Summary

The Seventh International Symposium on Eco-Evolutionary Dynamics was a success by many measures. The symposium was timely, given the increasing need to explore the interface of ecology and evolution (e.g. Schoener 2011). Symposium topics, such as Ecological Speciation & Radiation and Ecological Genetics & Genomics, lay at the cutting edge of eco-evolutionary research. Keynote speakers were geographically and scientifically diverse, and symposium participants spanned an impressive range of nationalities, career level, and scientific interests.

Scientific Context

Research at the interface of ecology and evolution developed largely independent of one another because ecological processes were assumed to operate on much shorter time scales than evolutionary processes. Only recently have reports of rapid evolution, substantial intraspecific variability in ecologically relevant traits, and genotypic effects that amplify across trophic levels called biologist's attention to the interaction of ecological and evolutionary processes (Whitham et al. 2003; Hairston et al. 2005; Fussmann et al. 2007; Pelletier et al. 2009). An increasing number of studies indicate substantial consequences of eco-evolutionary feedbacks for population persistence (Hanski & Mononen 2011), trophic interactions (Hairston et al. 2005), community assembly (Urban et al. 2008), and ecosystem properties (Harmon et al. 2009). However, only recently have some of the molecular mechanisms that underlie eco-evolutionary dynamics been identified (Becks et al. 2012).

Identification of the genetic mechanisms regulating rapid evolution remains an outstanding question with important implications. For example, interaction between ecological and evolutionary processes is more likely in the presence of factors that escalate the speed of evolutionary change, such as very strong selective pressures. Both natural and anthropogenic stressors can operate as strong selective pressures and drive populations and communities through rapid adaptive evolution. Combining eco-evolutionary dynamics and ecological and environmental genomics is critical to understand over what time-frame (years, decades, centuries) ecological dynamics drive evolutionary changes and eco-evolutionary feedbacks. Linking genomic mechanisms to eco-evolutionary dynamics is very much research in its early stages and would benefit from increased dialogue between the EUROCORES program Ecological and Evolutionary Functional Genomics (EuroEEFG) and a group focusing on eco-evolutionary dynamics.

Symposium Description

The ECO-EVO research network unites international teams exploring the interface of ecology and evolution and seeks to identify, understand, and predict eco-evolutionary dynamics (http://bio.kuleuven.be/de/evenet/index.php). This requires integrating research in population and landscape genetics, co-evolution, phylogenetics, and speciation with metacommunity ecology and ecosystem and global change biology. The network provides a critical hub among researchers in these distinct fields by assembling contacts, organizing workshops and seminars, and hosting a biannual symposium. The symposium especially serves as a forum for network members to share research progress and exchange ideas with invited attendees and interested junior researchers.

We hosted the International Symposium on Eco-Evolutionary Dynamics (EcoEvoVII) at KU Leuven's campus in Leuven, Belgium from February 5th to 7th 2013. 125 participants from twelve countries joined, contributing thirteen keynote talks, 32 research presentations, and 25 posters, as well as a stimulating intellectual environment enjoyed at coffee and lunch breaks, poster sessions, and the conference reception and dinner. Thanks to funding from EEFG, we expanded the intercontinental reach of our program by inviting keynote speakers from McGill University in Montreal (Canada), University of California at Berkeley (United States), Cornell University in Ithaca (United States), and State University of New York at Stony Brook (United States). Speakers from these locales joined European colleagues from The Netherlands (V.U. University Amsterdam, RU Nijmegen), Switzerland (University of Geneva), United Kingdom (Exeter University, University of Oxford), Germany (LMU Munich, University of Wuerzburg, Max Planck Institute for Evolutionary Biology), and Sweden (Uppsala University).

This year's program expanded its scope by adding a session on Ecological Genetics & Genomics with keynote addresses by Joop Ouborg and Frederick Chain. ECO-EVO network scientists blended with EEFG researchers and numerous postdocs and PhD students in the other seven sessions (Eco-evolutionary Dynamics, Eco-evolutionary Dynamics With *Daphnia*, Co-evolutionary Dynamics With parasites, Evolution Across Species Ranges, Dispersal and Evolution, Socio-evolutionary Dynamics, and Ecological Speciation & Radiation). We are especially grateful for EEFG members Joop Ouburg and Luisa Orsini for contributing to the Ecological Genetics & Genomics session and sharing a genomic perspective with scientists in attendence. Thanks to all participants, especially the graduate students and postdoctoral researchers that contributed a majority of presentations and posters, our symposium successfully shared information among participants and produced new interactions and potential collaborations sure to advance the study of eco-evolutionary dynamics. A complete listing of the participants concludes the attached symposium program.

References

Becks, L., Ellner, S. P., Jones, L. E., & Hairston, N. G. (2012). The functional genomics of an eco-evolutionary feedback loop: linking gene expression, trait evolution, and community dynamics. *Ecology Letters*, 15(5), 492–501.

Fussmann, G. F., Loreau, M., & Abrams, P. A. (2007). Eco-evolutionary dynamics of communities and ecosystems. *Functional Ecology*, 21(3), 465–477.

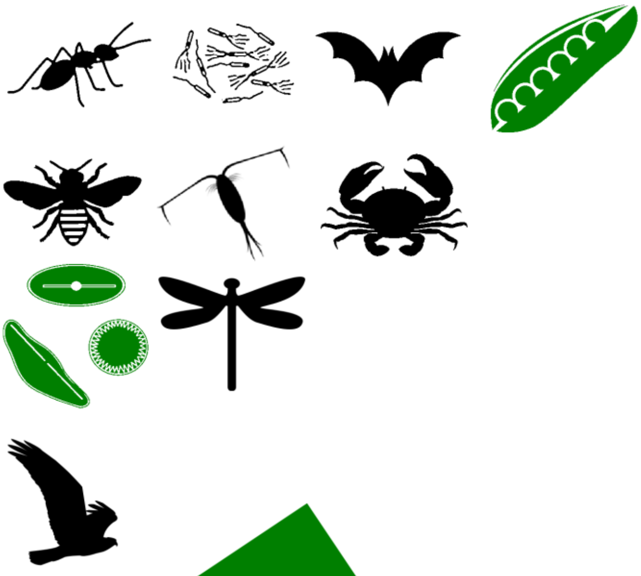
Hairston, N. G., Ellner, S. P., Geber, M. A., Yoshida, T., & Fox, J. A. (2005). Rapid evolution and the convergence of ecological and evolutionary time. *Ecology Letters*, 8(10), 1114–1127.

Hanski, I., & Mononen, T. (2011). Eco-evolutionary dynamics of dispersal in spatially heterogeneous environments. *Ecology letters*, 14(10), 1025–34.

Pelletier, F., Garant, D., & Hendry, A. P. (2009). Eco-evolutionary dynamics. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 364(1523), 1483–9.

Schoener, T. (2011). The newest synthesis: understanding the interplay of evolutionary and ecological dynamics. *Science*, 331(6016), 426-429.

Whitham, T. G., Young, W. P., Martinsen, G. D., Gehring, C. A., Schweitzer, J. A., Shuster, S. M., Wimp, G. M., et al. (2003). Community and ecosystem genetics: A consequence of the extended phenotype. *Ecology*, 84(3), 559–573.



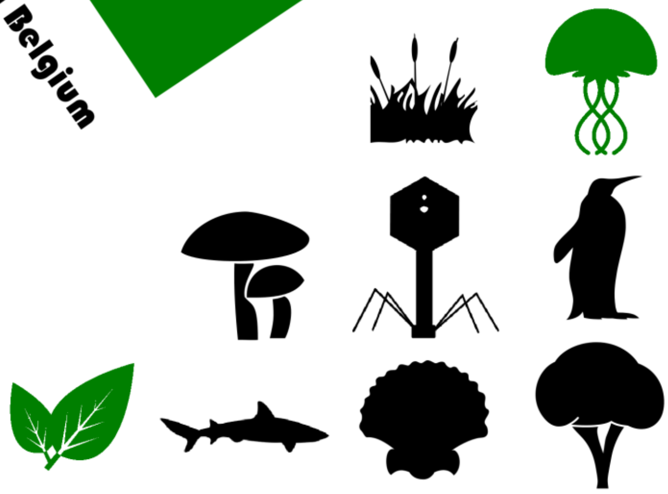
ECOEVO III

2013

Seventh
Symposium
Eco-Evolutionary
Dynamics

Feb 5 - 7

KU Leuven
3000 Leuven Belgium



EUROPEAN
SCIENCE
FOUNDATION
SETTING SCIENCE AGENDAS FOR EUROPE

KU LEUVEN

Universiteit
Antwerpen

UNIVERSITEIT
GENT

FWO
VLAANDEREN

images: Jacob Eckert, Christopher T. Howlett, Okan Benn, Megan Shrewsbury, Hernan D. Schlosman, Nicola Bridoux, Monika Ciapala, Felipe Silva, Kate Vogel, Christoffer Skogsmo - from The Noun Project

WELCOME

Welcome to Leuven and to the 7th Eco-evolutionary symposium. The roots of this symposium trace back to two former FWO Research Networks on *Ecological Genetics* (1997-2002 and 2002-2008). The last symposium in February 2011 (Leuven) and this symposium on *Eco-evolutionary dynamics* are embedded in the FWO Research Network *Eco-evolutionary dynamics in natural and anthropogenic communities*. It is coordinated by the Department of Biology of the KU Leuven, and includes national partners from the University of Antwerp and Ghent University. Sixteen international partners complement the network; we are very happy to welcome several of you. This year the symposium is co-organised with the *KU Leuven Excellence Center on Eco- and Socio-Evolutionary Dynamics* (SEEDS).

With the years the focus of the symposium has shifted from ecological genetics to eco-evolutionary and socio-evolutionary interactions. Ecology and social interactions influence evolution, and *vice versa*. In the philosophy of *small is beautifull* the number of participants to the symposium is limited to the Belgian scientific community reinforced with invited speakers from our international partners. Symposium costs for participants are minimal, while the chances for communication are maximal.

The registration list features 125 participants from 12 countries. The programme combining key note and regular talks complemented with posters looks very attractive. The local setting and the fine food should do the rest. We wish you a very pleasant, productive and scientifically invigorating stay in historical Leuven.

Filip Volckaert, Luc De Meester, Dries Bonte, Luc Brendonck, Ellen Decaestecker, Olivier Honnay, Hans Jacquemyn, Herwig Leirs, Luc Lens, Erik Matthysen, Robby Stoks, Stefan Van Dongen, Wim Vyverman and Tom Wenseleers

Leuven, 31 January 2013

ACKNOWLEDGEMENTS

This symposium was sponsored by the Fund for Scientific Research – Vlaanderen (http://www.fwo.be) through the network 'Eco evolutionary dynamics in natural and anthropogenic communities' and by the EUROCORES program Ecological and Evolutionary Functional Genomics (EuroEEFG).

We thank the administration and personnel of the Katholieke Universiteit Leuven for the excellent support and services they provide. In particular we would like to thank Alma for catering, Conny Coeckelberghs and Bart Hellemans for general organizational support, and the many doctoral and post doctoral students assisting with the organization.

FWO
VLAANDEREN
Fonds Wetenschappelijk Onderzoek
Research Foundation – Flanders

EUROPEAN
SCIENCE
FOUNDATION

KU LEUVEN
ARENBERG DOCTORAL SCHOOL

THE LABORATORIES HOSTING THE SYMPOSIUM

KU Leuven

- Laboratory of Animal Diversity and Systematics:
    - Filip Volckaert (coordinator), Jos Snoeks and Wim Van Neer
- Laboratory of Aquatic Ecology, Evolution and Conservation:
    - Luc Brendonck, Luc De Meester and Robby Stoks
- Laboratory of Plant Ecology:
    - Olivier Honnay, Hans Jacquemyn
- Laboratory of Socioecology and Social Evolution:
    - Tom Wenseleers, Johan Billen

KU Leuven-Kortrijk

- Laboratory of Aquatic Biology:
    - Ellen Decaestecker and Koenraad Muylaert

Ghent University

- Research Group Terrestrial Ecology:
    - Luc Lens and Dries Bonte
- Laboratory of Protistology and Aquatic Ecology:
    - Wim Vyverman

University of Antwerp

- Evolutionary Ecology Group:
    - Erik Matthysen, Stefan Van Dongen and Hedwig Leirs

PRACTICAL INFORMATION

- The meeting will be hosted in the facilities of the K.U. Leuven, in the Social Sciences Department, located in the city centre. Lectures take place in auditorium Jean Monnet AP 01.30 (Parkstraat 51). Coffee breaks and poster sessions will be held in the Hall in front of the auditorium.

- More information on transport, accommodation, … can be found on the Evolutionary Dynamics symposium website (http://bio.kuleuven.be/eeb/symposium/).

- Lectures include 13 invited talks (25 minutes) and 32 contributed talks (15 minutes), each with 5 minutes for discussion and change of speaker. For all speakers we ask to upload your presentations preferably upon registration, or at least one break ahead of your session. Mac users are encouraged to test their presentation in a Windows environment.

- People are invited to join for coffee breaks and lunches at the conference hall.

- The conference dinner is at Chess cafe; Fonteinstraat 1/A 3000 Leuven, a 15 minute (1km) walk from the conference venue.

- Internet Access: wireless internet access is available at the congress venue through the Eduroam network (http://www.eduroam.org/). For people who have no access to this Eduroam, a username and password can be provided at the registration desk. Each participant is assigned their own account and password. The account will work in all University buildings with a wireless connection.

- Closest bank and cash machine (ATM): KBC, Mgr. Ladeuzeplein, 15 or BNP Paribas, Naamsestraat 9.

- Certificate of attendance can be requested at the registration desk.

FOR ANY FURTHER INFORMATION PLEASE CONTACT ONE OF THE ORGANIZERS OR GO TO THE REGISTRATION DESK.

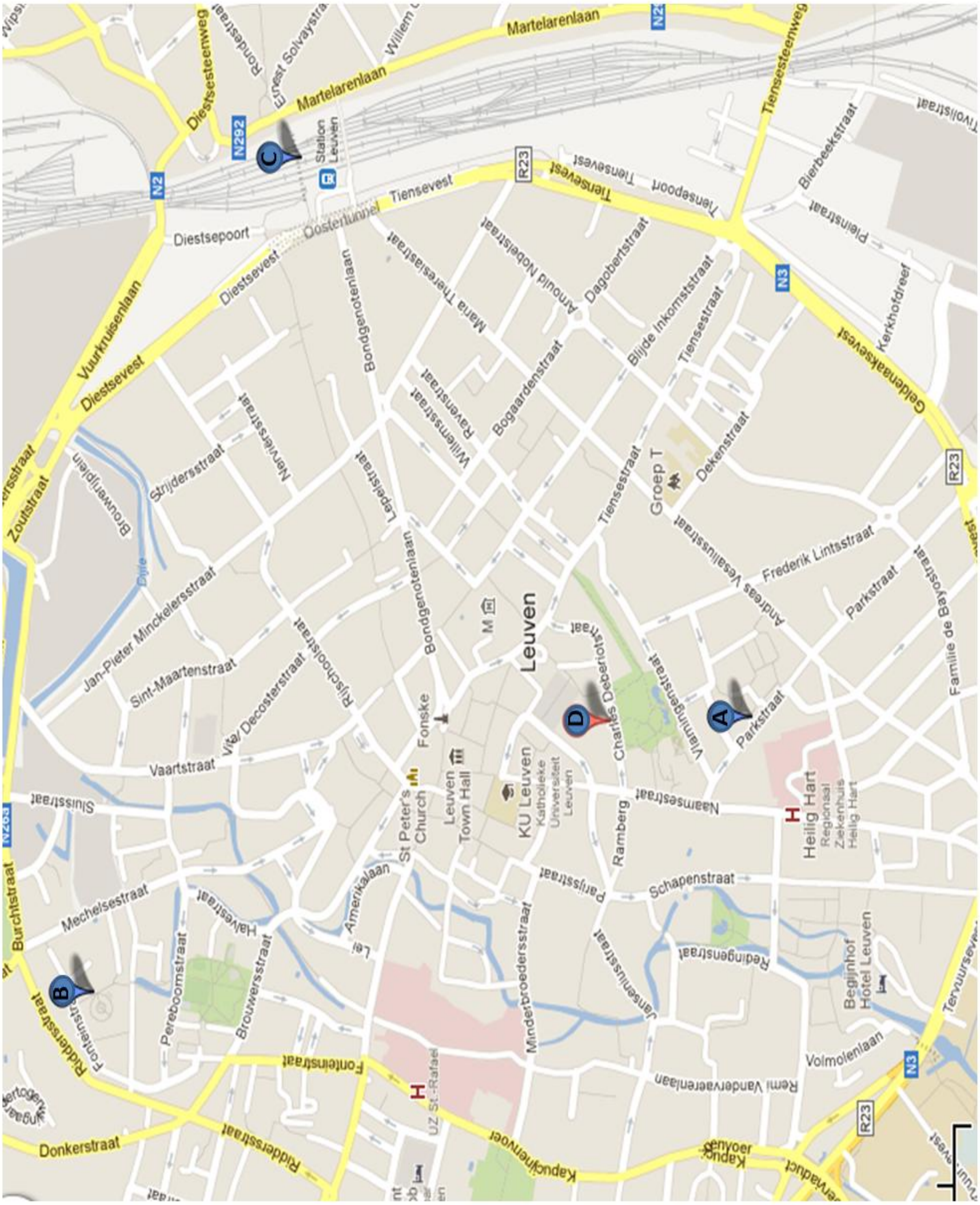
Symposium Secretariat:

Laboratory of Aquatic Ecology, Evolution and Conservation
Laboratory of Animal Diversity and Systematics
Ch. Deberiotstraat 32
B- 3000 Leuven
Belgium

E-mail: ecoevosymposium2013@bio.kuleuven.be

Phone: +32 16 32 37 17 & +32 16 32 39 66
Fax: +32 16 32 45 75

MAP


A
B
C
D
Leuven
Station Leuven
Martelarenlaan
Diestsesteenweg
Tiensesteenweg
Tiensevest
Diestsevest
Diestsepoort
Oostertunnel
Vuurkruisenlaan
Zoutstraat
Bondgenotenlaan
Maria Theresiastraat
Arnould Nobelstraat
Dagobertstraat
Bogaardenstraat
Ravenstraat
Willemsstraat
Brusselsestraat
Lepelstraat
Nerviersstraat
Strijdersstraat
Brouwerijplein
Dijle
Jan-Pieter Minckelersstraat
Sint-Maartenstraat
Vital Decosterstraat
Rijschoolstraat
Vaartstraat
Sluisstraat
Mechelsestraat
Halvestraat
Pereboomstraat
Brouwersstraat
Burchtstraat
Riddersstraat
Fonteinstraat
Donkerstraat
Kapucijnenvoer
Minderbroedersstraat
Parijsstraat
Schapenstraat
Naamsestraat
Ramberg
Janseniusstraat
Redingenstraat
Groep T
Dekenstraat
Tiensestraat
Blijde Inkomststraat
Andreas Vesaliusstraat
Frederik Lintsstraat
Parkstraat
Familie de Bayostraat
Vlamingenstraat
Charles Deberiotstraat
Geldenaaksevest
Bierbeekstraat
Pleinstraat
Kerkhofdreef
Tivolistraat
St Peter's Church
Fonske
Leuven Town Hall
KU Leuven
Katholieke Universiteit Leuven
Heilig Hart
Regionaal Ziekenhuis Heilig Hart
UZ St.-Rafaël
Begijnhof Hotel Leuven
Volmolenlaan
Remi Vandervaerenlaan
Tervuursevest
Amerikalaan
Lei
N2
N3
N292
R23
N263

PROGRAMME

Tuesday 5 February 2013

8:30 Registration

9:00 Opening of the Symposium – vice rector Peter Marynen

9:15 Practical information – Filip Volckaert

Session "**Eco-evolutionary dynamics**"
Chairman Luc De Meester

9:30-10:00
Eco-evolutionary dynamics in a three-species laboratory system: all hell breaks loose
Nelson Hairston, Stephen Ellner, Teppo Hiltunen, Lutz Becks, Laura Jones, Giles Hooker

10:00-10:30
How ecological interactions can drive evolutionary loss of traits
Jacintha Ellers

10:30 Coffee Break

11:00-11:20
Why rapid adaptive evolution matters
Lutz Becks

11:20-11:40
Ecosystem consequences of eco-evolutionary dynamics
Blake Matthews, Thierry Aebischer, Baenz Lundsgaard-Hansen, Karen E. Sullam, Ole Seehausen

11:40-12:00
The importance of pleiotropic costs on the evolution of persistence in the opportunistic human pathogen *Pseudomonas aeruginosa*
Tom Wenseleers, Frederic Muratori, Edgar Duenez-Guzman, Kristine Stepanyan, Jan Michiels

12:00 Lunch Time

Session "**Eco-evolutionary dynamics with *Daphnia***"

Chairman Jelena Pantel

14:00-14:20
Micro-evolutionary responses to climate change in the water flea *Daphnia magna*
Aurora Geerts, Joost Vanoverbeke, Bram Vanschoenwinkel, Wendy Van Doorslaer, Heidrun Feuchtmayr, Luc De Meester

14:20-14:40
Inbreeding and evolutionary potential for stress tolerance in the water flea *Daphnia magna*
Ine Swillen, Joost Vanoverbeke, Luc De Meester

14:40-15:00
Incidence of sex and evolution mediated priority effects in spatially heterogeneous environments
Joost Vanoverbeke, Mark Urban, Luc De Meester

15:00-15:20
Ripple effect through a simple freshwater food web: the bottom-up impact of priority effects in cyanobacteria on the zooplankton community
Veerle Lemaire, Kristien Brans, Wim Vyverman, Luc De Meester

15:20 Tea Time

15:50-16:10
Eco-evolutionary dynamics of predator-prey interactions: a case study with *Daphnia* and its predator *Triops*
Aline Waterkeyn, Nisse Van Pottelbergh, Luc De Meester, Luc Brendonck

16:10-16:30
Resurrecting complexity: Rapid multiple trait evolution in response to predation in the water flea *Daphnia*
Kevin Pauwels, Robby Stoks, Luc De Meester

16:30-16:50
Comparative responses of populations and communities to landscape properties
Jelena Pantel, Sarah Rousseaux, Steven Declerck, Pedro Peres-Neto, Luc De Meester

17:00 -19:00 Poster session & Reception

Wednesday 6 February 2013

Session "**Co-evolutionary dynamics with parasites**"

Chairman Ellen Decaestecker

9:00-9:30
Surviving chytrid assassins in changing lakes
Bas Ibelings, Alena Gsell, Silke Van den Wyngaert

9:30-10:00
Host-parasite coevolution at ecological time scales: bacteria-phage dynamics within a long-lived host
Britt Koskella

10:00-10:30
Parasites maintain host genetic diversity
Justyna Wolinska, Sabine Giessler, Mingo Yin

10:30 Coffee Break

11:00-11:20
Parasites as habitat-specific selection factors in sticklebacks
Martin Kalbe, Tina Henrich, Irene Samonte-Padilla, Per Jakobsen

11:20-11:40
Population dynamics and genetic structure of the tree-hole tick *Ixodes arboricola*
Raoul Van Oosten

11:40-12:00
Reconstructing genetic variation for historical changes in P-availability: a case-study using the *Daphnia*-parasite model system
Lien Reyershove, Thomas Beer, Koenraad Muylaert, Ellen Decaestecker

12:00-12:20
Host allelic diversity drives long-term host-parasite coevolutionary dynamics
Ellen Decaestecker, Herbert De Gersem, Yannis Michalakis, Joost Raeymaekers

12:20 Lunch Time

Session "**Evolution across species ranges**"

Chairman Luc Lens

14:00-14:20
The evolution of phenotypic plasticity in thermal sensitivity during range shifting
Jasmijn Hillaert, Jeroen Boeye, Robby Stoks, Dries Bonte

14:20-14:40
Vulnerability to a metal under global warming is shaped by thermal adaptation along a latitudinal gradient
Khuong Dinh Van, Lizanne Janssens, Sara Debecker, Robby Stoks

14:40-15:00
Rapid range expansion increases genetic differentiation while hardly reducing genetic diversity in a damselfly
Janne Swaegers, Joachim Mergeay, Lieven Therry, Maarten Larmuseau, Dries Bonte, Robby Stoks

15:00-15:20
Evolutionary changes in larval and adult phenotype at the expanding range edge of the damselfly *Coenagrion scitulum*
Lieven Therry, Robby Stoks, Dries Bonte

15:20-15:40
Vertebrate responses to spatial and environmental gradients reveal latitudinal differences in mechanisms of community assembly
Falko Buschke, Luc De Meester, Luc Brendonck, Bram Vanschoenwinkel

15:40-16:00
Niche conservatism among non-native birds: niche unfilling rather than niche expansion
Diederik Strubbe, Olivier Broennimann, Francois Chiron, Erik Matthysen

16:00-16:20
Geography, climate, and patterns of genetic diversity in a bdelloid rotifer
Diego Fontaneto, Cuong Tang

16:20 Tea Time

Session "**Dispersal and evolution**"

Chairman Erik Matthysen

16:50-17:20
If and how dispersal matters for bacterial diversity and function
Eva Lindström

17:20-17:50
Dispersal evolution and its consequences: From individuals to communities
Thomas Hovestadt

17:50-18:10
Ideal free distribution of fixed dispersal phenotypes in a wing dimorphic in heterogeneous landscapes
Frederik Hendrickx, Steve Palmer, Justin Travis

18:10-18:30
On the distribution of adaptive genetic variation in a sympatric mosaic of a salt marsh beetle
Steven Van Belleghem, Frederik Hendrickx

19:00 Conference Dinner

Thursday 7 February 2013

Session "**Socio-evolutionary dynamics**"

Chairman Tom Wenseleers

8:30-9:00
Social evolution of microbes
Kevin Foster

9:00-9:20
Low frequency of non-paternity events in historical human population of Flanders
Maarten Larmuseau, Joost Vanoverbeke, Anneleen Van Geystelen, Gilles Defraene, M. Vandezande, Nancy Vanderheyden, K Matthys, Tom Wenseleers, Ronny Decorte

9:20-9:40
Stable maintenance of uncooperative aphid mutualists in the black bean aphid *Aphis fabae*: hypotheses and tests
Sharon Schillewaert, Amelie Vantaux, Thomas Parmentier, Wim van den Ende, Tom Wenseleers

9:40-10:00
The altruistic cannibal: multilevel selection in *Arachnocampa fungus* gnats
Edgar Duenez Guzman, Suzanne Sadedin

10:00 Coffee Break

Session "**Ecological speciation & radiation**"

Chairman Joost Raeymaekers

10:30-11:00
Progress toward ecological speciation in Darwin's finches, threespine stickelback, and Trinidadian guppies
Andrew Hendry

11:00-11:30
Community assembly through adaptive radiation: spiders on islands
Rosemary Gillespie

11:30-12:00
Untangling the mechanisms influencing hummingbird assemblages: New tools to answer old questions
Catherine Graham

12:00-12:20
Repeated habitat occupancy through species sorting and parallel radiation are not always so different on islands
Frederik Hendrickx, Viki Vandomme, Carl Vangestel, Thierry Backeljau

12:20-12:40
Exploring introgression patterns within a wolf spider radiation
Charlotte De Busschere, Steven Van Belleghem, Frederik Hendrickx

12:40 Lunch Time

Session "**Ecological genetics & genomics**"

Chairman Filip Volckaert

14:00-14:30
Inbreeding depression in plants in a conservation genomic context
Joop Ouborg, Francesco Angeloni, Niels Wagemaker, Philippine Vergeer

14:30-15:00
Genomic patterns of ecological differentiation across stickleback populations
Frederick Chain, Philine Feulner, Mahesh Panchal, Yun Huang, Christophe Eizaguirre, Martin Kalbe, Tobias Lenz, Irene Samonte, Monika Stoll, Thorsten Reusch, Erich Bornberg-Bauer, Manfred Milinski

15:00 Tea Time

15:30-15:50
The role of selection in driving landscape genomic structure of the waterflea *Daphnia magna*
Luisa Orsini, Joachim Mergeay, Katina Spanier, Joost Vanoverbeke, Luc De Meester

15:50-16:10
The Eda gene as a target for selection and gene flow in three-spined stickleback
Joost Raeymaekers, Nellie Konijnendijk, Maarten Larmuseau, Gregory Maes, Bart Hellemans, Luc De Meester, Filip Volckaert

16:10-16:30
Genotypic diversity and differentiation among populations of benthic freshwater diatoms as revealed by microsatellites
Pieter Vanormelingen, Katharine Evans, David Mann, Sofie D'Hondt, Tine Verstraete, Ann-Eline Debeer, Koen Sabbe, Wim Vyverman

16:30-16:50
Genetic differentiation of Tanzanian suburban multimammate rats and their rural neighbours: an evolutionary event of synanthropy?
Sophie Gryseels, Joëlle Goüy de Bellocq, Jan Zima, Vladimir Mazoch, Kurt Van Mechelen, Jan Broeckhove, Rhodes Makundi, Herwig Leirs, Stuart Baird

17:00
Closing remarks of the symposium

End of the meeting

Eco-evolutionary dynamics

Eco-evolutionary dynamics in a three-species laboratory system: all hell breaks loose

Hairston N.[1.], Ellner S.[1.], Hiltunen T.[1,2.], Becks L.[1,3.], Jones L.[1.], and Hooker G.[4.]

[1.] Cornell University, Department of Ecology and Evolutionary Biology, Ithaca, NY, USA
[2.] Univ. of Helsinki, Dept. of Food and Environmental Sciences/Microbiology, Finland
[3.] Max-Planck Institute for Evolutionary Biology, Ploen, Germany
[4.] Cornell University, Department of Biological Statistics and Computational Biology, Ithaca, NY, USA

In 2-species predator-prey systems, antiphase cycles represent “smoking gun” evidence for eco-evolutionary dynamics. Evolutionary cycles, in which the peak in prey density coincides with the minimum in predator density (and vice versa) occur when conditions otherwise favor typical ecological predator-prey cycling, but when the prey population also has genetic variation for a tradeoff between defense and competitive ability. Under these conditions, prey-trait cycling accompanies the antiphase dynamics. This pattern is easily detected, highly reliable, and has been seen repeatedly in laboratory microcosms, including many studies where the original authors did not recognize the cause of the dynamics they observed.

A search for a “smoking gun” of eco-evolutionary dynamics in 3-species intraguild-predation systems, however, proves to be much more challenging. Although in the absence of prey evolution (i.e., no genetic variation), mathematical analysis suggests – and direct experimentation confirms – that a single pattern of cycling exists (peaks in prey are followed by those in the intermediate predator and then by those in the top predator), adding prey evolution results in as many as 11 distinct dynamical patterns of species abundance, depending upon the details of the prey defense-competitiveness tradeoff and the strength of the interaction between the two predators. Empirical results from 3-species laboratory chemostat systems display a diversity of dynamical patterns, and with 11 theoretically possible, it is challenging to identify any distinct signature for an effect of evolution. Nevertheless, all of the experimental dynamics seen when prey are genetically variable are clearly distinct from that observed in the absence of evolution, suggesting that a continued search for the smoking gun is worth pursuing, even if that evidence is almost certainly multifaceted.

How ecological interactions can drive evolutionary loss of traits

Ellers J.

V.U. University Amsterdam Department of Ecological Sciences, Amsterdam, The Netherlands

Loss of traits can dramatically alter the fate of species. Loss of morphological, behavioral, or physiological traits can occur if traits are selected against or if traits are no longer needed. At present, the prevalence of trait loss is likely to be grossly underestimated because trait loss is not always accompanied by loss of the external phenotype, provided the lost function is compensated for by species interactions. This is important because trait loss can tighten the ecological relationship between partners, affecting the maintenance of species interactions.

Here, I present a new perspective on so-called 'compensated trait loss' and how this type of trait loss may affect the evolutionary dynamics between interacting organisms. In the first part of the talk I will present a comprehensive literature survey to give an overview of known cases of trait loss, and identify factors promoting compensated trait loss. In the second part, I will focus specifically on compensated trait loss of an essential metabolic trait in parasitic insects. Using phylogenetic analyses, I show that parasitoids have repeatedly lost the ability to synthesize lipids as an evolutionary consequence of interactions with their host. I will also address the molecular mechanisms that underlie loss of lipogenesis. Despite its hidden nature, compensated trait loss is important in directing evolutionary dynamics of ecological relationships and has the potential to change facultative ecological interactions into obligatory ones.

Why rapid adaptive evolution matters

Becks L.

Max Planck Institute for Evolutionary Biology, Ploen, Germany

It is increasingly apparent that evolutionary dynamics that act on the same time scale as ecological processes might play an important role in determining population, community and ecosystem dynamics. I will present results of an algae-rotifer system showing that changes in adaptive genetic variance in a defense trait of a prey population can radically alter eco-evolutionary dynamics. I further explore how higher food web and spatial complexity affects the potential for eco-evolutionary dynamics. As another example of rapid adaptive evolution, I present first results of our work on how eco-evolutionary feedback dynamics could help explaining the evolution of sexual reproduction.

Ecosystem consequences of eco-evolutionary dynamics

Matthews B.[1], Aebischer T.[1], Lundsgaard-Hansen B.[1], Sullam K.E.[2] and Seehausen O.[3]

[1] Eawag, Luzern, Switzerland, Center for Ecology, Evolution, and Biogeochemistry, Kastanienbaum, Switzerland
[2] Drexel University, Department of Biology, Philadelphia PA, USA
[3] University of Bern, Institute for Ecology and Evolution, Bern, Switzerland

A hallmark of living organisms is their capacity to modify the physical, chemical, and biological properties of ecosystems. Organisms exhibit heritable variation in the traits causing such modifications, meaning that phenotypic evolution by natural selection can drive ecosystem change. In adaptive radiations, for example, the traits under divergent selection are often the same as those used to exploit resources in the natural environment, making them good candidates for exploring feedbacks between phenotypic diversification and ecosystem dynamics. Using stickleback and whitefish as model organisms, we did a series of common gardening experiments to test whether contrasting fish phenotypes, arising from either genetic or environmentally induced differences between or within closely related species, have different effects on aquatic ecosystems. Our results show that phenotypic differences among organisms can cause considerable divergence not only to the ecological structure and function of communities (e.g. prey communities, primary production), but also to the physical and chemical characteristics of ecosystems (e.g. dissolved organic matter, and light transmission). We found that the size of ecosystem-effect contrasts resulting from phenotypic plasticity tended to be smaller than those resulting from different species, but this depended somewhat on the ecosystem metric and the treatment organism. We also found that the ecosystem divergence, caused by organisms with contrasting phenotypes, persisted beyond the time period when the organisms were present in the system. Overall, this suggests that phenotypic diversification of organisms can generate divergent ecosystem conditions, and this might modify the form and strength of natural selection so as to facilitate or constrain further phenotypic divergence.

The importance of pleiotropic costs on the evolution of persistence in the opportunistic human pathogen *Pseudomonas aeruginosa*

Wenseleers T.[1.], Muratori F.[1.], Duenez-Guzman E.[1.], Stepanyan K.[2.] and Michiels J.[2.]

[1.] KU Leuven, Laboratory of Socioecology and Social Evolution, Leuven, Belgium
[2.] KU Leuven Centre of Microbial and Plant Genetics, Heverlee, Belgium

Bacterial persistence is a phenotypic trait which allows a small portion of an isogenic bacterial population to survive an antibiotic treatment, while the remaining cells are killed. Persister cells of *Pseudomonas aeruginosa*, an opportunistic human pathogen, represents one of most common sources of nosocomial infections and is a major cause of death for patients with cystic fibrosis. It has been hypothesized that persistence is a form of bet hedging, which allows bacteria to cope with unpredictable catastrophic events. Experimental evidence also shows that increased exposure to antibiotic treatments selects for mutants with higher fractions of persister cells (hip mutants), whereas the wild type with relatively low proportions of persister cells outcompetes the hip mutants under good, non-averse growing conditions.

We developed a mathematical model to (1) simulate the forementioned competition experiments and (2) determine the evolutionarily stable (ESS) level of persistence under a particular environmental regime. Our basic model consists of a system of ordinary differential equations, which considers the cellular processes (lag time, cellular division, phenotypic switch between persister and normal type and mortality). The model allows 2 different strains with specific parameters to compete for the same resource, using empirical estimates for all parameters.

Consistent with experimental data, the results of the model predict that high persister hip mutants outcompete the low persister wild type under a regime with frequent antibiotic exposure, unless the time between 2 antibiotic treatments is very long. We further confirmed these results by showing that the ESS level of persistence decreases with increasing time between treatments. Surprisingly, however, our basic version of the model shows that the observed level of persistence is three orders of magnitude lower than the one that is predicted by the ESS model, and that only the incorporation of pleiotropic costs, such as a correlation between higher persistence in increased lag times, lower carrying capacities during stationary phase, increased mortality of persister cells and reduced growth rate, for which we all found some empirical evidence, can actually replicate empirically observed levels of persistence. This shows the importance of considering the fact that different phenotypic traits frequently cannot evolve fully independently.

Eco-evolutionary dynamics with *Daphnia*

Micro-evolutionary responses to climate change in the water flea *Daphnia magna*

Geerts A.[1.], Vanoverbeke J.[1.], Vanschoenwinkel B.[1.], Van Doorslaer W.[1.], Feuchtmayr H.[2.], and De Meester L.[1.]

[1.] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2.] Lancaster Environmental Ctr, Ctr Ecol & Hydrol, Lancaster, UK

The rate of genetic adaptation of natural populations to climate change is key to predicting biological responses to this global challenge. Yet, the degree to which populations can genetically track climate change is unknown. We used an experimental evolution approach in mesocosms to test to what extent a natural population of the water flea *Daphnia magna*, a key ecological interactor in shallow freshwater ecosystems, harbours sufficient genetic variation in critical maximum temperature, CTmax, to genetically adapt to a strong increase in water temperature.

Our results show a significant genetic change in CTmax in response to a two-year exposure to a + 4°C treatment under seminatural conditions, and provide evidence that the studied natural population of the water flea Daphnia has the capacity to genetically track considerable changes in temperature.

Inbreeding and evolutionary potential for stress tolerance in the water flea *Daphnia magna*

Swillen I.[1.], Vanoverbeke J.[1.] and De Meester L.[1.]

[1.] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

When new populations are founded by one or a few individuals, the resulting population may suffer genetic drift and inbreeding depression, which may reduce its fitness and capacity to genetically adapt to changing environments. In the water flea *Daphnia*, populations can in principle be founded by one individual, as reproduction entails amictic parthenogenesis as long as conditions are favourable. Upon induction of sexual reproduction, however, this would result in strong inbreeding. Here, we investigated to what extent such inbred *Daphnia* populations might still show evolutionary potential to respond to environmental stressors. Strong inbreeding depression would promote the success of invading genotypes, irrespective of their numerical disadvantage. Starting from an outbred natural population of *D. magna*, we created three inbred families through selfing within clonal lineages. We used populations composed of either an inbred family or the outbred base population in a selection experiment involving exposure to three pulses of the pesticide carbaryl. Following this selection experiment, we performed a life table experiment in which we compared performance of clones from naive and selected inbred and outbred populations in the presence and absence of carbaryl. Inbred families did not show a higher overall mortality in the presence of carbaryl than the outbred population, and one inbred family showed a higher tolerance than the outbred population prior to selection. The outbred population did, however, show a stronger reduction in mortality upon selection. Overall, genetic variation for life history traits and responses to carbaryl was not reduced in inbred families compared to the outbred population. There is much variation among inbred families, but inbreeding itself did not necessarily reduce the capacity of the populations to cope with carbaryl stress.

Incidence of sex and evolution mediated priority effects in spatially heterogeneous environments

Vanoverbeke J.[1.], Urban M.[2.] and De Meester L.[1.]

[1.] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2.] University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, US

Evolution mediated priority effects occur when ecological priority effects are enhanced or stabilized by rapid evolution. During colonization of an (newly created) empty habitat, such evolution mediated priority effects may give the advantage to early colonizers at the expense of the establishment success of secondary immigrants. This advantage of early colonization will depend on the strength of priority effects and the speed of adaptation in relation to immigration. Whereas sexually reproducing organisms, may adapt more rapidly to the new environment due to recombination and segregation of available genetic material, asexually reproducing organisms avoid the 'cost of sex' and may therefore induce stronger priority effects when arriving early. Partially clonal organisms that engage only periodically in sexual reproduction, may incorporate the advantages of both sexual and asexual reproduction, by combining the release of hidden genetic variation with rapid population growth and efficient selection. Using an individual based model in which establishment is determined by lottery competition among offspring, we allow species that differ in their propensity for sexual reproduction to compete for establishment in an empty habitat to which they are not well adapted. We thus directly compare the effectiveness of different reproduction strategies in exploiting evolutionary mediated priority effects.

Eco-evolutionary dynamics of predator-prey interactions: a case study with *Daphnia* and its predator *Triops*

Waterkeyn A.[1,2], Van Pottelbergh N.[1], De Meester L.[1] and Brendonck L.[1]

[1] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2] Research Center for Mediterranean Wetlands Tour du Valat, Le Sambuc, France

Predators often fulfill a keystone role in communities, driving cascading effects across trophic levels and modulating relative abundances of species, alleles and adaptive trait values. Under such a strong selective force, evolutionary and ecological processes are expected to interact on the same time scales. As a model to empirically test this theory, we study the impact of the tadpole shrimp *Triops cancriformis*, a key invertebrate predator in temporary ponds, on a metacommunity of zooplankton prey including the focal prey species *Daphnia magna*. *Daphnia* is known to have evolved an arsenal of antipredator defenses. By integrating information on different prey endpoints (neutral genetic variation and adaptive trait variation (species level), trait variation among species, and variation in community composition (community level)), we aim at investigating ecological and evolutionary dynamics of predator-prey interactions in an evolving metacommunity context. In this presentation we give preliminary results on three endpoints (*Daphnia* antipredator traits, community trait and species composition), without taking a connectivity gradient into consideration.

Using large scale mesocosm-experiments, the impact of different *Triops* predation pressures on zooplankton communities was tested. On the community level, *Triops* caused a strong change in community structure and trait composition, while at the level of the prey species, there was an associated shift in *D. magna* population structure and shape distribution. In a life table experiment, we investigated patterns of local genetic adaptation by contrasting antipredator responses of *D. magna* populations from habitats differing in *Triops* predation pressure (French temporary ponds with/without *Triops* and Belgian temporary/permanent ponds without *Triops*). We found strong genetic variation in antipredator responses between populations and clones, with several strategies being represented. Results suggest local adaptation to *Triops* in ponds where this predator was very abundant. We also found a signature of past selection in Belgian *Daphnia*. These preliminary results show that *Triops* can, besides modifying the habitat itself, significantly alter relative abundances of species and adaptive traits within prey communities. In future experiments we will attempt to unravel how evolutionary changes can be linked to observed ecological patterns, and this in a metacommunity of temporary ponds with variable levels of connectivity.

Resurrecting complexity: Rapid multiple trait evolution in response to predation in the water flea *Daphnia*

Pauwels K., Stoks R. and De Meester L.

KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

Natural populations of organisms are facing a constantly changing environment and their capacity to adjust their phenotype is crucial for their persistence. Insight into the relative importance of phenotypic plasticity, genetic changes in constitutive responses and genetic changes in plasticity is crucial for our understanding of the dynamics of how trait matching in nature is achieved. In the present study we reconstructed the evolutionary response of a natural *Daphnia magna* population to a change in fish predation over time for a total of twelve morphological, life history and behavioural traits using a resurrection ecology approach. In the presence of fish kairomones, we observed plastic responses for almost all traits. Different genotypes responded with a different but integrated defence strategy, with the strongest plastic response as well as the most combinations of responsive traits observed in genotypes of the time period with the highest fish predation pressure. We thus show both strong phenotypic plasticity rapid adaptive evolution in response to a strong selection pressure.

Comparative responses of populations and communities to landscape properties

Pantel J.[1.], Rousseaux S.[1.], Declerck S.[2.], Peres-Neto P.[3.] and De Meester L.[1.]

[1.] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2.] Netherlands Institute of Ecology, Wageningen, The Netherlands
[3.] University of Quebec at Montreal, Canada

Though the conceptual and theoretical frameworks of evolution and ecology developed largely independent of one another, their organization is remarkably similar. However, the commonalities between population genetic and community structure remain underexplored. We investigated *Daphnia magna* populations and heterospecific zooplankton communities inhabiting shallow ponds in Belgium. The goal of our study was to compare the responses of four organismal properties - variability of *D. magna* populations at neutral loci, variability of *D. magna* populations in heritable life history traits, variability of zooplankton community composition among ponds, and variability in the aggregation of ecologically relevant traits observed in ponds when the entire zooplankton community is considered - to the mosaic of environmental gradients and spatial connectivity observed in a natural landscape. We arranged data collected from our pond survey into a series of site × property matrices, then used multivariate statistical techniques to describe common and unique relationships of the four organismal properties to the environmental and spatial landscape.

Co-evolutionary dynamics with parasites

Surviving chytrid assassins in changing lakes

Ibelings B.W.[1,2], Gsell A.S.[2] and Van den Wyngaert S.[3]

[1] University of Geneva, Versoix, Switzerland
[2] Netherlands Institute of Ecology, Wageningen, The Netherlands
[3] KU Leuven Kulak, Etienne Sabbelaan 53, 8500 Kortrijk, Belgium

Chytrids are highly virulent and abundant parasites of algae which really have the potential to alter the outcome of phytoplankton species sorting and succession in lakes. The outcome of disease, however, is not only determined by interactions between host and parasite, but is modulated by environmental factors. In our presentation two environmental factors in particular will be discussed, climate warming and low level, chronic aquatic pollution. Parasites and environmental variability may also interact to maintain host diversity at the genetic level. Genetic diversity in itself is an important mechanism that will aid phytoplankton to adapt to challenges in their environment, like the parasites, pesticides and climate change discussed in this presentation.

Host-parasite coevolution at ecological time scales: bacteria-phage dynamics within a long-lived host

Koskella B.

Exeter University Biosciences Centre for Ecology & Conservation, Tremough, UK

Plants and animals host a wide array of microbes and it is increasingly clear that these dynamic microbial communities affect host phenotype and resistance to disease. Microbiota should change over time due to immigration of new species, selection by the host immune system, and selection by bacteriophage viruses. However, very little is known about the speed and scale of bacteria-phage interactions in nature and there is yet to be direct evidence for coevolution of bacteria and phages within hosts. Using a tree-bacteria-phage system, I examine coevolutionary dynamics within a long-lived, natural host over one season. An experimental time-shift approach shows that bacteria are most resistant to phages from the past and least resistant to those from the future. These results are the first evidence that natural bacterial populations respond rapidly to local phage-mediated selection and that phages play a key role in shaping the microbiota of their eukaryotic hosts.

Parasites maintain host genetic diversity

Wolinska J., Giessler S. and Yin M.

LMU Munich, Evolutionary Ecology, Munich, Germany

I will present evidence that parasites maintain host genetic diversity through two processes: 1) the cost of being common, and 2) the cost of inducible defences. Regarding the first process, the coevolutionary hypothesis predicts that parasites drive oscillations in host genotype frequencies due to frequency dependent selection where common hosts are at disadvantage. We studied the genetic structure of natural populations and communities of the waterflea (*Daphnia*), in relation to their infection levels. So far, however, the genetic changes have been followed only for one of the players, the host. Recently, we have established tools to shed light on a so far hidden part of coevolutionary process: the genetic changes within parasite populations. This opens tremendous possibilities for future coevolutionary studies. Regarding the second scenario (i.e. the cost of inducible defences), theory predicts that defended morphs have greater fitness in the presence of predators, but lower fitness than undefended morphs in the absence of predators. If such costs did not exist, then a constitutively defended morph would be favored by natural selection; yet, evidence for such costs has been elusive. Our current work reveals that induced defended *Daphnia* morphs are significantly more vulnerable to infection than undefended morphs. Thus, by demonstrating a previously unknown and environmentally relevant cost to inducible defenses, this study enhances our understanding of adaptive phenotypic plasticity and its evolution.

Parasites as habitat-specific selection factors in sticklebacks

Kalbe M.[1.], Henrich T.[1.], Samonte-Padilla I.[1.] and Jakobsen P.J.[2.]

[1.] Max Planck Inst. for Evolutionary Biology, Dept. Evolutionary Ecology, Ploen, Germany
[2.] University of Bergen, Institute for Biology, Bergen, Norway

Parasites can be regarded as strong and rapidly changing selective factors in natural animal populations. Especially in macroparasites with complex life cycles the species composition of the parasite fauna can be very heterogeneous, depending on various ecological and environmental factors. Therefore, parasite communities can vary considerably between different habitats and populations of a given host species. Due to the continuous co-evolution with their parasites, hosts are expected to become locally adapted to their sympatric parasites fauna, providing a fitness advantage over immigrating individuals from other populations. This way, parasites probably play a role in the divergence of host populations.

Three-spined sticklebacks (*Gasterosteus aculeatus*) are ideal vertebrate model organisms to study the evolution of host-parasite interactions on a small geographical scale. In northern Germany sticklebacks e.g. from river and lake populations can be regarded as genetically distinct ecotypes, which have been also found to harbour different parasite communities. Infection experiments in the lab combined with comparative analysis of immune parameters indicated that sticklebacks are indeed pre-adapted to the parasite pressure in their native habitat type. This pre-adaptation was confirmed as well by transplantation experiments, where lab bred sticklebacks from both habitat types where kept in mesocosms in the waterbodies where either parental fish were caught.

Population dynamics and genetic structure of the tree-hole tick *Ixodes arboricola*

Van Oosten R.

Universiteit Antwerpen, Evolutionary Ecology Group, Antwerp, Belgium

The tree-hole tick Ixodes arboricola is a nidicolous tick specialised on hole-breeding birds, in particular blue (*Cyanistes caeruleus*) and great tits (*Parus major*). Consequently, it shows a strong tendency to detach in nest boxes (White et al. 2012) and at night (Heylen et al. 2010a).

Much is known about the biology of great tits, which allows for specific hypothesis predictions. In particular, it is known these birds tend to return to the same nest box (Matthysen 2002). As a result, ticks may have little opportunity to disperse and be subject to inbreeding.

Preliminary research indicates hierarchical structure of tick populations, with genetic differentiation increasing from nest boxes to areas (Van Oosten, in prep). Surprisingly, allelic richness within nest boxes is substantial. *I. arboricola* might utilise several behavioural adaptations to avoid inbreeding. For instance, it has been shown to remain attached to the host for extensive periods of time compared to other *Ixodes* species (Heylen et al. 2010b).

Alternatively, inbreeding might be reduced by inflow of genetic material from other sources. Nest boxes are perhaps sub-optimal habitat and a sink-source system with natural cavities has been proposed. Natural cavities have not been sampled as of yet but their existence as sources of allelic material would make this intricate system even more complex.

Reconstructing genetic variation for historical changes in P-availability: a case-study using the *Daphnia*-parasite model system

Reyershove L.[1.], Beer T.[2.], Muylaert K.[1.] and Decaestecker E.[1.]

[1.] KU Leuven Campus KULAK Aquatic Biology, Kortrijk, Belgium
[2.] University of Portsmouth, Hampshire, UK

These last decades, there has been a strong plea to merge biochemical and ecological insights into the field called ecological stoichiometry. Here, ecological interactions are depicted as a flow of essential elements from one level to another. One established principle is that *Daphnia* suffers a reduced growth and survival when fed on P-deprived algae. Moreover, it has been shown that the growth response of *Daphnia* towards P-availability depends on its genetic signature, a result of local adaptation. A few point of criticism arise. First, little is known about the genetic variation towards historical changes in N:P ratio within the same pond. Furthermore, other biological stressors such as parasites can act as an extra source of variation. At last, it remains to be seen how this G x E interaction applies to other life history traits such as mortality. Therefore, we set up a laboratory experiment to find out how a changing P-availability interacts with (i) the presence of parasites and (ii) within-species genetic diversity to influence *Daphnia* mortality. We selected two sets of six *Daphnia magna* clones and experimentally manipulated food P-availability and presence of the microparasite White Bacterial Disease (WBD). Both clonal sets were originally hatched from the same sediment core, and differ in their depth of isolation. As the selected depth range corresponds to a time span of about 40 years, we expected genetic differences between these clonal sets as a result of historical adaptation towards differences in P-availabiltiy. Our results show a significant three-way G x G x E interaction. An increasing N:P ratio positively correlated with *Daphnia* mortality. For old clones, the negative impact of WBD was independent of food quality. On the contrary, recent clones suffered more under reduced P-availability when parasites were present. We conclude that historical genetic variation in response towards changes in P-availability is more pronounced when considering the effect of parasites.

Host allelic diversity drives long-term host-parasite coevolutionary dynamics

Decaestecker E.[1], De Gersem H.[2], Michalakis Y.[3] and Raeymaekers J.[4,5]

[1] KU Leuven Campus KULAK Aquatic Biology, Kortrijk, Belgium
[2] KU Leuven Campus KULAK Dept Physics and Astronomy, Kortrijk, Belgium
[3] Maladies infectieuses et vecteurs : Ecologie, Génétique, Evolution et Contrôle, CNRS, Montpellier, France
[4] Laboratory of Biodiversity and Evolutionary Genomics, K.U.Leuven, Leuven, Belgium
[5] Zoological Institute, University of Basel, Basel, Switzerland

Hosts and parasites are involved in a coevolutionary interaction in which often hosts do not evolve as fast as their parasites. Yet, fast adaptive genetic changes occur upon infection, especially if host-parasite interactions are characterized by Red Queen dynamics. Red Queen dynamics between antagonists are caused by negative frequency-dependent selection and are assumed to have constant amplitudes. Here, a long-term time shift experiment, based on a unique historical reconstruction of a *Daphnia*-parasite coevolution, reveals that infectivity cycles with a smaller amplitude in experienced than in naive hosts. Experienced hosts were isolated from recent time periods, naive hosts from past time periods. A coevolution model, incorporating an increase in allelic diversity over time in the host explained the asymmetry in the infectivity cycles. In contrast, increased virulence over time did not confirm the observed experimental results. The accumulation of resistance alleles dampens long-term Red Queen dynamics, because introducing more host alleles in the coevolutionary arms race leads to more possible genotypes. As such, it becomes less probable that a parasite population would cause infection of a large number of hosts. Long-term effects in host-parasite coevolution have so far been neglected, but are important to extend current insight into the dynamics of co-evolutionary antagonistic interactions.

Evolution across species ranges

The evolution of phenotypic plasticity in thermal sensitivity during range shifting

Hillaert J.[1.], Boeye J.[1.], Stoks R.[2.] and Bonte D.[1.]

[1.] University of Ghent, Terrestrial Ecology Unit, Gent, Belgium
[2.] KU Leuven, Laboratory of Aquatic Ecology and Evolutionary Biology, Leuven, Belgium

Since climate change induces new and strong selection pressures, the need for understanding evolutionary dynamics and their feedback on population ecology is critical. An important but often ignored, adaptive response to withstand climate change is the evolution of phenotypic plasticity. We studied the evolution of phenotypic plasticity in thermal sensitivity during range shifting by means of an individual-based, spatially explicit model.

Our results highlight that the evolution of plasticity in thermal sensitivity is strongly affected by dispersal both in a static environment and during range shifting. In a static environment, differentiation in plasticity is only observed when dispersal ability is fixed at a low level. A minimum level of dispersal is necessary to survive range shifting and then, true specialists are never observed. When plasticity evolves simultaneously with dispersal in stable conditions, dispersal ability is overall low and the most specialized individuals occur near the center. After the start of range shifting, high dispersive and plastic individuals dominate the population.

These results highlight the importance of implementing the evolution of plasticity in thermal sensitivity in models prospecting the future range dynamics of species, to increase their reliability.

Vulnerability to a metal under global warming is shaped by thermal adaptation along a latitudinal gradient

Dinh Van K., Janssens L., Debecker S. and Stoks R.

KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

Global warming and pollution, two major threats to biodiversity, have the potential to interact synergistically. Yet, studies exposed organisms within a single generation to a higher temperature and were limited to a single latitude thereby ignoring the potential for gradual local thermal adaptation and northward dispersal mitigating the vulnerability to pollutants under global warming. Therefore, we studied the thermal dependence of the vulnerability of *Ischnura elegans* damselfly larvae to zinc in a common garden warming experiment with replicated populations from three latitudes spanning >1500 km. We observed a striking latitude-specific effect of temperature on the zinc-induced mortality pattern reflecting that local thermal adaptation along the latitudinal gradient made Swedish, but not French, damselfly larvae vulnerable to zinc at 24°C. This could not be explained by the internal zinc concentrations: these were higher at 24°C than at 20°C but consistently so across latitudes. More likely, the observed stronger zinc-induced reduction of food intake in Swedish larvae at 24°C reduced their ability to defend and repair damage. The pattern of local thermal adaptation indicate that the predicted temperature increase of 4°C will strongly magnify the impact of a pollutant such as zinc at northern latitudes unless there is thermal evolution and/or northward migration of southern genotypes. The here applied common garden experimental approach using animals from a natural temperature gradient spanning 4°C and where northern populations were tested at the current and predicted 4°C temperature allowed us to gain insights into how the vulnerability to pollutants will change under global warming thereby revealing insights that would not have been possible from traditional common garden heating experiments at a single latitude. Our results underscore the critical insights gained by studying the vulnerability to pollutants under realistic warming scenarios across natural temperature gradients.

Rapid range expansion increases genetic differentiation while hardly reducing genetic diversity in a damselfly

Swaegers J.[1], Mergeay J.[2], Therry L.[1], Larmuseau M.[3,4], Bonte D[5]. and Stoks R.[1]

[1] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2] Research Institute for Nature and Forest, Geraardsbergen, Belgium
[3] KU Leuven, Laboratory of Biodiversity and Evolutionary Genomics, Leuven, Belgium
[4] KU Leuven, Laboratory of Forensic Genetics and Molecular Archaeology, Leuven, Belgium
[5] Ghent University, Terrestrial Ecology Unit, Gent, Belgium

Many ectothermic species are currently expanding their geographic range due to global warming. This can modify the population genetic diversity and structure of these species because of genetic drift during the colonization of new areas. Despite its relevance, the genetic consequences of natural, contemporary range expansions have received little attention, with the only studies available focusing on range expansions along a narrow front. We investigate the genetic consequences of a natural range expansion in the Mediterranean damselfly *Coenagrion scitulum*, which is currently rapidly expanding along a broad front in different directions. We assessed genetic diversity and genetic structure using twelve microsatellite markers in five centrally located populations and five recently established populations at the edge of the geographic distribution. Furthermore, we genetically assessed the origin of the expansion wave using samples across a large part of *C. scitulum*'s range. We demonstrate that the recently established populations all originate from Spanish-French regions. Our results suggest that, although a marginal significant decrease in the allelic richness was found in the edge populations, genetic diversity has been preserved during the range expansion of this species. Nevertheless, edge populations were genetically more differentiated compared to core populations, suggesting genetic drift during the range expansion. The smaller effective population sizes of the edge populations compared to central populations also suggest a contribution of genetic drift after colonization. We argue and document that range expansion along multiple axes of a broad expansion front generates little reduction in genetic diversity, yet stronger differentiation of the edge populations.

Evolutionary changes in larval and adult phenotype at the expanding range edge of the damselfly *Coenagrion scitulum*

Therry L.[1], Stoks R.[1] and Bonte D[2]

[1] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2] Ghent University, Terrestrial Ecology Unit, Gent, Belgium

Climate change triggers northward range shifts in many animals. Rapid evolutionary changes have been documented in edge populations at the expansion front with most studies documenting an increase in dispersal ability and associated morphological traits in the adult stage. Less attention went to evolutionary changes in other adult traits, such as immune function, which also are expected to change due to genetic covariation with adult traits and/or changed selective regimes in the edge populations. Studies also largely ignored associated changes in the non-dispersive larval stage, such as larval activity and life history, which may be very relevant for interactions with other species. In this study, we compared several fitness-related adult and larval traits between replicated core and edge populations of the rapidly range-expanding damselfly *Coenagrion scitulum* using a common garden experiment where animals were reared from eggs until adults at two different food levels. In the dispersive adult stage, we found a higher investment in flight muscle mass and a higher immune response (encapsulation response) in the edge populations. In the non-dispersive larval stage, we documented a higher larval activity, faster development rates and higher mass growth rates in edge larvae reared at high food conditions, and overall higher size growth rates and higher mortality in the edge populations. Possible causes and ecological relevance for these trait difference between core and edge populations will be discussed.

Vertebrate responses to spatial and environmental gradients reveal latitudinal differences in mechanisms of community assembly

Buschke F., De Meester L., Brendonck L. and Vanschoenwinkel B.

KU Leuven, Laboratory of Aquatic Ecology and Evolutionary Biology, Leuven, Belgium

Although the latitudinal diversity gradient (LDG) is one of the most conspicuous patterns in nature, there is a lack of consensus regarding the processes underlying this pattern. The numerous proposed mechanisms for the LDG fit into two broad groups: niche-assembly mechanisms and dispersal-assembly mechanisms. Here we examine the relative importance of niche-based and dispersal-based processes across a latitudinal gradient. Using spatial data for vertebrate species distributions in sub-Saharan Africa, simulated Moran's Eigenvector Maps and climate variables, we decompose the variation in distribution patterns of individual species into independent environmental and spatial components by means of a variation partitioning associated with redundancy analysis. After correcting for the confounding effect of geographic range size, we examine latitudinal trends in the variation components for both individual species and communities. Results show that spatially-explained has a hump-shaped relationship with geographic range size while environmentally-explained variation increased with range size. Once the confounding effect of range size is removed, spatially-explained variation, and the dispersal-based processes it represents, increases with latitude whereas latitudinal patterns for environmentally-explained variation are inconclusive. The relative importance of processes which lead to the ecological sorting of species across environmental gradients, or the expansion of ranges after speciation, varies across sub-Saharan Africa. In conclusion, this study demonstrates that community assembly mechanisms are not uniform across a latitudinal gradient and suggests that biogeographical differences in metacommunity processes may contribute to the latitudinal diversity gradient.

Niche conservatism among non-native birds: niche unfilling rather than niche expansion

Strubbe D.[1.], Broennimann O.[2.], Chiron F.[3.], Matthysen E.[1.]

[1.] University of Antwerp, Evolutionary Ecology Group, Antwerp, Belgium
[2.] University of Lausanne,,Dept. of Ecology and Evolution, Lausanne, Switzerland
[3.] Muséum National d'Histoire Naturelle, Conservation des Espaces, UMR, Paris, France

Niche conservatism, or the extent to which niches are conserved across space and time, is of special concern for the study of non-native species as it underlies predictions of invasion risk. Based on the occurrence of 28 non-native birds in Europe, we assess to what extent that niches are conserved during biological invasion and formulate hypotheses to explain the variation in observed niche changes. Our results show that non-native birds in Europe tend to occupy a subset of the environmental conditions they inhabit in their native ranges and that niche expansion into novel environments is rare for most species, allowing species distribution models to accurately predict invasion risk. Niche changes were smaller for species having a higher propagule pressure and that were introduced longer ago, indicating that apart from purely ecological factors, patterns of niche conservatism during biological invasions may also be contingent on population-specific historical factors.

Geography, climate, and patterns of genetic diversity in a bdelloid rotifer

Fontaneto D.[1.] and Tang T.[2.]

[1.] National Research Council, Institute of Ecosystem Study, Verbania Pallanza, Italy
[2.] Imperial College London, Division of Ecology and Evolution, Ascot Berkshire, UK

The interplay between climate (current and past) and geography is known to be associated with spatial biodiversity patterns. Here we analyse genetic diversity in a bdelloid rotifer species complex along a latitudinal transect in Europe from ~40°N, Sardinia, to ~80°N, Svalbard. Contrary to what is described for larger organisms, none of the analysed patterns of diversity correlates with climate, and a strange relationship with geographical distances is present.

Dispersal and evolution

If and how dispersal matters for bacterial diversity and function

Lindström E.

Uppsala University Ecology and Genetics/Limnology, Uppsala, Sweden

For some time it has been debated whether bacterial communities follow similar ecological rules as greater organisms with regard to for instance their biogeography. A central matter of debate has been if bacteria and other microorganisms can be subject to dispersal limitation or if their biogeographic distribution relies exclusively on local contemporary environmental conditions. Beyond dispersal limitation two other dispersal mechanisms may also influence community structure and diversity; mass effects, when massive immigration of cells cause changes in community structure, and by seed banks when dispersed cells may become abundant in a community only after a disturbance. Based on data from inland water communities I will discuss if and in that case when and where these mechanisms may be of importance for bacterial community structure and diversity.

In previous experimental work it has been shown that dispersal among communities can also have impact on local community function due to changes in richness and functional diversity. I will show results from experimental work using diverse bacterial communities which show that other aspects than richness and diversity of the community may be more important for ecosystem functioning.

Dispersal evolution and its consequences: From individuals to communities

Hovestadt T.

University of Wuerzburg, Field Station Fabrikschleichach, Rauhenebrach, Germany

Dispersal is an ecological key process but it also is an important life-history attribute of individuals. Taking (appropriate) dispersal decisions may have severe fitness implications and thus underlies strong selection. Further, dispersal has important effects on the very ecological conditions under which selection takes place. A full appreciation of the selective mechanisms underlying dispersal evolution thus also requires considering the feedback effects between dispersal, population dynamics, and even emergent community structure.

In this talk I will first consider models for the evolution of informed dispersal, i.e. dispersal dependent on information about some environmental attributes. I will progress to some examples concerning the concurrent evolution of dispersal and other life-history attributes and then consider how such evolution may lead to and depend on emergent community attributes.

I will conclude with some ideas on what additional principles may govern dispersal evolution if we move from a single population to a community context.

Ideal free distribution of fixed dispersal phenotypes in a wing dimorphic in heterogeneous landscapes

Hendrickx F.[1.], Palmer S.[2.] and Travis J.[2.]

[1.] Royal Belgian Institute of Natural Sciences, Entomology Department, Brussels, Belgium
[2.] University of Aberdeen, Institute of Biological and Environmental Sciences, Aberdeen, UK

According to the ideal free distribution (IFD) theory, individuals that are able to perceive the quality of different patches in a landscape and disperse freely are expected to redistribute themselves proportionally to the carrying capacities of heterogeneous patches. Here, we argue that when dispersal is unconditional and genetically fixed, a coalition of both dispersal phenotypes can attain an IFD under spatio-temporally uncorrelated variation in fitness. This not only leads to a stable polymorphism of sedentary and dispersing strategies, but also implies that the number of dispersing individuals should on average be equal among patches and determined by the carrying capacity of the smallest local populations in the landscape. Differences in carrying capacity among patches are thus only reflected by changes in the number of sedentary individuals. Individual-based simulations show that this mechanism can be generalized over a wide range of spatio-temporal conditions and dispersal strategies. Moreover, these expectations are in strong agreement with empirical data on the density of both dispersal phenotypes within and among ten different metapopulations of the wing dimorphic ground beetle *Pterostichus vernalis*. Hence, for the first time, these results demonstrate that this mechanism serves as a plausible alternative to the competition-colonization model to explain the spatial distribution of fixed dispersal polymorphisms in heterogeneous landscapes. Understanding of the frequency distributions of individuals expressing discrete dispersal morphs in a metapopulation moreover improves our predictive and management capabilities for a broad range of species, for which we currently typically rely on using mean dispersal rates.

On the distribution of adaptive genetic variation in a sympatric mosaic of a salt marsh beetle

Van Belleghem S.[1.] and Hendrickx F.[2.]

[1.] Ghent University, Terrestrial Ecology Unit, Department of Biology, Ghent, Belgium
[2.] Royal Belgian Institute of Natural Sciences, Entomology Department, Brussels, Belgium

Adaptation to a particular environment requires the presence of adaptive gene variants that allow organisms to develop an optimal phenotype. Moreover, the distribution of these adaptive gene variants is expected not only to be influenced by environmental factors, but also by neutral dynamics such as gene flow and drift. Here, we investigate the distribution of putative adaptive allelic variation in the mitochondrial NADP+-dependent isocitrate dehydrogenase (mtIDH) gene locus of the wing-polymorphic ground beetle *Pogonus chalceus* in order to disentangle the roles of mutation, migration and selection on the population frequencies of adaptive alleles.

In P. chalceus, alleles of the mtIDH gene are strongly associated with dispersal power (i.e. wing development). Dispersal power, on its turn, is an adaptation to stability of the habitats occupied by this species. We characterized the DNA sequence variation at the mtIDH locus, revealing a striking pattern that seems to agree with both long term balancing selection (i.e. high number of fixed differences between alleles) and a selective sweep (i.e. little haplotype variation in the selected allele). Using coalescent simulations, we try to assess the parameter space in which this pattern may occur.

Next, using large scale mtIDH genotype data of Western European populations, we show that the mtIDH gene is not (or weakly) genetically linked to genes involved in wing development and argue that, across populations, divergence of the mtIDH alleles may result from similar selection pressures as the divergence in wing development. An association within populations between these physically unlinked genetic traits may be generated by migration between strongly differing habitats.

Together, these results confirm adaptation in multiple genetically unlinked traits in a system prone to gene flow and demonstrate that adaptation is more likely to occur through the sorting of adaptive gene variants according to habitat type after a single mutational event.

Socio-evolutionary dynamics

Social evolution of microbes

Foster K.

University of Oxford, Zoology, Oxford, UK

Since Darwin, evolutionary biologists have been fascinated by cooperative behaviour. For example, honeybee workers labour their whole life without reproducing, birds make alarm calls, and humans often help one another. But how cooperative are cells in microbial groups? We study this question using a diversity of systems, including simulation models, pseudomonad bacteria and budding yeast. We find that genetic similarity is an emergent property of microbial groups that grow through simple cell division, which creates favourable conditions for cooperation among cells of a single species. Moreover, we find that microbes can actively adjust both their genetic mixing and investment into social traits in a way that promotes cooperation within a species. However, our models and experiments on the interactions between different microbial species suggest that 'between species' the evolution of competitive phenotypes is more important than cooperation. This all suggests a model where microbes are nice to clone mates but not much else.

Low frequency of non-paternity events in historical human population of Flanders

Larmuseau M.H.D.[1,2,3]*, Vanoverbeke J.[4]*, Van Geystelen A.[5], Defraene G.[6], Vandezande M.[7], Vanderheyden N.[1], Matthys K.[7], Wenseleers T.[5] and Decorte R.[1,2]

[1] UZ Leuven, Laboratory of Forensic Genetics and Molecular Archaeology, Leuven, Belgium
[2] KU Leuven, Department of Imaging & Pathology, Forensic Medicine, Leuven, Belgium
[3] KU Leuven, Department of Biology, Laboratory of Biodiversity and Evolutionary Genomics, Leuven, Belgium
[4] KU Leuven, Department of Biology, Laboratory of Aquatic Ecology and Evolutionary Biology, Leuven, Belgium
[5] KU Leuven, Department of Biology, Laboratory of Socioecology and Social Evolution, Leuven, Belgium
[6] UZ Leuven, Radiation Oncology Department, Leuven, Belgium
[7] KU Leuven, Historical Demography, Centre for Sociological Research, Leuven, Belgium
* Both authors contributed equally to this study

Non-paternity rates in human populations are typically estimated based on data of currently living populations. Genealogical and surname data are seldomly taken into account when calculating these rates, although they are very useful. Due to a non-paternity event, the connection between the biological marker, i.e. the Y-chromosome and the cultural marker, i.e. the surname and therefore the paternal genealogy, disappears within a patriline. By analyzing surname origins, in-depth genealogies and extended Y-chromosomal genotypes, we were able to estimate the average non-paternity rate in the Flemish population over the last centuries.

We estimated the averaged non-paternity rate to lie between 0.5 and 5% per generation based on two different methods.

The first and most straightforward method consists of calculating the averaged rate based on couples of genealogically (surname) related males who are separated by 10 to 30 meioses/generations away from each other. Based on this analysis, the averaged non-reported non-paternity rate is estimated at around 1% per generation. This rate is nearly equal to the reported average rate in contemporary West-European populations for children of married couples.

The second method used modeling for the estimation of the non-paternity rate based on the fact that French surnames in Flanders still present the same Y-chromosomal subhaplogroup frequencies as in Northern France, even 500 years after the gene flow event. Although this method has a low resolution, it suggested that the average non-paternity rate is not larger than 5%.

Our results suggest that the non-paternity rate did not change significantly during the last 200-300 years in Flanders. Therefore there is a guarantee that a juridical genealogy rarely differs from the biological one. Consequently, these results are favorable for researchers in population genetics and historical demography in Western Europe, since they consider juridical genealogies as biological ones in their studies.

Stable maintenance of uncooperative aphid mutualists in the black bean aphid *Aphis fabae*: hypotheses and tests

Schillewaert S.[1.], Vantaux A.[1.], Parmentier T.[1.], van den Ende W.[2.] and Wenseleers T.[1.]

[1.] KU Leuven, Laboratory of Socioecology and Social Evolution, Leuven, Belgium
[2.] KU Leuven, Molecular Physiology of Plants and Micro-organisms Section, Heverlee, Belgium

The aphid *Aphis fabae* engages in a facultatively mutualism with *Lasius niger* ants, whereby the aphids secrete a sugary solution (honeydew) to the ants, and the ants protect them in return against natural enemies. Previously, however, we found that *A. fabae* clones display significant differences in the composition of their honeydew sugars, especially in the ant attractant sugar melezitose. These clonal differences could greatly impact the strength of the mutualistic interaction with ants as well as the aphids' fitness. Here we will present the results of a series of experiments in which we tried to test different hypotheses regarding the causes of this variation in this mutualistic trait. One set of results showed that the high-melezitose secreting clones had a higher mean relative growth rate on any given plant and therefore were likely to attract more ants thanks to their higher melezitose secretion. Nevertheless, they also produced fewer dispersing alates and were therefore likely worse at colonizing new plants. These results imply that a competition-colonization tradeoff may explain the stable coexistence of both types of clones. Several other explanations for the observed variation may, however, also still apply, such as variation in the degree to which different clones are adapted to particular host plants, and are currently being tested.

The altruistic cannibal: multilevel selection in *Arachnocampa fungus* gnats

Duenez Guzman E. and Sadedin S.

KU Leuven, Laboratory of Socioecology and Social Evolution, Leuven, Belgium

Multilevel selection has been shown to be plausible in spatially structured populations under certain conditions, implying that individual-level altruism may evolve. However, the importance of multilevel selection remains unclear because few natural examples are known. Here, we examine the potential for evolution of altruism through multilevel selection in cave-dwelling *Arachnocampa* fungus gnats. Adult *Arachnocampa* are often cannibalized by juveniles; if adults facilitate this, they are altruists. For juveniles, cannibalism leads to faster maturation time, so cannibalism may increase cave productivity. We built mathematical and individual-based models incorporating relevant behavioral and ecological data to test whether competition at the cave level could lead to the evolution of altruism. Results imply that multilevel selection is likely to lead to altruism in *Arachnocampa* under broad conditions.

Ecological speciation & radiation

Progress toward ecological speciation in Darwin's finches, threespine stickelback, and Trinidadian guppies

Hendry A.

McGill University Redpath Museum & Dept. of Biology, Montreal, Canada

Ecological speciation occurs when adaptation to different environments drives the evolution of reproductive isolation. This process is thought to have been very important in the evolution of biological diversity. I will discuss the diverse results I have obtained while studying progress toward ecological speciation in guppies adapting to different predation environments in Trinidad, threespine stickleback adapting to different foraging habitats in British Columbia, and Darwin’s finches adapting to different food types in Galapagos. Similar methods applied to these different systems have yielded divergent results, which has helped to generate new insights into the factors influencing progress toward ecological speciation.

Community assembly through adaptive radiation: spiders on islands

Gillespie R.

University Of California Berkeley, USA

Remote islands are heralded as "natural laboratories", with communities largely comprising species that have evolved within the islands as a result of adaptive radiation. I have been examining commonalities underlying patterns of adaptive radiation and how communities are filled in such situations, focusing on spiders in conjunction with other lineages of both animals and plants. Here, I examine patterns of morphological and ecological differentiation across the Pacific and how diversity can arise from a small sample of colonists. Specific topics will include: (1) *Patterns of diversification and species accumulation within an adaptive radiation*. What are the relative roles of colonization or dispersal versus parallel or convergent evolution and associated niche shifts, in shaping ecologically similar sets of species on different islands of the Hawaiian chain? (2) *Integrating population genetics and macroecological metrics to assess biodiversity dynamics*. How can we use the dynamic geology of the Hawaiian Islands to understand feedbacks between adaptation, population divergence, and associated community succession? Overall, this research promises insights into the interplay between selection and the biotic environment in the evolution of species within a community, and the nature and timing of species accumulation and equilibrium.

Untangling the mechanisms influencing hummingbird assemblages: New tools to answer old questions

Graham C.

Stony Brook University, Department of Ecology and Evolution, Stony Brook, USA

Evaluating the relative importance of ecological, evolutionary and biogeographic processes in the generation and maintenance of biological diversity remains a fundamental challenge in biodiversity science. I will combine taxonomic, phylogenetic and functional components of alpha and beta-diversity of hummingbirds across strong environmental gradients and varying degrees of isolation in northern South American to evaluate how different mechanisms, including dispersal limitation via geographic barriers, conservatism of functional traits and rapid radiation of lineages, might influence contemporary patterns of diversity. I will also demonstrate what can be learned by applying tools from the "original" community phylogenetics toolkit and evaluate some of the limitations of these tools and new directions in the field.

Repeated habitat occupancy through species sorting and parallel radiation are not always so different on islands

Hendrickx F.[1], Vandomme V.[1], Vangestel C.[1] and Backeljau T.[2]

[1] Royal Belgian Institute of Natural Sciences, Entomology Department, Brussels, Belgium
[2] Ghent University, Terrestrial Ecology Unit, Biology Department, Gent, Belgium

When environmental gradients are repeated on islands, habitat occupancy may result from either species sorting, wherein each ecotypic species colonizes the different islands, or through replicated and parallel adaptive radiation. However, the hypothesis to which island monophyly, often interpreted as evidence for in situ adaptive radiation, could be the result of a species sorting mechanism followed by high levels of introgression among ecotypes within islands is hard to demonstrate. This is important as it may strongly impact our understanding on the relative roles of determinism and contingency in evolution, niche lability and the role of adaptive radiation in the genesis of island communities. On the Galapagos, three distinct species of *Calosoma* caterpillar hunters that share similar traits are found exclusively on higher elevations of different islands, while lowlands are occupied by a fourth species. Although highland and lowland species are remarkably closely related on most islands, conflicting results from mitochondrial haplotypes demonstrate that highland species of the two oldest islands were initially monophyletic, but followed by extensive amounts of horizontal gene exchange with the lowland species. Hence, the close genetic relationship between highland and lowland species is due to within island introgression after species sorting, rather than resulting from a recent within island divergence. These findings not only relax the use of neutral gene genealogies to prove parallel evolution, but moreover indicate that interspecific gene exchange within as well as among islands makes the distinction between niche occupancy through adaptive radiation and species sorting less clear-cut as previously assumed.

Exploring introgression patterns within a wolf spider radiation

De Busschere C.[1.], Van Belleghem S.[2.] and Hendrickx F.[1.]

[1.] Royal Belgian Institute of Natural Sciences, Entomology Department, Brussels, Belgium
[2.] Ghent University, Terrestrial Ecology Unit, Biology Department, Gent, Belgium

Parallel radiations within island systems are often assumed to follow a simple scenario in which single colonization events are followed by in situ adaptive divergence. However, subsequent gene exchange after the initial colonization and during the divergence process might have important evolutionary impacts on species radiations. First, gene exchange among ecologically similar species from different islands may lead to introgression of adaptive genetic variation and, hence, influence the parallel divergence process. Second, hybridisation events among ecologically different species living on the same island may influence their genetic relationship due to the introgression of neutral genetic variation.

In this study, we estimate levels of gene exchange within a wolf spider radiation of the genus *Hogna* from the Galapagos, wherein habitat specialization into 'high elevation' and 'coastal dry' species apparently evolved repeatedly on two islands. By using a multilocus approach we show that low levels of inter island and relatively higher levels of intra island introgression have most likely been prevalent within this radiation. Using these estimates, we demonstrate by means of a coalescence simulation that adaptive gene genealogies, expected to better reflect the adaptive divergence process, may strongly differ from gene genealogies of neutral genes. As species phylogenies within radiations are frequently used to infer the divergence pattern, interspecific gene flow should not be neglected when interpreting parallel trait evolution.

Ecological genetics and genomics

Inbreeding depression in plants in a conservation genomic context

Ouborg J.[1.], Angeloni F.[1.], Wagemaker N.[1.] and Vergeer P.[1,2.]

[1.] RU Nijmegen, IWWR, Molecular Ecology, The Netherlands
[2.] Wageningen University, Nature Conservation and Plant Ecology Group, Wageningen, The Netherlands

Inbreeding depression, the reduced performance of inbred progeny as compared to their outbred kin, is playing an important role within theories of mating system evolution, in the design of breeding strategies and in conservation genetic evaluations of population viability.

Within the conservation biology context inbreeding depression is often treated as a population parameter. Yet, evidence is accumulating that inbreeding depression is a very complex phenomenon, with variation due to genotype, due to environmental differences and due to demographic history. Moreover, the causes of inbreeding depression are rather poorly understood.

Here we present data on long term research on inbreeding depression in plants. We will present evidence based on meta-analysis of the inbreeding depression literature, on detailed greenhouse experiments and on genomic approaches. Together these results urge us to adopt a more detailed perspective on inbreeding depression, its dynamics and the way we should incorporate this in conservation biological considerations.

Genomic patterns of ecological differentiation across stickleback populations

Chain F.[1.], Feulner P.[1.], Panchal M.[1.], Huang Y.[2.], Eizaguirre C.[1.], Kalbe M.[1.], Lenz T.[3.], Samonte I.[1.], Stoll M.[4.], Reusch T.[2.], Bornberg-Bauer E.[5.] and Milinski M.[1.]

[1.] Max Planck Institute for Evolutionary Biology, Evolutionary Ecology Department, Ploen, Germany
[2.] Helmholtz Center for Ocean Research (GEOMAR), Evolutionary Ecology of Marine Fishes, Kiel, Germany
[3.] Harvard Medical School, Brigham and Women's Hospital Division of Genetics, Boston, USA
[4.] Leibniz-Institute for Arteriosclerosis Research, Genetic Epidemiology of Vascular Disorders, Muenster, Germany
[5.] Westfaelische Wilhelms University, Institute for Evolution and Biodiversity, Muenster, Germany

The genetic architecture underlying adaptations remains a topic of broad interest in evolutionary biology. Most genomic studies on this subject focus on genetic model organisms wherein the impact of ecological context is often overlooked. Here, we characterize genomic differences across 10 natural populations of three-spined sticklebacks, a fish species that has recently colonized various habitats and undergone substantial and recurrent phenotypic divergence. Using 60 whole genome sequences from 5 lake-river population pairs (6 genomes from each population), we evaluated the relative importance of several types of genetic variation in the divergence of distinct ecotypes. We determined the most highly diverged genomic regions between lake-river pairs and assessed whether these loci are recurrently outliers across different pairs. We also investigated the extent of structural variations and lineage-specific duplication events and their potential impact on local adaptation. Our results help broaden our understanding of recurrent ecological adaptation at the genetic level, and offer perspective on the dynamics of genome evolution in natural populations in the wake of ecological differentiation.

The role of selection in driving landscape genomic structure of the waterflea *Daphnia magna*

Orsini L.[1], Mergeay J.[2], Spanier K.[1], Vanoverbeke J.[1] and De Meester L.[1]

[1] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2] Research Institute for Nature and Forest, Geraardsbergen, Belgium

The combined analysis of neutral and adaptive genetic variation is crucial to reconstruct the processes driving population genetic structure in the wild. However, such combined analysis is challenging because of the complex interaction among neutral and selective processes in the landscape. Overcoming this level of complexity requires an unbiased search for the evidence of selection in the genomes of populations sampled from their natural habitats and the identification of demographic processes that lead to present-day populations' genetic structure. Ecological model species with a suite of genomic tools and well-understood ecologies are best suited to resolve this complexity and elucidate the role of selective and demographic processes in the landscape genomic structure of natural populations. Here we investigate the water flea *Daphnia magna*, an emerging model system in genomics and a renowned ecological model system. We infer past and recent demographic processes by contrasting patterns of local and regional neutral genetic diversity at markers with different mutation rates. We assess the role of the environment in driving genetic variation in our study system by identifying correlates between biotic and abiotic variables naturally occurring in the landscape and patterns of neutral and adaptive genetic variation. Our results indicate that selection plays a major role in determining the population genomic structure of *D. magna*. First, environmental selection directly impacts genetic variation at loci hitchhiking with genes under selection. Second, priority effects enhanced by local genetic adaptation (cf. monopolization) affect neutral genetic variation by reducing gene flow among populations and genetic diversity within populations.

The Eda gene as a target for selection and gene flow in three-spined stickleback

Raeymaekers J.[1,2], Konijnendijk N.[1], Larmuseau M.[1,3], Maes G.[1], Hellemans B.[1], De Meester L.[4] and Volckaert F[1]

[1] University of Basel, Zoological Institute, Basel Switzerland
[2] KU Leuven, Laboratory of Biodiversity and Evolutionary Genomics, Leuven, Belgium
[3] UZ Leuven, Laboratory of Forensic Genetics and Molecular Archaeology, Leuven, Belgium
[4] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

A balance between diversifying selection and gene flow may maintain populations polymorphic for adaptive traits. Alternatively, relaxation of selection or opposing selection pressures might be maintaining adaptive polymorphisms. We investigated the maintenance of polymorphism for lateral plate number in three-spined stickleback populations from the lowlands bordering the North Sea. These populations consist of varying percentages of low-plated, partially plated and completely plated individuals. From spring 2008 until fall 2010, 15 polymorphic populations selected along a salinity cline were investigated in order to assess allelic fluctuations at the Ectodysplasin (Eda) locus, the major gene controlling plate number. We tested for signatures of differential environment-fitness correlations by comparing changes in Eda allele frequencies between seasons, and by comparing Eda genotypes for body size, reproductive investment and reproductive success. In addition, gene flow and recent migration between populations was determined using 15 neutral microsatellite markers. We observed a fitness advantage for the low-plated allele in freshwater, while the high-plated allele was favoured in brackish water. However, differentiation at the Eda locus was not correlated with salinity differences between sites, but with neutral genetic differentiation. This suggests that variation at the Eda gene, and hence variation in lateral plate number, is partially shaped by neutral genetic processes, and that gene flow counteracts selection by homogenizing Eda allele frequencies. A comparison of Eda allele frequencies between immigrants and residents suggested that high-plated individuals undertake more migration than low-plated individuals. We conclude that the combined effect of immigration (leading to maladaptive gene flow) and selection is responsible for the maintenance of lateral plate polymorphism in this stickleback system.

Genotypic diversity and differentiation among populations of benthic freshwater diatoms as revealed by microsatellites

Vanormelingen P.[1], Evans K.[2], Mann D.[3], D'Hondt S.[1], Verstraete T.[1], Debeer A.-E.[1], Sabbe K.[1] and Vyverman W.[1]

[1] Ghent University, Laboratory of Protistology & Aquatic Ecology, Gent, Belgium
[2] University of Edinburgh, School of Geosciences, Edinburgh EH9 3JW, United Kingdom
[3] UZ Royal Botanic Garden Edinburgh, Edinburgh, UK

Microsatellite-based studies of natural populations provide insight into the genetic and genotypic diversity within populations and patterns of gene flow between them. In diatoms and other microalgae, such studies are almost exclusively confined to the marine phytoplankton. Patterns for freshwater microalgae can be expected to be different due to the more fragmented and short-lived nature of their habitat. We developed and used 6 microsatellite loci for the epiphytic freshwater diatom *Eunotia bilunaris* 'robust' to investigate genotypic diversity and differentiation between populations at different spatial scales, from ponds within the same pond system, over the same region, to between regions on a Western European scale. 340 isolates from 9 populations were obtained, their species identity confirmed using morphology combined with rbcL sequences, and their microsatellite allelic composition determined. Analyses show that while in some populations there was a very high genotypic diversity with every strain belonging to a different genotype, in others one or a few genotype(s) made up half of the population. Population differentiation was low between ponds from the same pond system or for a single population sampled twice (Fst < 0.1) but could already be very high (Fst > 0.2) for populations from the same region, located some tens of kilometers from each other. Results from a similar dataset for the benthic freshwater diatom Sellaphora capitata are remarkably congruent, suggesting that this may be the general pattern for benthic freshwater diatoms. Moreover, this contrasts sharply with the limited differentiation between the same *E. bilunaris* 'robust' populations for temperature preference. Finally, possible causes for the observed large population differentiation for microsatellites will be discussed.

Incipient speciation in synanthropy? Genetic distinction between contiguous urban and rural multimammate mice in Tanzania

Gryseels S.[1.], Goüy de Bellocq J.[1.], Zima J.[2.], Mazoch V.[3.], Van Mechelen K.[4.], Broeckhove J.[4.], Makundi R.[5.], Leirs H.[1.] and Baird S.[6.]

[1.] University of Antwerp, Evolutionary Ecology group, Antwerp, Belgium
[2.] Institute of Vertebrate Biology, Academy of Sciences of the Czech Republic, Brno, Czech Republic
[3.] University of South Bohemia, Departement of Zoology, Ceske Budejovice 37005, Czech Republic
[4.] University of Antwerp, Department of Mathematics and Computer Sciences, B-2020, Antwerp, Belgium
[5.] Sokoine University of Agriculture, Morogoro, Pest Management Centre, Tanzania
[6.] Centro de Investigação em Biodiversidade e Recursos Geneticos, Aveiro, Portugal

By investigating the population genetic structure of a widespread organism, we can perceive how certain environmental variables trigger evolutionary genetic differentiation despite a seemingly continuous range. The multimammate rat, *Mastomys natalensis*, is the most widespread and abundant rodent in Sub-Saharan Africa, and is a notorious agricultural pest and a natural host for many zoonotic diseases. In this study we determined the population genetic structure of *M. natalensis* across a 180 km transect in central Tanzania along which the landscape alternated between agricultural land in a rural setting and natural woody vegetation, rivers, roads and a city. In a standardized way, we sampled at least 20 animals in maize fields of 10 localities spaced about 20 km apart (yielding a total of 951 *M. natalensis* samples), and genotyped 15 microsatellite loci from each individual. Minimising genetic disequilibria, STRUCTURE analyses revealed that our sample consisted of 3 clusters, of which 2 occur in the suburbs of Morogoro city (located in the centre of the transect) while the 3rd unites all 9 surrounding rural localities. Neither geographical isolation (through landscape analyses in Circuitscape) nor breeding asynchrony (through comparison of rainfall patterns and age structures) could explain the genetic differentiation of the suburban population. Using the Isolation-with-Migration model implemented in IMa2 we inferred that the split between the suburban and the rural population probably occurred very recently, the effective population density in suburban Morogoro is higher than in the rural areas, and suburbs versus rural areas act as a source-sink for effective migration. The observed genetic differentiation of multimammate rats in synanthropy is striking given the uninterrupted occurrence of the animal throughout the landscape. Future ecological studies may be able to identify the nature of the synanthropic niche in Morogoro.

Posters

Ecological niche predicts photoprotection capacity of microphytobenthic diatoms inhabiting intertidal mudflats

Blommaert, L.[1], Barnett A.[2], Meleder V.[3], Gaudin P.[3], Vyverman W.[1], Dupuy C.[2], Lavaud J.[2] and Sabbe K.[1]

[1] UGent, Protistology & Aquatic Ecology lab, Gent, Belgium
[2] UMR7266 LIENSs, Institut du Littoral et de l'Environnement, CNRS/Université de La Rochelle, France
[3] UPRES EA 2160 'Mer, Molécules, Santé', Université de Nantes, France

Despite being exposed to a highly fluctuating light climate, intertidal sediments belong to the most productive ecosystems on Earth. The main primary producers in this habitat are diatoms. They belong to two main functional groups: large motile diatoms (epipelon), which move freely in between sediment particles, and smaller diatoms which live in close association with individual sand grains (epipsammon). Within the epipsammon different growth forms can be distinguished. Non-motile forms live appressed to or stalked on sand grains. Other epipsammic species however are motile but only move within the sphere of individual sand grains. One of the main physiological mechanisms of photoprotection in diatoms is Non Photochemical Quenching (NPQ) which is associated with the xanthophyll cycle. In stressful light conditions the xanthophyll pigment diadinoxanthin is converted into diatoxanthin which safely dissipates excess energy as heat. It has been hypothesized that epipelic diatoms can migrate within a vertical light gradient to the most optimal light climate whereas epipsammic forms must be able to cope with a fluctuating light climate using mainly physiological mechanisms. NPQ would therefore be more performant in epipsammon than epipelon We tested the ability of a selection of representatives of each growth form to perform NPQ during 5min high light exposure (up to full sunlight, 2000 Âµmol photons m-2 s-1) and measured NPQ. We observed that epipelic diatoms have a lower NPQ potential than epipsammic ones. Interestingly, small motile epipsammic growth forms, despite being phylogenetically more closely related to epipelic taxa than to other epipsammic forms, have an intermediate NPQ photoprotection capacity. This suggests that ecological niche rather than phylogenetic relatedness predicts this photophysiological feature in microphytobenthic diatoms.

Linking parasite genetics with host disease phenotype, the case for human schistosomiasis

Nele Boon[1,2], Frederik Van den Broeck[1,2], Lynn Meurs[2], Filip A.M. Volckaert[1], Katja Polman[2] & Tine Huyse[1,2]

[1] Laboratory of Biodiversity and Evolutionary Genomics, Biology, University of Leuven
[2] Unit of Medical Helminthology, Institute of Tropical Medicine, Antwerp

Schistosomiasis is a major, poverty-related disease affecting more than 200 million people in developing countries, 85% of them in sub-Saharan Africa. It has a complex epidemiology with a large variation in infection intensity, immune responses to infection, and schistosome-related pathology. Besides host-related factors, there are numerous parasite and environmental factors involved, which have so far been largely overlooked in epidemiology and control-oriented research.

To untangle the importance of these factors, knowledge about the influence of parasite genetics on host's disease patterns is fundamental. We conducted a large epidemiological study in northern Senegal. We genotyped 1692 *S. mansoni* larvae collected from 45 human hosts with nine microsatellite loci and linked this with host data such as age, gender, infection intensity, liver and bladder morbidity. We found a positive relationship between schistosome infection intensity (measured as eggs per gram feces (epg)), and the frequency of a certain parasite allele. We corrected for age, sex, and co-infection with *S. haematobium*. This trend is found with linear regression and redundancy analysis. Two other alleles in this locus were negatively correlated with epg. If we divide infection intensity by worm burden (measured by parasite antigen levels in the blood serum of patients) , we have a measure of parasite fecundity. This parameter appeared also positively correlated with the specific allele. This microsatellite locus is located in the untranslated region (UTR) of a protein kinase gene cGMP. Inhibiting this gene in adult schistosomes resulted in declined egg production by 30%, and reduced muscle contraction.

The possible link with parasite fecundity might explain the correlation between the respective microsatellite allele with infection intensity in humans. The next step is to sequence the complete UTR region and the coding sequence to search for functional SNPs.

Metropole Flanders: spatial and environmental determinants of eco-evolutionary dynamics in zooplankton communities and populations along an urbanization gradient in Flanders

Brans K., Engelen J. and De Meester L.

KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

As mankind exerts an enormous pressure on natural systems (cfr. global warming, climate change, land use change etc.), we are eager to find out in which way urbanization influences metacommunity and metapopulation dynamics in different organismal groups of both aquatic and terrestrial ecosystems (e.g. bacteria, algae, zooplankton, fish, plants, butterflies, birds) and to what extend rapid evolution fuels the capacity of some organisms to cope with different anthropogenic stressors (e.g. high nutrient levels, pollution and toxicant exposure, habitat fragmentation, etc.). As zooplankton, and more specific the large bodied grazer *Daphnia magna*, plays a crucial and pivotal role in aquatic ecosystems and food webs we will conduct a large field survey in the region of Flanders. We will incorporate local as well as regional data by means of an hierarchically stratified GIS-based sampling design. Both population and community analysis as experimental lab and outdoor mesocosm studies will elucidate the impact of urbanization on zooplankton species diversity, metacommunity dynamics, genetic diversity, life history traits, stress responses, metapopulation structure and last but not least ecosystem functions and services. This project will be the first to address the multidimensional impact of urbanization on different organismal groups at a twofold spatial scale, with an ecological as well as an evolutionary line of approach. It will govern new and more precise valuable insights in the functioning of ecosystems and their different components in our current urbanized landscape, characterized by a geographic mosaic of anthropogenic stressors. Our results will not only fortify and clarify different (evolving) metacommunity scenarios, but will likely be translated in more accurate and organism-adjusted management strategies in nature conservation.

Impact of *Microcystis* on the symbiotic bacterial community of *Daphnia*

Callens M., Muylaert K. and Decaestecker E.

KU Leuven - KULAK, Laboratory of Aquatic Biology, Kortrijk, Belgium

The animal body forms a habitat for a diverse and dynamic symbiotic microbial community (SMC), which has an influence on the health and fitness of its host. Environmental factors can alter the composition of this SMC, which in turn can affect its functionality. We conducted an experiment to investigate the effect of the toxic cyanobacterium *Microcystis* on the composition of the SMC in *Daphnia*. We also aim at investigating the functional role of the SMC for *Microcystis* tolerance in *Daphnia*.

Identifying adaptive variation in the genome of three-spined stickleback along an environmental cline

Chaturvedi A., Raeymaekers J.A.M., Maes G. and Volckaert F.A.M.

KU Leuven, Laboratory of Biodiversity and Evolutionary Genomics, Leuven, Belgium

Three-spined sticklebacks live in a range of freshwater and marine habitats in the northern hemisphere, providing an exceptional opportunity for evolutionary biologists to identify genes responsible for its genetic adaption to those environments. Next generation sequencing technologies have made it feasible to study adaptive variation at the genome level in natural populations. Using Genotyping-By-Sequencing we identified and genotyped over 14,000 single nucleotide polymorphisms (SNPs) in three brackish water and three freshwater populations (each with at least 15 individuals per population). Pairwise genome scans between brackish and freshwater populations revealed that allelic diversity decreased inland and that the genes underlying adaptive variation change along the cline. Such results suggest local adaptation. Most genetic variation is found in intergenic and intronic sequences, hinting the important role of regulatory elements in shaping evolution. Further analysis is in progress to decipher the underlying functional causes of these putative signatures of selection.

Rapid evolution in rotifers under conditions of stoichiometric imbalance

Declerck S.A.J., van Donk E., Waasdorp D. and Papakostas S.

Netherlands Institute of Ecology. Wageningen, The Netherlands

Changed nutrient cycles forms one of the major drivers of global change in ecosystems and lead to the altered availability of biogenic elements, such as C, N, and P. Although consumer organisms tend to require biogenic elements in specific ratios, they have been shown to harbor substantial intra-specific genetic variation in their ability to cope with stoichiometric imbalances. An important implication is that such imbalances can represent an important selection factor causing rapid micro-evolutionary changes in natural consumer populations. Such evolution can allow populations to adapt and persist but may also have important consequences for food web interactions and ecosystem function. We present a chemostat study investigating the potential of rotifers (more specifically the species *Brachionus calyciflorus*) to adapt to stoichiometric imbalances and to investigate consequences of such adaptations for predator-prey interactions, elemental cycling and phytoplankton productivity. Another major focus is on the potential trade-off between adaptations in body stoichiometry and life history strategy. According to the "growth rate hypothesis" fast growing organisms are more phosphorus dependent than slowly growing organisms. We test if evolutionary changes in life history affect stoichiometric requirements.

Eco-evolutionary dynamics of antipredator defenses in temporally variable environments: An evolving metacommunity perspective

Frey H., Waterkeyn A., De Meester L. and Brendonck L.

KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

There is growing awareness that ecological and evolutionary processes 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.

The evolving metacommunity framework integrates both ecological and evolutionary processes. It focuses on more diverse communities and includes responses to all kinds of environmental gradients. Thus, it can help e.g. to improve our understanding of the impact that keystone species exhibit on aquatic ecosystems on the (meta-)community level.

In the course of this PhD, we will study the impact of a key invertebrate predator, the tadpole shrimp *Triops*, inhabiting isolated pond habitats along a connectivity gradient as a model of a selection pressure that impacts an evolving metacommunity of zooplankton prey. Our aim is to integrate data concerning different endpoints (regional variation in neutral genetic markers, antipredator traits, species composition and community trait values) to generate new insights in the structure and dynamics of evolving metacommunities. First, we will investigate the genetic metapopulation structure of both *Triops* and its focal prey species *Daphnia* in relation to environmental and connectivity gradients. Then, we will analyze patterns of genetic variation in *Daphnia* antipredator traits, prey communities structure and associated community trait values in relation to predation and connectivity gradients, both experimentally and in the field. Integrating these data will allow us to analyze the degree to which genetic variation in traits of a key species may impact species sorting or community trait responses to environmental gradients.

Pathogen-driven variation in MHC genes in natural populations under stress: house sparrows as a model

Ghysels L.

[1.] Ghent University, Terrestial Ecology Unit, Gent, Belgium

Explaining how functional genetic variation is maintained in natural populations constitutes a central question in evolutionary biology, especially when populations show strong signatures of genetic drift and natural selection. Populations in highly urbanized areas have been shown to decline and be exposed to novel evolutionary challenges, and hence provide good models to address this question. In this project, I aim to disentangle the roles of genetic drift and pathogen-driven selection in shaping variation at genes of the Major Histocompatibility Complex (MHC) in urban and rural house sparrows. MHC forms a highly polymorphic region of the vertebrate genome, and variation in MHC genes has been hypothesized to reflect local adaptation to pathogens. First, I will quantify neutral genetic variation among 36 sparrow populations that will constitute the basis for a null model of selection, and test for genetic signatures of recent population declines. Next, I will quantify genetic variation in MHC genotypes and test the hypothesis that MHC variation at landscape level is maintained through diversifying selection. Then, I will screen all genotyped populations for the presence of pathogens and test the hypothesis that relationships between MHC variation, pathogen load, and avian health vary with the population history of the host. Finally, I will conduct a common-garden experiment to test if pathogen-driven variation in MHC genotypes reflects local adaptation.

Parasite communities and population history predict immunogenetic diversity of natural populations of blunt-headed cichlids (*Tropheus* spp.) in Lake Tanganyika

Habluetzel P.I.[1.], Raeymaekers J.A.M.[1,2.] and Volckaert F.A.M.[1.]

[1.] KU Leuven, Laboratory of Biodiversity and Evolutionary Genomics, Leuven, Belgium
[2.] University of Basel, Zoological Institute, CH-4051, Basel, Switzerland

Cichlid fishes are emblematic models for the study of adaptive radiation, driven by natural and sexual selection. Their immune system is most likely involved in all these processes and its evolution therefore merits special attention. Among the vertebrate immunogenes, the highly polymorphic Mhc (major histocompatibility complex) is ideally suited to study many aspects of evolutionary host-parasite interactions. Here, we tested the hypothesis whether infection by multiple parasite species drive polymorphism of the host's Mhc class IIB genes in its natural environment. A preceding study showed that allopatric and genetically diverged color morphs of blunt-headed cichlids (*Tropheus* spp.) are infected by contrasting parasite communities. In this study, we could show that the Mhc gene pool of a host population is influenced by both parasite diversity and its genealogical history (reflected by neutral genetic diversity). Parasite diversity expressed as Simpson's diversity index is positively correlated with the number of Mhc alleles in a host population, but does not correlate with the host's neutral genetic diversity. We further found a positive relationship between neutral genetic diversity and Mhc allelic diversity, indicating that the population history parameters such as time since divergence, effective population size and migration rate significantly influence immunogenetic diversity. We conclude that allopatric color morphs of the philopatric blunt-headed cichlids responded adaptively to contrasting parasite communities, underpinning the role of adaptive divergence in the formation of these incipient species.

Rapid buildup of genetic diversity in founder populations of the gynodioecious plant species *Origanum vulgare* after semi-natural grassland restoration

Helsen K.[1], Jacquemyn H.[1], Hermy M.[2], Vandepitte K.[1] and Honnay O.[1]

[1] KU Leuven, Laboratory of Plant Conservation and Population Biology, Heverlee, Belgium
[2] KU Leuven, Division Forest, Nature and Landscape research, Department Earth and Environmental Sciences, Heverlee, Belgium

In most landscapes the success of habitat restoration is largely dependent on spontaneous colonization of plant species. This colonization process, and the outcome of restoration practices, can only be considered successful if the genetic makeup of founding populations is not eroded through founder effects and subsequent genetic drift. Here we used 10 microsatellite markers to investigate the genetic effects of recent colonization of the long-lived gynodioecious species *Origanum vulgare* in restored semi-natural grassland patches. We compared the genetic diversity and differentiation of fourteen recent populations with that of thirteen old, putative source populations, and we evaluated the effects of spatial configuration of the populations on colonization patterns. We did not observe decreased genetic diversity in recent populations, or inflated genetic differentiation among them. Nevertheless, a significantly higher inbreeding coefficient was observed in recent populations, although this was not associated with negative fitness effects. Overall population genetic differentiation was low (FST=0.040). Individuals of restored populations were assigned to on average 6.1 different source populations (likely following the 'migrant pool' model sensu Slatkin (1977)). Gene flow was, however, affected by the spatial configuration of the grasslands, with gene flow into the recent populations mainly originating from nearby source populations. This study demonstrates how spontaneous colonization after habitat restoration can lead to viable populations in a relatively short time, overcoming pronounced founder effects, even when gene flow is spatially structured. Restored populations can therefore rapidly act as stepping stones and sources of genetic diversity, likely increasing overall metapopulation viability of the study species.

Genetic basis of local and temporal adaptation in large lake *Daphnia* species

Herrmann M.[1,2.], Kreuzer P.[1.], Cordellier M.[1.], Henning N.[1.] and Schwenk K.[1.]

[1.] Molecular Ecology, Institute of Environmental Sciences, University of Koblenz-Landau, Landau in der Pfalz, Germany
[2.] LOEWE - Biodiversity and Climate Research Centre, Goethe-University, Frankfurt am Main, Germany

Ongoing global warming may cause long-lasting changes in local environmental conditions. If populations fail to adapt, e.g. due to the lack of evolutionary potential, they will be displaced or face extinction. We used the water flea *Daphnia galeata*, to get insights into the populations' ability to adapt to changed environmental conditions and to persist (over several decades) in their rapidly changing habitats. We used resting eggs of *D. galeata* obtained from multiple layers of sediment cores along a latitudinal transect across Europe. *Daphnia* populations were sampled over their geographic range as well as back in time. Presumably temperature relevant candidate genes *ERNA*, *TRY5F* and *MHC1* were sequenced and 11 putatively neutral microsatellite loci were analyzed in every population. Signals of local adaptation were detected using a comparison of genetic differentiation at functional and neutral loci and outlier tests. Mantel tests showed a correlation between functional genetic differentiation at the locus TF and temperature differences between habitats. These analyses provide evidence for local adaptation in *Daphnia* as a response to recent temperature changes. Future studies will link field observations (natural selection at temperature relevant genes) with genotypic architecture of clonal lineages (exposed to different temperature regimes) and gene expression analyses.

Micro-evolutionary response in a natural *Daphnia magna* population under Cu and Zn stress

Hochmuth J., Janssen C.R. and De Schamphelaere K.A.C.

Ghent University, Laboratory of Environmental Toxicology and Aquatic Ecology, Ghent, Belgium

A 10 week experimental evolution study was carried out under semi-field conditions to test for micro-evolutionary effects in a natural *Daphnia magna* population exposed to a control, 2 Cu, and 3 Zn concentrations. We investigated if the long-term exposures to Cu or Zn resulted in a higher organism fitness compared to that in control exposures and in the original (= start) population. At the end of the microevolution experiment a life-table experiment was initiated with clones from the start population, a control population and metal exposed populations to assess if metal acclimation had occurred in the exposed populations. The populations experimentally evolved at 180µg Cu/L and 760µg Zn /L had significantly higher reproduction at the corresponding concentrations than the lower metal or control treatments, i.e. evidence that metal acclimation had occurred. After 4 months of culturing under control conditions, thus eliminating any acclimation history, an additional life-table experiment was conducted to determine whether metal adaptation, measured as an increase in mean population fitness occurred. We observed a significantly higher total reproduction at 760µg Zn /L and at 180µg Cu/L in the respective long-term exposed populations compared to the long-term control exposed population and the start population. In long-term exposure to 760µg Zn/L acclimation and adaptation to the metal had enabled the population density to recover, matching that of the control, despite an initial reduction of 75% of the clones. Under long-term exposure to 180µg Cu/L, however, despite lesser initial mortality (50%), acclimation and adaptation effects were not sufficient to lead to a full recovery of the population density. Our results confirm that micro-evolution can occur after only a few generations but that adaptation in itself is not a guarantee for a complete recovery of the population density.

Effects of parasitism and food quality on host population dynamics in *Daphnia magna* populations

Lange B.[1], Reuter M.[2], Ebert D.[3], Muylaert K.[1] and Decaestecker E.[1]

[1] KU Leuven, Laboratory of Aquatic Biology, Kortrijk, Belgium
[2] University College London, Department of Genetics, Evolution and Environment, London, UK
[3] Universität Basel, Zoologisches Institut, Basel, Switzerland

Although host populations are commonly subjected to different environments, little is known about the contribution of habitat quality on host-parasite interactions. Especially the role of food quality in the interplay between hosts and their parasites is barely studied. To address this topic, experimental individuals and populations of the crustacean freshwater species *Daphnia magna* and two of its parasites, an unknown gut parasite (UGP) and White Bacterial Disease (WBD), were subjected to two different food qualities. The algae *Chlamydomonas reinhardtii* and *Cryptomonas* sp. were chosen as low and high quality food, respectively, based on their polyunsaturated fatty acids (PUFA) content. The results of our experiments showed that the fecundity of parasitized *Daphnia* differs depending on food quality, but survival does not. In a further step, a mathematical model was developed, which can be used to successfully predict host population equilibria. The model incorporated host population demography and can thus also be used to inversely predict individual level host parameters of parasite-driven fecundity decrease and excess in death rate of double infected host populations. Thus, we can predict both: population equilibria from single host parameters and the faith of host individuals within double infected populations.

TIPPINGPOND: from taxon and genetic diversity to ecosystem functioning and resilience

Lemmens P.[1], Hillebrand H.[2], Lindström S. E.[3], Wezel A.[4], Langenheder S.[3] and De Meester L.[1]

[1] K.U. Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2] Institute for Chemistry and Biology of the Marine Environment, Carl-von-Ossietzky University Oldenburg, Wilhelmshaven, Germany
[3] Uppsala University, Department of Ecology and Genetics, Uppsala, Sweden
[4] ISARA-Lyon, Lyon, France

Taxon and genetic diversity may play a key role in the resilience of ecosystems to regime shifts. Our research aims to identify early warning signals and tipping points for regime shifts, using ponds and shallow lakes as models and targets. We will combine an experimental approach with survey data on three types of water systems and in three countries to (1) quantify resilience and regime shift in natural ecosystems; (2) relate resilience and susceptibility to regime shift to the current state of environmental deterioration; (3) relate resilience to measures of taxon and genetic diversity; (4) identify reliable predictors for susceptibility to regime shifts; (5) develop guidelines to apply this knowledge to diversity management; (6) transfer knowledge on ecological regime shifts and tipping points of pond and lake systems to stakeholders and policy makers.

Can pesticides affect *Daphnia magna* dormant eggs? Effects on hatching characteristics and juvenile survival, growth and reproduction

Navis S., Waterkeyn A., Voet T., De Meester L. and Brendonck L.

KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

Many aquatic invertebrate species produce dormant stages that can accumulate in the sediment over different growing seasons to form a dormant egg bank, which can function as a reservoir of species and genetic diversity during fluctuating environmental conditions. Despite the importance of dormant egg bank dynamics in ecological and evolutionary processes, there is almost no information available on the effects of pollution on these dormant egg banks. Laboratory ecotoxicity tests and biomonitoring of invertebrates in aquatic systems are currently based on the active aquatic component.

In this study we investigated the effects of two pesticides on dormant eggs of *Daphnia magna*, a well established model organism in ecology and ecotoxicology, that reproduces by cyclical parthenogenesis. In a first series of laboratory experiments we studied the effects of two pesticides with a different mode of action (carbaryl and fenoxycarb) on embryonic development and hatching characteristics of the dormant eggs. In a second experiment we tested whether exposure to pesticides, during the time the eggs were also exposed to hatching cues, could have long term effects on survival and life history characteristics of the hatched individuals. Our results show that, depending on their mode of action, pesticides can have severe negative effects on hatching characteristics of *D. magna* dormant eggs, as well as on survival, growth and reproduction of the hatched neonates. This indicates that, in addition to inducing mortality of active individuals, pesticides can alter hatching dynamics and life history traits of hatched individuals. This can have far-reaching consequences for ecological and evolutionary dynamics of zooplankton communities in lakes and ponds.

From individual movement to population spread: movement and dispersal in *Tetrahymena thermophila* microcosms

Pennekamp F. and Schtickzelle N.

Université catholique de Louvain, Earth & Life Institute, Louvain-la-Neuve, Belgium

Movement is a fundamental characteristic of life. It is involved in important behavioural responses such as foraging, mate search or predator avoidance and consequently influences important ecological processes for example the dispersal between habitats and the resulting population dynamics. In order to understand movement and its ecological consequences we need a thorough knowledge of the biomechanics of the motion process, the navigation capabilities as well as the internal and external factors which influence the movement of organisms. Understanding the rules and constraints which underlie movement will help to better predict how organisms react to environmental change and better control of invasive species and pests.

Our model system consists of different genotypes of the unicellular aquatic eukaryote *Tetrahymena thermophila*. Populations are cultured under controlled conditions in the lab allowing easy manipulation of the environment. To quantify the movement behaviour we take video shots and extract two-dimensional movement trajectories of individual cells. The movement is then summarized into metrics such as net displacement, speed and path linearity to compare genotypes and treatments of conspecific density.

First, we show substantial intraspecific variation in the movement patterns and a relationship between the swimming speed and the cell shape. Second, our study shows a link between the movement behaviour expressed at the individual cell level and population level phenomena as the emigration rate. Third, changes in the individual movement due to different cell densities can partly explain density-dependent responses of the emigration rate.

Environmental change as a driver of diversification in Australian temporary aquatic habitats

Pinceel T., Brendonck L. and Vanschoenwinkel B.

KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

Over the past 65my, the Australian continent experienced a pronounced shift from predominantly tropical conditions to a much drier climate. Little, however, is known about the effect of this important continent wide event on freshwater organisms and ecosystems. Fairy shrimps (Crustacea; Anostraca) are ancient and specialist inhabitants of temporary and saline aquatic habitats that typically prevail under semiarid conditions. Therefore, they present suitable evolutionary models to study scenarios of historic environmental change and the impact of a drying climate on aquatic ecosystems in particular.

Focusing on both macro- and micro-evolution in the fairy shrimp genus *Branchinella* using mitochondrial DNA data (16S and COI) we evaluate whether patterns of contemporary genetic variation reflect events consistent with scenarios of historic climate change.

Our results indicate a close match between episodes of Cenozoic climate change and macro-evolutionary diversification in Australian fairy shrimps, presumably mediated by a progressive increase in the abundance and diversity of temporary aquatic habitats on the continent. Micro-evolutionary patterns reflect both range expansion and recent contraction, linked to extreme drying events during the Pleistocene glacial periods.

The current study effectively illustrates the potential long term effects of environmental change on the diversity and the evolutionary trajectories of the fauna of temporary waters. Moreover, it demonstrates the importance of adaptation to new environments and non-adaptive processes such as divergence in isolation for explaining extant diversity patterns in this particular environment.

Differences between sexual and asexual eggs of *Daphnia magna*

Putman A.[1.], Panis B.[2.] and De Meester L.[1.]

[1.] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2.] Laboratory of Tropical Crop Improvement, Department of Biosystems, KU Leuven, Heverlee, Belgium

Daphnia magna is an important model organism in ecological and evolutionary biological research and one of the most widely used model organism in ecotoxicology. For all of these applications, it would be a very big step forward if genetically well characterized lines of *Daphnia* could be safely stored, without keeping the clonal lines continuously in culture. Cryopreservation, the long-term preservation of living organisms via freezing at ultra low temperatures (-196°C), can be a solution, but so far no successful protocol has been developed for the cryopreservation of Daphnia eggs. The life cycle of *Daphnia* is characterized by an alternation of sexual and asexual reproduction, called cyclic parthenogenesis. The sexual eggs are more resistant to various stressors, but are not suitable for the preservation of clonal lines. Sexual eggs are, however, drought and freezing tolerant. Comparing characteristics of sexual and clonal eggs may thus provide insight in how to manipulate parthenogenetic eggs so that they become more suitable for cryopreservation. It is important to have a thorough understanding of the ecological, morphological and biochemical characteristics of these different types of eggs in order to understand the mechanisms that determine the differences in survival and sensitivity to dehydration and freezing. Freezing and dehydration tolerance is likely affected by membrane stabilization, changes in protein composition and the accumulation of cryoprotective substances. We observed that there are large differences in the fatty acid composition and amount of sterols between sexual and parthenogenetic eggs. Sugars can also play an important role in cryopreservation. More specifically, trehalose is known for its positive effect on freezing tolerance. This marks another important difference between sexual and parthenogenetic eggs: sexual eggs contain approximately double the amount of trehalose compared to asexual eggs. Through manipulating diet composition, we will try to incorporate higher levels of trehalose in asexual eggs.

Reproduction of *Rana temporaria* in variable environments

Reniers J., Vanschoenwinkel B. and Brendonck L.

KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

Under constant conditions, organisms are expected to optimize their life history traits, while in variable environments multiple life history optima can exist. When cues are informative of current and future environmental conditions, this environmental variation selects for plasticity of life history traits. However, when cues are uninformative, organisms are expected to hedge their bets and produce offspring with different or intermediate phenotypes to assure survival under any of the possible environmental conditions. Evidence has accumulated suggesting that such risk spreading strategies are common in a large diversity of organisms.

Anuran amphibians, which mostly reproduce in temporary fishless ponds, would greatly benefit from spreading reproductive effort in both space and time as successful reproduction is limited by the (often variable) duration of the aquatic phase of their offspring's habitat. Conversely, as tadpoles can correctly assess imminent drought, temporary pools should select for plasticity in development time of larvae. Making use of Belgian *Rana temporaria* populations, a generalist breeder, we investigated variable offspring provisioning (egg size), development time and developmental plasticity along a gradient of isolated ephemeral, semi permanent and permanent pools under common garden conditions. In addition, we determined tadpole fat body weight and corticosterone concentration, physiological mechanisms that could be involved in the different development strategies. Lastly we assessed possible costs and behavioral changes associated with these different strategies. Our results indicate that tadpoles from ephemeral pools intrinsically develop faster but still retain the same absolute amount of plasticity as tadpoles from permanent pools. Tadpoles from semi-permanent pools revealed an intermediate development time, not attributed to an intermediate development time per se, but to the existence of fast and slow developing clutches.

Our results show that environmental variation is an important driver for life history variation across species' ranges. Additionally, Amphibia can track their environment on relatively short timescales as some of the selected pools were relatively young. Further knowledge about variation in plasticity, its mechanisms and its costs, will shed light on the constraints on evolution and the resulting ecological consequences.

Indoor rivalry, alien invasions or evolution? Importance of local, regional and evolutionary processes for bacterial community composition in shallow lakes

Rummens K., Souffreau C. and De Meester L.

KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium

Microbial communities play a key role in many crucial ecosystem processes. Yet, the processes determining the species composition of natural bacterial communities are insufficiently known. Local (lineage sorting, i.e. local selection by (a)biotic factors) as well as regional (dispersal) and evolutionary dynamics might all play an important role in determining bacterial community composition, but the relative importance of, and interactions between these dynamics remain largely unknown. Also the (indirect) effect these dynamics have on the functional characteristics of bacterial communities isn't clear.

During this research we will quantify the relative importance of lineage sorting, mass effects, priority effects and evolution for the structuring of bacterial communities and investigate the impact of differential community composition on functionality. For this purpose, natural planktonic and biofilm communities from different pond types will be manipulated and cross-inoculated in specific experimental setups, including different immigration histories to test for the importance of priority effects. We will also characterize functional characteristics of lineages through time so that we will be able to answer questions like 'Are priority effects occurring due to a numerical advantage or mediated by evolution and genetic adaptation of the first colonist?' By using natural communities sampled from shallow lakes we aim at gaining insight in these processes in complex, species rich systems.

Identification of candidate genes for adaptive responses to environmental stress in *Daphnia magna*

Spanier K.[1.], Orsini L.[1.], De Meester L.[1.] and Aerts S.[2.]

[1.] KU Leuven, Laboratory of Aquatic Ecology, Evolution and Conservation, Leuven, Belgium
[2.] KU Leuven, Laboratory of Computational Biology, Leuven, Belgium

Understanding the genetic underpinning of adaptation of organisms to their natural environment is a key objective in the rapidly developing field of ecological and environmental genomics. However, assessing specific causes of natural selection in the wild is challenging because it is nearly impossible to unambiguously determine selective forces in a multidimensional natural context.

Capitalising on the fast development of genomic tools, the genome sequence and the rich ecological background available for *D. magna*, we identify candidate genes underlying adaptive responses to key selection pressures in the wild.

The use of next generation sequencing techniques for genome scans and transcriptome analyses yields a high number of candidate genes. Part of those genes show homology to genes with known function in other organisms, whereas for the rest there is no functional annotation. We target the latter genes for prioritisation using firstly integrated information from parallel experiments and secondly a purely sequence-based approach to identify putative gene regulatory networks.

We here present a bioinformatics approach for analysing genomic data in a non-genetic model species which can be applied to other species with similar data background and therefore contributes to advances in ecological genomics.

Coevolution in the mutualism between N-fixing bacteria and leguminose plant species

Van Cauwenberghe J.

KU Leuven, Plant Conservation and Population Biology, Heverlee, Belgium

Based on the geographic mosaic of coevolution theory, it can be expected that in different communities symbiotic partners will be locally coadapted in a different manner. Hence, locally coadapted symbionts will only match well in their local habitat and will mismatch in allopatric habitats. This hypothesis will be tested on the mutualistic interaction between a leguminose (*Vicia cracca*) and *Rhizobium leguminosarum* biovar *viciae (Rlv).*

First the diversity or presence of certain genotypes between *Rlv* populations will be checked by multilocus sequence typing. At present we are analyzing a pilot of 50 isolates in 4 neighboring populations. Sequencing of the 16S rRNA gene showed that *Rlv* is the only species present. Further analysis of the chromosomal genes (glnII, recA and atpD) and plasmid genes (nodC, nodE and nifD) would show deeper genetic differentiation. A preliminary cluster analysis of the glnII gene seems to indicate that most genotypes are omnipresent, but the abundance seems to vary among populations. It will be tested if environmental differences (e.g. pH, phosphate level, nitrogen deposition) can explain this variation.

Additional sampling will be conducted through a trap plant experiment in which plants are allowed to nodulate with rhizobia from allopatric soils. This experiment can provide indications of specific selection and possibly give evidence for local adaptation. Next objective is to combine several genotypes of *Rlv* with plants from different *Vicia cracca* populations in *in vitro* conditions in order to test for local coadaptation. Finally the effects of different *Rlv* – *Vicia cracca* combinations on intraspecific competitions, the entire plant community and higher trophic levels will be examined.

Impact of treatment with PZQ on the evolution of the human parasite *Schistosoma mansoni*

Van den Broeck F.[1], Volckaert F.A.M.[1], Polman K.[2] and Huyse T.[1]

[1] KU Leuven, Laboratory of Biodiversity and Evolutionary Genomics, Leuven, Belgium
[2] Institute of Tropical Medicine, Unit of Medical Helminthology, Antwerp, Belgium

Schistosomiasis or bilhar*zia* is a major poverty-related disease, caused by parasitic worms of the genus *Schistosoma*. Praziquantel (PZQ) is the drug of choice to treat schistosomiasis because of the absence of toxicity, low cost and the activity against all schistosome species. Whereas cure rates are usually 78-88%, the observed cure rate at the onset of the epidemic in Senegal reached only 18-32%, indicating the possible existence of PZQ resistance/tolerance. Here we aim to study the impact of treatment with PZQ on the neutral and adaptive evolution of *Schistosoma mansoni* in Senegal. We hypothesized that treatment will reduce the overall neutral genetic diversity of parasite populations (bottleneck effect) in combination with a selection for drug resistant genotypes that confer parasite survival (adaptive evolution).

This study is part of a larger project where the Senegalese village Nder was treated with PZQ and followed in time to study re-infection rates. We collected schistosome miracidia of individuals at the start of the study and six months after repeated PZQ treatment. First, *S. mansoni* parasites were genetically characterized using 9 neutral microsatellite DNA markers. In a second step, the same parasites will also be genotyped using a panel of ~50 adaptive SNP markers to identify signatures of selection.

Thorough population genetic analysis of the neutral marker dataset revealed no significant differences in the genetic diversity of, and genetic differentiation between parasite populations before and after repeated treatment. As rapid-reinfection alone cannot explain the sustained high genetic diversity, these results suggest that some strains may survive PZQ treatment. In the following steps, it will be important to test for signatures of selection based on adaptive genetic markers and to conduct larger field studies with short-term follow-up after treatment together with in depth snail surveys.

Inferring genetic population structure in contemporary house sparrow populations along an urbanization gradient: a plea for individual-based analysis.

Vangestel, C., Matheve H., Vandomme V. and Lens L.

University of Ghent, Terrestrial Ecology Unit, Ghent, Belgium

House sparrow (*Passer domesticus*) populations have suffered major declines in highly urbanized areas. Yet, to date no exhaustive attempt has been made to examine how, and to what extent, spatial variation in population demography is reflected in genetic population structuring along contemporary urbanization gradients. Here we use information from 16 polymorphic microsatellite DNA markers to study if and how genetic variation can be partitioned in a hierarchical way among different urbanization classes. Population-based analyses such as principal coordinate analyses and MANOVA did not support the hypothesis that urbanized and rural populations comprise two distinct genetic clusters. In contrast, monitoring individual-based measures of genetic relatedness along the urbanization gradient revealed small-scale patterns of genetic structure. Average levels of relatedness were higher among urban individuals than among individuals from rural areas, suggesting lower rates of dispersal in more built up habitats. Comparison of observed levels of relatedness with simulated distributions of known kinship values showed that central urban individuals had the highest proportion of closely-related conspecifics in their immediate neighbourhood. Spatial auto-correlograms supported this small-scale genetic structure and further indicated stronger effects of genetic drift and/or limited dispersal in urban populations. This study underscores the importance of individual-level analyses as a complementary approach to traditional population-level analyses when studying genetic population structure over small spatial scales. Results shown here can be used as baseline information for future genetic monitoring programmes and provide additional insights into contemporary house sparrow dynamics along urbanization gradients.

β-proteobacteria beyond legumes: endophytic *Burkholderia* in Rubiaceae

Verstraete B.[1], Janssens S., Smets E. and Dessein S.[2]

[1] Plant Conservation and Population Biology, KU Leuven, Leuven, Belgium
[2] Naturalis Biodiversity Center, Leiden University, Leiden, The Netherlands
[3] National Botanic Garden of Belgium, Meise, Belgium

Symbiotic β-proteobacteria not only occur in root nodules of legumes but are also found in leaves of certain Rubiaceae. The discovery of bacteria in plants formerly not implicated in endosymbiosis suggests a wider occurrence of plant-microbe interactions. Several β-proteobacteria of the genus Burkholderia are detected in close association with tropical plants. This interaction has occurred three times independently, which suggest a recent and open plant-bacteria association. The presence or absence of *Burkholderia* endophytes is consistent on genus level and therefore implies a predictive value for the discovery of bacteria. Only a single *Burkholderia* species is found in association with a given plant species. However, the endophyte species are promiscuous and can be found in association with several plant species. Most of the endophytes are part of the plant-associated beneficial and environmental group, but others are closely related to B. glathei. This soil bacteria, together with related nodulating and non-nodulating endophytes, is therefore transferred to a newly defined and larger PBE group within the genus *Burkholderia*.

PARTICIPANTS

Job	Aben	job.aben@gmail.com
Jacek	Bartlewicz	bartlewiczjacek@gmail.com
Lutz	Becks	lbecks@evolbio.mpg.de
Lander	Blommaert	lander.blommaert@ugent.be
Wim	Bonckaert	wim.bonckaert@gmail.com
Nele	Boon	nele.boon@kuleuven.be
Kristien	Brans	kristienbrans@bio.kuleuven.be
Luc	Brendonck	Luc.Brendonck@bio.kuleuven.be
Falko	Buschke	falko.buschke@bio.kuleuven.be
Evelyn	Buyze	evelyn.buyze@Ugent.be
Martijn	Callens	martijn.callens@kuleuven.be
Frederic	Chain	chain@evolbio.mpg.de
Anurag	Chaturvedi	anurag.kuleuven@gmail.com
Marlies	Coopman	marlies.coopman@kuleuven-kulak.be
Charlotte	De Busschere	charlotte.debusschere@naturalsciences.be
Olivier	De Clerck	odclerck@gmail.com
Hanne	De Kort	hanne.dekort@bio.kuleuven.be
Luc	De Meester	Luc.DeMeester@bio.kuleuven.be
Annelies	De Roissart	annelies.deroissart@ugent.be
Ellen	Decaestecker	Ellen.Decaestecker@kuleuven-kulak.be
Steven	Declerck	S.declerck@nioo.knaw.nl
Khuong	Dinh Van	khuong.dinhvan@student.kuleuven.be
Eveline	Diopere	eveline.diopere@bio.kuleuven.be
Edgar	Duenez Guzman	duenez@bio.kuleuven.be
Jacintha	Ellers	j.ellers@vu.nl
Jessie	Engelen	jessie.engelen@student.kuleuven.be
Diego	Fontaneto	d.fontaneto@ise.cnr.it
Kevin	Foster	kevin.foster@zoo.ox.ac.uk
Hendrik	Frey	hendrik.frey@bio.kuleuven.be
Aurora	Geerts	Aurora.Geerts@bio.kuleuven.be

Lies	Ghysels	lies.ghysels@ugent.be
Pieter	Gijbels	Pieter.Gijbels@bio.kuleuven.be
Rosemary	Gillespie	gillespie@berkeley.edu
Catherine	Graham	catherine.graham@stonybrook.edu
Sophie	Gryseels	sophie.gryseels@ua.ac.be
Pascal Istvan	Habluetzel	pascal.habluetzel@bio.kuleuven.be
Tsegazeabe	Haileselasie	tsegazeabehadush.haileselassie@student.kuleuven.be
Nelson	Hairston	ngh1@cornell.edu
Bart	Hellemans	bart.hellemans@bio.kuleuven.be
Kenny	Helsen	kenny.helsen@bio.kuleuven.be
Frederik	Hendrickx	frederik.hendrickx@naturalsciences.be
Andrew	Hendry	andrew.hendry@mcgill.ca
Maike	Herrmann	herrmann@bio.uni-frankfurt.de
Dieter	Heylen	Dieter.Heylen@ua.ac.be
Jasmijn	Hillaert	Jasmijn.Hillaert@ugent.be
Jasmien	Hillen	jasmienhillen@gmail.com
Jennifer	Hochmuth	jennifer.hochmuth@ugent.be
Marie-Jeanne	Holveck	marie-jeanne.holveck@uclouvain.be
Olivier	Honnay	olivier.honnay@bio.kuleuven.be
Thomas	Hovestadt	hovestadt@biozentrum.uni-wuerzburg.de
Tine	Huyse	tine.huyse@bio.kuleuven.be
Marie	Huysman	Marie.Huysman@UGent.be
Bas W.	Ibelings	bastiaan.ibelings@unige.ch
Mieke	Jansen	Mieke.Jansen@bio.kuleuven.be
Martin	Kalbe	kalbe@evolbio.mpg.de
Xavier	Karreman	xavier.karreman@biw.kuleuven.be
Gunter	Kathagen	gunter.kathagen@gmail.com
Nellie	Konijnendijk	Nellie.Konijnendijk@bio.kuleuven.be
Britt	Koskella	B.L.Koskella@Exeter.ac.uk
Milica	Lakovic	milica.lakovic@ugent.be
Benjamin	Lange	benjamin.lange@kuleuven-kortrijk.be
Maarten	Larmuseau	maarten.larmuseau@bio.kuleuven.be

Veerle	Lemaire	veerle.lemaire@bio.kuleuven.be
Pieter	Lemmens	pieter.lemmens@bio.kuleuven.be
Luc	Lens	Luc.Lens@UGent.be
Eva	Lindström	Eva.Lindstrom@ebc.uu.se
Gregory	Maes	gregory.maes@bio.kuleuven.be
Veronika	Martinova	Veronika.martinova@student.kuleuven.be
Blake	Matthews	Blake.Matthews@eawag.ch
Erik	Matthysen	erik.matthysen@ua.ac.be
Sofie	Meeus	sofie.meeus@bio.kuleuven.be
Sabine	Navis	Sabine.Navis@bio.kuleuven.be
Caroline	Nieberding	caroline.nieberding@uclouvain.be
Dagmar	Obbels	dagmar.obbels@ugent.be
Isabelle	Olivieri	isabelle.olivieri@univ-montp2.fr
Luisa	Orsini	luisa.orsini@bio.kuleuven.be
Joop	Ouborg	j.ouborg@science.ru.nl
Jelena	Pantel	Jelena.Pantel@bio.kuleuven.be
Kevin	Pauwels	Kevin.Pauwels@bio.kuleuven.be
Frank	Pennekamp	Frank.Pennekamp@uclouvain.be
Tom	Pinceel	tom.pinceel@bio.kuleuven.be
Adinda	Putman	adinda.putman@bio.kuleuven.be
Viktoriia	Radchuk	viktoriia.radchuk@uclouvain.be
Joost	Raeymaekers	joost.raeymaekers@unibas.ch
Jane	Reniers	jane.reniers@bio.kuleuven.be
Lien	Reyserhove	Lien.Reyserhove@kuleuven-kulak.be
Koen	Rummens	koen.rummens@bio.kuleuven.be
Sharon	Schillewaert	sharon.schillewaert@bio.kuleuven.be
Klaus	Schwenk	schwenk@uni-landau.de
Melanie	Serruys	melanie.serruys@uclouvain.be
Caroline	Souffreau	caroline.souffreau@bio.kuleuven.be
Piet	Spaak	spaak@eawag.ch
Katina	Spanier	katina.spanier@bio.kuleuven.be
Frederique	Steen	frederique.steen@ugent.be

Kristine	Stepanyan	Kristine.Stepanyan@biw.kuleuven.be
Robby	Stoks	robby.stoks@bio.kuleuven.be
Diederik	Strubbe	diederik.strubbe@ua.ac.be
Janne	Swaegers	Janne.Swaegers@bio.kuleuven.be
Ine	Swillen	ine.swillen@bio.kuleuven.be
Lieven	Therry	Lieven.Therry@bio.kuleuven.be
Anne	Tielsch	thielsch@uni-landau.de
Vania	Torrez Flores	VaniaWendy.TorrezFlores@bio.kuleuven.be
Steven	Van Belleghem	Steven.VanBelleghem@UGent.be
Jannick	Van Cauwenberghe	jannick.vancauwenberghe@bio.kuleuven.be
Frederik	Van de Perre	frederik.vandeperre2@student.ua.ac.be
Evelien	Van de Vyver	evelien.vandevyver@ugent.be
Frederik	Van den Broeck	frederik.vandenbroeck@bio.kuleuven.be
Sascha	van der Meer	sascha.vandermeer@bio.kuleuven.be
Hans	Van Dyck	hans.vandyck@uclouvain.be
Anneleen	Van Geystelen	anneleen.vangeystelen@bio.kuleuven.be
Raoul	Van Oosten	raoosten@gmail.com
Katrien	Van Petegem	katrien.vanpetegem@ugent.be
Sara	Vandamme	sara.vandamme@ilvo.vlaanderen.be
Carl	Vangestel	carl.vangestel@ugent.be
Pieter	Vanormelingen	Pieter.Vanormelingen@UGent.be
Joost	Vanoverbeke	joost.vanoverbeke@bio.kuleuven.be
Brecht	Verstraete	brecht.verstraete@bio.kuleuven.be
Filip	Volckaert	filip.volckaert@bio.kuleuven.be
Guy	Vranckx	guy.vranckx@bio.kuleuven.be
Aline	Waterkeyn	aline.waterkeyn@bio.kuleuven.be
Tom	Wenseleers	tom.wenseleers@bio.kuleuven.be
Joel	White	joel.white@educagri.fr
Justyna	Wolinska	wolinska@bio.lmu.de