol has since been optimized to increase yield and nucleic acid integrity.

3.2 Scientific Activities

Scientific Retreat

In June 2014, the second URPP Evolution in Action Retreat took place in Diessenhofen am Rhein, with 50 participants. All research projects of the URPP Evolution in Action were presented; the PhD students conducting the projects held the presentations. A special focus was laid on the scientific background of the research topics as well as on the progress made since the first annual retreat in 2013. 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 indeed followed by lively discussions.

- The keynote talk "Functional Evolution of Mammalian Genomes" was held by Henrik Kaessmann (University of Lausanne)
- An input talk was given by Balthasar Bickel, from the Department of Comparative Linguistics:
 "Linguistics and Biology: New Avenues for Interdisciplinary Research"
- Brainstorming session as a first step in generating new interdisciplinary research ideas
- Similar to the first annual meeting in 2013, the retreat 2014 was also the opportunity to meet all other members and PhD students of the URPP Evolution in Action and 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 further support the PhD students such that they can benefit fully from the networking possibilities within the URPP, continuation of the bioinformatics support, etc. Meetings were held during the retreat to discuss 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.
- Election of the Search Committee for the Academic Fellow Position

Bioinformatics tutorials

The successful series of bioinformatics tutorials was continued in 2014, 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 Lischer, who joined as a second embedded bioinformatician in February 2014. In the retreat, an interactive session 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:

- Next Generation Sequencing Part 2: lab tour Functional Genomics Center Zurich (FGCZ), BAM preprocessing, variant calling
- Next Generation Sequencing Part 3: Variant calling 2 using GATK, variant effect prediction
- Next Generation Sequencing Part 4: RNA-Seq and making sense of gene lists
- Linux Bash Shell Part 3: Writing bash scripts, control structures, parallelizing jobs, awk extension

In addition, the following one-day tutorials were offered:

- Introduction to R Part 1: Using R as a calculator, variables, subsetting, reading in data, writing functions, apply functions, missing data, plotting (base::plot)
- Introduction to R Part 2: Programming exercises, plotting using ggplot2, writing clean code

Each of the tutorials was held twice (with the exception of the RNA-Seq tutorial) such that all interested persons could participate. Every tutorial consisted of a theoretical introduction to the topic, followed by guided exercises. The tutorials were very well attended, with five to 13 participants in every class. The students generally gave a very positive feedback, 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 institutes attended the tutorials. The series is being continued in 2015. In 2014, we also started quarterly one-to-one meetings between each PhD student and an embedded bioinformatician to discuss the project design and methods. 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 (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 and FGCZ), Rie Shimizu-Inatsugi (IEBES, UZH), Heidi Lischer (URPP Evolution in Action).
- New courses for the PhD Program in Evolutionary Biology were in the conceptual or preparatory phase in 2014 and will be held in 2015.
- Several of the professors who as a result of the URPP Evolution in Action are newly associated with the PhD Program in Evolutionary Biology participated in the course "Topics in Evolutionary Biology" (Bio554).

Open Call for Research Projects

To promote young scientists, the URPP Evolution in Action called 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 were 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 this call was to fund pilot projects necessary for subsequent larger grant applications. Alternatively, high-risk experiments that could potentially open up new avenues within ongoing projects were equally eligible. Among the 18 applications received, the Steering Committee of the URPP Evolution in Action funded six projects:

Applicant: Sinisa Bratulic, PhD Student

Title of project: Measuring phenotypic mutation rates using mass spectrometry-based proteomics

Granted funding: CHF 4'400

Applicant: Dr. Christine Grossen

Title of project: Genomic signatures and mechanisms of introgression in Alpine ibex

Granted funding: CHF 19'873

Applicant: Dr. Mélissa Lemoine

Title of project: Assessing hidden diversity of Borrelia pathogens along altitudinal gradients in the Swiss Alps

Granted funding: CHF 19'730

Applicant: Marta Pinto, PhD Student

Title of project: Estimation of effective population sizes and identification of possible transmission bottlenecks

of obligate leaf nodule symbionts of Psychotria

Granted funding: 12'090

Applicant: Dr. Yolanda Schaerli

Title of project: Evolution of duplicated genes

Granted funding: 20'000

Applicant: Dr. Samuel Wuest

Titel of project: Characterization of mutant loci affecting fitness through altered reproductive allocation

patterns in an annual plant Granted funding: 15'000

Search for an Academic Fellow

We advertised the Academic Fellow Position in November 2014. The advertisement was aimed at young scientists who have recently received their PhD degree or have completed a short, first postdoctoral position to pursue a period of independent research before taking a faculty position. The research topic of the Academic Fellow was requested to be linked to the research themes of the URPP Evolution in Action, and preferably include an integrative/interdisciplinary approach. For this position we received 39 applications and the Search Committee (Ueli Grossniklaus (Chair), Giada Ferrari, Frederic Guillaume, Anna Lindholm, Jakob Pernthaler, Frank Rühli, Kentaro Shimizu, and Andreas Wagner) invited 5 applicants for interviews on March 2, 2015.

Initiation of Recruiting Process for the Assistant Professor Position

The structural issues/search commission, including members from the URPP Evolution in Action, members of the other "Fachbereiche", "Ständevertreter", as well as external members, has written the structural issues report for the non-tenure track Assistant Professor Position "URPP Evolution in Action". The Executive Board of the Faculty of Science has approved the structural issues report, which has been forwarded to the Executive Board of the University for consideration. The application procedure for the Assistant Professor Position "URPP Evolution in Action" is scheduled for 2015.

Membership Applications

Group leaders addressing evolutionary questions at the organismal, molecular, and/or conceptual level at UZH can apply for membership in the URPP Evolution in Action. Applications are subject to approval by the Steering Committee. In 2014 the Steering Committee approved the following membership applications:

Prof. Dr. Rolf Kümmerli, Institute of Plant Biology

Prof. Dr. Frédéric Guillaume, Institute of Evolutionary Biology and Environmental Studies

Dr. Erik Postma, Institute of Evolutionary Biology and Environmental Studies

Prof. Dr. Hans-Johann Glock, Chair of Theoretical Philosophy, Philosophisches Seminar

Dr. Philipp Schlüter, Institute of Systematic Botany

Scientific Minisymposium

A first scientific minisymposium, which offer an opportunity to postdocs and PhD students to invite international colleagues in a specific field, was held in March 2014 in Zurich Talks on conservation biology and the detection of signatures of selection were held by Mark Beaumont (University of Bristol) and Mike Bruford (Cardiff University) who also taught a half-day practical course.

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 13 PhD students and two postdocs, 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 bioinformaticians of the URPP Evolution in Action support 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, that 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 works one day per week in the von Mering (IMLS) and Wagner (IEBES) 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. In 2014, the second embedded bioinformatician started her tenure, allowing an expansion of the bioinformatics services, as well as tutorials and courses in bioinformatics within the URPP Evolution in Action.

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).

We are in the process of setting up a series of Minisymposia, where the PhD students and postdocs 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 first such minisymposium focusing on population genetics and conservation biology held place in March 2014.

The PhD students in the URPP Evolution in Action have the possibility to bring in their view in various ways. At our retreats, they were invited to formulate their needs in a workshop specifically dedicated to this aim. Furthermore, the PhD students have elected a representative to serve on the Steering Committee of the URPP Evolution in Action and also the Search Committees for the Academic Fellow position.

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. Wherever possible, we support efforts to create a family-friendly work environment, for instance by enabling part-time work.

- Within the PhD student peer group of the URPP Evolution in Action, female students represent the large majority (9/13).
- In the first open call for pilot projects of the URPP Evolution in Action, all young UZH researchers in the field were eligible to apply. We received 18 applications, whereof nine were submitted by women.
 Of the six projects that were funded, four are led by women.
- For the Academic Fellow position of the URPP Evolution in Action, we received 39 international applications, whereof 14 were handed in by women. Among the five shortlisted candidates three were women.

5 Publications

5.1 Peer-reviewed publications

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, Balčiauskas 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 immun receptor Toll-like receptor 2 (TLR2) across bank vole populations and lineages in Europe. *Biological Journal of the Linnean Society*, in press.

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.

5.2 Poster abstracts

Cornetti L, Lemoine M, Tschirren B: Genomic insights into the evolution of Borrelia resistance along altitudinal gradients in the Alps. Congress of the European Society for Evolutionary Biology (ESEB) 2015, Lausanne, Switzerland

Ferrari G, Rühli FJ, Bouwman AS: Optimization of DNA extraction protocols from historic soft tissues for palaeomicrobiological studies. International Symposium on Biomolecular Archeology (ISBA) 2014, Basel, Switzerland

Kropivšek K, Heichinger C, Züst T, Turnbull L, Schmid B, Grossniklaus U: Epigenetic variation and selection by aphids in *Arabidopsis thaliana*. Congress of European Society for Evolutionary Biology (ESEB) 2015, Lausanne, Switzerland

Ferrari G, Akgül G, Rühli FJ, Bouwman AS: Optimization of DNA extraction protocols from historic formalin-fixed soft tissues for palaeomicrobiological studies. Annual Meeting of the Paleopathology Association 2015, St. Louis, Missouri.

Giesen A, Schäfer MA, Blanckenhorn WU: The evolution of reproductive isolation between the two hybridizing dung flies *Sepsis cynipsea* and *S. neocynipsea* (Diptera: Sepsidae). System Genetics and Evolution of Non-human (Model) Organisms SGE2014, Ascona, Switzerland.

Giesen A, Schäfer MA, Blanckenhorn WU: Quantitative analysis of population structure of the closely related sister species *Sepsis cynipsea* and *S. neocynipsea* (Diptera: Sepsidae) shows high inter-specific and intercontinental genetic differentiation. biology15, Dübendorf, Switzerland.

Giesen A, Schäfer MA, Blanckenhorn WU: The evolution of reproductive isolation between two hybridizing dungfly species *Sepsis cynipsea* and *S. neocynipsea* (Diptera: Sepsidae). Congress of European Society for Evolutionary Biology (ESEB) 2015, Lausanne, Switzerland

Pinto-Carbó M, Eberl L, Carlier A: Comparative genomics of *Burkholderia* leaf nodule symbionts. Congress of European Society for Evolutionary Biology (ESEB) 2015, Lausanne, Switzerland

Pinto-Carbó M, Eberl L, Carlier A: Genome evolution of *Burkholderia* leaf nodule symbionts. XVth European Society for Evolutionary Biology 2015, Lausanne, Switzerland.

Pinto-Carbó M, Eberl L, Carlier A: Genome evolution of *Burkholderia* leaf nodule symbionts. 10th International Symposium on Phyllosphere Microbiology 2015, Monte Verità, Ascona, Switzerland.

Menardo F, Wicker T and Keller B: Genomics of formae specialis in Blumeria graminis. 4th International Powdery Mildew workshop 2014, London, UK.

Leigh D, Grossen C, Wagner A, and Keller L: Post-bottleneck genetics in wild populations: Do we see what we expect and do patterns differ from neutrality? Congress of European Society for Evolutionary Biology (ESEB) 2015, Lausanne, Switzerland

6 Structures

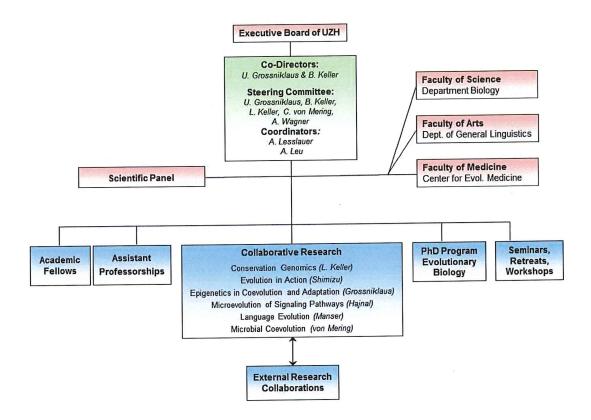


Figure 1: Organizational chart of the URPP Evolution in Action

7 Third-Party Funds

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

Data obtained through this URPP project helped setting up the basis of an SNF Sinergia grant proposal (number CRSII3_154430) to investigate the functional aspects of leaf nodule symbiosis. CHF 1'037'274 were awarded to the group of Leo Eberl, and to the co-PIs Prof. K. Gademann (University of Basel) and Dr. T. Wicker (UZH). (Subproject 1.2)

Mélissa Lemoine obtained a Marie-Heim-Vögtlin grant to work in the project. Grant from the Baugarten Foundation for fieldwork and consumables. (Subproject 2.2)

The Claraz Foundation spoke lump sums of CHF 4'500 and 2'500 to Barbara König and co-workers (Subproject 2.5) and Wolf Blanckenhorn and colleagues (Subproject 2.6), respectively.

De novo sequencing and bioinformatics of four Sepsis species at the Beijing Genomics Institute was funded via grants to Bonn University (Subproject 2.6).

PSC Syngenta Research Fellowships were obtained for projects that are thematically related to Project 3 of the URPP Evolution in Action. Ueli Grossniklaus and Bernhard Schmid obtained CHF 150'000 for the PhD project "Epigenetic Contributions to Hybrid Vigor in Apomictic Offspring" (related to Subproject 3.1) and Florian Schiestl, Heather Kirk, and Ueli Grossniklaus CHF 50'000 for the project "Causes and Consequences of Epigenetic Variation in Plant Interactions with Pollinators and Herbivores" (related to Subproject 3.2).

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

- Subproject 1.1: Microbial Networks in Lake Zurich
 - o Project leader: Jakob Pernthaler
 - o Funding: CHF 65'700
- Subproject 1.2: Evolutionary Degeneration of an Obligate Symbiont
 - o Project leader: Leo Eberl
 - o Funding: CHF 65'700
- Subproject 2.1: Virulence evolution in past human pathogens
 - o Project leader: Frank Rühli
 - o Funding: CHF 65'700
- Subproject 2.2: Understanding Variation in Borrelia Resistance in Swiss Natural Host Populations
 - o Project leader: Barbara Tschirren
 - o Funding: CHF 65'700
- Subproject 2.3: Adaptation of a Fungal Pathogen to New Host Species
 - o Project leader: Beat Keller
 - o Funding: CHF 65'700
- Subproject 2.4: Hybrid Speciation and Male Invasion in Action in Switzerland
 - o Project leader: Kentaro Shimizu
 - Funding: CHF 32'900
- Subproject 2.5: Speciation through Chromosomal Rearrangements in Wild House Mice in Switzerland
 - o Project leader: Barbara König
 - o Funding: CHF 65'700
- Subproject 2.6: Incipient Speciation Due to Thermal Adaptation or Sexual Selection in Sepsid Flies
 - o Project leader: Wolf Blanckenhorn

- o Funding: CHF 65'700
- Subproject 3.1: Epigenetic Variation and Selection
 - o Project leader: Ueli Grossniklaus
 - o Funding: CHF 131'500
- Subproject 3.2: Epigenetics in Plant Adaptation
 - o Project leader: Florian Schiestl
 - o Funding: CHF 32'900
- Subproject 3.3: Epigenetics in Microbial Adaptation
 - o Project leader: Owen Petchey
 - o Funding: CHF 32'900
- Subproject 4.1: Microevolution of the Ras, Wnt and Notch Signaling Pathways in C. elegans
 - o Project leaders: Alex Hajnal, Michael Hengartner
 - o Funding: CHF 65'700
- Subproject 4.3: Systems Genetics of Growth and Size Regulation
 - o Project leader: Ernst Hafen
 - Funding: CHF 65'700
- Subproject 5.1: The evolutionary origins and selective conditions promoting the evolution of human language
 - Project leader: Marta Manser
 - o Funding: CHF 65'700
- Subproject 6.1: Conservation Biology of the Alpine Ibex (Genomic Aspects)
 - Project leader: Lukas Keller
 - o Funding: CHF 65'700
- Subproject 6.2: Conservation Biology of the Alpine Ibex (Transcriptomic Aspects)
 - o Project leader: Andreas Wagner
 - o Funding: CHF 65'700