

MEETING STEVE 2017

Annual meeting of
Students in **E**volution and **E**cology

Tübingen
10 November 2017



EBERHARD KARLS
UNIVERSITÄT
TÜBINGEN



Meeting StEvE 2017

The meeting of Students in Evolution and Ecology (Meeting StEvE) is a yearly opportunity for postgraduate students from the Evolution and Ecology Research School at the University Tübingen (EVEREST) as well as for advanced MSc students and young postdocs from Tübingen to present their work and exchange ideas.

Meeting StEvE 2017 is organized by the Plant Evolutionary Ecology group. This year we have participants from EVEREST as well as from collaborating institutes (see list below). Oral and poster presentations will cover multiple interdisciplinary fields within evolution and ecology. Our keynote speaker, Prof. Virpi Lummaa from the University of Turku, will give a fascinating talk on how natural selection works on modern human evolution. Our meeting is held in the Alte Aula, a historic monument which once served as the main building of the University Tübingen. Afterwards we offer an evening Apéro in the Evangelisches Stift, another historic attraction located in the beautiful old town of Tübingen.

We hope you enjoy your time at Meeting StEvE 2017 !

The organisers -- Anna Kirschbaum - Bence Gáspár - Franziska Willems - Javier Morente - Madalin Parepa - Niek Scheepens – Ying Deng - Svenja Block



Participating working groups (from the University of Tübingen unless stated otherwise):

Animal Evolutionary Ecology

Biogeology / Senckenberg Centre for Human Evolution and Palaeoenvironment

Comparative Zoology

DFG Center for Advanced Studies "Words, Bones, Genes, Tools"

Earth System Dynamics

Evolutionary Biology of Invertebrates

Molecular Biology, Max Planck Institute for Developmental Biology, Tübingen

Paleoanthropology

Parasitology

Plant Ecology

Plant Evolutionary Ecology

Zooarchaeology

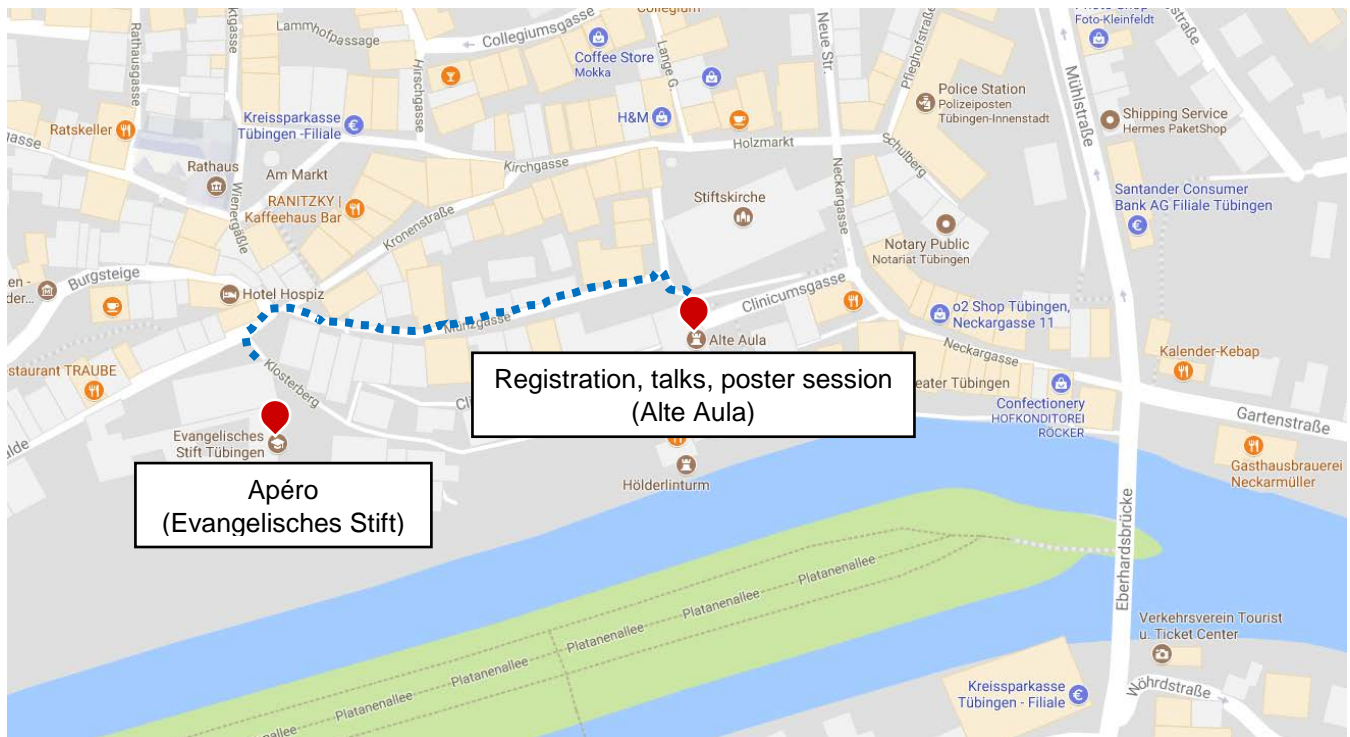
Practical information

Locations

Main venue: (9:00-18:00) Festsaal of the **Alte Aula**, Münzgasse 30

- **Presentations:** Festsaal, ground floor
- **Coffee break:** Entrance hall & Festsaal, ground floor
- **Poster sessions:** Festsaal, ground floor

Apéro: (start 18:15) Speisesaal of the **Evangelisches Stift**, Klosterberg 2



Posters

Portrait, format A0, to be put up in Festsaal of the Alte Aula on Friday during registration. Poster stands will not be numbered. Please choose your own.

Talk preparation and presentation

All presentations will run from a single computer to prevent time loss while changing speakers. Prepare your presentation in PowerPoint or export it as a pdf (to be shown in full-screen mode). Note that PDFs will run more reliably across platforms than PowerPoint presentations. You can “animate” your pdf by building up changes over several slides rather than within a slide (as you would in ppt). Please use font sizes ≥ 18 pt. Presentations will be run from a Windows computer. We provide a remote control with laser pointer.

Please hand in your presentation on a USB-Stick **well in time before** your session starts to check that your presentation runs properly.

Presentations are 15 min followed by 5 min discussion. The session chair keeps track of time.

Beverages during the meeting

We offer free drinks, coffee and snacks during the breaks in the entrance hall.

Apéro

All participants are invited to attend the Apéro in the Evangelisches Stift in the evening, from 18:15 till 21:00. Drinks and snacks are offered.

Emergency

For medical and fire emergencies, call 112 (mobile) or 70112 from fixed university phones.

Meeting Program - Friday 10 November 2017 - Morning

8:15 – 9:00 Registration

Session I

Chair: Svenja Block

| | | |
|---------------|------------------------|---|
| 9:00 – 9:15 | Niek Scheepens | Welcome |
| 9:15 – 9:35 | Robert Rauschkolb | Does ex situ cultivation of rare plant species in botanical gardens lead to loss of adaptation to the wild? |
| 9:35 – 9:55 | Anubhav Mohiley | Herbivory induces foraging for poison in plants |
| 9:55 – 10:15 | Lara Braun | More is less: the effect of soil depth on species richness |
| 10:15 – 10:35 | Liesbeth van den Brink | Connecting the green and the grey world through a soil-seed transplant experiment |

10:35 – 11:10 Coffee break

Session II

Chair: Javier Morente

| | | |
|---------------|----------------------|--|
| 11:10 – 11:30 | Eleanor Gibson-Forty | Reproductive strategies, not pollinator activity, determine the reproductive success of crucifer species along a steep rainfall gradient |
| 11:30 – 11:50 | Viktoría Ferenc | Mating systems of annual crucifer species along a rainfall gradient |
| 11:50 – 12:10 | Peter Pogoda | Flesh and bone: an integrative approach towards sexual size dimorphism of a terrestrial salamander |
| 12:10 – 12:30 | Julia Staggenborg | Evidence-based biodiversity conservation in the agricultural landscape - the corn bunting (<i>Emberiza calandra</i>) as model species |

12:30 – 13:40 Lunch break

Meeting Program - Friday 10 November 2017 - Afternoon

Session III

Chair: Bence Gáspár

| | | |
|---------------|----------------|---|
| 13:40 – 14:00 | Sergio Latorre | Estimating methylation levels In historic plant specimens |
| 14:00 – 14:20 | Abel Bosman | A virtual approach to the investigation of the suprainiac depression in the Eyasi 1 and Aduma crania |
| 14:20 – 14:40 | Jessica Starke | Latitudinal variation in denudation rates along the Andean Western margin (Peru and Chile): Insights from cosmogenic ¹⁰ Be |
| 14:40 – 15:00 | Gillian Wong | Human subsistence and environment during the Magdalenian at Langmahdhalde: Preliminary evidence from a rock shelter in the Lone Valley, Southwest Germany |

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| 15:00 – 16:30 | Poster session | [16:00-16:30 EVEREST student & supervisor meeting] |
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| 16:30 – 17:30 | Virpi Lummaa | KEYNOTE: Natural selection in contemporary human populations |
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| 17:30 – 17:45 | Awards of best talk and poster and closing remarks | |
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|---------------|--|--|
| 18:15 – 21:00 | Apéro in the Evangelisches Stift with free drinks and snacks | |
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List of participants (in alphabetical order)

| Participant | | Lab | Presentation |
|-------------|--------------------------|---|--------------|
| Claudia | Adolphi | <i>Plant Evolutionary Ecology</i> | |
| Korinna | Allhoff | <i>Plant Ecology</i> | |
| Nils | Anthes | <i>Animal Evolutionary Ecology</i> | |
| Tamara | Ayoub | <i>Plant Ecology</i> | |
| Catherine | Bauer | <i>Biogeology</i> | |
| Chris | Baumann | <i>Zooarchaeology</i> | |
| Alex | Bertacchi | <i>Zooarchaeology</i> | Poster |
| Paul | Bilinski | <i>MPI, Molecular Biology</i> | |
| Mark | Bilton | <i>Plant Ecology</i> | |
| Pierre-Paul | Bitton | <i>Animal Evolutionary Ecology</i> | |
| Svenja | Block | <i>Plant Evolutionary Ecology</i> | |
| Hervé | Bocherens | <i>Biogeology</i> | |
| Abel | Bosman | <i>DFG Center for Advanced Studies “Words, Bones, Genes, Tools“</i> | Talk |
| Oliver | Bossdorf | <i>Plant Evolutionary Ecology</i> | |
| Lara | Braun | <i>Plant Ecology</i> | Talk |
| Maximilian | Collenberg | <i>MPI, Molecular Biology</i> | Poster |
| Ying | Deng | <i>Plant Evolutionary Ecology</i> | |
| Dorothee | Drucker | <i>Biogeology/Senckenberg Centre HEP</i> | |
| Sireen | El Zaatari | <i>Paleoanthropology</i> | |
| Nasim | Farahani Zayas | <i>MPI, Molecular Biology</i> | |
| Viktoria | Ferenc | <i>Plant Ecology</i> | Talk |
| Katharina | Foerster | <i>Comparative Zoology</i> | |
| Bence | Gáspár | <i>Plant Evolutionary Ecology</i> | Poster |
| Hannah | Gelaudie | <i>Plant Ecology</i> | Poster |
| Ellie | Gibson-Forty | <i>Plant Ecology</i> | Talk |
| Alba | Gonzalez Hernando | <i>MPI, Molecular Biology</i> | Poster |
| Uta | Grünert | <i>Plant Evolutionary Ecology</i> | |
| Michal | Gruntman | <i>Plant Ecology</i> | |
| Ulrike | Harant | <i>Animal Evolutionary Ecology</i> | |
| Ingeborg | Haug | <i>Plant Evolutionary Ecology</i> | |
| Stefanie | Herbst | <i>Evolutionary Biology of Invertebrates</i> | |
| Susanne | Hermann | <i>Plant Evolutionary Ecology</i> | |

| | | | |
|-------------------|-------------------------|---|---------|
| Melania | Ioannidou | <i>Paleoanthropology</i> | |
| Yun-Ting | Jang | <i>Comparative Zoology</i> | |
| Fotios Alexandros | Karakostis | <i>Paleoanthropology</i> | |
| Anna | Kirschbaum | <i>Plant Evolutionary Ecology</i> | Poster |
| Christian | Kubica | <i>MPI, Molecular Biology</i> | Poster |
| Anna | Lampej Bucharova | <i>Plant Evolutionary Ecology</i> | |
| Patricia | Lang | <i>MPI, Molecular Biology</i> | |
| Sergio | Latorre | <i>MPI, Molecular Biology</i> | Talk |
| Nicola | Lechner | <i>Plant Ecology</i> | Poster |
| Shanghai | Li | <i>Plant Ecology</i> | |
| Virpi | Lummaa | <i>University of Turku, Department of Biology</i> | KEYNOTE |
| Deike | Lüdtke | <i>Comparative Zoology</i> | Poster |
| Nico | Michiels | <i>Animal Evolutionary Ecology</i> | |
| Anubhav | Mohiley | <i>Plant Ecology</i> | Talk |
| Javier | Morente | <i>Plant Evolutionary Ecology</i> | Poster |
| Rebecca | Peters | <i>Plant Ecology</i> | |
| Peter | Pogoda | <i>Comparative Zoology</i> | Talk |
| Ronja | Ratzbor | <i>Plant Ecology</i> | |
| Robert | Rauschkolb | <i>Plant Evolutionary Ecology</i> | Talk |
| Alfons | Renz | <i>Parasitology</i> | |
| Mirjam | Rieger | <i>Plant Evolutionary Ecology</i> | |
| Carolin | Röding | <i>Paleoanthropology</i> | Poster |
| Fernanda | Ruiz Fadel | <i>Comparative Zoology</i> | |
| Niek | Scheepens | <i>Plant Evolutionary Ecology</i> | Poster |
| Julia | Staggenborg | <i>Animal evolutionary ecology</i> | Talk |
| Jessica | Starke | <i>Earth System Dynamics</i> | Talk |
| Katja | Tielbörger | <i>Plant Ecology</i> | |
| Manuela | Unger | <i>Evolutionary Biology of Invertebrates</i> | |
| Antonia | Uthoff | <i>Animal Evolutionary Ecology</i> | |
| Liesbeth | van den Brink | <i>Plant Ecology</i> | Talk |
| Eva | Vennemann | <i>Plant Evolutionary Ecology</i> | |
| Clemens | Weiss | <i>MPI, Molecular Biology</i> | |
| Franziska | Werner | <i>Plant Evolutionary Ecology</i> | |
| Franziska | Willems | <i>Plant Evolutionary Ecology</i> | |
| Gillian | Wong | <i>Zooarchaeology</i> | Talk |

KEYNOTE

Prof. Dr. Virpi Lummaa¹

1 - Department of Biology, University of Turku, Finland

Natural selection in contemporary human populations

Recent social and cultural adaptations have cast doubt on the continued relevance of Darwinian selection in humans. Yet, in both traditional and industrialized societies, differences among individuals still lead to selection favouring certain heritable traits because although survival to old age can be high, not everyone has the same family size and many forego reproduction altogether. This coupled with heritable traits linked to differences in reproductive rate might lead to rapid changes in the genetic makeup of populations. However, few studies have examined how the modern environment itself fuels evolution, and how the recent drastic demographic shifts to low birth and death rates have affected the opportunity for selection or specific trait selection. I use longitudinal demographic data from Finland spanning 300 years and >12 generations to investigate how the strength and direction of selection on key fitness traits changed with the modernization of society.

Abstracts of oral presentations

R. Rauschkolb¹, L. Szczeparska², J. F. Scheepens¹, A. Kehl¹

1 - University of Tübingen

2 - University of Warsaw

Does ex situ cultivation of rare plant species in botanical gardens lead to loss of adaptation to the wild?

Anthropogenic environmental factors caused rapid declines in global plant diversity during the last decades. To prevent extinction of plant species, numerous botanical gardens responded with creating ex situ collections of threatened species. These collections function as a source for seeds and plant material for restocking natural populations if they are threatened by extinction or after they already have gone extinct in the wild.

Since environmental conditions in botanical gardens likely differ from those in the original habitats of cultivated plant species, ex situ collections may lose adaptation to the wild and instead adapt to the cultivation environment.

In this study, we compare three plant populations cultivated in the Botanical Garden of the University of Tübingen with their original wild populations. In summer 2016 we collected seeds from the botanical garden and the original wild populations, and in February 2017 we started germination experiments. After germination we performed common garden experiments in the greenhouse.

Rapid evolution under cultivation conditions may seriously compromise efforts to preserve our biodiversity. The results of our experiments may increase the understanding of such evolutionary processes and may help to optimize cultivation conditions from an evolutionary point of view.

A. Mohiley¹, K. Tielbörger¹, S. Höreth², S. Clemens², M. Gruntman¹

1 - Plant Ecology, Institute of Evolution and Ecology, University of Tübingen

2 - Lehrstuhl Pflanzenphysiologie, Universität Bayreuth

Herbivory induces foraging for poison in plants

Plants can exhibit foraging behaviour in response to resource heterogeneity. However, a yet unexplored hypothesis is that such foraging responses could be induced by environmental stressors, such as herbivory, which might alter the demand for particular resources, e.g. those required for herbivore defense. In this study, we examined the effect of simulated herbivory on clonal foraging in the metal hyperaccumulating plant *Arabidopsis halleri*, which uses heavy metals for herbivore defense. Two connected *A. halleri* ramets were grown with one ramet in high-Cd pot and the other in a low-Cd pot with or without herbivore induction. Foliar herbivory was simulated by both piercing holes in the leaves as well as applying jasmonic acid. Plants subjected to simulated herbivory exhibited clonal foraging for Cd, enhanced Cd uptake and enhanced Cd sharing among ramets. Moreover, these induced foraging responses were exhibited particularly in ramet pairs originating from non-metalliferous soils, which have lower metal tolerance. Our findings demonstrate that the uptake as well as sharing of a harmful compound could be stimulated when its benefits of protection from herbivory outweigh its costs.

L. Braun¹, R. Kadmon¹, K. Tielbörger¹

1 - Plant Ecology, Institute of Evolution and Ecology, University of Tübingen

More is less: the effect of soil depth on species richness

How a diversity of competing plant species can coexist is a major unresolved question in community ecology. An important determinant of species coexistence and richness may lie below-ground, and soil depth could be key. Yet, previous studies investigating the role of soil depth on species richness have yielded mixed results. On the one hand, deeper soils provide more space, thus below-ground competition should be reduced, allowing more species to coexist. On the other hand, deeper soils provide more resources and support more productive communities, which could lead to an increase in competition and result in the exclusion of weak competitors (i.e. decreased species richness). We tested these two alternative hypotheses in a large common garden experiment where both soil depth and fertility were manipulated within a full factorial design. Species richness and above-ground biomass were estimated after 2 years. Species richness was greatest on shallow, unfertilized soils and decreased on deep, unfertilized soils, which supported the same number of species as all fertilized soils. Our study demonstrates that soil depth affects species richness mainly by regulating above-ground competition and less by the provision of below-ground niche-space.

L. van den Brink¹, R. Canessa², L. Cavieres³, H. Neidhardt⁴, Y. Oelmann⁴, K. Tielbörger¹

1 - Plant Ecology, Institute of Evolution and Ecology, University of Tübingen

2 - Faculty of Geography, Philipps University of Marburg

3 - Departamento de Botánica, Universidad de Concepción and Instituto de Ecología y Biodiversidad (IEB)

4 - Geoecology, University of Tübingen

Connecting the green and the grey world through a soil-seed transplant experiment

Space-for-time approaches, where spatial gradients are taken as a proxy for temporal change, are often used in ecological and geological research. I use manipulation experiments to disentangle the relationships between climate, vegetation and geochemical effects on nutrient cycling along a climate gradient.

To test the possibility for plants to establish in another climate, a reciprocal soil-seed transplant was conducted between the semiarid- and Mediterranean zone in Chile. Similar transplants between north- and south facing slopes within these zones were done to investigate the influence of soil humidity and exposure on the establishment within the climate areas. Preliminary results show that there was no home-site advantage but that plants performance was generally higher in the wetter site.

E. V. J. Gibson-Forty¹, K. Tielbörger¹, M. Seifan²

1 - Plant Ecology, Institute of Evolution and Ecology, University of Tübingen

2 - Mitrani Department of Desert Ecology, Swiss Institute for Dryland Environmental and Energy Research, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Midreshet Ben-Gurion

Reproductive strategies, not pollinator activity, determine the reproductive success of crucifer species along a steep rainfall gradient

Environmental conditions drive plant adaptations at every life-stage. Reproductive assurance by self-fertilisation is a common evolutionary mechanism which guarantees reproductive success by releasing plants from dependencies on pollinators. We hypothesize that annual plants self more in harsh environments because of severe pollinator-limitation than in benign environments. We tested our hypothesis along a rainfall gradient observing pollinator activity and using a pollinator-exclusion treatment to compare the seed set of three annual crucifer species. Pollinator activity was lowest in arid regions and increased along the gradient, yet the reproductive success of each species did not change. None of the species relied more on self-pollination in harsher environments; rather, each species maintained the same reproductive strategy in all sites, irrespective of pollinator activity or reproduction mode. Overall, our results show that varying pollinator activity is not the main selective force which determines the mode of reproduction in these species, suggesting that reproductive success of plants is not pollinator-limited as expected, particularly in harsh environments.

V. Ferenc¹, E. Gibson-Forty¹, K. Tielbörger¹

1 - Plant Ecology, Institute of Evolution and Ecology, University of Tübingen

Mating systems of annual crucifer species along a rainfall gradient

The mating system of hermaphroditic plants ranges from fully outcrossing to fully self-fertilized. Though the advantages and disadvantages of each mating system have been studied theoretically and with respect to environmental conditions, experimental evidence for clinal variation and local adaptation in mating system expression is still rare. It has been suggested that the degree of self-incompatibility is a function of pollinator abundance and conspecific density. Namely, populations should be predominately selfing in habitats with few mates and/or pollinators and vice-versa. Here, we tested this hypothesis using three annual crucifers growing along a steep aridity gradient in the Eastern Mediterranean Basin. Inbred lines of plants were grown in a greenhouse, outcrossing (resp. selfing) enforced via hand-pollination, and flower abortion and seed set estimated. Our results suggest that populations from more arid regions, i.e. regions with fewer conspecifics and fewer pollinators, have a higher fitness when forced to self than populations from wetter regions. This suggests that the species across the gradient are locally adapted to environmental severity. The findings also suggest that populations from wetter climates may be particularly vulnerable to predicted increasing aridity and suffer from pollinator limitation.

P. Pogoda^{1,2}, A. Kupfer^{1,3}

1 - Department of Zoology, State Museum of Natural History Stuttgart

2 - Comparative Zoology, Institute of Evolution and Ecology, University of Tübingen

3 - Institute of Zoology, University of Hohenheim

Flesh and bone: an integrative approach towards sexual size dimorphism of a terrestrial salamander

Males and females face different selection pressures due to a sexually biased investment into reproduction. This does often result in different morphologies. Sexual size dimorphisms (SSD) can give us important hints on the evolution and biology of a species. Salamanders are a well suited system investigating SSD including a diversity of reproductive modes and behaviors and patterns of SSD combined with life history traits including phylogeny help us to understand the evolution behind these processes. The genus *Salamandrina* as the phylogenetically most basal taxon of the Salamandridae have a key role for reconstructing the evolutionary pattern of SSD. Extensive morphological measurements on *S. perspicillata* gave us an overall overview of the expressed SSD in the external morphology and osteology, latter accessed by applying high resolution mCT scans. Analysis showed that males generally had larger cloacae, heads and limbs relative to body size, while females had larger trunks. Analysis of osteology revealed also new dimorphisms in the skull and the pelvic girdle. The dimorphic characters are likely linked to the different reproductive roles of the sexes of the salamanders.

J. Staggenborg¹, N. Anthes¹

1 – *Animal Evolutionary Ecology, Institute of Evolution and Ecology, University of Tübingen*

Evidence-based biodiversity conservation in the agricultural landscape - the corn bunting (*Emberiza calandra*) as model species

Farmland biodiversity is declining at unprecedented rates, primarily due to large-scale habitat deterioration, in particular to invertebrate and herb suppression, the corresponding elimination of food sources and to the loss of breeding areas. Dedicated agri-environmental schemes (AES) largely failed to revert this trend, calling for fine-grained studies on their regional efficiency. Using the corn bunting as model species, we critically evaluate how different AES affect local habitat conditions, habitat selection and bird fitness, which will be recorded repeatedly in distinct project areas throughout the next three years. AES should be established first time or supplementary to previous ones in each area and in collaboration with nature conservation authorities. By comparing population dynamics along that spatial and temporal gradient (presence and absence of AES, before and after their implementation), changes in habitat selection, bird abundance, survival and breeding success will allow evaluating AES efficiency. Management concept designs based on the study results can ensure the future promotion of evidence-based habitat quality improving AES.

S. Latorre¹, H. A. Burbano¹

1 - Ancient Genomics and Evolution, Department of Molecular Biology, Max Planck Institute for Developmental Biology

Estimating Methylation Levels in Historic Plant Specimens

Ancient DNA (aDNA) and the time-stamped meta-information associated with it provide a direct way of detecting variation in DNA sequence through history. Epigenetic changes such as cytosine methylation are an additional source of variation. In plants, it occurs in three different contexts: CG, CHG and CHH (where H = A, T or C).

Despite the impact of epigenetics, it has barely been studied using historic samples. This is mainly because conventional methods for assessment of methylation degrade DNA, and aDNA is already fragmented. We implemented an approach that can accurately assess methylation in plant historic genomes without exposing the molecules to further DNA degradation.

We investigated the methylation status of 42 *Arabidopsis thaliana* genomes retrieved from herbarium specimens collected from 1863 to 1993. Comparisons between inferences produced by our approach and traditional methylation calling using bisulfite sequencing on modern samples, showed that we are able to recover typical genomic features. Through inferred epimutation rates we can now understand the evolutionary dynamics of differentially methylated regions through time in plant populations.

A. M. Bosman¹

1 - DFG Center for Advanced Studies "Words, Bones, Genes, Tools," University of Tübingen

A virtual approach to the investigation of the suprainiac depression in the Eyasi 1 and Aduma crania

Even though our understanding of the phenotypic variation of the earliest members of *H. sapiens* is steadily increasing, there is an unresolved discussion about which traits define anatomical modernity. One such trait is the suprainiac depression. While some scholars argue that this anatomical trait is a Neandertal autapomorphy, it has been described for several fossils that do not belong to this species. In this study, we provide a combined quantitative and qualitative approach, using μ CT imaging, to investigate the suprainiac depressions on the African Eyasi 1 and Aduma crania. While the external morphology of the depressions on these fossils appears to be similar to the standard Neandertal appearance, their internal morphology does not. Our measurements of the cranial vault thickness corroborate this result, as there is no decrease in the relative thickness of the diploic layer in these crania. This study demonstrates that we need to employ approaches that rely on several lines of evidence when discussing the expression of phenotypic traits, their character state, and the relationships between the taxa for which these traits have been described.

J. Starke¹, T. Ehlers¹, M. Schaller¹

1 - Department of Geosciences, University of Tübingen

Latitudinal variation in denudation rates along the Andean Western margin (Peru and Chile): Insights from cosmogenic ¹⁰Be

This study quantifies latitudinal variation in denudation rates along the Andean Western and Coastal Cordillera in South America to understand the interactions between climate and tectonic processes in localizing denudation rates. The controls on the denudation rates are evaluated with a multivariate statistical factor analysis that identified correlations and covariation between denudation rates with climate, vegetation, topography, and fluvial steepness index (among other things). Measured cosmogenic derived denudation rates range from 0.5 - 168 m/Myr. The denudation rates generally decrease from the 15°S (near Nasca, Peru) to 23°S (near Antofagasta, Chile) and from the Western Cordillera to the Coastal Cordillera. Results from the factor analysis indicate that (1) the main controls on denudation rates are local tectonic driven processes indicated by the strong correlation and covariation of the denudation rate to the channel steepness in the arid northern Chile. (2) In southern Peru the denudation rates are mainly controlled by the intensity of vegetation and show strong covariation of denudation rates, vegetation cover and precipitation.

G. L. Wong¹, B. M. Starkovich^{1, 2}, N. J. Conard^{2, 3}

1 - Institut für Naturwissenschaftliche Archäologie, Eberhard-Karls-Universität Tübingen

2 - HEP Senckenberg

3 - Ur- und Frühgeschichte und Archäologie des Mittelalters, Eberhard-Karls-Universität Tübingen

Human Subsistence and Environment during the Magdalenian at Langmahdhalde: Preliminary Evidence from a Rock Shelter in the Lone Valley, Southwest Germany

The archaeological sites in the Swabian Jura of Southwest Germany have been studied for over a century and are world-famous for their contributions to our understanding of Paleolithic cultures. Research on the Magdalenian from this region has documented exchange systems, human subsistence patterns, technological innovations, and the re-settlement history of the area. Work at Langmahdhalde, a newly excavated rockshelter in the Lone Valley of the Swabian Jura, continues this research tradition with the application of modern tools and methods. Here, we present a preliminary analysis of the faunal remains from the site. We find that the microfaunal assemblage is ideal for reconstructing paleoenvironments and we discuss some initial interpretations of the data from this assemblage. Further, we discuss the origin of the macrofaunal assemblage and find that a significant portion of this assemblage was likely deposited as a result of human activity. Our results indicate that the faunal remains from Langmahdhalde have great potential to address questions of Magdalenian settlement patterns and site use.

Abstracts of poster presentations (in alphabetical order)

A. Bertacchi¹, B. Starkovich^{1,2}, H. Bocherens^{2,3}, N. Conard^{2,4}

1 - Institute of Archaeological Sciences, University of Tübingen

2 - Senckenberg Center of Human Evolution and Palaeoecology, University of Tübingen

3 - Institute of Geosciences, University of Tübingen

4 - Department of Early Prehistory and Quaternary Ecology, University of Tübingen

Small game exploitation in the Upper Palaeolithic at Sirgenstein, Swabian Jura

In the last years, archaeological excavations conducted with modern methods and comprehensive faunal analyses have showed that Upper Palaeolithic foragers in the Swabian Jura (SW Germany) exploited a wide range of small game. This contradicts earlier views of continuity across the Middle and Upper Palaeolithic. Here we present taxonomic and taphonomic evidence for small game exploitation at Sirgenstein cave, Ach Valley. We also hypothesize that the intensification of avian resources associated with the Gravettian technocomplex may signal technological and social developments in the forager community.

M. Collenberg¹, F. Bemm¹, D. Weigel¹

1 - Department for Molecular Biology, Max Planck Institute for Developmental Biology

Transcriptome Analysis in Hybrid Plants using Platinum Genomes

Heterosis is the deviation of the F1 progeny from the phenotypic mean of the parental plants, especially in cases where both parents are inbred and homozygous. Three genetic models explaining heterosis have been proposed without reaching a consensus, yet. A recent study in maize suggested structural genome variation as an important factor. Gene expression with regard to heterosis has been analyzed in several plants. However, the majority of these studies relied either on microarray data, which are limited to transcripts present on the chip, or on RNA-seq data that have been processed using a single reference genome, thus not accounting for structural genome variation. We now have access to high quality genome sequences of six *A. thaliana* genotypes. Two of them have been used in a reciprocal crossing. Transcriptomes of F1 hybrids and parental plants have been sequenced. RNA-seq reads were processed using a trans-reference genome, containing full length genome sequences of both parental plants and accounting for orthologous assignment. Here we present a way of how to process a double reference genome in for improving the analysis of hybrid transcriptomes regarding heterosis.

B. Gáspár^{1,2}, W. Durka², O. Bossdorf¹

1 - *Plant Evolutionary Ecology, Institute of Evolution and Ecology, University of Tübingen*

2 - *Department of Community Ecology, Helmholtz Centre for Environmental Research UFZ*

Natural epigenetic diversity in the common grassland plant *Plantago lanceolata*

Evidence from model systems suggests that, even in the absence of genetic variation, within-species diversity in ecologically important traits can also be created by underlying epigenetic variation. However, it is still unknown whether this is relevant in natural populations. Here, we present work based on 60 natural grassland populations of *Plantago lanceolata*, distributed across three regions in Germany, and covering various environmental gradients and different land-use types and intensities. We analysed genetic and epigenetic diversity using fingerprinting methods (AFLP and MSAP). To assess the heritability of epigenetic differences, we used leaf tissue collected directly from the field as well as from the F1 generation grown in a common greenhouse environment. Our first results show that there was only weak but nevertheless significant epigenetic population structure, and that epigenetic variation was generally lower in the greenhouse than in the field, indicating a significant environmentally-induced component of epigenetic variation. However, the observed epigenetic diversity or epigenetic distances between the studied populations were unrelated to their geographic, genetic or environmental differences.

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Herbivory induces clonal foraging for nutrient in plants

In response to resource heterogeneity, plants have shown to exhibit foraging behaviour, by the selective placement of resource-acquiring organs within resource-rich patches. It is still unclear if herbivory can affect foraging behaviour in plants. This study examined how simulated herbivory affects clonal foraging in the plant *Arabidopsis halleri*, from Brassicaceae family, which use nitrogen based compounds as herbivore defence. Additionally, we asked if these foraging responses to herbivory and clonal sharing of labelled nutrient would differ between plants originating from either metalliferous or non-metalliferous soils. Two connected *A. halleri* ramets were grown with one ramet in high-nutrient pot and the other in a low-nutrient pot with or without herbivore induction. Foliar herbivory was simulated by both piercing holes in the leaves as well as applying jasmonic acid, with water as control. We expect plants subjected to simulated herbivory to exhibit higher clonal foraging for nutrients, enhanced nutrient uptake and enhanced nutrient sharing among ramets. Additionally, we expect pairs that originate from non-metalliferous soils to show a higher response.

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Investigating the role of adaptive introgression of disease resistance genes in a recent plant colonization

During colonizations, founder populations experience a genetic diversity lost due to bottlenecks. New mutations or later colonizers could bring genetic variants that are adaptive. To test this, we are using a *A.thaliana*, which recently colonized North America experiencing a bottleneck. Its genetic diversity increased over time evidencing the arrival of later colonizers. In this context, we are investigating the adaptive role of new mutations and introgression from later lineages looking at disease resistance to the pathogen Hpa. For doing so, individuals from North America and its native range were screened for Hpa resistance. Results show that individuals from the Hpg1 lineage are susceptible, suggesting that de-novo mutations that causes resistance to these Hpa lines have not arisen. Then, GWA analysis identified major Hpa resistance loci. Comparing genomic locations of introgression and resistance loci will determine the adaptive potential of introgression in Hpa disease resistance.

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Evolution of plant phenotypic plasticity in response to grassland management

Phenotypic plasticity (PP) is one of the key mechanisms by which plants respond to environmental changes. One such situation might be grassland management: Mowing, grazing and fertilization create temporally variable environmental conditions, which should favour and thus select for PP, in particular the ability of plants to rapidly exploit temporary nutrient pulses, and the ability to regrow after damage.

We will carry out controlled common garden experiments with three widespread grassland species to test relationships between PP and land-use management. Seeds for these experiments have been sampled from 65 grassland plots from the Biodiversity Exploratories, which vary in mowing, grazing and fertilization intensity.

We will measure trait responses to fertilization and clipping treatments as well as plant fitness to investigate whether plastic responses are adaptive and whether they have a fitness cost.

Furthermore, we will test for correlations of PP with plot-level spatial and temporal heterogeneity. Finally, we will link our phenotypic data to existing molecular marker data to examine correlations of PP with neutral genetic diversity and gene flow.

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Building usable full genome variation graphs

The 1001 Genomes Project generated a polymorphism (SNP) and short structural variant (short SV) map for well over 1000 wild strains (accessions) of *Arabidopsis thaliana*. In addition, transcriptome, methylation and phenotypic data for most of the accessions was collected. By utilising long read sequencing technologies to generate de novo assemblies of diverse *A. thaliana* accessions, we are launching the next phase of this project, in which we will detect and genotype large SVs. Firstly, we will shift from a single reference based approach to a multiple genome graph, representing a set of highly diverse *A.thaliana* accessions. Based on this, we will detect SVs and subsequently genotype these in the 1001 Genomes Project short read data set.

Building a genome graph, however, is not trivial, and its quality depends on the number of shared regions that form informative nodes and (super-) bubbles in the graph. Here we propose a way to cope with diverse sequences for graph construction. We use Maximum Unique Matches (MUMs) to semi-globally glue the input genomes into a rough genome graph and locally resolve bubbles into a base precision graph which we use for read mapping and variant calling.

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Drought impacts on herbaceous plants – separating resistance and resilience mechanisms

Changing precipitation patterns make it important to look at drought responses of different ecosystems. To test what happens to temperate herbaceous vegetation in decreasing summer precipitation we use a gradient of natural water availability on the Swabian Alb. We established field experiments in beech forests and nutrient-poor grasslands in sites with low and high water availability. We want to disentangle resistance and resilience mechanisms in plant responses and find out if adaptation of plant populations to higher variability results in different responses to different types of drought. To simulate different drought scenarios we established rainout shelters, which simulate mild and extreme drought. We hypothesize that forests and grasslands that grow in regions with naturally low water availability will exhibit more resistance to permanent drought than plant communities that grow under high water availability. Plant communities that grow in regions with variable conditions of water availability would exhibit higher resilience to extreme drought than plant communities that grow under constant water availability.

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Male mate choice for female body colouration in Alpine newts

Traditionally, females are considered to be the choosy sex, while males compete for access to females and advertise themselves through extravagant colourations and decorations. However, we can also observe similar conspicuous traits in females. Depending on the specific sex roles in a species, also males may benefit from choosing to mate with the best available female. Male choosiness is expected to evolve also in non sex-role reversed species as a response to individual variation in female fecundity or maternal ability. In that case, male mate choice might select for ornamental traits or honest signals in females. Many ectothermic vertebrate species show brightly coloured females but little attention has been directed to the hypothesis that female colouration in this group evolved in response to sexual selection through male mate choice. I will present results from a study on the adaptive significance of the carotenoid-based belly colouration of female alpine newts (*Ichthyosaura alpestris*). In a mate choice experiment, we found that males invest more resources when courting more colourful females. Thus, we expect the female's body colouration to be a sexually selected trait. We found that less colourful females can compensate through more responsiveness, to attain similar attention from males as the more colourful females.

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Identification of phenology characters under genetic differentiation and selection in Mediterranean high mountain plant populations under different adaptive pressures

Silene ciliata Pourret (Caryophyllaceae) is a late flowering plant of the Mediterranean high mountain psicro-xerophile grasslands that represents one of the most vulnerable habitats to global change. In this context, populations of the species that are in the southern limit of distribution are under different environmental conditions related with their geographical location. In this study we analyze the phenological traits genetic differentiation of nine populations under different adaptive pressures using a common garden experiment. The patterns founded are indicators of genetic differentiation in flowering timing between populations under different environmental conditions. This differentiation could be related to divergent selection of phenological characters, but also neutral evolutionary processes can be happening.

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Ontogenetic and Adult Variation in the Morphometry of the Cerebellar Area

In this study, GMM was used to document the variation in modern human and chimpanzee cerebellar morphometry and to interpret ontogenetic changes within this framework. Three shape components with the largest variation in the sample were documented for the adult individuals of modern humans and three shape components for the adult chimpanzees. The axes of greatest variation are not identical in both species but show similarities. A common factor of the shape components of both species is a shift in proportions of the anterior part of the posterior cranial fossa relative to the posterior part. At the time of reaching a complete deciduous dentition species-specific differences between modern humans and chimpanzees are already established. However, during late phases of ontogeny only chimpanzees show a cerebellar shape change comparable to the main axis of variation in adult individuals. The combination of these results suggests a link to an already present axis of cerebellar shape variation in the population ancestral to modern humans and chimpanzees or to a change in cerebellar function in modern humans.

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GrENE-net – a global evolution experiment

The recent recognition that rapid evolutionary processes occur widely in nature gave impetus to investigate adaptation of populations to dynamic environmental conditions, which is of utmost relevance to understand adaptation to rapid climate change. To this aim, experimental evolution under natural conditions would strongly increase our understanding of evolutionary processes.

Here we present GrENE-net – Genomics of rapid Evolution in Novel Environments – a global evolution experiment with *Arabidopsis thaliana* involving over 40 institutions worldwide with the aim to understand how climate drives natural selection and shapes spatio-temporal genetic variation.

In autumn 2017, participants sowed replicates of a seed mixture of 231 natural genotypes of *A. thaliana* into 12 small plots. Every year, plant tissue of flowering individuals will be sampled for sequencing to track temporal changes in allelic abundances. These sequence data will be combined with previously obtained phenotypic trait data related to growth and phenology and with in situ climate data to study the “genome-phenotype-environment map”.

Interested? Check out our poster or visit us on <http://GrENE-net.org>!

