

## 'Adaptation in natural populations: tools and mechanisms'

Tuesday, May 31 , 2011

**Luc De Meester**

**Title: Life in a mosaic of stressors: an evolving metacommunity approach**

Laboratory of Aquatic Ecology and Evolutionary Biology, K.U.Leuven, Belgium

### Abstract

Ecological and evolutionary processes have largely been studied separately, yet there is growing evidence that ecological and evolutionary dynamics can occur at the same time scale and can strongly interact. Ignoring these interactions may distort our view on population, community and ecosystem responses to environmental change, including human impact. The evolving metacommunities framework tries to disentangle the relative importance of species and genotype sorting in determining community trait responses to environmental gradients locally and regionally. A key aspect that determines the outcome of eco-evolutionary interactions is the rate of local species sorting and genetic adaptation versus immigration rates. I will illustrate these concepts using our own research, using the water flea and its responses to natural and anthropogenic stressors as main model system. I will discuss evolution-mediated priority effects and responses to climate change, and provide some perspectives on potentially interesting approaches to study evolving metacommunities in nature.

**Ellen Decaestecker**

**Title: 'The Red Queen in action in Daphnia-parasite interactions'**

Laboratory of Aquatic Ecology and Evolutionary Biology, K.U.Leuven, Belgium

### Abstract

Fast evolving parasites are a key structuring force in host ecosystems. In their 'arms race' with fast evolving parasites, there will be selection in Daphnia populations against defense mechanisms that are abundant in the momentary interaction, as parasites adapt to the most abundant host genotypes. The resulting antagonism produces an ongoing co-evolutionary dynamic that maintains genetic variation in infectivity traits. It is, however, notoriously difficult to study co-evolutionary dynamics in nature, because time series over many generations are needed. Consequently, empirical evidence for the process of host-parasite co-evolution in natural systems is lacking. To obtain insight in the fundamental processes that drive the co-evolutionary dynamics of antagonistic host-parasite interactions, the water flea Daphnia and its parasites were used as an evolutionary and experimental model. A historical reconstruction of a natural Daphnia-parasite interaction was realized using what amounts to a time machine in a shallow pond, as this pond contains layered sediments with both Daphnia resting eggs and spores of her bacterial parasites. These resting stages remain dormant for many years, but can be revived and thus provide an archive of past evolutionary dynamics in a natural system. Our results revealed Red Queen host-parasite dynamics. These specific host-parasite interactions are further investigated in a wider ecological framework investigating the link of these interactions with defenses towards predation and dynamic environments.

**Anke Schwarzenberger & Eric v. Elert**

**Title: Seasonal and local adaptation of *Daphnia magna* to cyanobacterial protease inhibitors? – Comparison of three natural populations.**

Aquatic Chemical Ecology, Zoological Institute, University of Cologne, Germany

Abstract

Cyanobacteria are known to produce a variety of toxic secondary metabolites. Many of these metabolites have been shown to be grazer toxins, among them the wide-spread protease inhibitors (PIs). These PIs have been demonstrated to negatively affect *Daphnia* by reducing their growth and decreasing the activity of the direct targets of the PIs, i.e. digestive gut proteases. Here we compare different *D. magna* populations from three European lakes that differ with respect to the presence of cyanobacteria. Microsatellite analyses show distinct differences in FST values of the three populations. Direct inhibition of the gut proteases of different *D. magna* genotypes with natural lake seston demonstrates a higher resistance of the *D. magna* population from the lake with cyanobacteria, hinting at local adaptation to PIs. Seston from the lake with cyanobacteria proved to contain PIs with a maximum in PI content in early summer. Analysis of neutral markers reveals differences in *D. magna* genotype composition in the periods before, during and after this maximum of PI content. Additionally, a conspicuous change in haplotype frequencies was observed in early summer. Further investigations have to test if these changes in genotype frequencies can be attributed to seasonal selection by PIs in the seston.

**Christian Küster & Eric v. Elert**

**Title: High Resolution Melting Analysis (HRMA) – A powerful and cost effective tool for large scale genotyping projects**

Aquatic Chemical Ecology, Zoological Institute, University of Cologne, Germany

Abstract

HRMA is based on monitoring the melting of whole PCR amplicons. Due to saturating concentrations of dye that bind at high concentrations to double stranded DNA it is possible to genotype a high number of samples rapidly. Even single SNPs within a 200 bp amplicon can be detected. HRMA is easy to apply, very accurate and cost effective vs. other genotyping techniques such as sequencing. In the present study HRMA was used to analyse the polymorphism of a chymotrypsin locus within *Daphnia* populations.

**Christoph Effertz & Eric v. Elert**

**Title: Relative expression of actine genes in *D. magna* – Possible targets for fish kairomones?**

Aquatic Chemical Ecology, Zoological Institute, University of Cologne, Germany

Abstract

In response to cues released by predators *Daphnia* shows a high degree of phenotypic plasticity that has been shown to vary within and among species. The molecular level of these responses is nearly unknown. It has been shown that the actine protein concentration in *D. magna* is influenced by fish kairomones. Here we hypothesize that these changes in actine protein are caused by changes in gene expression and investigate the effect of fish kairomones on the relative expression of four paralogous actine genes in *D. magna* via qPCR .

**Patrick Fink, Wiebke Bindemann, Anke Schwarzenberger & Eric von Elert**  
**Title: Variation in gene expression in *Daphnia pulex* - a key to understand competition for essential fatty acids**

Aquatic Chemical Ecology, Zoological Institute, University of Cologne, Germany

Abstract

The diet's content in semi-essential polyunsaturated fatty acids (PUFAs) is a major determinant of nutritional quality of phytoplankton for herbivorous zooplankton; in particular the PUFA eicosapentaenoic acid (EPA) has been shown to limit growth of the herbivorous cladoceran genus *Daphnia* in the field. Recently, in *Daphnia* intraspecific variability has been shown with regard to clonal sensitivity to EPA-limitation. This can probably be explained by differences in the genotypes' ability to convert dietary precursor PUFAs into EPA. We here used a target gene approach to quantify the expression of an enzyme crucial for the conversion of a common dietary precursor-PUFA into EPA. We experimentally manipulated the dietary availability of PUFAs for two *Daphnia pulex* clones and subsequently compared the expression of the elongase-2 gene in these animals. Daphnids on a diet rich in a precursor PUFA, but without EPA showed higher expression levels of the elongase gene compared to animals on a diet rich in EPA. Furthermore, the two investigated *D. pulex* clones differed in the diet-dependent changes in elongase-2 expression. This indicates that the ability to regulate the expression of genes involved in the biosynthesis of EPA is a variable trait within populations. This trait is a potential target for selection and could help to explain competitive interactions and evolutionary divergence within natural *Daphnia* populations.

**Wednesday, June 01, 2011**

**Andrew Beckerman**

**Title: Phenotypic plasticity, local adaptation and high dimension phenotypes**

Department of Animal and Plant Sciences, University of Sheffield, UK

Abstract

Phenotypic plasticity, and its role in adaptation, is frequently evaluated in single traits. However, it remains imperative to evaluate whole phenotypes in order to understand the role of plasticity in adaptation. By examining multiple traits, it is possible to investigate fundamental issues relating to evolution in variable environments such as phenotypic convergence/divergence, genetic constraints and trade-offs, phenotypic integration and the stability/differentiation of the G-matrix. Here, using *Daphnia* as a model system, I present insight into these core topics based on the implementation of modern, multivariate statistical tools.

**Luisa Orsini**

**Title: Approaches and molecular tools to study adaptation in natural populations**

Laboratory of Aquatic Ecology and Evolutionary Biology, K.U.Leuven, Belgium

Abstract

Genetic variation is the raw material of evolution and the one component that allows populations to adapt to changing environments. Adaptation is mediated by selection, gene flow, mutation and genetic drift. I will briefly discuss how these forces affect genetic diversity

and how the introduction of an additional variable to the mix, natural or anthropogenic stress, can interfere with the dynamic equilibrium in which natural populations live. Stress, natural or human induced, moves organisms away from their physiological optimum. This triggers a range of responses in natural populations ranging from adaptation to extinction. I will show a number of genetic/genomic approaches and molecular tools that can be used to measure adaptation in natural populations in response to environmental stress. I will discuss several examples from case studies including both model and non-model genetic species. The case studies will exemplify the application of genetics and genomics to ecology, evolution, adaptation and conservation. I will conclude the tutorial with an overview on the most recent technological developments in the 'omics' era.

**Veerle Lemaire, S. Brusciotti, I. van Gremberghe, J. Vanoverbeke, W. Vyverman & L. De Meester**

**Title: Genotype-genotype dependent interactions between the cyanobacterium *Microcystis* and its grazer, the waterflea of the genus *Daphnia***

Laboratory of Aquatic Ecology and Evolutionary Biology, K.U.Leuven, Belgium

Abstract

*Microcystis* are cyanobacteria inhabiting many of the freshwater systems we use for recreation, drinking water, or fisheries worldwide. *Microcystis* blooms have a pervasive impact on their abiotic (e.g. low light levels, hypoxia) and also impact their biotic environment by producing secondary metabolites (e.g. microcystin-LR, protease inhibitors), which can poison or kill organisms spanning the entire foodweb, including humans and livestock. Large-bodied *Daphnia* are capable of ingesting cyanobacteria, but can *Daphnia* control *Microcystis* blooms or, is it rather *Microcystis* that suppresses *Daphnia*? Recent studies report *Daphnia* physiologically acclimatizing and genetically adapting to cyanotoxins. We hypothesized that interactions between *Daphnia* and *Microcystis* are genotype-genotype specific, the outcome of the interaction depending on the genetic identity of both. To test this, we exposed two-day old juveniles of ten *Daphnia* clones for 48 hours to increasing concentrations of ten *Microcystis* strains (supplemented with *Scenedesmus* to 1mgC/l). We observed a significant *Microcystis* strain effect on *Daphnia* mortality. These differences could only partly be attributed to differences in microcystin-LR content between the strains. We also observed a significant effect of *Daphnia* genotype on mortality caused by *Microcystis*. Finally, we confirm our hypothesis: there are genotype-genotype dependent interactions between *Microcystis* and *Daphnia*, indicating that there is scope for local co-adaptation of *Microcystis* and *Daphnia*, suggestive of a geographic mosaic of co-evolution. *Microcystis* evolved a portfolio of anti-grazer defenses, and in response *Daphnia* acquired different resistance mechanisms to circumvent defenses of *Microcystis* strains. We conclude that locally adapted *Daphnia* may be able to control cyanobacteria and prevent blooms.

**Lutz Becks**

**Title: Adaptation and the evolution of sex in facultative sexual rotifer**

Zoological Institute, University of Cologne, Cologne, Germany

Abstract

One of the oldest and most enduring hypotheses for the evolution of sex is based on the idea that sexual reproduction facilitates adaptation. While previous empirical work showed that sexual reproduction can accelerate adaptation, evidence that sex can evolve during times of adaptation is still lacking. Using facultatively sexual rotifers, we present direct experimental

evidence that adaptation can drive the evolution of sex itself. We find that sex is favoured in novel environments. Rates of sex evolved within adapting populations to higher levels, but declined when populations were close to their fitness optimum. We found a similar, but consistent decline in the control populations that stayed in the environment they previously were adapted to. We link these changes in the rate of sex to their underlying population genetic mechanisms by experimentally inducing sex in a subsample of the populations. Specifically, we find that long-term advantages of sex became large in populations adapting to novel environments, but not in control populations. Compared to non-adapting control populations in which sex is disfavoured, we find that sex has both a larger long-term advantage and a smaller short-term disadvantage in adapting populations.