DEPARTMENT BIOLOGICAL SCIENCES
ECOLOGY AND GENETICS
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ESF report:

Conference 11-14 April 2010

Evolutionary potential in natural populations

Organizers: Trine Bilde, Torsten Nygaard Kristensen, Volker Loeschcke, Dept. Biological Sciences, Aarhus University, Ny Munkegade Building 1540, 8000 Aarhus C, Denmark.

Venue: Sandbjerg Estate, Sandbjergvej 102, 6400 Sønderborg, Denmark
http://www.sandbjerg.dk/eng/welcome.aspx

Summary: The meeting aimed to bring together world class researchers working on various aspects of evolutionary potential in natural populations. We focused on three major topics (see below), and had an impressive list of invited speakers to address each of these topics, and to discuss the overall theme. In addition to 11 invited speakers, we accepted 8 contributed talks. We also offered a PhD course, where students were obliged to read contributed papers from each invited speaker, to attend all the talks and present posters, and finally to submit an essay within one of the three topics covered at the meeting. There was great interest in the meeting, and 101 people including 50 PhD students attended the meeting.

Scientific content and invited speakers

There is increasing focus on the effect of environmental change on survival and sustainability of natural populations. The ability to adapt to changing ecological conditions and track environmental changes crucially relies on standing genetic variation in the population and hence on evolutionary potential. However, processes that maintain genetic variation in natural populations are enigmatic and poorly understood, and this constrains our ability to understand population responses to environmental impacts.

For this meeting we brought together researchers with a primary focus on evolutionary processes in wild populations and processes affecting evolutionary potential. We organized three main topics that covering the following subjects

1) Investigating evolution in wild populations using molecular and quantitative genetic tools
2) Understanding the processes that lead to loss / generate and maintain genetic variation in natural populations
3) What constrains evolution in natural populations? plasticity, genetic and environmental constrains

List of invited speakers:

Ary A. Hoffmann, University of Melbourne, Australia.
Anna Qvarnstrom, Uppsala University, Sweden.
Ben Sheldon, University of Oxford, UK.
Charles W. Fox, University of Kentucky, USA.
Ilka Hanski, Helsinki University, Finland.
Jacintha Ellers, Vrije University Amsterdam, The Netherlands.
Jon Slate, University of Sheffield, UK.
Martin Lascoux, Uppsala University
Mikkel Schierup, Aarhus University, Denmark.
Ruth Shaw, University of Minnesota, USA.
Tom Tregenza, University of Exeter, UK.

Ph.D. course: Ph.D. students had the possibility of attended the conference as a 5 ECTS Ph.D. course. Students received a compendium with original research articles on current research within the three major topics prior to the conference. They were further required to write an essay related to one of the main topics. Full attendance of the entire meeting, preparation through background reading and submission of an essay was required to obtain 5 ECTS.

Conference report:

The persistence and adaptation of organisms to changing environmental conditions relies on standing genetic variation, and phenotypic plasticity. The first topic “Studying evolution in wild populations using molecular and quantitative genetic tools” focused on the estimation of genetic variation and understanding the genetic architecture underlying fitness traits in natural populations, and studies investigating signals of adaptation in organisms originating from environmental gradients. The second topic “Understanding the processes that lead to loss / generate and maintain genetic variation in natural populations” specifically focused on the dynamics of genetic variation and underlying adaptation with examples from plant and animal populations. The third topic, “What constrains evolution in natural populations? plasticity, genetic and environmental constrains” aimed to understand factors that determine evolutionary constraints such as genetic correlations, and the evolution of

phenotypic plasticity. Finally, a plenary talk on “Climate change adaptation: where does evolution fit in?” was presented. This was followed by a plenary discussion on how a better understanding of evolutionary processes can be implemented in understating and predicting adaptation of organisms to changing environments. Much time was allocated to discussions and networking between researchers and Ph.D. students, and this was very well received among the delegates.
40 PhD students attended the meeting also as an PhD course. The invited speakers had all provided scientific papers that were compiled for the students to read before the meeting. Subsequently to the meeting students submitted an essay where they summarized the major take home messages from one of the major three topics and outlined a research project within the chosen topic. Students also presented posters in two poster sessions during the meeting.

CONFERENCE PROGRAMME

Evolutionary potential in natural populations - 11-14 April 2010

Sunday 11 April – arrival afternoon/evening – dinner at 18.00

Monday 12 April

Breakfast 8-9

Topic 1: Studying evolution in wild populations using molecular and quantitative genetic tools.

9.45 Natural and Sexual selection in wild crickets
Tom Tregenza, Exeter University

10.30 – coffee

11.10 Thermal adaptation in the butterfly *Lycaena tityrus*
Klaus Fischer, Greifswald University

11.30 Footprints of selection on candidate genes in seven populations along a latitudinal cline in the tropical butterfly *Bicyclus anynana*.
Maaike de Jong, Steve Collins, Niklas Wahlberg, Patricia Beldade, Paul Brakefield and Bas Zwaan, Leiden University

12.00 - lunch

13.30 Speciation in *Ficedula* flycatchers
Anna Qvarnström, Uppsala University

14.15 Eco-evolutionary dynamics in heterogeneous landscapes
Ilka Hanski, Helsinki University

15.00 - coffee and cake

15:30 Phenotypic plasticity and local adaptation in life history traits of natural populations
Frank Johansson and Martin Lind, Umea University Sweden

15.50 Q_{ST} – F_{ST} comparisons reveals local adaptation in sea trout
Björn Rogell, Johan Dannewitz, Erik Petersson, Stefan Palm and Anssi Laurila, Uppsala University

16.10 - break and soft drinks

Topic 2: Understanding the processes that lead to loss / generate and maintain genetic variation in natural populations

16:30 Understanding the dynamics of genetic variation and adaptation
Ruth Shaw, University of Minnesota

17.30 History, flowering time variation and circadian rhythms of the shepherd's purse (*C. bursa-pastoris*)
Martin Lascoux, Uppsala University

18.00 - dinner

19.30 Poster session
Odd numbered poster authors will be by their posters

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Tuesday 13 April
Breakfast 8-9

9.00 Origins and evolution of a coat colour polymorphism in wild sheep
Jon Slate, Sheffield University

9.45 Evolutionary processes of the great apes inferred from genome sequences
Mikkel Schierup, Aarhus University

10.30 – coffee

11.00 Latitudinal and voltinism compensation shape thermal reaction norms for growth rate
Lisa NS Shama, Melina Campero-Paz, Marjan De Block, K. Mathias Wegner & Robby Stoks, Alfred Wegener Institute

11.20 Variation in male traits and female preferences in natural hybrid zones: disentangling cause and effect
[123]Machteld N. Verzijden and [12]Gil G. Rosenthal
[1]Texas A&M University, USA, [2]Centro de Investigaciones Científicas de las Huastecas Colonia Aguazarca, Calnali, Mexico, [3]Lund University, Sweden

12.00 - lunch

Topic 3: What constrains evolution in natural populations? - plasticity, genetic and environmental constrains

13.30 Genetic correlations and evolutionary constraints
Charles W. Fox, University of Kentucky

14.15 The plasticity paradox: opposite effects of environmental variation on the evolution of phenotypic plasticity
Jacintha Ellers, Vrije University Amsterdam

15.00 - coffee and cake

15.45 Contrasting patterns of phenotypic plasticity in reproductive traits in two great tit (*Parus major*) populations
[1]Arild Husby, [1]Dan H. Nussey, [2]Marcel E. Visser, [1]Alastair J. Wilson, [3]Ben C. Sheldon & [1]Loeske E. B. Kruuk
[1]University of Edinburgh, Edinburgh, [2]Netherlands Institute of Ecology, [3]University of Oxford

16.05 Evolutionary constraints – small populations and environmental stress
Torsten Nygaard Kristensen, Aarhus University, Denmark

16.30 - Poster session
Even numbered poster authors will be by their posters

19.00 - Conference dinner

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Wednesday 14 April

Breakfast 8-9

9.00 Seasonal timing in a warming world
[1]Marcel E. Visser, [1]Luc te Marvelde, [1]Sonja Schaper, [2]Alistair Dawson, [3]Simone Webber & [4]Arild Husby
[1]Netherlands Institute of Ecology, [2]CEH, Edinburgh, UK
[3]University of Birmingham, [4]University of Edinburgh

9.20 Temperature-induced life-history adaptations in a polymorphic damselfly: no differences between female morphs
Niels Bouton, Arne Iserbyt, Hans van Gossum , University of Antwerp

9.40 – coffee

10.00 Climate change adaptation: where does evolution fit in?
Ary Hoffmann, University of Melbourne

11.00 coffee and discussion

12.00 - lunch
End of meeting

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Poster presentations by:

1. Anders Kjærsgaard, Aarhus University
   The effect of maternal age on migration in *Drosophila melanogaster* - preliminary results

2. Anna Lundhagen, Peter Kanuch, Berrit Kiehl, Swedish University of Agricultural Sciences
   Influences of gene flow on local adaptation in an expanding species, the Roesel´s bush cricket

3. Anthony Bouétard , UMR INRA-Agrocampus
   Evolutionary potential of molecular responses to xenobiotics : a project on *Lymnaea stagnalis* exposed to pesticides

4. Antoine Millet, Holar University College
   Determinants of spatial and temporal phenotypic variation in threespine stickleback from Myvatn

5. Berrit Kiehl, Uppsala University
   Patterns of polyandry in the bush cricket *Metrioptera roeselii* along a latitudinal gradient

6. Camilla Kalvatn Egset, Norwegian University of Science and Technology
   Effects of predation and body size on the allometry between tail area and body area in Trinidadian guppies (*Poecilia reticulata*)

7. Camille Madec, Uppsala University
   Evolution of floral display in *Primula farinose*

8. Dirk Schaerlaekens, Katholieke Universiteit Leuven
   On the importance of historical otolith collections in evolutionary eel research

9. Emma Dahl, Uppsala University
   Predator induced corticosterone stress response along a latitudinal gradient

10. Esa Aalto, Oulu University
    Is low variation in flowering time genes in *Arabiopsis lyrata* due to natural selection?

11. Friederike Schulz, Uppsala University
    Adaptation to rapid climate change in snails of the Baltic Sea

12. Gemma Calabria, Universitat de Barcelona
    Genetic variation linked to chromosomal inversions in natural populations of *Drosophila subobscura*
13. Grethe Robertsen, Eli Kvingedal & Sigurd Einum, Norwegian University of Science and Technology
    Does relative family-specific performance depend on competitive intensity in juvenile brown trout?

14. Hallvard Haanes[1,3], K. H. Røed[1], E. Solberg[2], I Herfindal[3], B. E. Sæther[3]
    [1]Norwegian School of Veterinary Science, [2]Norwegian Institute for Nature Research, [3]The Norwegian University of Science and Technology
    Genetic discontinuities in a continuously distributed population of a highly mobile ungulate

15. Ilaria Milano, University of Bologna
    Advances and perspectives in evolution of the Atlantic Bluefin Tuna: is the small scale population structuring linked to local adaptation?

16. Jacquelin DeFaveri, University of Helsinki
    Parallel Evolution of Freshwater Adaptation in Three-spined Stickleback (*Gasterosteus aculeatus*)

17. Janine Helms, Institute for Zoo and Wildlife Research, Berlin
    A rapid natural colonization: *Argiope bruennichi* as a successful founder

18. Jenni Kesäniemi , University of Jyväskylä
    Population structure and connectivity in the poecilogonous polychaete *Pygospio elegans*

19. Jonathan Barnaby, Uppsala University
    Social consequences of winter ranging behaviour on the social system of a cooperative breeding bird species, the apostlebird (*Struthidea cinerea*)

20. Kristian Meier, Technical University of Denmark
    Local adaptation and adaptive potential in brown trout (*Salmo trutta* L.)

21. Laura Vesala, University of Jyväskylä
    Response to cold: plastic changes in resistance to low temperatures

22. Lina Lehndal, Uppsala University
    Effects of herbivory on population dynamics and evolution of resistance in purple loosestrife (*Lythrum salicaria* L.)

23. Line Ugelvig, Copenhagen University
    Genetic consequences of fluctuating population size

24. Marcus Ljungqvist, Lund University
Molecular inference of inbreeding: which estimate to use?

25. Maria Uscka-Perzanowska, Uppsala University
Selection on the self-incompatibility locus in *Arabidopsis lyrata*

26. Mat Seymour, Holar University College
Accessing small scale population divergences in the threespine stickleback

27. K. Mathias Wegner, AWI Waddenseastation Sylt
Evolutionary potential of host-parasite systems in coastal ecosystems facing global change

28. Melanie Christiansen, Reading University
An Approximate Bayesian Computation model for the Phylogenomics of *Pongo ableii* from Sumatra and *Pongo pygmaeus* from Borneo – preliminary results

29. Miyako Kodama, University of Washington
Evolution of Life History Traits in a Wild Population of Coho Salmon at Big Beef Creek, Washington, USA

30. Nina Annika Pekkala, University of Jyväskylä
Effects of inbreeding and hybridization on fitness of small populations under normal and stressful conditions

31. Nina Overgaard Therkildsen, Technical University of Denmark
Using the candidate gene approach to search for direct evidence of fisheries-induced evolution

32. Reiko Akiyama, Uppsala University
Variation in adaptive traits in natural populations of *Arabidopsis thaliana*

33. Richard Fautley, Imperial College London
Population genetics of range expansion in roe deer

34. Robert Hegna, University of Jyväskylä
Polymorphism in *Parasemia plantaginis*

35. Sandra Hangartner, Aquatic Ecology, Eawag
Phenotypic divergence and its quantitative genetic basis in the Swedish moor frog (*Rana arvalis*)

36. Silwia Czarnomska, Mammal Research Institute, Białowieża
Spatial genetic structure of yellow- necked mouse *Apodemus flavicollis* in NE Poland - the impact of heterogeneous landscape or isolation by distance?

37. Sofia Hemmilä, Uppsala University
Conservation genetics of medicinal tree species in India

38. Tiina S. Salminen, University of Jyväskylä
Adaptation to Northern Latitudes: photoperiodicity shaping life-history strategies

39. Venera Tyukmaeva, University of Jyväskylä
Reproductive diapause of *Drosophila montana* in Finnish cline populations

40. Viktor Nilsson, Umeå University
Genetic variation in phenotypic plasticity across species' ranges: are all damselflies ready for climate change?

Talk abstracts received in order of presentation

Natural and Sexual selection in wild crickets

Tom Tregenza, Exeter University

Attempts to understand natural and sexual selection have become polarized into field and laboratory studies on completely different groups. Invertebrates dominate laboratory evolutionary biology, but we know astonishingly little about what determines individual reproductive success in wild invertebrates. Using advances in video technology combined with DNA fingerprinting of all the members of a population and all their offspring, we have captured the lives of a wild field cricket population. Our study confirms the fundamental prediction that males vary more in their reproductive success than females. It shows that both males and females leave more offspring when they mate with more partners and reveals that the factors that predict the success of a male in gaining matings are not the same as those that predict how successful he will be in producing offspring.

Thermal adaptation in the butterfly *Lycaena tityrus*

Klaus Fischer, Greifswald University

Understanding how organisms adapt to complex environments lies at the very heart of ecology and evolutionary biology. We here analyze clinal variation in traits related to fitness in the butterfly *Lycaena tityrus*, as such variation suggests a contribution of directional selection. We first 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 environmental variation in the expression of stress-inducible heat-shock proteins as opposed to low-altitude butterflies. Using allozyme markers, we next show that high- and low-altitude populations are genetically differentiated to a remarkable degree (F_{ST}: 0.065), 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.

Footprints of selection on candidate genes in seven populations along a latitudinal cline in the tropical butterfly *Bicyclus anynana*.

Maaike de Jong, Steve Collins, Niklas Wahlberg, Patricia Beldade, Paul Brakefield and Bas Zwaan, Leiden University

Understanding the mechanisms of adaptation by natural selection is crucial for predicting the ability of natural populations to adapt to environmental change. As past evolutionary change is recorded in the genome, we can use this information to make predictions about the evolutionary potential in response to future changes. Latitudinal clines are a powerful tool in demonstrating patterns of past natural selection. The butterfly *Bicyclus anynana* occurs in East Africa from the equatorial Kenya to subtropical South Africa, an area with considerable climatic differences between regions. To investigate geographical patterns of local adaptation to climate, we sequenced regions of 30+ candidate genes, for 40-50 individuals for each of seven populations along a latitudinal cline spanning the species range. The majority of the studied genes are associated with temperature or stress adaptation, and include metabolic enzymes (including *Treh*, *Sod*, *UGP*, *Pglym78* and *Cat)*, other metabolic genes (e.g. *Catsup, Vg*) and several heat shock proteins. Furthermore, we sequenced candidate genes involved in development (e.g. *Dll*, *Wg*) and several pigmentation genes. We found significant clines in allele frequencies of amino acid polymorphism (non-synonymous SNPs) for several of the metabolic enzymes, indicating a role of these genes in temperature and/or climate adaptation. To contrast these patterns of selection with neutral population divergence we present population genetic parameters based on putatively neutral SNPs, as well as haplotype networks for the mitochondrial COI gene

Speciation in *Ficedula* flycatchers

Anna Qvarnström, Uppsala University

Speciation in animals often requires that population divergence goes through three major evolutionary stages, i.e. ecological divergence, development of sexual isolation and the build up of genetic incompatibility. There is theoretical consensus regarding favourable conditions required for speciation to reach its final and irreversible stage, but empirical tests remain rare. Here I present recent research on processes of speciation, based on studies in hybrid zones between collared (Ficedula albicollis) and pied flycatchers (F. hypoleuca). A major advantage of this study system is that questions concerning all three major sources of reproductive isolation and their interconnections can be addressed. I conclude that (1) ecological divergence is caused by divergence in life history traits, (2) females prefer mates of their own species based on differences in both plumage and song characteristics, (3) male plumage characteristics have diverged but their song has converged in sympatry, (4) there is genetic incompatibility in accordance with Haldane?s rule, and (5) the Z- chromosome appears to be a hotspot for genes involved in sexual isolation and genetic incompatibility. I will discuss how identification of the genes underlying the three major sources of reproductive isolation can be used to draw conclusions about links between the processes driving their evolution.

Phenotypic plasticity and local adaptation in life history traits of natural populations

Frank Johansson and Martin Lind, Department of Ecology and Environmental Science, Umea University Sweden

Environmental heterogeneity is predicted to select for phenotypic plasticity in organism. However, little empirical evidence is available to support this prediction. We have invested local adaptation and phenotypic plasticity in development time in island populations of the common frog (*Rana temporaria*) which breeds in pools on islands. Pools on islands differ in their degree of pool drying and it is important for frogs to adjust their development to pool drying. F_{st} (from microsatellites) and Q_{st} (life history characters) from common garden experiments were estimated for 14 island populations. We found evidence of divergent selection both in phenotypic plasticity and local specialisation. Despite gene flow among island populations, this local adaptation has occurred within less than 300 generations, suggestion that the evolutionary potential in wild population sometimes is high.

Q_{ST} – F_{ST} comparisons reveals local adaptation in sea trout

Björn Rogell, Johan Dannewitz, Erik Petersson, Stefan Palm and Anssi Laurila, Uppsala University

It is generally assumed that local adaptation is responsible for much of the phenotypic variation observed among wild salmonid populations. This raises concerns for the preservation of salmonid stocks since they are frequently managed through translocation programmes and by sea ranching. If translocated stocks are adapted to specific conditions, target populations may be affected by outbreeding depression. Here we present results from a large-scale experiment on local adaptation in sea-migrating brown trout (*Salmo trutta*) from Sweden, conducted during two successive years. A Q_{ST}-F_{ST} approach was used in two rearing environments - one laboratory and one experimental (close to natural) stream. In both years, trout originating from two east coast and two west coast populations were included. In addition, the first year included 2 stocks of river Dalälven, one seventh- and one first- generation of sea ranching. All parents were genotyped and the eyed eggs were introduced to the experimental settings (a semi natural stream and a ranching facility) during autumn. The following autumn all fish were caught, measured, and DNA was sampled for parentage assessment. We found that size differed amongst the populations. Additionally, Q_{ST} was greater than F_{ST} indicating that among population divergence may be attributed to divergent selection. In general, the east coast populations reached a larger size as when compared to the west coast populations. The differences between the two Dalälven stocks indicate that increasing size appears to be a sign of selection under sea ranching conditions. Assuming that the divergence amongst the Dalälven stocks is due to selection for increased growth rate, it would have required a standardized selection differential of 0.54. In addition, the relative length of the pectoral fin differed amongst the populations. Both size (growth) and pectoral fin length are important fitness traits in salmonid fishes. Since populations are adapted to local conditions, release of maladapted stocks may lower the overall fitness through outbreeding depression. The relevance of our findings are emphasized by the fact that the sea ranched stocks from River Dalälven seem adapted to hatchery rearing, questioning release of hatchery trout into the wild.

Latitudinal and voltinism compensation shape thermal reaction norms for growth rate

Lisa NS Shama, Melina Campero-Paz, Marjan De Block, K. Mathias Wegner & Robby Stoks, Alfred Wegener Institute

Relationships between life history traits and latitude can be directly translated to the predicted response of populations to global change. Here, we assessed the relative importance of additive genetic, environmental, and neutral genetic effects on latitudinal variation of thermal reaction norms of growth rate for populations of the damselfly, *Ischnura elegans*. At the interpopulation level, reaction norms differed primarily in elevation, suggesting that shorter growth seasons in both high latitude and bivoltine populations select for faster growth rates regardless of environmental temperature. Within populations, heritable variation for growth rate, as well as broad sense (family) genetic variance for plasticity suggests that reaction norms are not constrained. However, partitioning of genetic variance into additive (V_A) and non-additive effects revealed no significant additive (sire) genetic variance for plasticity, indicating that reaction norms are not free to evolve. Heritability of growth rates were lower in unfavourable conditions (high temperature), likely due to the combined effects of reduced V_A and increased environmental and non-additive genetic variance. Quantitative trait divergence (Q_{ST}) was greater than neutral genetic divergence (F_{ST}) in all cases, showing that selection rather than drift is the main contributor to population divergence in growth rate. Additionally, Q_{ST} estimates increased with experimental temperatures, indicating the presence of genotype by environment interactions.

Variation in male traits and female preferences in natural hybrid zones: disentangling cause and effect

[123]Machteld N. Verzijden and [12]Gil G. Rosenthal
[1]Texas A&M University, USA, [2]Centro de Investigaciones Científicas de las Huastecas Colonia Aguazarca, Calnali, Mexico, [3]Lund University, Sweden

Hybridization can increase variation in genotypes and subsequently phenotypes, and is thus an important factor in the evolution of a species. Mate choice plays a crucial role in hybrid zones in whether the gained variation is subsequently maintained or lost.
We study the effects of hybridization on sexual selection in several independent natural hybrid zones in Swordtail fish (*Xiphophorus birchmanni* and *X.malinche*) . These hybrids occur in intermediate ‘ecozone’ to their parental species, show intermediate phenotypes for ecological measures, and show no diminished survival. Male secondary sexual traits in these hybrid zones show a larger variation than in populations of the parental species, and even show transgressive segregation, indicating an increased genetic variation. Hybridization can also directly change female preferences, by two proximate mechanisms: first, it can change the preference landscape of genetically determined preferences by decoupling preferences for trait combinations. Second, it can change the preference landscape of socially (learned) determined preferences, through the change in phenotypic variation that an individual may encounter.
We have determined the shape of wild caught female preference landscapes in 3 male sexual trait dimensions of two independent hybrid populations and populations of their parental species. We will also show the effect of early (as young) experience as well as recent (as adults) experience with hybrids of heterospecific males on female preferences. We show that variation in male traits and female preferences is different in hybrid populations than in parental populations, and that female preferences for male secondary sexual traits are at least partly learned. This indicates that variation in male traits can indirectly create variation in female preferences.

Contrasting patterns of phenotypic plasticity in reproductive traits in two great tit (*Parus major*) populations

[1]Arild Husby, [1]Dan H. Nussey, [2]Marcel E. Visser, [1]Alastair J. Wilson, [3]Ben C. Sheldon &
[1]Loeske E. B. Kruuk
[1]University of Edinburgh, Edinburgh, [2]Netherlands Institute of Ecology, [3]University of Oxford

Phenotypic plasticity is an important mechanism via which populations can respond to changing environmental conditions, but we know very little about how natural populations vary with respect to plasticity. Here we use random-regression animal models to understand the multivariate phenotypic and genetic patterns of plasticity variation in two key life history traits, laying date and clutch size, using data from long-term studies of great tits in the Netherlands (HV) and UK (WW). We show that, whilst population-level responses of laying date and clutch size to temperature were similar in these populations, between-individual variation in plasticity differed markedly. Both populations showed significant variation in phenotypic plasticity (IxE) for laying date, but IxE was significantly higher in HV than in WW. There was no significant genotype-by-environment interactions (GxE) for laying date, yet differences in GxE was marginally non-significant between HV and WW. For clutch size, we only found significant IxE and GxE in WW but no significant difference between populations. From a multivariate perspective, plasticity in laying date was not correlated with plasticity in clutch size in either population. Our results suggest that generalisations about the form and cause of any response to changing environmental conditions across populations will be difficult.

Seasonal timing in a warming world

[1]Marcel E. Visser, [1]Luc te Marvelde, [1]Sonja Schaper, [2]Alistair Dawson, [3]Simone Webber &
[4]Arild Husby
[1]Netherlands Institute of Ecology, [2]CEH, Edinburgh, UK
[3]University of Birmingham, [4]University of Edinburgh

Climate change is affecting avian reproduction as is shown by well documented shifts in seasonal timing. This seasonal shift is however often not sufficient to maintain synchrony with the also shifting seasonal peak in food abundance. The resulting mistiming will have negative fitness effects and one of the key questions is whether natural selection will lead to micro-evolutionary changes in seasonal timing to reduce this loss in fitness. We will present data on the selection on, and heritability of, timing of reproduction in great tits (*Parus major*). To forecast micro-evolution it is important to understand genetic variation among individuals. This variation can be due to variation in cue sensitivity or to variation in the energetics associated with reproduction (such as the costs of egg production). We will present data from aviary experiments using genetically related individuals which show that there is genetic variation in cue sensitivity and present data from energetic measurements from females in the wild that show that early and late individuals do not differ in the costs of egg production. Finally, we will argue that although there will be micro-evolution in reproductive traits, the rate of micro-evolution will not be able to keep up with the rate of climate change with possible severe consequences for avian population viability.

Temperature-induced life-history adaptations in a polymorphic damselfly: no differences between female morphs

Niels Bouton, Arne Iserbyt, Hans van Gossum , University of Antwerp

The maintenance of three female morphs in the damselfly *Ischnura elegans* has been explained from frequency-dependent sexual conflict, but a recent study also showed a correlation of morph frequency with environmental temperature. We measured egg survival and hatching time of eggs of three female morphs of the damselfly *I. elegans* of a coastal and inland population from the Netherlands using a split-brood design and two temperature regimes (cold and warm) in the laboratory. The coastal and inland populations differ in climate conditions, the inland population experiencing larger differences in day/night and summer/winter temperatures and slightly higher summer temperatures. We found considerable thermal plasticity in hatching time but not in egg survival of the aquatic eggs between the cold and warm treatment. We also found significant differences in both hatching time and egg survival between the inland and coastal population, suggesting local adaptation. Individuals from the coastal population hatched faster, but had lower survival in both treatments. This suggests the operation of a natural selection force other than temperature to establish fast hatching, possibly crowding of the aquatic habitat at the coastal site. In our experiment individuals born to mothers belonging to different colour morphs did not differ in their response to temperature treatment. Thus, there is no interaction effect of maternal morph and temperature on the traits measured here and no temperature-induced life-history variation that could explain morph frequency variation.

Poster abstracts received

Grethe Robertsen, Eli Kvingedal & Sigurd Einum, Norwegian University of Science and Technology

Does relative family-specific performance depend on competitive intensity in juvenile brown trout?

Spatial heterogeneity in population density can be hypothesised to contribute to the maintenance of within-population genetic variation through its influence on local levels of intraspecific competition and hence on selection pressures. This depends on different genotypes being optimal under different levels of competition. In the current study we tested for effects of intraspecific competitive intensity on the relative performance (growth and dispersal) of juvenile brown trout (Salmo trutta) originating from nine different families. This was done experimentally in tanks and in semi-natural streams. Both growth and dispersal differed consistently among families, indicating genetic variation in these traits. However, there were no significant interaction effects between competitive intensity and family on performance in either of the two experimental systems. Thus, genetic variation in responses to competitive intensity appeared to be limited in the population from which these juveniles originated. One possible reason is that this population has evolved under ecological conditions which may provide limited spatial variation in levels of early-life competition (large and highly fecund adults breed within restricted areas). Yet, studies of maternal effects in salmonid fishes have shown certain trait values to be particularly favourable under high competition. It would therefore be surprising if offspring genetics played no role in determining their response to competitive intensity. Thus, it may prove fruitful to test for genetically based variation in response to competitive intensity in populations or species that have evolved under ecological settings different from the population used in the present study.

Hallvard Haanes[1,3], K. H. Røed[1], E. Solberg[2], I Herfindal[3], B. E. Sæther[3]
[1]Norwegian School of Veterinary Science, [2]Norwegian Institute for Nature Research, [3]The Norwegian University of Science and Technology

Genetic discontinuities in a continuously distributed population of a highly mobile ungulate

Many species have populations with histories of geographic range shifts or successive shifts between fragmentation, growth, spatial expansion and a continuous distribution. The genetic effects are of great concern, given the present major shifts in many species. We assess the distribution of genetic variation of 15 microsatellite loci in the abundant and continuous Norwegian moose population, which has a history of colonisation and recent fragmentation. Bayesian clustering methods both without and with spatial information suggests that genetic discontinuities divide the population into at least three subpopulations along a latitudinal axis, separated by convergence zones of high admixture. Approximate Bayesian Computation estimates suggest the structure is old, and that postglacial colonisation has followed both southern and northern routes.

K. Mathias Wegner, AWI Waddenseastation Sylt

Evolutionary potential of host-parasite systems in coastal ecosystems facing global change

How global change and increasing physical stress interact with emerging marine diseases is largely unexplored in coastal ecosystems. Evolutionary consequences for such altered interactions between hosts and bacterial pathogens are even less known. To exemplify the complex community structures host and pathogens evolve in I use ubiquitous bacterial pathogens (genus *Vibrio)* from the Wadden sea ecosystem that can potentially cause severe mortalities in hosts from different key groups (bivalves and fish). I characterised bacterial symbionts and especially shared pathogens of members of both groups (Pacific oysters *Crassostrea gigas* and plaice *Pleuronectes platessa*). This correlative approach will be complemented by experimental work on established model species. Here, Pacific oysters and marine sticklebacks, will be studied in closer detail because their projected selective responses to rising temperatures point in opposite directions. By exploring the effects and evolutionary trajectories of bacterial pathogens and the genetic architecture of resistance in corresponding hosts, potential consequences of global change and bacterial disease for the ecosystem as a whole can be derived in an integrated community level approach.

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Evolution of Life History Traits in a Wild Population of Coho Salmon at Big Beef Creek, Washington, USA

In order to understand selective pressures and the process of natural selection, it is critical to determine the factors that shape mating system and affect variation in reproductive success among individuals. In salmonids, a number of studies have shown that body size and arrival dates affect reproductive success and mating system, yet many of these studies are based on behavioral observations. However, recent development of molecular genetic tools enabled direct kinship analysis, thus allowing us to examine the parent-offspring relationship in traits affecting individuals' reproduction and survival, as well as to accurately measure reproductive success and describe mating system. In this study, reproductive success, mating system and effective population size of a wild population of coho salmon (Oncorhynchus kisutch) will be estimated using microsatellite markers, and the direction and strength of selection on several life-history traits will be examined. Returning adults have been sampled every year since 2006, and sampling will continue until 2010. For each individual, body length, age, arrival date and sex, as well as fin clips are collected. Using 10 microsatellite loci, a pedigree of the wild population will be constructed over five consecutive years. Relative influence of measured fitness-related traits on reproductive success and mating system will be investigated, and natural selection acting on these traits will be quantified. In addition, effective population size will be estimated in order to examine the rate of genetic drift. This study provides baseline information on evolution in the wild population and has implications on management practices throughout the State.

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Determinants of spatial and temporal phenotypic variation in threespine stickleback from Mývatn

Understanding the processes and factors that determine phenotypic variation, and how these feed back to population level processes in natural populations is of fundamental importance for understanding how biological diversity emerges, is maintained and changed. We explore how spatial and temporal variation in agents of natural selection (e.g. prey availability and habitat quality) and potential for dispersal/gene flow influence phenotypic variation (e.g. body size and feeding morphology) of the threespine stickleback (*Gasterosteus aculeatus*) in Mývatn (NE Iceland). To address this question, we use spatial (multiple sampling sites across the lake) and long-term data on ecological variables (e.g. chironomids densities and major habitat types) and stickleback populations (population density and phenotypic variation), as well as molecular genetic methods (microsatellite markers). Our first results on body size variation indicate that stickleback phenotype (body size)
varies both among sites within the lake, as well as over years, possibly due to differences in habitats and/or fluctuations in food availability, and that the extent of gene flow varies among the sites. This is a first step towards a more complete insight in the ecological and evolutionary process involved in Mývatn stickleback population dynamics.

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Accessing small scale population divergences in the threespine stickleback

Rapid adaptive radiations are divergences in related lineages, often in response to different ecological habitats, which occur over a short period of time, and rely greatly on standing genetic variation and phenotypic plasticity. The most readily method for individuals and populations to acclimate to changing or new environments is through phenotypic plasticity. However, recent studies also suggest, standing genetic variation plays an important role in species divergence. Whereas mutation relies on new alleles arising and fixating within a population, standing genetic variation utilizes existing allelic variation. This allelic reserve allows for rapid adaptation radiation to ecological changes. Using a known adaptive radiated species, coupled with ecological recordings we can assess relationship between ecological variation, adaptation and other evolutionary processes. Threespine sticklebacks are a model species for studying adaptive radiation based on their ability to rapidly acclimate and adapt to new environments over a wide geographical range. The Belgjaskógur woodlands northeast of Lake Mývatn, Iceland includes over a hundred lakes and ponds of various sizes from a few square meters to over 520 m^2 within 7.5km^2. The main objective of this study is to assess the effects of environmental factors on intraspecific diversity. This study is divided into three main parts. We will 1) determine phenotypic diversity of sticklebacks over a small spatial scale in Belgjaskógur woodland using morphometrics techniques 2) develop a genetic structuring comparison of nineteen ponds using neutral genetic markers 3) compare our phenotypic and genetic findings with ecological data to infer potential links to evolutionary processes, including phenotypic plasticity, parallel adaptation, gene flow, and genetic drift.