

SECTION OF GENETICS AND ECOLOGY
DEPARTMENT OF BIOLOGICAL SCIENCES
UNIVERSITY OF AARHUS



Final Report of the ESF funded workshop “evolutionary and physiological adaptation to climate induced environmental changes”

The Congen and Thermadapt programs funded by the European Science Foundation have financed the workshop entitled “Evolutionary and physiological adaptation to climate induced environmental changes”. This workshop was held in Białowieża (Poland) from the 28 June (date of arrival) to the 1 of July (departure: 2 July early in the morning) in the EU Centre of Excellence Mammal Research Institute, Polish Academy of Sciences (MRI PAS).

The main goal of this workshop, which has been organized by Cino Pertoldi and Torsten Nygaard Kristensen (Department of Biological Sciences, Ecology and Genetics, Aarhus University, Denmark), Marek Konarzewski, and Paulina A. Szafrńska (Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland) was to use a cross-disciplinary approach to increase our understanding of thermal adaptation in space and time in poikilotherms and small homeotherms. The selection of participants was done according to applicants’ interests, CV, statement of interest quality, recommendation letters, and applicants’ projects. Priority was given to applicants who come from countries that financially support the ConGen and ThermAdapt programme. However, a balanced geographical representation, sex ratio among the participants, and broad project organism taxonomy coverage was ensured.

By bringing together people with different expertise within this field, we improved our understanding of the genetic and physiological basis of thermal adaptation from individual molecules and cells to whole ecological systems. We invited leading researchers in physiology, conservation genetics, evolutionary biology, ecology and genomics, working on various levels of biological organization from molecules to populations and species (list of participants and lecturers, and program are available at the web page: www.congen.biz and www.esf.org/congen and www.esf.org/thermadapt). The invited speakers use a wide variety of methodological approaches in their research, which provided an inspiring setting for discussions on cutting edge approaches for studying thermal adaptation in free living as well as laboratory model organisms, particularly from a cross-disciplinary perspective. To understand the mechanisms behind thermal adaptation insight is needed from several biological levels, and to understand what limits the ability of species to adapt to climate induced changes, there is a need to integrate (local) short-term and long-term changes and to increase our knowledge on the importance of genetic and environmental components on the variability of ecological relevant traits. It was acknowledged during the workshop that this can be achieved by applying a multidisciplinary approach: *1) experimental population genetics, 2) collection and analysis of empirical field data, and 3) computational population genetics*. Thus, in this workshop, we tried to merge knowledge from population genetics and molecular and evolutionary physiology in a multidisciplinary fashion and discussed possible approaches to get a deeper understanding of mechanisms behind adaptation to thermal changes.

The workshop was organized in three different sessions (1st Session: *POPULATION GENETICS, PLASTICITY AND THEORETICAL ASPECTS*, 2nd session: *EXPERIMENTAL POPULATION GENETICS*, 3rd session: *COLLECTION AND ANALYSIS OF EMPIRICAL FIELD DATA*)

During these sessions several issues were discussed:

1. How close are tropical organisms really to thermal thresholds? Can this be predicted? Can predictions be validated?
2. Plastic responses occur for phenological responses and for resistance traits. To what extent do these allow organisms to cope with climate change? When are the limits reached? What role might patterns of resource distribution play?
3. Genetic limits appear to apply to climate specialist *Drosophila*. Is this also the case for other groups?
4. Observed evolutionary changes under climate change depend on biotic interactions. Can these ever be predicted? Do we need to simulate each situation to get realistic predictions?
5. Warm adapted genotypes may move into areas and displace local genotypes. Can in situ microevolution be strong enough to compete with this process?
6. What are the implications of the above for management? When should genetic translocation occur (with multiple individuals) to maximise adaptive responses? When should a species/population be considered to be facing extinction based on physiological data and warrant dramatic management responses?
7. Are associations between size components and temperature due to selection within immature developmental stages or to selection at the adult stage?
8. To what extent is niche conservation determined by what other species do?
9. Is adaptation to temperature a blessing or a problem?
10. To what extent do predictions derived from abundant species apply to rare species (and are the latter more vulnerable to climate change due to abundance per se or traits)?
11. Is the genomics and transcriptomics carried out so far “bits and pieces”?
12. What are the relative roles of the three alternative response processes to climate change: adaptation / phenotypic plasticity / dispersal? What do we need to measure (V_g / V_{gxe} / V_e) to decide?

Additionally, the assumptions on which several models have been built have been criticized as they often assume: a) No dispersal b) No evolutionary change c) Physiological limits not explicitly defined d) No interaction among species. Emphasis has been put on more complex models that can incorporate additional components like: space complexity, species interactions, evolutionary constraint, physiological limits. An open question remains: individual based, demographic or mechanistic models? Which work best?

In the three sessions several talks were presented, and below there is a preliminary list of papers which have been presented and have been offered as potential papers for a special issue of Climate Research. There will be some additional papers (one from Ary Hoffman, one from Kuke Bijlsma, one from myself and other from other invited speakers). We set a deadline for submission the first of October 2009.

Michael J. Angilletta Jr.: The role of theory in predicting ecological and evolutionary responses to climate change.

Scharf, Inon; Blanckenhorn, W.U.; Schäfer, Martin; Bauerfeind, Stephanie: Effect of maternal and offspring temperature and photoperiod on life-history traits in five European populations of the yellow dung fly.

Hywel Williams: Pleiotropic constraints on species adaptation affect ecosystem response to environmental forcing

Klaus Fischer, Isabell Karl: Exploring plastic and genetic responses to temperature variation using copper butterflies

Bahrndorff, S., Mariën, J., Loeschke, V. and Ellers, J.: Genetic variation for stress resistance and Hsp70 expression in inbred isofemale lines of the springtail *Orchesella cincta*.

Cindy Canale and Pierre-Yves Henry: Adaptive phenotypic plasticity in unpredictable environments: an advantage to withstand rapid climate changes?

Kyle G. Dexter: Evolution of Climatic Adaptation in Tropical Trees

Anders Kjaersgaard: Temperature specific locomoter activity in *Drosophila melanogaster*

M.A. de Jong: Coping with climate: geographic variation in plasticity responses of life history and wing pattern traits to temperature in *Bicyclus anynana*

Trotta V.: Thermal plasticity of wing size and shape in *Drosophila melanogaster*, *D. simulans* and their hybrids

Tejedo, M., Marangoni, F., Pertoldi, C., Richter-Boix, A., Nieceza, A., Gómez- Mestre, I., Alvarez, D., Laurila, A. Orizaola, G.: Contrasting effects of temperature and resource level variations in the larval environment on morphological plasticity in postmetamorphic frogs.

J. Balanyà, F. Rodriguez-Trelles, L. Serra, M. Matos, E. L. Rezende, M. Santos, I. Fragata, C. Rego: Potential title: Using chromosomal inversions to study climatic selection: latitudinal clines.

Below there is the full program and the final budget:

PROGRAMME

Day 1 (Monday, 29 June 2009)

7.45-8.45



Registration at the Information Point (main hall of the Institute)

1st Session (all sessions at the conference hall)

COMPUTATIONAL POPULATION GENETICS, THEORETICAL ASPECTS AND STATE OF THE ART

8.45-9.00

Opening of the Workshop

Welcome address – presentation of the Mammal Research Institute PAS

Jan M. Wójcik and

Presentation of ThermAdapt and ConGen programs

Wolf Blanckenhorn and Kuke Bijlsma

9.00-9.30

Functional tests of selected alleles-a case study in *Drosophila*

Christian Schlötterer

9.30-10.00

System-based approaches to the identification of thermotolerance mechanisms

Andrew Cossins

10.00-10.30

Thermal adaptation in Copper butterflies

Klaus Fischer

10.30-10.45



Coffee break



10.45-12.30

PRESENTATIONS by the young scientists (7 persons)

10.45-11.00

Evolutionary and environmental triggers for nonlinear change in simulated ecosystems

Hywel Williams

- 11.00-11.15** **Adaptation to environmental stress in soil organisms – Plastic responses**
Simon Bahrndorff
- 11.15-11.30** **Flexible adjustments of daily torpor in response to climate-driven environmental: explorations with food availability experiments**
Pierre-Yves Henry
- 11.30-11.45** **Comparative analysis of thermal performances curves in a tropical and temperate amphibian tadpoles communities. Are tropical taxa living on the edge?**
Marco Katzenberger
- 11.45-12.00** **Phylogeny and evolution of sex-determining mechanisms: From dependency on thermal environment to genetic control**
Lukáš Kratochvíl
- 12.00-12.15** **Standard metabolic rate and diapause behaviour in the Colorado potato beetle (*Leptinotarsa decemlineata*)**
Saija Piironen
- 12.15-12.30** **Temperature-induced phenotypic plasticity in growth, body size and sexual size dimorphism in the gecko *Paroedura picta***
Zuzana Starostová
- 12.30-14.00**  Lunch break
- 14.00 -14.45** **Adaptation to thermal heterogeneity: bridging the gap between theory and data**
Michael J. Angilletta Jr.
- 14.45-15.15** **title.....**
Nils Christian Stenseth
- 15.15 -15.45** **Singing in the rain? Response of the water frog *Rana esculenta* complex to climate change**
Piotr Tryjanowski
- 15.45 -16.00**  Coffee break
- 16.00-16.30** **Local adaptation to thermal variation: an integrated approach**
Maartje Liefing
- 16.30-17.15** **Macrophysiology as an approach to understand the impacts of environmental change**
Steven L. Chown

17.15 -17.30  Coffee break

17.30-18.45 **PRESENTATIONS** by the young scientists (5 persons)

17.30-17.45 **Comparative analysis of thermal performances curves in larval and juvenile stages in frogs. Are tadpoles more sensitive to global warming?**
Miguel Tejedo

17.45-18.00 **Tropical species of *Drosophila* fail to respond to sudden temperature changes**
Johannes Overgaard

18.00-18.15 **Fundamental limits in ecologically important traits shape species distributions**
Vanesa Kellerman

18.15-18.30 **Seasonal variability of body mass and Resting Metabolic Rate (RMR) in free ranging weasels (*Mustela nivalis*)**
Paulina A. Szafrńska

18.30-18.45 **Latitudinal clines in life history and immune function in a damselfly**
Ine Swillen

19.00  Supper

Day 2 (Tuesday, 30 June 2009)

2nd session

EXPERIMENTAL POPULATION GENETICS

8.30-9.15 **Experimentally evaluating the evolutionary and ecological susceptibility of species to climate change: can it be done?**
Ary A. Hoffmann

9.15-9.45 **Risks of genetic rescue in a changing world**
Kuke Bijlsma

9.45-10.15 **The effect of body mass and metabolic rate variation on mortality and breeding success of the root vole *Microtus oeconomus***
Karol Zub

10.15-10.30  Coffee break

10.30-11.00 **Thermal preference and heat stress resistance in clinally varying inversion polymorphisms of *Drosophila subobscura***
Mauro Santos

11.00-11.30 Metabolic correlates of selection on basal and maximum metabolic rates in laboratory mice: a cross-test of the model of the evolution of endothermy
Marek Konarzewski

11.30-12.30 PRESENTATIONS by the young scientists (4 persons)

11.30-11.45 Latitudinal Variation and Temperature Plasticity in a Polymorphic Sperm Storage Organ
D. Berger

11.45-12.00 Cold tolerance and its genetic basis in *Drosophila montana*
Laura Vesala

12.00-12.15 Phenotypic Plasticity and Evolutionary adaptations
Kyle Dexter

12.15-12.30 Comparative thermal tolerances in tropical and temperate tadpole communities. Can tropical tadpoles take the heat?
Helder Duarte

12.30-14.00  Lunch break

14.00-14.30 Thermal Adaptation in *Drosophila*: an Eco-Evo-Devo Approach
Jean R. David

14.30 -15.00 Experimental thermal evolution in water fleas
Robby Stoks

15.00-15.30 Temperature-mediated evolution makes a difference – an evolving metacommunity perspective
Luc De Meester

15.30 -15.45  Coffee break

15.45-16.15 Developmental acclimation affects clinal variation in heat resistance traits in *Drosophila buzzatii*
Volker Loeschcke

16.15 -16.45 Out of the frying-pan, into the fire: brown trout populations under anthropogenic pressure
Michael Møller Hansen

16.45-17.15 Responses to climate change: microevolution or phenotypic plasticity and how can we disentangle them?
Phillip Gienapp

17.15 -17.30  Coffee break

17.30-18.45 PRESENTATIONS by the young scientists (5 persons)

- 17.30-17.45** Evolutionary and physiological adaptation to climate induced environmental changes
Katarzyna Tarnowska
- 17.45-18.00** Phenotypic evolution in spatially-structured populations: implications of local adaptation for evolutionary responses to climate change
Richard John Walters
- 18.00-18.15** Coping with climate: adaptation and plasticity of life history traits in the tropical butterfly *Bicyclus anynana*
Maaike de Jong
- 18.15-18.30** Global warming and the evolution of virulence in infectious diseases
Gisep Rauch
- 18.30-18.45** Costs and benefits of cold acclimation in field-released *Drosophila*
Torsten N. Kristensen

18.45-19.15 Communication in science: poster presentations

19.15  Supper

Day 3 (Wednesday, 1 July 2009)

8.00  EXCURSION to Białowieża National Park

12.30-14.00  Lunch break

3rd session

COLLECTION AND ANALYSIS OF EMPIRICAL FIELD DATA

14.00-14.30 Plasticity is no panacea: maladaptive phenotypic responses to climate change will be common
Josh Van Buskirk

14.30-15.00 Impacts of a rapid climate warming event on forest plant species distribution along the elevation gradient
Jonathan Lenoir

15.00-15.30 Colder, warmer, colder, warmer, ...: Evolutionary significance of body size and cell size in ectotherms under different thermal conditions
Marcin Czarnołęski and Jan Kozłowski

15.30-15.45  Coffee break

15.45-17.00 PRESENTATIONS by the young scientists (5 persons)

15.45-16.00 More capital or income breeding – optimal strategies for indeterminate growers in the seasonal environment

Maciej Jan Ejsmond

16.00-16.15 Life history responses to nutritional limitation in a tropical butterfly *Bicyclus anynana*

Marjo Saastamoinen

16.15-16.30 Environment specific heterosis in *Drosophila melanogaster*

Anders Kjærsgaard

16.30-16.45 Learning about populations history using an approximate bayesian computation

Joao Lopes

16.45-17.00 Evolutionary relationships between the common bean *Phaseolus vulgaris* and closely related bean species

Angela Mina-Vargas

17.00-18.30 CONCLUSION AND DISCUSSION



19.00 Dinner & Party (in the garden of Hotel “Białowieski” in Białowieża)

DEPARTURE FROM BIAŁOWIEŻA (Thursday, 2 July 2009)



06.00 Departure of the 1st bus to Warsaw Airport
Arrival between (09.00 and 11.00)

12.00 Departure of the 2nd bus to Warsaw Airport
Arrival between (15.00 and 17.00)

List of Speakers

Michael J. Angilletta Jr., *USA*

Kuke R. Bijlsma, *The Netherlands*

Wolf Blanckenhorn, *Switzerland*

Steven L. Chown, *South Africa*

Marcin Czarnołęski, *Poland*

Andrew Cossins, *UK*

Jean R. David, *France*

Luc De Meester, *Belgium*

Klaus Fischer, *Germany*

Phillip Gienapp, *Finland*

Michael Møller Hansen, *Denmark*

Ary A. Hoffmann, *Australia*

Marek Konarzewski, *Poland*

Jan Kozłowski, *Poland*

Jonathan Lenoir, *Denmark*

Maartje Liefting, *The Netherlands*

Volker Loeschcke, *Denmark*

Cino Pertoldi, *Denmark*

Mauro Santos, *Spain*

Christian Schlötterer, *Austria*

Nils Christian Stenseth, *Norway*

Robby Stoks, *Belgia*

Piotr Tryjanowski, *Poland*

Josh Van Buskirk, *Switzerland*

Karol Zub, *Poland*

Abstracts of lectures

(Alphabetical order by the lecturers' surnames)

Michael J. Angilletta Jr.

Adaptation to thermal heterogeneity: bridging the gap between theory and data

Indiana State University, USA
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Thermal biologists have amassed thousands of data sets, but have generated only a handful of theoretical models to explain these data. The few models that we have rely on the concept of a performance curve to predict the evolution of thermosensitivity or thermoregulation. These models predict a close match between the modal body temperature and the temperature that maximizes performance (the thermal optimum). Yet thermosensitivity, and its capacity for acclimation, often differs from that predicted by current models. Likewise, a recent comparative analysis suggests that thermoregulatory behavior does not accord with existing theory. To advance our understanding, we need more complex models of thermal adaptation. These models should account for the spatial and temporal structure of thermal heterogeneity, the coadaptation of thermosensitivity and thermoregulation, and the ecological interactions among species. Models that incorporate one or more of these factors yield novel predictions about thermal adaptation. My collaborators and I are currently testing such models experimentally in the lab and the field.

Kuke (R.) Bijlsma

Risks of genetic rescue in a changing world

Population & Conservation Genetics, Theoretical Biology, University of Groningen,
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Fragmented populations of endangered species often show considerable signs of genetic erosion, impeding their fitness and consequently greatly increasing their extinction probability. To alleviate the negative effects of genetic erosion it is becoming practice to genetically rescue such populations by introducing some unrelated individuals from another population (the rescuers) into the affected population. It is thought that this measure will decrease the homozygosity in the population concerned thereby reducing the effect of inbreeding depression and thus significantly increase the fitness of the population. The expectations, however, may depend significantly on (i) the genetic make up of the rescuers as they will certainly also carry deleterious alleles and their genome often becomes highly overrepresented in the population, (ii) whether the environmental conditions are benign and constant or are changing and stressful (e.g. high temperature stress, global warming scenarios), (iii) the long-term size of the rescued population, as renewed inbreeding may exaggerate the effects of genetic erosion. In this talk I will explore a number of possibilities using *Drosophila* as a model organism

Steven L. Chown

Macrophysiology as an approach to understand the impacts of environmental change

Centre for Invasion Biology, Department of Botany and Zoology, Stellenbosch University, Private Bag X1, Matieland
7602, South Africa

A growing number of modelling studies are demonstrating that assemblage level characteristics, such as the species abundance distribution, species-area relationship, and the species occupancy distribution can be derived from patterns of aggregation at multiple spatial scales. At several of these scales, aggregation is dependent on the autocorrelation structure of the environment and the way in which this is translated through individual responses to spatial autocorrelation of abundance. The relationship between the environment and abundance is a function, *inter alia*, of physiological and behavioural variation. Macrophysiology provides a way of exploring physiological variation across space and time, and across a range of hierarchical levels, to understand the ecological implications thereof. By using an $r \times c$ matrix approach it provides an explicit connection to other matrix-based approaches such as mechanistic niche modelling, spatially explicit population viability assessment, and metacommunity models. This large-scale physiological perspective also provides new insights into the realized and likely impacts of the major global change drivers. Here, I explore the macrophysiological approach in the context of environmental change, highlighting both its strengths and some of the challenges faced when implementing it.

Marcin Czarnoński and Jan Kozłowski

Colder, warmer, colder, warmer, ...: Evolutionary significance of body size and cell size in ectotherms under different thermal conditions

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Adult body size increases with latitude and altitude in many species of ectotherms; similar clines exist for cell size in some species. These two traits respond to temperature in lab experiments in a manner consistent with the geographic patterns, though our knowledge on the cell size responses is less complete. Evolutionary significance of such reactions at different biological levels remains unclear, and we are not sure to what extent the two types of responses are causally inter-related. First, we use modeling of optimal resource allocation to growth and reproduction to identify conditions that lead to the responses of life histories to temperature observed in nature. In particular, we show how a temperature-dependence of mortality and that of the size-scaling exponents of biomass production contributes to the origin of the observed patterns in growth rates and body size across temperature gradients. Second, we integrate current knowledge from physiology and biophysics to discuss the role of cell size in coping with challenges set by thermal conditions of the environment. In particular, we focus on the role of cell membranes in intra- and inter-cellular transport, as both transport barriers and enhancers, and in generating physiological and life history costs (maintenance of ion gradients, remodeling of membranes in response to changing temperature, damage by free radicals). Finally, we underline the need for a deeper integration of the responses to temperature at different levels of biological organization to form coherent theoretical basis for our better understanding of thermal evolution.

Andrew Cossins

System-based approaches to the identification of thermotolerance mechanisms

University of Liverpool, UK.

Animals display an impressive ability to enhance tolerance to warm and cold lethal stress simply by prior exposure to sub-lethal thermal conditions. A number of proximate mechanisms have been identified including heat shock proteins, desaturases, cryoprotectants etc, but little is known about how the induction of these factors is regulated. We have identified a clearcut cold tolerance phenotype in the nematode *C. elegans* that is induced by culturing at reduced temperature, and is rapidly lost by culturing at normal temperatures. We have identified ~200 genes whose transcript expression is affected by altered growth temperature, and approximately 40 metabolites whose concentrations are affected by conditioning including trehalose, glycerol and glycerol-3-phosphate. Using interference RNA we have screened ~700 genes, including the transcriptionally cold-responsive genes and ~500 genes with a nominal regulatory function, to identify those whose ablation interferes with the induction of the phenotype. Finally we have modelled these genes and metabolite using gene network models to identify pathways and processes that might lay upstream in an extended regulatory pathway controlling cold tolerance.

Jean R. David

Thermal Adaptation in *Drosophila*: an Eco-Evo-Devo Approach

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Temperature tolerance and adaptation is probably the major feature explaining the distribution and abundance of ectotherms. All biological processes are temperature sensitive but in various ways. Moreover, the thermal environment is variable according to day time, season or geographic location. A way to investigate thermal adaptation of a morphometrical trait is to investigate its Phenotypic Plasticity which implies an interaction between environment and development, that is Eco-Devo. The reaction norm (RN) approach is convenient for describing plasticity and, since most RN are not linear, quadratic or cubic polynomial functions are used. A given RN can be characterized by the trait value but also by its reactivity to temperature, that is its plasticity. Comparing different traits reveals very different shapes of the RN, suggesting at first sight some unknown developmental constraints, so that plasticity would be deprived of any adaptive or evolutionary interest. For a given trait, however, RN are genetically variable when comparing populations of the same species adapted to different climates, and a geographic adaptation can be proposed. Similar results are also observed when comparing different species clearly adapted to different climates. In such cases, an evolutionary dimension is introduced in the analysis of plasticity, and the adaptive significance of RN shape variations is demonstrated by this Eco-Evo-Devo- analysis.

Temperature-mediated evolution makes a difference – an evolving metacommunity perspective

Luc De Meester, Wendy Van Doorslaer & Robby Stoks

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A change in temperature represents a selection pressure, which can translate in micro-evolutionary changes as well as in changes in species composition (species sorting). Experimental evolution trials show temperature-mediated genetic changes in the water flea, *Daphnia magna*, within a time frame of a few months. We here ask the question whether these changes impact ecological interactions. More specifically, we quantified to what extent genetic adaptation to a temperature increase changes the capacity of a local population to reduce establishment success of immigrant genotypes that are pre-adapted to higher temperatures. We show that 1.5 years of micro-evolutionary change significantly reduces competitive superiority of genotypes derived from southern Europe when invading a U.K. population in a high temperature mesocosm. Our results reveal a significant impact of micro-evolution on the relative importance of local and regional processes in the response of populations to climate change.

Thermal adaptation in Copper butterflies

Klaus Fischer

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Variation in environmental conditions is a significant source of mortality in nature. In particular variable thermal environments may pose substantial challenges for key elements of fitness such as survival and reproduction. Against this background we have investigated thermal adaptation in Copper butterflies using altitudinal clines and environmental manipulations. I will first explore the significance of temperature-mediated plasticity in body size and the mechanistic basis of the temperature-size rule. Then, I will demonstrate altitudinal variation in life-history and stress resistance traits, with high-altitude animals showing e.g. increased cold- but decreased heat-stress resistance, but little variation in the expression of stress-inducible heat-shock proteins in response to different ambient temperatures as opposed to low-altitude butterflies. Using allozyme markers, I will next show that high- and low-altitude populations are genetically differentiated to a remarkable degree, which is basically caused by variation at a single locus, PGI. Finally, I will demonstrate that PGI genotype significantly affects growth patterns and cold stress resistance. The PGI genotype dominating in high-altitude populations showed patterns consistent with those found in high-altitude animals. Thus, PGI is likely to contribute significantly to thermal adaptation in the butterfly species investigated.

Responses to climate change: microevolution or phenotypic plasticity and how can we disentangle them?

Phillip Gienapp

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Changes in phenology, the timing of life-cycle events, as bud burst, hibernation, hatching or breeding, are among the most prominent effects of climate change. Rising spring temperatures

have led, for example, to an advancement of flowering in plants, appearance in spring of insects or breeding time in birds. These phenotypic changes are sometimes interpreted as an evolutionary response to climate change but they can also be the result of phenotypic plasticity. Disentangling these processes will contribute to our general knowledge of evolution in natural populations and also to assessing possible negative impacts of climate change. While phenotypic plasticity allows a quick response to a changing environment, genetic changes will happen more slowly but are more likely to enable population or species persistence in the long term. However, disentangling these two processes can be logistically and methodologically challenging. In this presentation, I will first give a general overview of the evidence of microevolution in wild populations and how (and how not) we are able to disentangle phenotypic plasticity from genetic change. Apart from directly and indirectly assessing possible genetic changes, testing whether the observed phenotypic changes are consistent with ‘sustainable evolution’ offers another indirect way to address this question. Selection always reduces population mean fitness and too strong selection can hence lead to population extinction. This means that there is a maximum rate of ‘sustainable evolution’, which cannot be exceeded over longer time. Using this approach we will look at the evidence for climate change induced evolution by reviewing the literature on, e.g. avian breeding time or insect phenology.

Out of the frying-pan, into the fire: brown trout populations under anthropogenic pressure

Michael M. Hansen

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Organisms throughout the biosphere are faced with negative consequences of anthropogenic pressure. In brown trout and other salmonids, one of the most pressing problems consists in spawning intrusion by stocked or escaped hatchery strain fish into wild populations, thereby swamping indigenous adaptive variation. Moreover, future climate change is expected to significantly affect populations. Through a series of studies based on contemporary and historical samples, we have shown that hatchery strain trout generally exhibit reduced fitness in the wild, and many wild populations are surprisingly little introgressed. Based on analysis of 61 microsatellite loci in historical samples (archived scales from the 1940s), hatchery strains and contemporary populations of brown trout subject to stocking, we identify loci under possible hitch-hiking selection in stocked vs. wild fish. Patterns of differentiation suggest that selection acts against stocked trout, but introgression rate may become too strong for selection to override immigration. Nevertheless, even in strongly introgressed populations, Bayesian clustering analysis using linked loci demonstrates the presence of non-admixed individuals. A common garden experiment comparing early life history traits among four trout populations incubated at three different temperatures (2, 5 and 6 degrees) shows significant Q_{st} values for two traits. Additionally, temperature reaction norms suggest that populations are adapted to their local temperature regimes. On one side, the results suggest that current adaptation to temperature regimes may be maladaptive under future climate change scenarios, but on the other side the results demonstrate an evolutionary potential that may enhance adaptation to a warmer climate. Collectively, brown trout shows some resilience towards introgression by hatchery strain trout and also exhibit some climate change adaptability. However, the fate of the populations ultimately depends on the severity of the anthropogenic pressure they experience.

Experimentally evaluating the evolutionary and ecological susceptibility of species to climate change: can it be done?

Ary A. Hoffmann

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The long term resilience of populations of insects and other organisms under climate change will depend on their ability to genetically adapt and/or to respond through plastic changes. Species that are living close to physiological limits and with limited adaptive potential may be particularly susceptible even when they currently have a large population size. In this talk I use a range of *Drosophila* species to evaluate whether susceptibility can be assessed from experimental studies. I discuss difficulties associated with measuring physiological limits but suggest ways this might be done more effectively. I also outline findings that have emerged from a comprehensive evaluation of genetic variation in molecular markers and quantitative traits across populations and species. I suggest surrogates that might serve as indicators of evolutionary potential and physiological limits in species.

Metabolic correlates of selection on basal and maximum metabolic rates in laboratory mice: a cross-test of the model of the evolution of endothermy

Marek Konarzewski 1, 2 and Andrzej Gębczyński 2

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The aerobic capacity model postulates that high basal metabolic rates (BMR) underlying endothermy evolved as a correlated response to the selection on maximal levels of oxygen consumption associated with locomotor activity (V_{O2max}). The recent assimilation capacity model specifically assumes that high BMR evolved as a by-product of the selection for effective parental care, which required long-term locomotor activity fueled by energy assimilated from food. To test both models we compared metabolic, anatomic and behavioral correlates to two independent artificial selections on (1) body mass-corrected BMR and (2) maximum body mass-corrected metabolism elicited by swimming (V_{O2swim}) in laboratory mice. V_{O2max} elicited by running on the treadmill (V_{O2run}) did not differ between lines selected on BMR. Likewise, BMR of mice selected on V_{O2swim} did not differ from that of the controls, despite significant differences in V_{O2run} , duration of running (a measure of stamina, t_{run}), and the distance run to exhaustion (d_e). Higher V_{O2max} in selected animals was positively correlated with higher masses of gastrocnemius muscles and heart but not to other visceral organs (intestine, stomach, liver and kidneys), which in turn were much larger in mice selected for high BMR. These findings point to the lack of genetic correlation between BMR and V_{O2max} , which is supported by observed patterns of organ size variation.

In contrast, selection on BMR resulted in the elevation of spontaneous long-term locomotor activity and food intake, which were not found in animals selected on V_{O2swim} . Our results therefore corroborate predictions of the model of evolution of endothermy invoking selection on assimilation capacity rather than the aerobic capacity.

Impacts of a rapid climate warming event on forest plant species distribution along the elevation gradient

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Do plant species shift their ranges in pace with the rapidly changing climate? Here we aimed to assess the magnitude of current changes in plant species distribution to answer this question for a currently understudied ecosystem, namely temperate forest. We worked in mountain environments below the tree-line limit since it provides an ideal environment for detecting shifts in temperate plant species distribution in response to climate warming because of steep and unidirectional climatic gradients across elevation. We addressed our study question at two spatial scales (whole of France and individual mountain ranges within France) and for three different range measures (overall species distributions, life-stage specific distributions, and community composition). At the scale of France, we estimated an upward shift in plant species optimum elevation averaging 65 m for 171 forest species between 1971 and 1993, with a larger shift for herbs, probably reflecting their faster generation turnover. For 13 out of 17 tree species, we found that the mean altitude of presence records for the seedling life stage was higher than for the adult life stage during the studied warm period (1986-2006). At scale of individual mountain chains, we documented changes in plant community composition towards warmer and dryer conditions between 1989 and 2007. A synthetic analysis linking the three range measures to species' biological, ecological and biogeographical characteristics confirmed generation turnover as the most important life trait determinant of the magnitude of the realized range shift. Overall these results give new insights supporting a significant upward shift in plant species distribution coherent with climate warming. It also highlights that warming-driven range shifts are already now occurring in temperate ecosystems.

KEYWORDS: climate change, climatic niche, community, elevation, forest plant species, global warming, mountains, range shift

Local adaptation to thermal variation: an integrated approach

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Changes in temperature due to global climate change are expected to have a major effect on species performance. Especially since temperature is considered one of the main mediators of phenotypic plasticity in organisms. We can make use of existing geographic variation in temperature regimes to study adaptation to thermal changes, and thereby predict possible effects of climate change. In field populations, consistent ecotypic variation in level of thermal plasticity of ectotherms is found. These differences exist for different species and across different scales. I will

discuss how the plastic responses differ for life history and morphological traits. The physiological mechanisms and costs associated with adaptation to thermal variation are addressed in laboratory experiments, using artificial thermal regimes and various proxies for temperature tolerance. A better understanding of selection on phenotypic plasticity in habitats with high thermal variation is not only of interest to evolutionary ecology, but can also aid in identifying the vulnerability of species and ecosystems to global warming.

Developmental acclimation affects clinal variation in heat resistance traits
in *Drosophila buzzatii*

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We studied the possible change of patterns of clinal genetic variation in longevity, starvation and knock-down resistance after development at fluctuating as compared to constant temperatures in *Drosophila buzzatii*, using 9 populations that originated from an altitudinal gradient on the island of Tenerife, Spain. Genetic variation along the gradient was found in both stress resistance traits, with higher stress resistance in flies developing at the fluctuating temperature. The clinal pattern differed among rearing regimes and sexes, with differences among populations generally being larger when developing at fluctuating temperatures. The clinal pattern in heat knock-down resistance at fluctuating temperatures disappeared when the flies were reared at constant temperatures. This emphasises the environment dependency of plastic responses to thermal variation.

Thermal preference and heat stress resistance in clinally varying inversion polymorphisms of
Drosophila subobscura

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Latitudinal clines in the frequency of various chromosomal inversions are well documented in *D. subobscura*. Because these clines are roughly parallel on three independent continents, they have undoubtedly evolved by natural selection. The simple idea that latitudinal gradients in climate favor different inversions at different latitudes results attractive, and several lines of evidence suggest that temperature may be the underlying selective factor. However, laboratory natural selection experiments rendered some conflicting results with the natural patterns, which could

simply reflect a “fault” in the experiment due to a mismatch between the thermal regimes and the actual optimum temperatures of the various gene arrangements. Here we explore whether the thermoregulatory behavior of *D. subobscura* has a genetic component. To be more specific, we analyzed whether or not individuals carrying different chromosomal arrangements also vary in their thermal preferences (Tp: the body temperature an organism chooses when provided with a range of potential temperatures). Furthermore, because *D. subobscura* can occasionally experience injurious or lethal effects of very high body temperature, we have also assessed heat resistance (Tko: the temperature required to knock out a fly in a water-bath) in the same flies that had been scored for Tp. Our results show that although Tp and Tko are uncorrelated, flies carrying “cold-adapted” gene arrangements tend to choose lower temperatures in the laboratory or have a lower heat stress tolerance, in line with what could be expected from the natural patterns. Different chromosomes are mainly responsible for the underlying genetic variation in both traits, which explains why they are linearly independent. If Tp corresponds closely with temperatures that maximize fitness, a more focused prediction comes up from our present data regarding the evolution of the chromosomal inversion polymorphism in laboratory cage populations since temperature was the only driving force there, something that is far from clear when dealing with natural populations along a latitudinal gradient. Consistent patterns between the population cages outcomes and our results here emerge, which suggest that thermoregulation does affect fitness in *D. subobscura* but also that there is more to latitudinal clines than thermoregulatory behavior. Also consistent with data from the regular tracking of the inversion polymorphism ever since the colonization of the Americas by *D. subobscura*, we tentatively conclude that selection on tolerance to thermal extremes is more important in the evolution and dynamics of clinal patterns than the relatively “minor” adjustments from behavioral thermoregulation.

Functional tests of selected alleles-a case study in *Drosophila*

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The question of how organisms cope with changes in the environment has been of long standing interest to both ecologists and evolutionary biologists. More recently, in the light of global warming, this question has also received considerable interest from governmental agencies. Nevertheless, despite the longstanding interest, very little is known about the genetic changes required for adaptation to a changing environment. Using the genetic model organism *D. melanogaster*, I will discuss how population genetic methods can be used to identify genes contributing to the adaptation of natural populations to their environment. Using the example of the cramped locus, I show how genetic tests could be designed that allow the functional comparison of naturally occurring alleles.

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Experimental thermal evolution in water fleas

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We present two experimental evolution studies in which we evaluated genetic responses of *Daphnia* to simulated global warming. In both experiments, a thermal selection part was followed by a life table experiment under laboratory conditions at different temperatures to quantify micro-evolutionary changes. In a first experiment, *Daphnia* populations were exposed for six months to different temperature treatments in outdoor mesocosms that mimicked small pond systems. We found a fast evolutionary response in size at maturity showing that *Daphnia* is able to genetically adapt to increased temperature within one growing season. In a second selection experiment in the laboratory, after three months of selection, we found a micro-evolutionary response to temperature in performance, but only in one of two culling regimes, highlighting the importance of population dynamics in driving micro-evolutionary change within populations. The results of the competition experiment were in agreement with predictions based on performance as quantified in the life table experiment and illustrate that micro-evolution within a short time frame has the ability to influence the outcome of intraspecific competition. When comparing the results of both experiments, we can conclude that the ecological context is very important in determining with which traits species adapt to global warming.

Singing in the rain? Response of the water frog *Rana esculenta* complex to climate change

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Recent studies on climate responses in ectothermic (cold-blooded) vertebrates have been few in number and focussed on phenology rather than morphology and population genetic structure. Although amphibians are ectothermic vertebrates, weather and climatic conditions may also impact on their morphology, and thereby affect their survival rates and population dynamics. Here I show, in a unique long-term study during the period 1963-2003 in an agricultural landscape in western Poland, that the body length of two water frog parental species (males of both *Rana ridibunda* and *R. lessonae*) increased significantly. However, their hybridogenetic hybrid *R. esculenta* did not show similar changes. A significant relationship with a large-scale climatic factor, the winter North Atlantic Oscillation index, was found: positive for *R. ridibunda* males and *R. lessonae* females, and negative for *R. esculenta* females. The obtained findings, the first for amphibians, are consistent with other studies reporting that recent climate change had affected the

morphology of animals. However, we also show that changes in amphibian phenotype linked to climate may vary independently between (even very similar) species, and I plan to discuss some genetical consequences of climate to hybridogenetic breeding type of water frogs.

Plasticity is no panacea: maladaptive phenotypic responses to climate change will be common

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There is much hope that phenotypic plasticity will enable organisms to adjust to rapid anthropogenic change in the Earth's climate in the coming decades. Indeed, individuals of many species routinely respond to changing environmental conditions by facultatively adjusting their phenotype, and some studies implicate plasticity as a primary cause of phenotypic change associated with climate change. Of course, plasticity must be adaptive if it is to counteract detrimental impacts of climate change. Is it? In a review of published experiments, I used two criteria to evaluate the adaptive value of temperature-induced plasticity: (1) Does the change result in improved individual fitness components as judged from demographic theory, and (2) Is the phenotypic response to warming congruent with observed genetic divergence among populations evolving within different climates? Overall, the data suggest that phenotypic plasticity will not generally benefit organisms under climate change. Some responses to warm conditions, such as higher developmental rates, do appear adaptive. But these are outweighed by many other maladaptive responses. Moreover, because countergradient variation is prevalent in many taxa and traits, induced responses to temperature are often opposite to those that have evolved in warm climates. These findings suggest that plasticity is no panacea for the challenges posed by climate change.

The effect of body mass and metabolic rate variation on winter mortality of the root vole
Microtus oeconomus

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Body mass and metabolic rate are individual traits of great interest to both ecology and physiology. The main goal of our investigation was to estimate the strength and direction of natural selection on individual body mass, maximum (or peak) metabolic rates (PMR), and resting metabolic rates (RMR) in a population of root voles *Microtus oeconomus* in a fenced enclosure in natural habitat. Winter is characterized by food shortages and low temperatures, and overwinter survival of root voles is related to energy expenditures, which are determined by metabolic rates and body mass. Therefore we expected that small individuals, or those with low resting metabolic rates, would be more likely to survive winter. Moreover, harsh winter conditions should favor individuals characterized by higher maximum metabolic rates.

Beginning in autumn 2006, we investigated the mortality of root voles during three consecutive winters. The density of voles was highest during the first season, which was followed by a 'crash' year (low population density) and then a year of population increase. In the first winter surviving individuals had lower body mass than the pre-winter population mean, but higher RMR (corrected for the effects of body mass). In the second winter we also found significant selection favoring high RMR, but there was no selection on body mass. Mean RMR increased during the second year, but decreased while population density increased during the third year. In both of the first two seasons PMR were inversely related to RMR. During the third winter, survival rates were the highest observed in the study, but we did not detect selection on either metabolic rate or body mass.

Our results demonstrate that selection for both body mass and metabolic rates was strongest at high and low population densities, and weakest when population density was recovering after a 'crash' year. This pattern may result from food availability or quality favouring different phenotypes in consecutive years, or an interaction between food and population density.

Abstracts of students' lectures and posters (Alphabetical order by the participants' surnames)

**Laila Hanghøj Andersen^a, Torsten N. Kristensen^{a,b}, Volker Loeschcke^a, Søren Toft^a
and David Mayntz**

Nutritional impacts on stress resistance, development and fecundity
in *Drosophila melanogaster*

[POSTER]

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Dietary nutrient composition may continuously influence stress resistance and life history traits of organisms. We addressed this issue by raising male and female fruit flies of the species *Drosophila melanogaster* under two nutritional regimes: a sucrose enriched growth medium and a protein enriched growth medium. We studied nutritional responses of males and females to chill coma recovery, heat knockdown resistance and tolerance to desiccation as well as flies' ability to recognise and avoid predation from a wolf-spider. In addition, we examined differences in activity. We also compared egg-to-adult viability and productivity within the two nutritional regimes. We found a clear connection between a high protein intake and heat and desiccation tolerance and increased productivity. On the contrary, a sucrose enriched growth medium increased cold resistance (decreased recovery time from chill coma in adult flies) compared to a protein enriched diet. Female flies were more tolerant to chill coma, heat knockdown and desiccation stress compared to males. Males were quicker than females to recognize and/or avoid a predator. This may partly have been explained by a lower level of activity in the males compared to the females. We found viability from egg to adult to enhance males development on the sucrose enriched medium, while female survival was highest when developed on the protein enriched medium. We also found females developed on the protein enriched medium to produce more eggs than females developed on the sucrose enriched medium. Our results indicate that nutrition have high effects on the ability to cope with stress, but that optimal nutrient composition for coping with stress depends on the type of stress.

Simon Bahrndorff

Adaptation to environmental stress in soil organisms – Plastic responses

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Plasticity has important implications for the ability of organisms to acclimate to future conditions and it has been argued that species living under unpredictable thermal conditions need to have more flexible physiological capabilities to meet with thermal stress than species living in thermally stable environments. However, rather few studies have looked at plastic responses and adaptation

in soil organisms. We have looked at plastic responses, especially induced heat hardening in the collembola, *Orcehesella cincta*. The relationship between thermal resistance and expression of inducible heat shock proteins, especially Hsp70, depends on the species and temperature treatments. The induction of Hsp70 has been shown to be essential for heat stress survival in a number of species, yet the maximum protein expression levels do not coincide with peak survival after heat hardening in *Drosophila*.

In the present study we compared heat-induced expression of the heat shock protein Hsp70 and thermal resistance. Hsp70 gene and protein expression levels were measured at time points 2, 4, 6, 23, 27, 49 h after a heat hardening treatment.

Thermotolerance increased over time after heat hardening until 49 h after exposure when the experiment ended. However, the expression of *hsp70* messenger RNA reached a peak within the first 2 h and then sharply decreased after 6 h. Within 23 h *hsp70* expression was back to control levels. Surprisingly, protein levels of Hsp70 followed thermotolerance and reached the highest levels 49 h after heat hardening and a significant positive association was found between thermotolerance and Hsp70 protein levels, but not with *hsp70* mRNA levels.

Our results support a strong correlation between Hsp70 expression levels and thermal resistance following a heat hardening treatment. They also show that gene and protein expression follow different dynamics. Other studies have shown population differences in other plastic traits in *O. cincta*, although the evolutionary consequences of the present results are yet to be tested.

D. Berger, M.A. Schäfer, S.S. Bauerfeind and W.U. Blanckenhorn

Latitudinal Variation and Temperature Plasticity in a Polymorphic
Sperm Storage Organ

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In the yellow dung fly *Scatophaga stercoraria*, laboratory reared females possess either three or four sperm storage organs (spermathecae). Common garden rearing in three different temperatures revealed that six European populations lacking significant population structure at 'neutral' markers are genetically differentiated regarding this polymorphism. Interestingly, northern populations tended to show higher frequencies of four spermathecae than southern populations, suggesting that selection varies systematically with latitude. Furthermore, at low temperatures, reflecting natural developmental conditions, the frequency of females with four spermathecae was very low in all of the six studied populations whereas the frequency strongly increased at high temperatures. The observed variation of the rare four spermatheca phenotype could be explained by spatio-temporal differences in the relative strength of sexual versus natural selection as suggested by previous work. However, additional dissections of field caught females indicate that the overall frequency of four spermatheca expression in the wild is next to zero, lending support to the alternative hypothesis that the four spermatheca phenotype reflects a slightly deleterious developmental distortion which is purged out in southern climates, but due to its recessive nature and temperature dependent expression, remains hidden and maintained in northern climates.

Resurrection ecology and genetics of biological archives: the response to climate
in space and time
[POSTER]

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Biological archives of aquatic microcrustaceans offer the unique opportunity to study evolutionary and physiological adaptation to climate induced environmental changes.

Many zooplankton species produce resting stages which can be “resurrected”. This natural phenomenon allows us to study the population genetic and phenotypic response to environmental changes. Previous studies showed that *Daphnia* species and genotypes differ in their somatic growth rate and fitness if subjected to different water temperatures. In order to unravel the process of adaptation to temperature in different climate zones and under different levels of anthropogenic disturbance, it is necessary to sample biological archives of lakes along a latitudinal gradient in Europe. Daphnids of past and contemporary decades will be subjected to different temperature regimes in common garden experiments. In addition to the measurement of genetic variation in neutral molecular markers (microsatellites and mitochondrial DNA) we will also identify candidate genes associated with variation in temperature. This approach, using field and experimental data in combination with molecular genetic markers will allow us to determine the strength and rate of adaptation to current global changes. Our project contributes to the recently established Research Center on Biodiversity and Climate which aims to explain the interactions of organismal biodiversity and climate.

Impact of landscape structure on the population genetics
[POSTER]

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The Agent-Based Model (ABM) ALMaSS has been developed with a view to realistically address the spatio-temporal configuration of populations and to assess how the population is affected by the spatio-temporally explicit landscape structure and management. We investigated neutral evolution during landscape shifts in the ecologically and behaviourally realistic field vole model (*Microtus agrestis*) in the ALMaSS system. Using heritable, neutral genes each vole was diploid with Mendelian transmission of genes. Each individual's genes and location was recorded once per simulation year and the population genetic structure was evaluated in three different landscapes

with varying degrees of fragmentation. Results indicate that the system is very sensitive to landscape topography. A shift in the level of fragmentation influences the landscape connectivity and affects the spatial spread of mutations. We argue that climate change can affect the genetic structure of populations through its affect on the level of landscape fragmentation.

Phenotypic Plasticity and Evolutionary adaptations

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Global climate change is expected to alter precipitation patterns in the tropics. It is uncertain how or if tropical forest communities, and the tree species which comprise them, can adapt to these changes. To address this question, we examine the plasticity and evolutionary lability of tree species in French Guiana for traits related to adaptation along a precipitation gradient (from 2000 to 4000 mm rainfall/year). Some species are restricted to either end of the gradient while other species occur across its entire breadth. We first show that species at opposite ends of the gradient differ in certain traits (e.g. specific leaf area, sapwood density). We then show that widespread species have greater intraspecific variation for these traits than restricted species and that the pattern of variation within species along the gradient reflects that found among species. These results suggest that the widespread species will be able to cope with changing precipitation patterns while restricted species may not. We next use phylogenetic analyses to assess the evolutionary lability of these traits. Our preliminary results show that close relatives can differ greatly for these traits. This in turn suggests that at longer time scales, species can readily adapt to different precipitation regimes.

Comparative thermal tolerances in tropical and temperate tadpole communities.

Can tropical tadpoles take the heat?

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The impact of climate change on terrestrial ectotherms is predicted to be higher in tropical communities. Assuming upper thermal tolerances are homogeneous along a latitudinal gradient, their proximity to environmental temperatures suggests a higher vulnerability to extinction compared to temperate regions, where warming would actually be beneficial. In this communication we tested this prediction by collecting environmental temperatures and critical thermal maxima of two larval amphibian communities: a subtropical community from the Chaco, Argentina with high environmental temperatures ranging from 20°C to 42°C where we studied 18 species comprising five different amphibian families, and a temperate Iberian community with lower pond temperatures ranging from 5°C to 34°C with 8 species comprising six families. Results indicate that tropical tadpoles species can tolerate much higher temperatures (average species $CT_{max} = 42,3$ °C, range 40,6°C - 44,7°C) than temperate species ($CT_{max} = 37,9$ °C, range 36,6°C - 39,7°C). These results suggest that latitudinal differences exist in tadpole thermal tolerances, considering that some lineages are shared between both amphibian communities (*Bufonidae* and *Hylidae*), thus suggesting adaptive evolutionary divergence within clades. Also, it is clear that tropical species are closer to their physiological limit than temperate ones and therefore at higher risk of extinction to global warming.

More capital or income breeding – optimal strategies for indeterminate growers
in the seasonal environment

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We use dynamic optimization algorithm to find adaptive schedules of energy allocation to growth and reproduction in the seasonal environment for an organism that can be capital or income breeder. Value of newborns in our model is related to the timing of reproduction. Our results show that the relationship between newborns value and storing reserves for reproduction can be highly negatively correlated. Importantly the reliance on reserves in reproduction may be optimal without the stochastic changes in environmental conditions usually assumed in the models of capital breeding evolution. Our results confirm also the idea that optimality of capital breeding strategy depends on efficiency of energy channeling from reserves to reproduction.

Flexible adjustments of daily torpor in response to climate-driven environmental:
explorations with food availability experiments

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There is an increasing interest in understanding how organisms adapt to changing environments. Extreme climatic events are increasing and have profound demographic and evolutionary impacts. To which extent climate-driven food shortages could be compensated by physiological plasticity? We tested with a food restriction experiment, how captive Grey Mouse Lemurs modify torpor-based energy savings in response to contrasted regimes of food availability. Twelve individuals were fed *ad libitum* (“good year”), and 12 were exposed to a 40% caloric restriction (“bad year”). Afterwards, six of each group were exposed to a 80% caloric restriction (“extreme event”). Energetic, plastic modulations were characterised by changes in daily torpor. Overall, daily torpor appeared to be flexible and adjusted to food availability, with a greater flexibility of the passive drop of body temperature. Our results suggest that facultative, heterothermic organisms could partly overcome climate-driven, sudden changes in food availability by a flexible modulation of energy savings. However, this may have costs that remain to be evidenced.

Coping with climate: adaptation and plasticity of life history traits
in the tropical butterfly *Bicyclus anynana*

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The afro-tropical butterfly *Bicyclus anynana* shows striking seasonal plasticity for wing patterns and life history traits, which functions as an adaptation to contrasting wet-dry seasonal environments. Temperature is the single most important climatic variable determining *B. anynana* seasonal phenotype for our well-studied population from Malawi, where temperature is highly correlated with rainfall and thus a reliable indicator for the adaptive seasonal forms. However, patterns of temperature-rainfall correlation vary strongly throughout the geographical distribution of *B. anynana*, and different regions therefore pose different selection pressures on the species’ plastic responses to temperature. The outcome of past adaptation can be used as a proxy for the potential for future adaptation of this organism to climate change. We explored the nature and extent of developmental plasticity and genetic adaptation to temperature by comparing various life history (related) traits and wing pattern for a Malawian population and a South African population at three common garden temperatures in a family design. Results revealed very similar reaction norms for the two populations, and indicate the importance of phenotypic plasticity over genetic adaptation in coping with local climate. This was especially the case for traits that can be regulated by acclimation during the butterfly’s adult life span.

Comparative analysis of thermal performances curves in a tropical and temperate amphibian
tadpoles communities. Are tropical taxa living on the edge?

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Amphibian physiological performance is highly affected by environmental thermal characteristics. With expected global warming, the ability to perform ecologically relevant functions may be compromised, affecting their general fitness. Assessing how a species performs at a range of temperatures will highlight its susceptibility to temperature changes and subsequently its risk of extinction. Tropical ectotherms are considered to be more vulnerable to warming than higher latitude species, because environmental temperatures are closer to their optimum. To verify this hypothesis, we analyzed the swimming performance of anuran larvae of 9 species from the Gran Chaco, Argentina (water temperatures: 20°C - 42°C) and 7 species from the Iberian Peninsula (pond temperatures: 5°C - 34°C), to obtain their specific thermal performance curves (TPCs). We determined neotropical species have their maximal and optimal performance shifted towards higher temperatures. Some species tend to follow the “jack-of-all-temperatures” strategy (e.g. *Pelobates cultripes*, *Pseudis paradoxa*), and others have a well defined maximum peak of performance (e.g. *Alytes cisternasii*, *Hypsiboas raniceps*). While most tropical species are already operating very near or even above their physiological optimum, any increase in warming may have catastrophic consequences, temperate species, generally living in sub-optimum cooler environments or with a wider breadth TPC, may in fact benefit or not be affected at all.

Fundamental limits in ecologically important traits shape species distributions

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A lack of genetic variation is rarely proposed as an explanation for distribution limits of species. Consequently, little is known about why or how frequently low levels of genetic variation in ecologically important traits may limit species distributions. Here we collect and collate data on mean resistance and genetic variation (narrow-sense heritability) across *Drosophila* species to determine whether species with narrow distributions are constrained by a lack of genetic variation in traits associated with distribution limits. Under a model of low genetic variation limiting distributions we predicted low genetic variance coupled with low trait means for these resistance traits. This association was detected for both desiccation and cold resistance where narrowly distributed tropical species consistently had low trait means and low genetic variation whereas widely distributed species had high trait means and high levels of variation. These results suggest narrowly distributed *Drosophila* species are constrained in their evolutionary responses through a low level of genetic variation in ecologically important traits.

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Using four highly inbred lines of *D. melanogaster* and their F1 crosses we tested the impact of an outbreeding event on several fitness components of flies developed at three temperatures (20, 25 and 30°C) as the detrimental effects of inbreeding as well as heterotic effects are generally believed to be most pronounced in environments that are stressful to the organism. Fitness components investigated were resting metabolic rate (RMR) at different life-stages and the ability to locate resources in a Hirsh maze, egg-to-adult viability, and developmental time. Maze performance may be seen as an alternative to release experiments and test the time and ability of flies to reach a food source. The metabolic rate integrates fundamental aspects of the physiology of an organism and theoretically inbred genotypes could be expected to have a higher RMR because of higher maintenance costs to the genetic machinery. New measuring devices offer the opportunity to measure respiration of even a single drosophilid egg. Preliminary results are presented and the potential of high precision measurements of metabolic rate using microsensors is discussed.

Phylogeny and evolution of sex-determining mechanisms: From dependency on thermal environment to genetic control

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The decision of an individual concerning its sex is an important determinant of lifetime fitness. These decisions have a dramatic effect at the population level as well, because sex ratio is an important population characteristic directly influencing evolvability and susceptibility to extinction. In this respect, facing the recent global climatic changes, the most vulnerable seem to be animals where sex depends on environmental factors such as temperature during embryonic development (“temperature-dependent sex determination”, TSD). Many animal lineages possess alternative sex-determining mechanism, “genotypic sex determination” (GSD) characterized by presence of sexually dimorphic genomes. Animals with GSD usually have equal sex ratio under various thermal regimes, although extreme temperatures lead even in them to biased sex ratio due to development of sex reverted individuals or sex-specific mortality. The evolution of sex-determining mechanisms and their mutual transitions are a matter of current discussions. I will present and discuss the results of our phylogenetic analysis in amniotic tetrapods suggesting that TSD was the ancestral state and that within this clade, GSD have evolved from TSD many times. Moreover, GSD have probably never been reverted back to TSD. These unidirectional transitions could reflect superiority of GSD guaranteeing higher resistance to climatic fluctuations.

Costs and benefits of cold acclimation in field-released *Drosophila*

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One way animals can counter the effects of climatic extremes is via physiological acclimation, but acclimating to one extreme might decrease performance under different conditions. Here, we use field releases of *Drosophila melanogaster* on two continents across a range of temperatures to test for costs and benefits of developmental or adult cold acclimation. Both types of cold acclimation had enormous benefits at low temperatures in the field; in the coldest releases only cold-acclimated flies were able to find a resource. However, this advantage came at a huge cost; flies that had not been cold-acclimated were up to 36 times more likely to find food than the cold-acclimated flies when temperatures were warm. Such costs and strong benefits were not evident in laboratory tests where we found no reduction in heat survival of the cold-acclimated flies. Field release studies, therefore, reveal costs of cold acclimation that standard laboratory assays do not detect. Thus, although physiological acclimation may dramatically improve fitness over a narrow set of thermal conditions, it may have the opposite effect once conditions extend outside this range, an increasingly likely scenario as temperature variability increases under global climate change.

Interpopulation hybridisation and developmental stability in *Drosophila subobscura*

[POSTER]

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Fluctuating asymmetry (FA), the increased variation of bilateral symmetry in a sample of individuals, can point to disturbance in developmental stability at molecular, chromosomal and epigenetic level. The aim was to study different genetic causes of FA, such as interpopulation hybridization as genomic stress and find out whether coadaptations or heterozygosity are probable mechanisms which maintain developmental homeostasis in populations. We focused on coadaptive aspect of inversion polymorphism in *Drosophila subobscura* and its relation with genomic stress, such as interpopulation hybridization and developmental stability. We analysed the effect of interpopulation hybridization through the variability of fluctuating asymmetry (FA) of two wing size parameters (wing width and wing length) and of sternopleural bristle number of *D.subobscura* from three ecologically distinct populations, presuming that they possess a certain degree of genetic differentiation due to their different evolutionary histories. The FA analysis and

statistics was done on samples from P, F1 and F2 generations of inter- and intrapopulation crossings.

Learning about populations history using an approximate bayesian computation

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Approximate Bayesian Computation (ABC) is a recent developed Bayesian technique that can be used to extract information from DNA data. This method has been firstly introduced to Population Genetics in 1999. It relies in two major approximations: the use of a simulated step that substitutes the need for using an explicitly likelihood function; and the summarization of DNA data with a set of summary statistics. This Bayesian approach can be used to estimate several demographic historic parameters from populations using DNA data. Its main advantages are the decrease on computation time demanding and the increase on efficiency and flexibility when dealing with multiparameter models. A particular ABC method, similar to the one used by Beaumont (2007), was applied to published data of bonobos and chimpanzees (Won and Hey, 2005). This data has been studied using several flavours of MCMC. The ABC studies confirm the competitiveness of this recently explored Bayesian method when compared to a standard MCMC approach. Its potential role on researches with more complex, therefore more realistic, models is emphasized.

Coping with changing environments: genetic and physiological mechanisms of adaptive plasticity [POSTER]

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Organisms are expected to have some intrinsic capacity to respond to changing environmental conditions; in the form of ecological (i.e. physiological and/or behavioural plasticity), dispersal to suitable habitats elsewhere, or evolutionary adaptation. Of special interest in the study of how organisms cope with changing environments is phenotypic plasticity. Adaptive phenotypic plasticity leads to a better phenotype/environment match and can represent a potential solution to the problems posed by fluctuating environments. One of its most compelling examples is seasonal polyphenism in butterfly wing patterns. The adaptive value of such alternative seasonal phenotypes and their relation to hormone cycles has been previously established. However, little is known about how the environmental cues modulate development to produce those phenotypes, and about the evolution of plasticity. In this project will be used laboratory populations of *Bicyclus anynana* that differ in genetic background and in their wing plasticity in relation to temperature. I plan to investigate how developmental temperature and hormone manipulations affect quantitative levels and spatial patterns of gene expression which produce alternative phenotypes. In the end, I

hope to combine information from genes, to development, to physiology, to different phenotypes (wing patterns and life histories), and finally to fitness in natural populations.

Angela Mina-Vargas¹; Nicola Flanagan^{1,2}; Daniel Debouck²; Joe Tohme²; and Spillane, Charles¹

Evolutionary relationships between the common bean *Phaseolus vulgaris* and closely related bean species

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The common bean, *Phaseolus vulgaris*, is the most widely cultivated species of bean, representing 90% of all bean production worldwide. Valuable genetic variation for bean breeding programs is held within the secondary gene pool of *Phaseolus vulgaris*. The secondary gene pool consists of the closely related species of *P. vulgaris*, comprising *P. albescens*, *P. coccineus*, *P. costaricensis*, and *P. dumosus*. Understanding the phylogenetic relationships between these species is important in order to assess and prioritise efforts for inter-specific crosses between the secondary and primary gene pools for crop improvement.

Phylogenetic relationships have been estimated amongst *P. vulgaris* and closely related species based on combined morphological and molecular markers (Delgado-Salinas et al 1999). In the former study, *P. vulgaris* forms a sister clade to the remaining species, which cluster together, while in a latter study (Delgado-Salinas et al 2006), the phylogenetic relationships between the species remain mainly unresolved. We have conducted phylogenetic analysis using the chloroplast trnK sequence data available in GenBank and also have generated DNA sequence data from the chloroplast genome for almost 10,500 bp across 12

highly variable loci using several individuals for each species within the *P. vulgaris* clade. The samples were obtained from the *Phaseolus* germplasm collection in CIAT, Colombia, and represent wild relative samples collected across Central and South America. Initial chloroplast sequence analysis indicates that *P. dumosus* seems more closely related to *P. vulgaris* than *P. coccineus*, indicating that *P. dumosus* could be one of the closest relatives of *P. vulgaris*. We will discuss the implications of this and ongoing sequence analysis for understanding the phylogenetics of common bean and its close relatives.

Tropical species of *Drosophila* fail to respond to sudden temperature changes

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Ectothermic animals may employ a suite of physiological or behavioural adjustments to maintain organismal function relatively stable in the face of the fluctuating environmental temperatures. Such adjustments may be especially relevant for the ectotherms inhabiting temperate climates where temperature variability is high on both a seasonal and daily time scales. In the present study we test the hypothesis that the ability to physiologically adjust organismal performance must have evolved particularly in temperate species. We addressed this question by a comparative approach where we compare the thermal tolerance limits of 9 species of either generalist or tropically restricted species of *Drosophila*. These measures were performed after the flies had been exposed to various long or short term acclimation protocols. Initial results indicate three major findings from this study. Firstly we found that generalist species had considerable wider temperature tolerance limits than tropically restricted species. Secondly we found that, in contrast to our hypothesis, tropical and temperate species showed a similar level of plasticity of thermo-tolerance limits when exposed to long term acclimation. However when we examined the short term acclimation response the temperate species showed an almost twice as large response indicating that a major difference between the tropical restricted and temperate species may be their ability to deal with rapid (daily) temperature changes through hardening responses.

Standard metabolic rate and diapause behaviour in the Colorado potato beetle
(*Leptinotarsa decemlineata*)

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Standard metabolic rate (SMR) describes the cost of living, and thus, is closely related to fitness. A high metabolic rate is suggested to be adaptive at high latitudes but could be maladaptive if overwintering period is long. We investigated the age-dependence of SMR and the role of SMR in diapause behaviour, i.e. digging into the soil for overwintering, in the invasive pest species, the Colorado potato beetle. In the first experiment SMR (CO₂ production) was measured for ten consecutive days after adult emergence by using flow-through respirometry (n = 108). Age affected SMR significantly. A substantial increase in SMR occurred during the first two days of adult life after which SMR decreased with age relatively more slowly. The observed pattern in SMR can be explained by the development of flight muscles, accumulation of lipids and the preparation for overwintering. In the second experiment, the diapause behaviour and overwintering survival were examined using beetles whose SMR had been measured at age 6 (n = 1541). Beetles that digged into the soil for diapause had lower SMR, higher body mass and overwintering survival than beetles that stayed on the surface. The implications of the results for range expansion potential will be discussed.

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The potential impact of global warming on infectious diseases has recently attracted much attention. In particular, the effect of global warming on virulence, the host fitness reduction caused by a parasite, is of central interest. Temperature is known to variably affect virulence in the short-term. However, how virulence evolves in the long-term under global warming is unresolved. I present here a theoretical model where a temperature increase led to a change in virulence in the short-term. In the long-term however, the short-term effects of a temperature rise on virulence either disappeared or were even reversed, when evolutionary adaptations were incorporated. I further present here a suitable host-parasite system to test these model predictions in an experimental evolution approach. Using *Paramecium tetraurelia* infected with *Caedibacter taeniospiralis* bacteria, I will analyse how virulence evolves in the long-term under increased temperatures. With a QTL-mapping approach I plan to identify the molecular genetic basis of a possible temperature dependent host defence evolution. Finally, I present here experimental results analysing the short-term effect of a temperature increase on virulence. This theoretical and experimental evolution approach may underline the importance of evolutionary dynamics to reliably predict the effect of global warming on infectious diseases.

Life history responses to nutritional limitation in a tropical butterfly *Bicyclus anynana*

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Organisms in the wild are constantly faced with environmental variation due to human induced changes. Even though the ability to cope with environmental variation such as limited nutrient availability is essential for individual survival, very little is known about the possible strategies and mechanisms involved in such processes. In species with complex life cycles, such as butterflies, stressful environmental conditions during the juvenile stage can influence life histories via changes in development time as well as altering allocation of body resources to the life history traits during metamorphosis. These alterations may be scaring (non-adaptive) and result in negative consequences for the individuals' fitness. Under some circumstances, however, individuals may be able to alter their body composition or life history after short-term nutritional stress so that it helps them to buffer against poor environmental conditions later in life (adaptive phenotypic plasticity). These questions were assessed in the tropical butterfly, *Bicyclus anynana*. In particular we were interested in how nutritional stress during larval stage shapes the adult physiology (body composition and metabolic rate) and fitness (fecundity and lifespan), and whether the observed alterations in the physiology helped individuals to cope with stressful conditions later on in life.

Adaptation to rapid climate change in the snail guild of the Baltic Sea
[POSTER]

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Faced with a rapid climate change, organisms can either adapt to the warming climate, move to other regions or die out. Adaptation can occur through phenotypic plasticity or via genetic microevolution. Numerous examples show adaptive responses to the ongoing climate change, but mostly through phenotypic plasticity; only very few studies have found microevolution. We are studying whether aquatic snails have been able to adapt to a warming climate. Some of our study populations have experienced a consistently warmer environment during the past 30 years. By studying life history variation in the laboratory and performing reciprocal transplants, we want to disentangle phenotypic plasticity and microevolution. To assess the effect of climate on species interactions, we plan to compare snail performance in competition with an invasive thermo-tolerant species in environments with different temperatures. Lastly, we want to study the physiological aspects behind adaptation to a warmer environment. We plan to test thermal tolerance and the variation in heat shock protein expression in snails originating from populations experiencing different climate regimes.

Temperature-induced phenotypic plasticity in growth, body size and sexual size dimorphism
in the gecko *Paroedura picta*

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Temperature-induced phenotypic plasticity in body size as well as in other life-history traits has been demonstrated in dozens of species of ectotherms. Here we report results of an experiment studying effect of three different temperatures (24°C, 27°C, 30°C) on several life-history traits in the Madagascar ground gecko (*Paroedura picta*). Freshly-laid eggs were randomly distributed into three climatic chambers differing in constant temperatures. Approximately 35 individuals were kept in the each climatic chamber till adulthood and their snout-to-vent length and body mass was measured regularly. Hatchlings at 24°C were significantly smaller than those at 27°C and 30°C. Growth rate (regardless of sex) and asymptotic body size in females followed similar pattern. Males were smallest at the lowest temperature, the largest at 27°C, while the highest temperature

produced medium-sized males. Consequently, sexual size dimorphism was also temperature-dependent. Our results question the generality of temperature-size rules such as Bergmann's or converse Bergmann's rule for ectotherms and suggest temperature optimum for *P. picta* at about 27°C - both lower and higher temperatures affect body size negatively. We thus also support recent findings that tropical animals may be particularly vulnerable to climate changes.

Latitudinal clines in life history and immune function in a damselfly

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Many species show latitudinal variation in life history traits such as size (e.g. the well-known Bergmann cline), development time or growth rate. Many studies have been conducted to assess latitudinal variation in life history traits. However, only few studies additionally looked at such variation in important physiological traits such as immune function. Here, we wanted to assess latitudinal variation in both life history traits and immune function and how these are affected by temperature. Therefore, we reared individuals of the damselfly *Ischnura elegans* from Southern Sweden, Belgium and Southern France in a common-garden experiment at 18°C, 21°C and 24°C. We found that mass at emergence decreased with increasing temperature in all populations, in line with the temperature-size rule. Development time also decreased with increasing rearing temperature. In line with Bergmann's rule, the Swedish took the longest to develop and were consistently the heaviest, whereas the French emerged the most quickly and were the smallest at emergence. The Swedish showed highest activity of phenoloxidase (a measure of immune function), except at 24°C. The French consistently have the lowest immune defense, probably as a cost of their fast life history. Across temperatures, immune defense seems to trade off against growth rate in Belgians.

Seasonal variability of body mass and Resting Metabolic Rate (RMR) in free ranging weasels (*Mustela nivalis*)

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Ongoing global warming as well as short-term thermic perturbations significantly influence marine communities. Therefore, in order to predict consequences of those events it is crucial to know the species capacity to cope with environmental temperature changes. *Cerastoderma glaucum* is a lagoon specialist living in water temperatures varying from almost 0°C to above 30°C. Some morphometrical and physiological parameters of this species have been studied in contrasting thermic and salinity conditions. Water temperature seems to be a main factor influencing a reproductive cycle and oxygen consumption. Differences in physiological performance in different environmental conditions could be provoked by acclimatizations or genetically fixed adaptations. Genetic structure of European populations of *C. glaucum* has been studied as well using markers which are assumed to be neutral, mitochondrial DNA (COI) and microsatellites. We found that genetic structure, which evidences strong differentiation among regions, seems to be shaped mostly by historical climatic conditions and a present restricted gene flow among populations. Therefore local adaptations had the possibility to arise (evolve) by natural selection in different environments, since dispersal appears restricted in this species. Additional studies are necessary to check if this was actually the case. To understand a molecular background of physiological performance of *C. glaucum* in different often extreme temperatures and reactions to temperature changes further studies on heat shock proteins need to be undertaken.

Comparative analysis of thermal performances curves in larval and juvenile stages
in frogs. Are tadpoles more sensitive to global warming?

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An important issue in the analysis of the consequences of global change on ectotherms with complex life cycle is to determine which stage will be more sensitive to the expected warming. The locomotor performance of ectotherms is highly sensitive to acute changes in body temperature. Decreases in locomotor performance as a result of increases or decreases in

temperature can affect an ectotherm's ability to escape from predators and to capture prey. Amphibian anurans are vertebrates with striking differentiated stages both at the ecological niche (aquatic/terrestrial) and locomotor mode (swimming/jumping). We compare thermal locomotor performance curves throughout a thermal gradient (10°C-35°C) for several frog species from the Iberian peninsula. The comparison encompasses both old lineages (*Alytes* sp, *Discoglossus galganoi*, *Pelobates cultripes*, *Pelodytes ibericus*) and some modern frog clades (*Bufo* sp., *Hyla* sp., and *Rana* sp.). We estimate phylogenetic correlations for locomotor performance between stages. In addition, we also estimate phenotypic correlations between phases for some species. Although preliminary, some species tend to follow the “jack-of-all-temperatures” strategy (e.g. *Pelobates cultripes*), and others have a well defined maximum peak of performance (e.g. *Alytes cisternasii*). The main result showed that in general aquatic larval stages have lower optimal temperature than terrestrial juveniles. This is important since tadpoles are more constrained to behavioral thermoregulation especially during acute heating of pond environment.

Thermal plasticity and genetic variability of wing size and shape
in *Drosophila melanogaster*, *D. simulans* and their hybrids
[POSTER]

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Genetic differences in body size and shape are naturally occurring in populations of *Drosophila melanogaster* and *D. simulans*, however developmental constraints seem to exist resulting in similar wing shape and size between related species. Wing size and shape can be analyzed using geometric morphometric approaches, which separate morphological variation into these two components. The overall shape may, in turn, be separated into two distinct components: an allometric component (size dependent) and a non-allometric one (size independent). Variation in the non-allometric component is suggested to reflect the evolutionary potential for shape variation. To dissect the evolutionary relevance of the different components, genetic variability for wing size and shape was estimated at four different rearing temperatures in *D. melanogaster* and *D. simulans*. Interspecific hybrids were also analyzed. The hybrids display diverse types of abnormalities attributed to a breakdown of coadapted gene complexes. In this context, the analysis of shape variation in hybrids could reveal the past evolutionary history of the two species and give insight into their evolutionary potential.

Cold tolerance and its genetic basis in *Drosophila montana*

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Environmental stresses have a strong effect on species distribution and evolution. Accordingly, it is important to pay attention to the strategies that organisms use to survive in cold environments when tracing factors limiting the species distribution in seasonally changing environments at high latitudes. In this project adaptation to cold is studied on different levels from physiology to gene expression using *Drosophila montana* as a study species. *D. montana* flies overwinter in reproductive diapause which also improves their cold tolerance. Possible differences in cold tolerance between populations originating from different locations (Oulanka (Finland, 66°N), Colorado (USA, 39°N, 3000m above the sea level) and Vancouver (Canada, 49°N)) are determined as well as the effect of reproductive diapause on cold tolerance in these populations. Also the effect of annual (acclimation) and diurnal (hardening) rhythms on cold tolerance will be studied. In addition, DNA-microarray technique will be used to trace expressional changes in cold tolerance candidate genes during acclimation to cold, cold shock and recovery from it. On the basis of microarray results one or two of the most interesting genes will be sequenced. Finally, cold tolerance and sequence variation in chosen genes along a newly collected latitudinal cline in Finland are studied.

Phenotypic evolution in spatially-structured populations: implications of local adaptation for evolutionary responses to climate change

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Thermal adaptation is ubiquitously observed among ectotherms from protists to trees. The implications of such local adaptation for future adaptation and extinction risk under climate change are explored in an individual-based allelic simulation model. Building upon the analytical model of Bürger and Lynch (1995), phenotypic evolution of performance curve optima are modeled in a spatially-explicit environment. Heritability and the extent of local adaptation in the model are emergent properties of migration-mutation-selection-drift balance. Realistic landscapes are generated using a fractal algorithm to replicate varying levels of habitat fragmentation. An interaction between habitat fragmentation and population size leads to divergent effects of gene-flow on local adaptation and resulting genetic variance across the landscape. Local adaptation is found to play an increasingly disproportionate role in extending mean time to extinction as the rate of climate change increases beyond the critical rate k_c . These results support recent calls to focus conservation measures on preserving local adaptations, particularly for longer-lived and less abundant species.

Hywel Williams

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Throughout Earth history, life has coevolved with its physical environment. In the current period of rapid climate change, understanding the evolutionary response of ecosystems to environmental forcing is of key importance. Ecosystems are complex adaptive systems that integrate nutrient and energy cycles through trophic structure and physical processes. Predicting ecosystem-level responses to perturbation requires consideration of the lower-level responses of constituent species, as well as species-species and species-environment interactions. Here we use an individual-based, evolutionary model of interconnected microbial ecosystems to analyze nonlinear changes in global state resulting from internal and external perturbations. We show that local adaptation and speciation can trigger sudden change across the ecosystem when new traits allowing rapid growth of biomass cause abrupt environmental change, driving incumbent species extinct. These internally generated perturbations can result in ecosystem collapse, followed by recovery to an alternate stable state, or even system-wide extinction. Similarly extreme disruptions can be caused by external forcing of the environment, which can overcome the stabilising tendency of an established community and push key variables beyond resilience thresholds. We analyse the internal and external triggers for ecosystem collapse and examine possible methods for their prediction.

BUDGET

		Euro	
Categories	Details	PLN	(1 Euro = 4,4157 PLN, exchange rate from 1st July 2009)
Transport	Travel of invited speakers, transport of all participants from Warsaw to Bialowieza, students' support grants	77 595,41	17 572,62
Accommodation	Participants (double rooms), Invited speakers (single rooms)	37 614,00	8 518,24
Food	Lunches and dinners, coffe breaks, ceremonial evening closing workshop	34 337,35	7 776,20
Cost of extra labour of MRI PAS staff		27 389,84	6 202,83
Costs of workshop organization	Printing of conference materials, insurance, administrative costs of MRI PAS	21 803,52	4 937,73
TOTAL		198 740,12	45 007,62