



cornwall 2013

empseb  
19

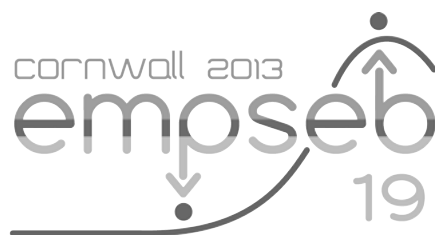
BMC

Evolutionary Biology

Abstract book sponsored by

# 19th European Meeting of PhD students in Evolutionary Biology

3rd - 8th September 2013, Cornwall, England





---

Dear PhD students in Evolutionary Biology,

I would like to offer you the warmest welcome to Cornwall and to the University of Exeter's Centre for Ecology & Conservation, in Penryn.

This is the 2nd time EMPSEB has been held in England, although some Cornish folk dispute that Cornwall is part of England at all! Cornwall proudly retains a distinct cultural identity and we hope you will embrace it by stuffing yourself with Cornish pasties, enjoying a cream tea with our famous clotted cream, tasting some Cornish ciders, and experiencing some of the most unspoilt and breath-taking scenery in the UK!

This years meeting promises to be truly memorable, and we hope it will equip you with skills and experiences you will value throughout and beyond your PhD. EMPSEB is unique in that you'll get helpful and constructive feedback from the top evolutionary biologists in our field on a friendly and personal level. You and your peers will help each other along the way, and friendships will be formed that will last your entire career.

Science is changing, and our innovative workshops and public engagement event reflect this. There is now an expectation to invite the public to be interested in our science and we scientists must learn how to explain what we do in a way that is relevant to society. It is too easy for us to become wrapped up in our research and forget about the bigger picture. The public must understand not only what is being done but why we do it.

I hope you enjoy the full EMPSEB experience!

On Behalf of the Organising Committee,

Siobhan

## Contents

---

|                                                       | page |
|-------------------------------------------------------|------|
| People                                                | 5    |
| Organising committee                                  | 9    |
| Invited speakers                                      | 17   |
| Wednesday talks                                       | 29   |
| Thursday workshops                                    | 59   |
| Friday talks                                          | 63   |
| Public engagement event<br>(For the Love of Science!) | 86   |
| Saturday talks                                        | 87   |
| Sunday excursion                                      | 117  |
| BMC Evolutionary Ecology abstracts                    | 121  |
| Timetable                                             | 132  |

## Contents

| first name                  | last name   | e-mail                        | page |
|-----------------------------|-------------|-------------------------------|------|
| <i>Organising committee</i> |             |                               |      |
| Siobhan                     | O'Brien     | eso201@exeter.ac.uk           | 10   |
| Beatrice                    | Downing     | bd249@exeter.ac.uk            | 10   |
| Christopher                 | Beirne      | cb441@exeter.ac.uk            | 10   |
| David                       | Fisher      | dnf201@exeter.ac.uk           | 11   |
| Emma                        | Wood        | ew261@exeter.ac.uk            | 11   |
| Eoin                        | Duffy       | E.M.K.Duffy@exeter.ac.uk      | 11   |
| Helen                       | Leggett     | helen.leggett@zoo.ox.ac.uk    | 12   |
| Katy                        | Scott       | ks334@exeter.ac.uk            | 12   |
| Lindsay                     | Walker      | lw356@exeter.ac.uk            | 12   |
| Lucy                        | Ovens       | lo212@exeter.ac.uk            | 13   |
| Matthew                     | Silk        | mjs234@exeter.ac.uk           | 13   |
| Martin                      | Grunnill    | mdg206@exeter.ac.uk           | 13   |
| Michael                     | Hawkes      | M.F.Hawkes@exeter.ac.uk       | 14   |
| Robyn                       | Manley      | rm418@exeter.ac.uk            | 14   |
| Sarah                       | Paul        | scp210@exeter.ac.uk           | 15   |
| Sheridan                    | Willis      | sw360@exeter.ac.uk            | 15   |
| <i>Invited speakers</i>     |             |                               |      |
| Andy                        | Gardner     | andy.gardner@zoo.ox.ac.uk     | 18   |
| Britt                       | Koskella    | B.L.Koskeller@exeter.ac.uk    | 26   |
| Geoff                       | Parker      | Gap@liverpool.ac.uk           | 21   |
| Johanna                     | Mappes      | johanna.mappes@jyu.fi         | 20   |
| Judith                      | Mank        | judith.mank@ucl.ac.uk         | 23   |
| Laurent                     | Keller      | Laurent.Keller@unil.ch        | 22   |
| Paula                       | Stockley    | p.stockley@liv.ac.uk          | 25   |
| Tom                         | Currie      | T.Currie@exeter.ac.uk         | 19   |
| Troy                        | Day         | tday@mast.queensu.ca          | 24   |
| <i>Delegates</i>            |             |                               |      |
| Akash                       | Sharma      | a.sharma@rug.nl               | 30   |
| Alexis                      | Sullivan    | arsulliv@mtu.edu              | 31   |
| Alison                      | Cotton      | alison.cotton.10@ucl.ac.uk    | 71   |
| Anasuya                     | Chakrabarty | anasuya.chakrabarty@gmail.com | 64   |
| Ann Kathrin                 | Huylmans    | huylmans@bio.lmu.de           | 65   |
| Anna                        | Campbell    | alc218@exeter.ac.uk           | 93   |

## Contents

---

|               |             |                                   |     |
|---------------|-------------|-----------------------------------|-----|
| Anne          | Winters     | e.anne06@gmail.com                | 89  |
| Anni          | Hämäläinen  | anni.m.hamalainen@gmail.com       | 34  |
| Antoine       | Stier       | antoine.stier@iphc.cnrs.fr        | 32  |
| Ben           | Ashby       | ben.ashby@zoo.ox.ac.uk            | 66  |
| Benja         | Fallenstein | benja.fallenstein@gmail.com       | 67  |
| Charlie       | Ellis       | cde204@exeter.ac.uk               | 91  |
| Charlotte     | Récapet     | charlotte.recapet@univ-lyon1.fr   | 35  |
| Chen          | Hou         | chen.hou@su.se                    | 33  |
| Christine     | Tansey      | C.J.Tansey@sms.ed.ac.uk           | 49  |
| Christopher   | Culbert     | c.culbert12@imperial.ac.uk        | 68  |
| Christopher   | Quickfall   | acp12cgq@shef.ac.uk               | 88  |
| Diamanto      | Mamuneas    | dmamuneas@rvc.ac.uk               | 69  |
| Dimitri       | Stucki      | dimitri.stucki@helsinki.fi        | 92  |
| Eduard        | Solà        | edu.sola@gmail.com                | 39  |
| Elizabeth     | Duxbury     | emlduxbury@gmail.com              | 38  |
| Eryn          | McFarlane   | eryn.mcfarlane@ebc.uu.se          | 72  |
| François      | Renož       | francois.renož@uclouvain.be       | 73  |
| Gaëlle        | Pontarotti  | gaelle.pontarotti@gmail.com       | 96  |
| Georgina      | Brennan     | g.l.brennan@sms.ed.ac.uk          | 97  |
| Gwennaël      | Bataille    | gwennaël.bataille@uclouvain.be    | 43  |
| Ilka          | Vosteen     | ivosteen@ice.mpg.de               | 41  |
| Isabel        | Mück        | isabel.mueck@uni-tuebingen.de     | 74  |
| Isabel        | Winney      | isabel.winney@googlemail.com      | 98  |
| Isabel Salome | Keller      | ikeller@geomar.de                 | 40  |
| Iwona         | Giska       | iwona.giska@uj.edu.pl             | 99  |
| Jana          | Wolf        | Jana.Wolf@helsinki.fi             | 42  |
| Jenni         | Paviala     | jenni.paviala@helsinki.fi         | 75  |
| Joanna        | Sudyka      | joanna.sudyka@uj.edu.pl           | 78  |
| Jonathan      | Henshaw     | jono.m.henshaw@gmail.com          | 76  |
| Juan          | Ramirez     | acq11jcr@sheffield.ac.uk          | 100 |
| Julien        | Amouret     | jua6@hi.is                        | 101 |
| Kati          | Saarinen    | kati.m.saarinen@jyu.fi            | 90  |
| Katrine       | Lund-Hansen | k.lund-hansen@sussex.ac.uk        | 48  |
| Konstanze     | Schiessl    | konstanze.schiessl@eawag.ch       | 77  |
| Lien          | Reyserhove  | Lien.Reyserhove@kuleuven-kulak.be | 79  |
| Louise        | Christensen | r01llc12@abdn.ac.uk               | 102 |

## Contents

---

|              |               |                                                                                      |     |
|--------------|---------------|--------------------------------------------------------------------------------------|-----|
| Lucas        | Marie-Orleach | <a href="mailto:l.marie-orleach@unibas.ch">l.marie-orleach@unibas.ch</a>             | 103 |
| Maarit       | Mäenpää       | <a href="mailto:M.I.Maenpaa@sms.ed.ac.uk">M.I.Maenpaa@sms.ed.ac.uk</a>               | 46  |
| Małgorzata   | Grzesiuk      | <a href="mailto:m.grzesiuk@uw.edu.pl">m.grzesiuk@uw.edu.pl</a>                       | 47  |
| Marie        | Rescan        | <a href="mailto:marie.rescan@sb-roscoff.fr">marie.rescan@sb-roscoff.fr</a>           | 80  |
| Marine       | Pouget        | <a href="mailto:marine.pouget@imbe.fr">marine.pouget@imbe.fr</a>                     | 81  |
| Mark         | Harrison      | <a href="mailto:mch44@le.ac.uk">mch44@le.ac.uk</a>                                   | 104 |
| Martin       | Vallon        | <a href="mailto:martin.vallon@uni-tuebingen.de">martin.vallon@uni-tuebingen.de</a>   | 105 |
| Merel        | Breedveld     | <a href="mailto:merelbreedveld@mncn.csic.es">merelbreedveld@mncn.csic.es</a>         | 45  |
| Naga Apoorva | Kasala        | <a href="mailto:nagaapoorva@evolbio.mpg.de">nagaapoorva@evolbio.mpg.de</a>           | 44  |
| Nina         | Wale          | <a href="mailto:nina.wale@gmail.com">nina.wale@gmail.com</a>                         | 82  |
| Nolwenn      | Fresneau      | <a href="mailto:nolwenn.fresneau@gmail.com">nolwenn.fresneau@gmail.com</a>           | 83  |
| Pablo        | Valverde      | <a href="mailto:pablo.valverde@uni-bielefeld.de">pablo.valverde@uni-bielefeld.de</a> | 106 |
| Pascal       | Milesi        | <a href="mailto:pascal.milesi@univ.montp2.fr">pascal.milesi@univ.montp2.fr</a>       | 107 |
| Paul         | Saunders      | <a href="mailto:paul.alan.saunders@gmail.com">paul.alan.saunders@gmail.com</a>       | 50  |
| Pepijn       | Kamminga      | <a href="mailto:pepijn.kamminga@naturalis.nl">pepijn.kamminga@naturalis.nl</a>       | 51  |
| Raïssa       | de Boer       | <a href="mailto:raissa.deboer@ua.ac.be">raissa.deboer@ua.ac.be</a>                   | 85  |
| Ramith       | Nair          | <a href="mailto:ramith.nair@env.ethz.ch">ramith.nair@env.ethz.ch</a>                 | 84  |
| Rebecca      | Jones         | <a href="mailto:bs0u916d@liverpool.ac.uk">bs0u916d@liverpool.ac.uk</a>               | 108 |
| Rebecca      | Watson        | <a href="mailto:rebecca.watson@ed.ac.uk">rebecca.watson@ed.ac.uk</a>                 | 110 |
| Richa        | Joag          | <a href="mailto:richajoag@gmail.com">richajoag@gmail.com</a>                         | 52  |
| Robert       | Griffin       | <a href="mailto:robgriffin247@hotmail.com">robgriffin247@hotmail.com</a>             | 54  |
| Roslyn       | Henry         | <a href="mailto:r01rch12@abdn.ac.uk">r01rch12@abdn.ac.uk</a>                         | 53  |
| Sarah        | Bouchemousse  | <a href="mailto:sbouchemousse@sb-roscoff.fr">sbouchemousse@sb-roscoff.fr</a>         | 55  |
| Saskia       | Wutke         | <a href="mailto:wutke@izw-berlin.de">wutke@izw-berlin.de</a>                         | 109 |
| Silvio       | Waschina      | <a href="mailto:silvio.waschina@uni-jena.de">silvio.waschina@uni-jena.de</a>         | 111 |
| Simon        | Uphill        | <a href="mailto:sjuphill@hotmail.com">sjuphill@hotmail.com</a>                       | 57  |
| Sophie       | Reichert      | <a href="mailto:reichert.sophie@gmail.com">reichert.sophie@gmail.com</a>             | 56  |
| Stefania     | Meconcelli    | <a href="mailto:stefania.meconcelli@unito.it">stefania.meconcelli@unito.it</a>       | 114 |
| Tanya        | Pennell       | <a href="mailto:t.pennell@sussex.ac.uk">t.pennell@sussex.ac.uk</a>                   | 113 |
| Tess         | Driessens     | <a href="mailto:tess.driessens@ua.ac.be">tess.driessens@ua.ac.be</a>                 | 112 |
| Timotheé     | Bonnet        | <a href="mailto:timothee.bonnet@ieu.uzh.ch">timothee.bonnet@ieu.uzh.ch</a>           | 115 |
| Uttaran      | Maiti         | <a href="mailto:uttaranmaiti@gmail.com">uttaranmaiti@gmail.com</a>                   | 37  |
| Valentina    | Botto         | <a href="mailto:valentina.botto@unito.it">valentina.botto@unito.it</a>               | 36  |
| Virginie     | Thuillier     | <a href="mailto:virginie.thuillier@uclouvain.be">virginie.thuillier@uclouvain.be</a> | 70  |
| Wolfgang     | Reschka       | <a href="mailto:wolfgang.reschka@helsinki.fi">wolfgang.reschka@helsinki.fi</a>       | 94  |
| Yun          | Huang         | <a href="mailto:yun.huang@evolbio.mpg.de">yun.huang@evolbio.mpg.de</a>               | 95  |



---

'It is not the strongest or the most intelligent  
who will survive but those who can best  
manage change.'

Charles Darwin

---

## Organising committee



**Siobhan O'Brien (president)**

My PhD looks at the evolution and ecology of social behaviour in pseudomonad bacteria. Specifically, whether rapid evolution of social interactions are important in 'natural' settings, and if it can have a significant impact on the structure and function of natural microbial communities.



**Beatrice Downing**

I study social behaviour by chasing wild geese across England and am interested in intraspecific variation, its causes, evolution, and effects at group, population and landscape scales. My PhD uses social network analysis to decipher patterns in social groups and links these to disease parameters. The ultimate aim is to elucidate disease transmission in a wild, heterogeneous population.



**Christopher Beirne**

I am exploring the causes of variation in senescence rates in the European Badger using a combination of molecular lab work and longitudinal database analysis. I also try and sneak in a bit of citizen science and Neotropical herpetology when my supervisor isn't looking! Twitter @Chris\_Beirne.

### David Fisher

The social encounters an animal has affect everything from its behaviour to its fitness. By watching every move a cricket makes in its entire life, I hope to understand how what you do determines what kids you have and how you affect the wider community. Roll cameras, its big-bug brother!



### Emma Wood

My PhD focuses on how social environment affects ageing rates of a cooperatively breeding bird, the white-browed sparrow weaver. I am investigating age-related declines in performance and the roles that telomere dynamics and immunosenescence play in mediating such declines.



### Eoin Duffy

I investigate aspects of sexual selection and sexual conflict using the fruit fly *Drosophila simulans*. One of the fundamental questions in evolutionary biology concerns the adaptiveness of sexual selection; does sexual selection reinforce or act in opposition to natural selection? Utilizing experimental evolution techniques I examine the combined and independent effects of natural and sexual selection during adaptation to a novel, stressful environment. I am also investigating different aspects of intralocus sexual conflict in my model species





**Helen Leggett**

I work on the evolutionary ecology of microbes by primarily studying evolution in real-time in controlled lab experiments (experimental evolution) with various strains of bacteria (*Pseudomonas spp.*) and viruses (bacteriophages). My research focuses on social evolution and virulence in parasites.



**Katy Scott**

I study the behaviour and physiology of meerkats in zoos, and find the differences between captive and wild animals fascinating. I worked at Paignton Zoo in Devon during and after my bachelor's degree at the University of Durham, and then continued using zoo-based research in my PhD at the University of Exeter.



**Lindsay Walker**

I am fascinated by apparently 'altruistic' behaviours - why help others at a cost to yourself? I aim to examine the mechanistic underpinning of the considerable variation in individual contributions to cooperative behaviour using the white browed sparrow weaver (*Plocepasser mahali*) as a model system.

### Lucy Ovens

I am a first year PhD student studying the social networks of badgers, researching how social behaviour impacts disease dynamics. I hope to use this information to test the efficacy of alternative bovine tuberculosis control strategies.



### Matthew Silk

I'm a behavioural ecologist using social network analysis to investigate fission-fusion social dynamics in a population of light-bellied brent geese. Frequent trips to cold, wet places are used to study social network structure in staging populations of this long distance migrant, hoping to explore the link between site use, sociality, behaviour, condition and success.



### Martin Grunnill

My research is in vertical transmission of viruses (transmission from parent to offspring) and disease persistence. I study a moth (*Plodia interpunctella*), virus system in the lab, which I use to test theory. As well as vector borne diseases (such as Dengue), through mathematical models and possible field work.





**Michael Hawkes**

My PhD will explore intralocus sexual conflict (IASC) over insecticide resistance in the fruit fly *Drosophila melanogaster*, where resistance is conferred by upregulation of the cytochrome P450 gene Cyp6g1. This upregulation is caused by transposable element-derived enhancer sequences inserted upstream of Cyp6g1. I aim to elucidate the mechanism of this IASC and understand its evolutionary consequences. Twitter @mfhawkes



**Robyn Manley**

Viruses are important pathogens of honeybees, but have recently been discovered in bumblebees and other pollinators. I am researching the factors that influence transmission and disease emergence. These factors include host-specificity and pathogenicity of viruses, host phylogenetics and ecology, and host-virus co-evolution.

### **Sarah Paul**

My PhD focuses on the costs of chemical defence in the context of intraguild predation, using the native/ naturalised 2-spot ladybird and 7-spot ladybird and the invasive harlequin ladybird as a study system. The main aim of my research is to understand the intrinsic and extrinsic factors that affect the levels of toxins in individuals, and the costs and benefits associated with being toxic.



### **Sheridan Willis**

I research intra-locus sexual conflict in Indian meal moths. Although sexual dimorphism has evolved in these moths, there is still strong evidence for conflict over life-history traits. I will be looking at the mechanisms that may help overcome this conflict, such as sex-biased gene expression.





---

'Nothing in biology makes sense  
except in the light of evolution'

Theodosius Dobzhansky

---

## Invited speakers

**Dr. Andy Gardner**

University of Oxford, UK



Andy is a Royal Society University Research Fellow at the Department of Zoology at the University of Oxford. His work is on Darwinian adaptation, addressing fundamental questions such as whether natural selection explains the appearance of design in the living world, at what level this design is expected to manifest itself – gene, individual, society – and what its function is? Using a wide range of biological systems such as viruses, bacteria, protozoa, crustaceans, insects, fish and humans he develops general theory on the topics of inclusive fitness and multilevel selection, and also tailors general theory to the biology of particular species to facilitate empirical testing. There has been significant media interest in his recent collaborative work applying evolutionary genetics theory to the controversial Cosmological Natural Selection hypothesis.

**Tuesday 3rd 18:00 - 19:00**

**Dr. Tom Currie**

University of Exeter, UK



Tom is a Post-Doctoral Research Fellow and lecturer in cultural evolution at the University of Exeter, having recently moved to Exeter from University College London. Tom's research utilizes evolutionary theory and methods from biological sciences to understand human behavior and evolution. In particular his interests lie in testing hypotheses about human pre-history and cultural evolution using quantitative techniques such as phylogenetic methods. His research examines how cultural traits and societies change over time, and also what ecological and social factors drive the evolution of social and political organization. Some of this research involves global-scale analyses, while other aspects have focused on Island Southeast Asia and the Pacific and sub-Saharan Africa, which represent ideal testing grounds for comparative studies of social and cultural evolution. Furthermore Tom is also interested in practical applications of his research to aid in the development of social policy to help solve real-world problems.

**Wednesday 4th 09:00 - 10:00**

**Professor Johanna Mappes**

University of Jyväskylä, Finland



Johanna is a Professor of Evolutionary Ecology at the University of Jyväskylä, Finland. Her work is rooted in evolutionary ecology and biological interactions. In recent years Johanna's research has focused on studying aposematism and mimicry, particularly studying interspecific interactions associated with the evolution of warning signals and mimicry in chemically defended prey. Research areas also covered by Johanna and her team include parental care, the evolution of bacterial virulence and the evolution of sexual and asexual reproduction. Her study animals include moths, snakes, birds and beetles. Johanna and her research team have also extensively described sexual selection in the drumming wolf spider.

**Wednesday 4th 14:00 - 15:00**

**Professor Geoff Parker**

University of Liverpool, UK



Geoff is a Fellow of the Royal Society and Emmiritis Professor of Biology at the University of Liverpool. He has made so many significant contributions during the course of his career to evolutionary biology and behavioural ecology that we cannot list them all here! Notable firsts include: introducing the concept of sperm competition, theoretical analysis of sexual conflict, and the first theory explaining the evolution of anisogamy. He has done extensive work on applying game theory to various biological problems. Geoff's broad research interests include: sperm competition, evolution of the two sexes, evolutionary theory of sexual conflict, mating strategies, sexual selection, competitive mate searching, competitive resource use and animal distributions, coercion and punishment, evolution of sibling rivalry and intra-familial conflict, and the evolution of complex life cycles in helminthes. In 2008 he won the Darwin Medal for his lifetime contribution to the foundations of behavioural ecology.

**Thursday 5th 10:00 - 11:00**

**Professor Laurent Keller**

University of Lausanne, Switzerland



Laurent is an evolutionary biologist, myrmecologist and a Professor of Evolutionary Ecology at the University of Lausanne in Switzerland. His research has made significant contributions to the study of eusociality in ants. At the University of Lausanne his research group aims to ‘understand the principles governing the evolution of animal societies and the ecological and evolutionary consequences of social life’. The numerous topics his research covers include understanding genes associated with aging, experimental tests of kin selection theory and understanding the genetic, ecological and molecular bases of transitions in social structure. Laurent and his team have recently sequenced the fire ant genome, an important step in addressing questions related to social behavior and aging.

**Thursday 5th 18:00 - 19:00**

**Professor Judith Mank**

University College London, UK



Judith is Professor and Chair of Evolutionary and Comparative Biology at University College London. At UCL her research group focuses on how selection acting on a phenotype enacts change within the genome by applying population and molecular genetic tools to genomic and transcriptomic data. Using avian and insect models her research includes genome and transcriptome evolution, examining gene expression patterns associated with sexual conflict and the different ways that the genome responds to selection. She has collaborated in examining the evolution of alternative sex-determining mechanisms in teleost fishes. Judith's current research projects include investigating the genomic and transcriptomic locus of sex-specific selection in birds and the expression of the chicken W chromosome and the evolution of female phenotypes.

**Friday 6th 09:00 - 10:00**



**Professor Troy Day**  
Queens University, Canada



Troy is a mathematical biologist specializing in evolutionary ecology and a Professor at Queen's University in Kingston, Canada. His broad areas of interest include evolutionary medicine, genomic conflict, imprinting, sexual selection and sexual conflict. Troy's research focuses on developing theory to explain the evolution of the genotypic and phenotypic attributes of individual organisms, as well as the evolution of intra- and inter-specific interactions between these organisms. He is the co-author of the text book 'A Biologist's Guide to Mathematical Modeling' a required read and reference book for any biologist interested in applying mathematics to biology.

**Friday 6th 14:00 - 15:00**

**Dr. Paula Stockley**  
University of Liverpool, UK



Paula is a reader in Mammalian Behaviour & Evolution at the Institute of Integrative Biology at the University of Liverpool's Leahurst Campus. Her research, primarily using mammals such as bank voles, mice and shrews but also fish and insects aims to explain the diversity in animal reproductive traits. Her work has made significant contributions in describing the mechanisms and evolutionary consequences in sperm competition biology. Paula also has broad interests in the fields of behavioural and evolutionary ecology relating to reproductive strategies, life history evolution and social behavior. Other research areas covered in her work include chemical communication in rodents, the evolution of parental care in mammals and welfare of laboratory animals.

**Saturday 7th 09:00 - 10:00**

**Dr. Britt Koskella**

University of Exeter, UK



Britt is a Postdoctoral Independent Research Fellow at the University of Exeter. She is an evolutionary biologist whose research is primarily on host - parasite co-evolution and the effects of parasitism on population dynamics. Her work combines laboratory based experimental evolution techniques with field studies of natural interactions between hosts and pathogens. She has examined host-parasite co-evolution between fungi and plants as well as trematodes and snails. Britt's recent work has incorporated controlled selection experiments and surveys of natural populations to explore the influence of environmental heterogeneity on the trajectory of coevolution for a tri-trophic interaction between plants, plant-pathogenic bacteria and lytic bacteriophages.

**Saturday 7th 14:00 - 15:00**



---

'Perhaps our greatest distinction as a species  
is our capacity, unique among animals, to  
make counter-evolutionary choices.'

Jared Diamond

---

Wednesday

## Testing theories of sex determination in houseflies *Musca domestica*

Sex determination is a universal developmental process ranging from unicellular organisms to humans. Nonetheless, sex determination mechanisms are not evolutionarily conserved, but are bewilderingly diverse and have rapid turnover rates during evolution. Evolutionary biologists seek explanations for this conundrum. What drives the evolution of the diversity behind such a fundamental developmental process with the same outcome: two sex types, male and female? The genetic mechanisms and regulation of sex determination, as well as the evolutionary processes responsible for the observed variation by applying the latest genomics technology in housefly (*Musca domestica*) genetics. The housefly is an exceptional organism in having populations with different sex determination mechanisms, including the standard male heterogametic (XX-XY) system, location of the dominant male determiner (M) on different autosomes, or female heterogamety. We will exploit the Housefly Genome Project to develop dense marker linkage maps and identify candidate genes for functional analyses. Results are expected to lead to a better understanding of the mechanisms and evolution of sex determination systems and early stages of sex chromosome evolution.



**Akash Sharma**

University of Groningen

1st year PhD student

## Genomic diversity within managed spruce stands

Forest trees are drivers of community and ecosystem processes. By extension, their genotypes comprise a key ecological property involved in community diversity, structure, and persistence. In principle, genetically-sound silvicultural practices should not impose directional selection, impede natural admixture and migration, nor cause a loss of genetic diversity. While sustainable forest management recommendations establish criteria to ameliorate potential evolutionary consequences of harvest, little is actually known about the patterns of genetic diversity arising from currently employed techniques. To address this knowledge-gap, we are conducting a high-throughput, landscape-level study of Norway spruce genetic structure and diversity. Primeval forest and managed stands subjected to contrasting silvicultural treatments and regeneration strategies will be sampled to allow comparison of genetic diversity resulting from varying stand histories. In addition, recently colonized Baltic island populations of different ages and sizes will provide a reference model to which spatial genetic structure in reforested spruce stands can be compared. These populations will be genotyped via exome sequencing and an association-genetics approach will be used to identify genetic polymorphisms putatively involved in edaphic and climatic adaptation. Together, these data will be used to assess whether current and putatively sustainable management techniques successfully avoid imposing directional selection, genetic drift, and reproductive isolation.

**Alexis Sullivan**

Umeå University  
1st year PhD student





## Uncoupling to survive? Lessons from an experimental study in zebra finches.

The understanding of ageing and lifespan determinants has always been of tremendous interest both for evolutionary biologists and gerontologists. In this context, oxidative stress (i.e. the imbalance between the production of reactive oxygen species (ROS) during normal energy processing and the level of antioxidant defences) has been suggested as a key determinant of ageing. Mitochondrial uncoupling (i.e. a decreased efficiency to produce ATP per unit of O<sub>2</sub> consumed) has been suggested as a way to reduce ROS production and therefore ageing rate. Because resources are limited, life-history theory predicts a trade-off in terms of resources allocation between key life-history traits. In this context, our goal was to investigate if mitochondrial uncoupling might be an effective way of reducing oxidative stress in birds, and if such an increased energy allocation toward self-maintenance will be associated with a decreased allocation in other life-history components (e.g. reproduction). Adults zebra finches (*Taeniopygia guttata*) treated chronically with an artificial uncoupler (2,4-Dinitrophenol) exhibited elevated ( $\approx +15\%$ ) resting metabolic rate on the long-term. Unexpectedly, oxidative stress levels remained similar to those of control birds, and similarly reproductive investment was not affected by the treatment. Our study illustrates that the “uncoupling to survive theory” validated in mammals does not seem to apply for birds, since an experimental uncoupling did not influence oxidative stress. Considering remarkable characteristics of birds (long lifespan, high metabolism, high body temperature), our study raises the question of a natural uncoupling state of birds, which could contribute to explain the inefficiency of our un-coupling treatment.



**Antoine Stier**

University of Strasbourg  
3rd year PhD student

## Evolutionary study of Gnetum (Gnetales)

Gnetum comprises about 40 species of evergreen trees or lianas in rain forests of Asia, Africa and South America. They are superficially similar to angiosperms in gross vegetative morphology with broad pinnate-veined leaves, but their close affinity to the other members of the gymnospermous group Gnetales is clearly supported by molecular data as well as reproductive morphological data. The study will focus on evolutionary diversification patterns, pollination biology and biogeography of Gnetum and will be based on molecular laboratory work as well as field studies and experiments. A key to all further studies of evolution is a well-resolved phylogeny of the group of interest and I will therefore start there. I aim to resolve phylogenetic relationships within Gnetum and make a first assessment of species delimitations, using a dense sampling of taxa (all extant species and several specimens of each whenever possible), and molecular data from seven loci (18S, 26S, ITS, matK, rbcL, and trnL-F). The major aims of this first part are: a) to test classification schemes in Gnetum and the generally poorly supported phylogenetic results of previous molecular studies. b) to test the monophyly of species and resolve the systematic position of species not included in previous studies.

**Chen Hou**

Stockholm University  
2nd year PhD student



## Survival of the “fittest”? Comparing patterns of physical aging between captive and wild gray mouse lemurs (*Microcebus murinus*)

Physical aging often manifests as a decline in body mass, caused mainly by the loss of muscle mass. Decreases in strength and body condition can impair functioning but the actual implications of these processes depend on the individual's environment and can be different for the sexes. In this study, we compare the age trajectories of physical condition between the natural situation and the neutral, safe conditions of captivity by measuring two indicators of physical condition (long term body mass data and cross-sectional measurements of physical strength) in captive and wild gray mouse lemurs (*Microcebus murinus*) of both sexes. The results indicate significant differences between the environments and between sexes in survival and in the maintenance of physical condition into old age. In captivity, where most environmental stressors are absent, both sexes can survive to old age and exhibit a decline in muscle strength with age. Additionally, in captive males but not in females, body mass and the ability to regain mass are impaired at old age. In the wild, only very old females show declined body mass and strength, while in males the body mass decline begins in midlife. A greater proportion of males than females disappears from the population by the average age of peak physical performance. This discrepancy between captive and wild animals suggests that environmental stressors may accelerate senescence and promote selective mortality of senescent individuals. The earlier onset of senescence in males may reflect differing life history strategies between the sexes.



**Anni Hämäläinen**

University of Göttingen  
3rd year PhD student

**Do dispersing and philopatric individuals exhibit similar responses to changes in their flight costs? An experiment in the collared flycatcher *Ficedula albicollis*.**

The role of oxidative balance in shaping life histories has been recently re-emphasized. Studies of wild populations have indeed shown that oxidative balance could create trade-offs between life-history traits and mediate environmental effects, through macromolecular damage and modification of cell-signalling pathways. However, the question remains whether metabolism could functionally link behavioural choices and life-history strategies. Potentially, lifelong metabolic differences in relation to behaviour could generate different senescence dynamics and thus different selective pressures on major life-history traits. Behaviour would not only indirectly impact life histories through physical and biotic environment, but also directly through physiology. The aim of my project is to investigate whether dispersal, i.e. the movement of individuals between breeding sites, could be physiologically related to life-history strategies. Not only a key process in determining breeding environment, dispersal is also a good candidate to study the integration of behaviour and life-history traits through oxidative stress. In fact, recent studies have linked dispersal to other phenotypic traits. Typically, dispersers exhibit higher levels of aggressiveness, exploration, hormone production and immunity. All these traits are energetically demanding. Because energy production through proton-motive force produces oxidative compounds, dispersal might be associated with a shift in oxidative balance. To characterize the metabolic correlates of dispersal, I tested how breeding birds respond to an experimental manipulation of their flight costs, in a naturally fragmented population of the collared flycatcher *Ficedula albicollis*. I will specifically report on differences in metabolism, oxidative balance, reproductive success and local survival between dispersing and non-dispersing individuals following such manipulation.

**Charlotte Récapet**

University Claude Bernard - Lyon 1 //  
University of Lausanne  
2nd year PhD student



## Heritability of secondary sexual traits under favorable vs. unfavorable environmental conditions

Sexual signals have an important function both in intra-sexual and inter-sexual communication, because they allow to assess the quality of a competitor or a mate. In order to ensure effective communication, such signals must be reliable, i.e. they must provide honest information about the sender. These traits can be inherited, but it is well known that heritability of traits can be different under adverse vs. favorable conditions. Some reviews have demonstrated that heritability is usually lower under stressful conditions and that life history and behavioral traits tend to have lower heritability than morphological traits. However, the empirical evidence about heritability of secondary sexual traits under different ecological conditions has not been systematically reviewed yet; therefore, a comprehensive framework for such problem is still lacking. Thus, the aims of this work are: (1) to investigate how favorable vs. unfavorable environmental conditions affect the heritability of secondary sexual traits, and (2) to discuss how these trends can impact on the maintenance of secondary sexual signal reliability and on the dynamics of evolutionary processes. I will pursue these goals by performing both a “vote counting review” and a meta-analysis on the available published data about the subject.



**Valentina Botto**

University of Turin

1st year PhD student

## Exploratory performance of artificially selected bank voles in an Open field test

Among the various theories about evolution of complex physiological adaptations, one of the most recent one propose that such evolution could be driven by natural selection acting primarily on behaviour. Behavioural traits interpreted as "personality" of individuals, influence habitat preference, attitude to novel objects or situations, which in turn could lead to the variation in physiological traits such as metabolic rate; however, empirical evidence for the hypothesis remains ambiguous. To test such a hypothesis, an open field environment is a popular experimental condition to assess anxiety and exploratory drive in a quantitative manner. Open field is a novel situation to semi fossorial rodents like bank voles (*Myodes glareolus*). By measuring performance in such novel environment we can estimate 'proactive' or 'reactive' personality, in bank voles selected for high aerobic metabolism (A), predatory tendencies (P), ability to grow on low quality herbivorous diet (H), and unselected control (C). The working hypothesis is that the selection lines will differ in exploratory performances. One of the main predictions is that A-line individuals, which have high locomotor activity, will also score high in exploratory behaviour when compared to the control (C). P- line individuals, which are also hyperactive in cages, and often aggressive may show high exploratory behaviour as well. However, the H-line individuals may show lesser exploration. This is equivalent to testing the hypothesis that personality traits are heritable and genetically correlated with the traits under selection.

**Uttaran Maiti**

Jagiellonian University  
2nd year PhD student



## Sex, diet, health and lifespan: the role of antagonistic pleiotropy in the fruit fly, *Drosophila melanogaster*

Ageing is the intrinsic deterioration of individuals over time, reflected in populations by an increased likelihood of mortality and a decline in reproductive output. In evolutionary terms ageing can be considered as the declining strength of natural selection on genes which show Antagonistic Pleiotropy, that is opposing beneficial and deleterious effects of single genes over the lifetime of an organism. An example is a single gene with beneficial effects early in life on growth and reproduction but deleterious later life effects on healthy ageing. Where the benefits outweigh the costs, in evolutionary terms, these genes persist, allowing the surprisingly high occurrence of genes linked to later life problems and pathologies. In the work presented we extend the mechanistic idea of Antagonistic Pleiotropy to mismatched environments, to investigate the interplay between phenotype and early versus late life environment. The Thrifty Phenotype hypothesis proposes that mismatches between the environment adapted to in early life development and that experienced in adult life can influence later susceptibility to disease and lead to later life pathologies and reduced fitness. Using the powerful model system, fruit fly *Drosophila melanogaster*, we test this hypothesis. The fitness effects on adult reproductive output and lifespan in populations which experienced a mismatched in nutritional environment between larval diet and adult diet were compared with populations maintained on a constant nutritional environment over lifetime. The results from this work will be presented and plans for future work, involving experimental evolution, briefly outlined.



**Elizabeth Duxbury**

University of East Anglia  
1st year PhD student

## Tracing the origin and spread of the freshwater planarian genus *Dugesia* (Platyhelminthes, Tricladida, DugesIIDae)

*Dugesia* is a genus of freshwater flatworm best known because its regeneration capacities and its triangle-shaped head, being frequently depicted in text-books. Beyond this, *Dugesia* is the most specious member of the DugesIIDae family with almost 80 known species, and there probably are many more to be discovered. Freshwater flatworms are animals of slow dispersion, depending on contiguous freshwater bodies to survive and spread. However, *Dugesia* species present a wide distribution range, including Africa, Europe, Middle East, Oriental Region, Far East and Australasia. Some researchers have speculated that *Dugesia* has an African origin, placing it in a post-Gondwana scenario, when Africa and South America were split (130-100 Mya). But the origin of this genus could be even older, taking into account that Madagascar, inhabited by three endemic *Dugesia* species, was split from Africa much before (183-158 Mya). In this case, the present absence of this genus in South America could be explained by geographical barriers already present in Gondwana before its breakup or by a posterior *Dugesia* extinction. After the closure of the Tethys Sea, *Dugesia* would have spread into Palaearctic and towards eastern Asia. Up-to-date, the molecular phylogeographic studies of these animals have been limited to the Mediterranean Basin. Here we have expanded the range of study to different localities along its whole distribution range. By the use of molecular data, we have investigated where and when *Dugesia* appeared and how their species have dispersed through all the present distribution.

**Eduard Solà**

University of Barcelona  
4th year PhD student





## Trans-generational immune priming via mouthbrooding in African cichlids

Trans-generational immune priming (TGIP), i.e. the non-genetic transfer of immunity from parents to offspring, is widely acknowledged in vertebrates and invertebrates. TGIP serves to protect the newborn in a phase where its own adaptive immune system is not yet fully developed. TGIP was so far suggested to be limited to mothers, because eggs are as opposed to sperm large enough for the transport of antibodies and as offspring is usually born in the maternal environment and thus exposed to a similar parasite pressure as the mothers. In systems with paternal or bi-parental care, however, this pattern may be challenged. Recently, we demonstrated that in sex-role reversed pipefish *Syngnathus typhle* both maternal and paternal transfer of immunity exists, potentially via the paternal placenta-like structure during male pregnancy. Species with intense paternal care such as some mouth brooding cichlids are potentially exposed to similar selection pressures as sex role reversed species, which could have resulted in the parallel evolution of bi-parental TGIP. With a cross-fostering experiment we want to assess transfer of immunity via bucal mucosa of cichlids. In a second experiment we aim to examine whether TGIP can occur from both parents via mucosa. These results could potentially allow the comparison of two model systems with bi-parental TGIP (pipefish and cichlids) to answer questions about the costs and benefits for the parents as well as the mechanisms behind bi-parental TGIP.



**Isabel Salome Keller**

Geomar - Helmholtz Centre for Ocean Research Kiel  
1st year PhD student

## Potential role of hoverfly – plant species interaction in sympatric speciation of the pea aphid complex

The pea aphid (*Acyrtosiphon pisum*) complex is a well studied model for sympatric speciation. It consist of at least 11 genetically distinct host races which are native to specific host plants, but can all develop on the universal host plant *Vicia faba*. The factors that gave rise to and maintain these host races are not yet known. If natural enemies prefer certain plants for prey searching or oviposition, this might cause aphids to favour other plants (enemy free space) as hosts and thus help to maintain the host races. The attractiveness of a certain plant for natural enemies might depend on plant architecture, volatile profile and chemical composition which may alter the nutritional value and toxin content of aphids, thereby influencing natural enemy performance. We tested for the existence of enemy free space by exposing three pea aphid host races feeding either on their respective native host plants, *Medicago sativa*, *Trifolium pratense*, or *Pisum sativum*, or on the universal host plant to natural predator populations in the field. For each aphid host race we found a strong oviposition preference of hoverflies (*Episyrphus balteatus*) for the universal host plant. Since hoverfly larvae are important aphid predators we conclude that they may force pea aphids to use other hosts. Now we are investigating the cause of this enemy free space and weather it is temporally stable to evaluate its importance in the process of sympatric speciation of the pea aphid complex.

**Ilka Vosteen**

Max Planck Institute for Chemical Ecology  
3rd year PhD student



## Size-assortative mating in the ant *Myrmica ruginodis* and its implication for speciation

Size-assortative mating occurs widely in animals - increasing the frequency of desirable traits and enhancing fitness. In queens of the myrmecine ant *Myrmica ruginodis*, two distinct morphs exist, larger (macrogyne) and smaller (microgyne) queens. However, whether the occurrence of these morphs is maintained by size-assortative mating is unknown. Females are considered to choose their mating partner during nuptial flights, while males compete over females and large males usually regarded as higher quality will find a mating partner more likely. Nevertheless, whether a bi-modal size distribution exists in males at all, and whether small males participate in a nuptial flight has not been confirmed so far. To test whether assortative mating occurs in the two queen-morphs in *M. ruginodis*, individual males as well as males and females engaged in copula were collected during nuptial flights, and measured for size. Furthermore, queens of excavated nests and their offspring were analyzed to investigate if size characteristics are heritable and therefore fulfill preconditions for an on-going speciation. We investigated whether size-assortative mating occurs for the mating couples, as well as if spatial and temporal isolation of macrogyne and microgyne morphs during the mating flights exist. This study provides insight into the composition of nuptial flights of *Myrmica ruginodis* and their mating behavior in connection to the queen size dimorphism and its implications on speciation in this ant.



**Jana Wolf**

University of Helsinki  
2nd year PhD student

## Playing with dispersal rules: Which strategies are selected according to the landscape and do they promote connectivity?

Dispersal, i.e. individual movements away from their native population, is a key process in ecology. Since it allows gene flow among populations, dispersal is of primary importance for meta-population long-term persistence. Dispersal can be seen as a three-stage process with departure, transience and settlement, and natural selection can thus fashion dispersal at several stages. Though lot of work has been done already to study the emigration process, little is known about what shapes the transience and settlement stages, how it links to emigration, and how this can impact population connectivity. Particularly, some traits can prove to be beneficial for individual's success, but detrimental at the (meta-)population level. For example, one may predict that a higher perceptual range, both with a high settlement probability, would increase local connectivity but decrease long-distance dispersal. It is then crucial to obtain a more precise understanding about the evolution of dispersal to avoid bad management decisions in natural populations. Here, we first investigate the influence of perceptual range and other behavioural rules on connectivity in different landscape contexts, with a modelling approach. We then allow the evolution of traits to see what in the environment influences the evolution of dispersal syndromes, and the co-existence of distinct dispersal strategies. The model organisms we consider here are butterflies, but conclusions could be extended to other organisms.

**Gwennaël Bataille**

Université catholique de Louvain  
2nd year PhD student



## Analysis of MHC class I genes in Three-spined sticklebacks

The genes of major histocompatibility complex (MHC) are the most poly-morphic genes in vertebrates that encode for cell-surface proteins involved in the recognition of parasite-specific antigens. The evolution and maintenance of this extensive polymorphism are believed to be mediated by parasites. Parasites are major ecological agents that contribute to the divergence of host populations by imposing strong selection pressures. Different habitats support distinct parasite communities that mediate hosts to evolve varying local immunogenetic adaptation. The three-spined stickleback (*Gasterosteus aculeatus*) is a good model system to investigate parasite-mediated local adaptation mainly because of its wide distribution in both freshwater and marine ecotypes that harbour contrasting parasite communities. Extensive research has already been carried out in this species showing the significant role of MHC Class II genes in mate choice, kin recognition, and in elucidating parasite-mediated local adaptation. However, not much information is known about MHC class I genes which play an equally important role. Using three lake-river pairs and one ancestral marine population, we will first determine the MHC Class I allelic diversity and the bacterial communities of each of these populations. Secondly, we will correlate our findings from MHC Class I with what we expect to find in MHC Class II i.e., selection pressure exerted by intracellular parasites like bacteria on their host will also be reflected in the MHC Class I allelic polymorphism. For the determination of MHC Class I and II diversities and for identification of bacterial communities, we will use next generation sequencing strategy.



**Naga Apoorva Kasala**

Max Planck Institute for Evolutionary Biology

1st year PhD student

## A copulation induced mating window and adaptive mate choice strategies in the common lizard

Mate encounter rates may crucially constrain reproduction and are determined by the spatial distribution of potential mates, population density, and reproductive characteristics, such as length of the mating season and sexual selection. Annual breeders with a short time window for mating, may suffer more from reduced mate encounter than species in which females ovulate every month. On the other hand, evolution can favor adaptations to overcome situations of low mate encounter and guarantee reproductive success. Determining the existence of mating windows and reproductive strategies that allow mitigating their effects is essential for understanding interactions between mating systems and population dynamics. Here, we test the effect of time until mate encounter on female reproductive success and strategies, using the common lizard, *Lacerta vivipara*. In this species mating starts shortly after emergence from hibernation and previous work suggests it may be time limited. We determined date of emergence from hibernation, and manipulated time until mating and re-mating. We examined treatment effects on female copulation probability and mate choice. Results indicate a mating window exists, which is initiated at first copulation, since re-mating probability depends on the time passed since first copulation, but neither on emergence date, nor on time passed between emergence and first copulation. Additionally, longer time delay until mating reduced female choosiness, showing that females may hedge against remaining unmated. This strategy of adaptive choice, as well as the copulation induced mating window, may increase reproductive success in situations of reduced mate encounter.

**Merel Breedveld**

Museo Nacional de Ciencias Naturales (CSIC)  
4th year PhD student



## The effects of the intensity of begging to the life history traits of the parent in the burying beetle *Nicrophorus vespilloides*

According to life history theory, costly behaviours, such as parental care, are moulded by natural selection to maximise the fitness of the parent. For species capable of breeding more than once during their lifetime, investment in the current reproduction depletes the resources available for future reproduction, creating a trade off between the two events. The burying beetle, *Nicrophorus vespilloides*, provides elaborate parental care. The larvae solicit food from their parents with conspicuous begging displays. Previous studies have shown that larvae beg less as they become more proficient in feeding themselves, whereas the parent's response to begging does not change over time. Larval begging peaks 24 hours after hatching, after which they start begging less, until the behaviour ceases all together 72 hours after hatching. Thus the age of the larvae importantly affects the intensity of begging in a brood. I will be presenting data from an experiment where I manipulated the begging intensity parents are subjected to by manipulating the age of the larvae they were caring for, for a given amount of time, subjecting the parents to larvae that were constantly older or younger than their natural brood. The life history consequences for the parent were estimated by obtaining information on the parent's future survival and reproductive success. The aim of the study is to uncover how parent-offspring communication influences the trade off between current and future reproduction, as well as to determine whether the cessation of provisioning is under parental or larval control.



**Maarit Mäenpää**

University of Edinburgh

1st year PhD student

## Effects of fluoxetine on behavior of *Carassius carassius*

Fluoxetine is a selective serotonin reuptake inhibitor widely used as an antidepressant (Prozac, Sarafem) in clinical depression, eating disorders and many more. Fluoxetine was shown to be present in the discharge of waste water and surface waters in low concentrations up to 540 ng/l. In this study, the effect of fluoxetine, at realistic concentrations detected in the environment, on behavior of crucian carp (*Carassius carassius*) was examined. Crucian carp was exposed to a concentration of fluoxetine at 360 ng/l, 720 ng/l and 1440 ng/l for at least 30 days. To examine the chronic effect of exposure to this drug, four behavioral patterns have been examined: schooling, refuge seeking, reaction distance towards prey and feeding rate. Significant difference in the reaction distance with a small prey (juvenile *Daphnia magna*) was measured when comparing fish exposed to fluoxetine with the control group. The total amount of prey caught, and the number of juvenile and mature *D. magna* eaten by fish significantly differed between fluoxetine and control treatments. . During the experiments, fish changed their color repeatedly after transfer to the experimental tanks. Fish mimicked the color of the background. Fluoxetine effect on the rate of color in fish from different experimental groups will be also demonstrated.

**Małgorzata Grzesiuk**

University of Warsaw  
2nd year PhD student





---

## FLX experiment

It is by now well-established that sexually antagonistic genetic variation is important for the fitness in *Drosophila melanogaster* and data suggest that the X-chromosome should be enriched for sexually antagonistic genetic variation. So far investigation of the response of X-linked genetic variation to sex-limited selection has been done in males. The aim of my PhD is to test this response in a female-limited X-chromosome (FLX) experimental evolution experiment. The FLX experiment protocol will use female flies with a FM balancer chromosome that will force female-limited transmission of the X-chromosome. Based on results from the male-limited X-chromosome experiment, it is predicted that FLX females should have higher fitness than control females.



**Katrine Lund-Hansen**

University of Sussex

1st year PhD student

## **The effects of plasticity and local adaptation on spring phenology of UK plant species.**

Patterns of phenological change have been observed for numerous taxa, and in many plant species, spring flowering and leafing occurs earlier in warmer years. The timing of such events affects the biotic and abiotic conditions that individuals are exposed to, and consequently can impact on fitness. Long term changes in spring temperature may expose populations to conditions that they are less adapted to. Interactions between species may also be disrupted by changing seasonal timing, causing ecological mismatch. Using data from the UK Phenology Network, the effects of plasticity and local adaptation on spring phenological events of UK plant species can be investigated. Records of spring phenological events across the UK and over a period of years are combined with daily temperature data to find the optimal cues for seasonal timing. By examining the slopes of phenology over time and space it is possible to estimate the contribution of plasticity and local adaptation to different seasonal events. This can help identify populations locally adapted to temperature that may be at higher risk from shifts in climate. These techniques use data collected by citizen scientists to explore macroecological processes and look for signals of evolutionary change. A growing area of interest is how citizen scientists can be asked to collect more complex data. To answer questions on possible ecological mismatch in UK tree and understory species, I have developed a citizen science scheme, and will report on the pilot season of 'Track a Tree'.

**Christine Tansey**

University of Edinburgh  
1st year PhD student



## Sex chromosome transmission bias in a Mammal species with XY females, *Mus minutoides*

Mammals have an extremely conserved sex determination system (XY/XX) and any deviation from it usually leads to sterility. However, a dozen species harbour unconventional sex determination systems. In *Mus minutoides*, the African pygmy mouse, males are XY, and females XX, XX\* or X\*Y (the asterisk designates a sex reversal mutation on the X). Different approaches are used to understand the evolutionary causes and the mechanisms involved in the transition between the usual XX/XY and the weird system harboured by *M. minutoides*. One assumption about this system is that sex-ratio should be female-biased as some “potential males” are turned into females. Data from our laboratory colony reveals that the three types of females produce more males than expected under the Mendelian transmission hypothesis. Further investigation suggest that males mated with XX or XX\* females see their Y chromosome transmitted more often (Y transmission ratio: 0.75), whereas in couples with X\*Y females, male’s X chromosome is favoured (0.33). Previous theoretical studies showed that a sex chromosome distorter may induce change in the sex determination mechanism: we therefore believe the transmission distortion of males’ sex chromosomes may be involved in the evolution of the system. It is surprising to see that transmission of male sex chromosomes depends on the female’s genotype, and as far as we know, it’s the first time that such transmission distortion is documented. In order to gain more insight into the mechanisms involved and influence of each parent, different analyses (sperm-FISH, embryonic mortality analysis) are currently being carried out.



**Paul Saunders**

Université Montpellier II  
1st year PhD student

## Evolution of morphological diversity of extant sharks

Variation in overall external shape, fin morphology, jaws and jaw suspension determine the mode of locomotion and feeding in fishes. Biomechanical studies in fishes have focused on correlations of fin and tail morphology with types of locomotion and on correlations of jaw and hyoid arch morphology with feeding types. Sharks display an array of morphologically diverse forms. The combination of our biomechanical knowledge with the diversity of sharks species and available phylogenies provides a system for studying the evolution of ecomorphological diversity in marine vertebrates. The research goals comprise: (1) recording the range of diversity in morphological characters relevant to feeding and locomotory mechanics in extant shark species; (2) investigating the covariation between feeding mechanics and features of body shape important for locomotion (3) studying the distribution of this diversity through phylogeny. We use computed tomography (CT) scanning to produce 3D reconstructions of the jaw and hyoid arch of 47 extant shark species covering 16 families. To document the external body shape we use 2D digital photography of 62 species covering 14 families. Using 2- and 3D morphometrics we quantify functional aspects of the feeding and locomotory apparatus. Combining this data with phylogenetic comparative methods and ecological parameters shows functional evolutionary patterns of shape diversity. We compare the morphotypes to study their arrangement in the morphospace and use phylogeny to investigate phylogenetic signal. The results will provide a deeper understanding of the ecological indicators determined from morphology their influence on the evolution of sharks in their marine ecosystems.

**Pepijn Kamminga**

Naturalis Biodiversity Center  
2nd year PhD student



## Transcriptomics of adaptation in *Drosophila simulans* and *Drosophila melanogaster*

The main objective of this research is to study the molecular basis of adaptation to a thermally stressful environment, in the presence or absence of sexual selection. We are using a fully factorial design for experimental evolution of *Drosophila simulans* in replicate populations, in both standard (25°C) and novel (27°C) environments, with two different mating regimes in each environment. After 30 generations of experimental evolution, progeny flies will be used to identify genes whose expression patterns and sequence divergence are associated with thermal adaptation and the presence/absence of sexual selection. Instead of looking at global changes, we will focus on genes for accessory gland proteins (Acps); male reproductive tract proteins transferred to females during mating; which alter their reproductive physiology and behaviour. Additionally, we are studying gene expression levels of sex peptide, one of the Acps, in males from selection populations of *D. melanogaster* in which females do not express the sex peptide receptor. We want to study whether production of this sexually antagonistic protein is costly to males and also whether males compensate by increasing production of other Acps/ seminal proteins such as Ovulin and DUP99B, since these proteins have some overlapping functions with SP. RT-qPCR will be used to study gene expression levels of the Acps in males and ELISA to quantify the proteins transferred to the female reproductive tract during mating. This will indicate whether there is a correlation between gene expression levels and the amount of protein retained in the females an hour after mating.



**Richa Joag**

Jagiellonian University  
2nd year PhD student

## **Eco-evolutionary dynamics of range shifts: Evolutionary rescue and elastic margins**

It is widely recognised that the response of a population to environmental change will be determined by the eco-evolutionary dynamics of dispersal. In my recent work modelling the evolution of dispersal distance within a species structured across environmental gradients yielded some important general insights. In particular, the evolution of greater dispersal distances resulted in evolutionary rescue at a macro-ecological scale. However, critical survival thresholds exist; beyond which even the evolution of greater dispersal distance is unlikely to rescue a population. The position of such thresholds depends on a combination of demographic and environmental parameters. Should similar thresholds exist for real species aggressive conservation actions are likely to be required to reduce the risk of extinction. Despite their simplicity, models such as the one presented here, will be essential for providing a theoretical underpinning for more tactical eco-evolutionary modelling.

**Roslyn Henry**

University of Aberdeen  
1st year PhD student



## The shared genome is a pervasive constraint on the evolution of sexual dimorphism

Males and females share most of their genomes, and differences between the sexes can therefore not evolve through sequence divergence in protein coding genes. Sexual dimorphism is instead restricted to occur through sex-specific expression and splicing of gene products. Evolution of sexual dimorphism through these mechanisms should also be constrained, however, when the sexes share the genetic architecture for regulating gene expression. Despite these obstacles, sexual dimorphism is prevalent in the animal kingdom and commonly evolves rapidly. Here, we ask whether the genetic architecture of gene expression is plastic and easily molded by sex specific selection, or, if sexual dimorphism evolves rapidly despite pervasive genetic constraint. To address this question we explore the relationship between the intersexual genetic correlation for gene expression (rMF - which captures how independently genes are regulated in the sexes), and the evolution of sex-biased gene expression. Using transcriptome data from *Drosophila melanogaster* we find that most genes have a high rMF, and that genes currently exposed to sexually antagonistic selection have a higher average rMF compared to other genes. We further show that genes with a high rMF have less pronounced sex-biased gene expression than genes with a low rMF within *D. melanogaster*, and that the strength of the rMF in *D. melanogaster* predicts the degree to which the sex-bias of a gene's expression has changed between *D. melanogaster* and *D. simulans*. In sum our results show that a shared genome constrains both short and longterm evolution of sexual dimorphism.



**Robert Griffin**

Uppsala University  
2nd year PhD student

## Human-assisted contact between two cryptic species : invasion and hybridization within the complex *Ciona intestinalis* in the English Channel

Biological invasions are excellent model systems for studying on-going eco-evolutionary processes. The role of hybridization between native and introduced species has recently been highlighted as a potential important process to facilitate the establishment of invaders (adaptive introgression). In this context, the recently described species complex of the vase tunicate, previously known as *Ciona intestinalis*, is particularly relevant: type A (introduced in Europe) and type B (native) are morphologically similar but with 14% genome divergence and are shown to hybridize in the wild. We investigated the spatial occurrence of these two cryptic species in 11 populations along Brittany coasts in 2012, repeating the survey over two seasons. Both morphological criteria and diagnostic genes were used to monitor the presence of the two taxa. Type A corresponded to 5% of spring populations against 35% in autumn. This variation may indicate an overall increase of type A or a seasonal effect with different environmental optimum for the two taxa. The survey is pursued. A comparative population genetic study was also carried out using one mitochondrial gene. Low haplotypic diversity was observed in type A as compared to type B. This is supporting the hypothesis of a founder event in the introduced species, a scenario which is not commonly reported in invasive marine invertebrates. The work will be continued by an in-depth investigation of the genome diversity, by means of SNPs, to better describe the permeability of type A and type B genomes in the wild.

**Sarah Bouchemousse**

University Pierre et Marie Curie (Paris)  
1st year PhD student





## Telomere length inheritance in the king penguin (*Aptenodytes patagonicus*)

Evidence is accumulating that telomeres, a non coding repetitive DNA sequence triggering replicative senescence, could be implicated in different life history trade-offs. For instance, telomere length with which one starts in life has been recently shown to be linked with life-long survival at the individual level, suggesting that telomere dynamics can be a proxy of individual fitness and thereby be implicated in evolutionary trade-offs. To tackle this question, the first step is to quantify the importance of the heritable component that determines telomere length. In humans, the mode of telomere length inheritance appears to be paternal. Even though several studies focused on this matter in humans, only one examined it in birds. It shows that in the kakapo (*Strigops habroptila*), telomere length seemed to be maternally inherited, suggesting a heterogametic-related inheritance. We propose to test telomere inheritance in a population of king penguins, where both parents and the only chick can be both sampled early in life and followed over the growth period. We can then check paternal and maternal influence on chick starting telomere length, and followed how these relationships change with time over growth. We found that telomere length of the offspring was positively correlated with maternal telomere length. With this study, we confirmed that telomere length in birds is most likely maternally inherited. These results suggest that in birds, as in humans, telomere length is inherited from the heterogametic sex, but intimate mechanisms and evolutionary implications of telomere inheritance remains an open and stimulating question.



**Sophie Reichert**

University of Strasbourg  
3rd year PhD student

## Biological prerequisites of the reintroduction of endangered salmon populations with implications to captive breeding programmes

Atlantic salmon reintroduction programmes in the Baltic area are based on the assumption that generations in captivity have not reduced genetic variability or weakened fitness-related traits. However, recent studies by our research group and others have shown that this assumption is not valid. Genetic structures of animal populations are often altered and genetic variability reduced due to captive breeding. Studies on salmonid fishes have shown considerable deterioration of fitness-related traits due to genetic changes in captive breeding within few generations (Araki et al. 2008). Earlier studies have also indicated that hatchery fish are slower in switching to new prey (Olla et al. 1998; Sundström & Johnsson 2001) and slower to start feeding on natural prey (Vehanen et al. 2009) compared with wild conspecifics. Learning to forage efficiently is directly linked to brain size and structure in fishes (Kotrschal et al. 1998; Striedter 2005). Recent results of studies by our research group indicate that lowered genetic variability in the captive stock after few generations the hatchery leads to inferior development of salmon brains which consequently lowers ability to learn to forage on natural prey after wild release. The situation is only made worse by the unnatural standard rearing method. As the underlying mechanisms leading to dramatically reduced performance and survival of salmon released to the wild have been revealed, the focus is on the mechanisms producing maladaptive traits and how these mechanisms can be altered to produce salmon that are fit enough to allow re-establishment of new self-reproducing natural populations.

**Simon Uphill**

University of Helsinki  
1st year PhD student



---

'A man has no reason to be ashamed of having an ape  
for his grandfather. If there were an ancestor whom I  
should feel shame in recalling it would rather be a man  
who plunges into scientific questions with which he has  
no real acquaintance, only to obscure them by an  
aimless rhetoric....'

Thomas Henry Huxley

---

## Thursday

| Time        | Event                           |
|-------------|---------------------------------|
| 08:50       | coach to the Eden Project       |
| 10:00-10:10 | arrival and introduction        |
| 10:10-11:10 | invited speaker: Geoff Parker   |
| 11:10-13:00 | break and discussion groups     |
| 13:00-14:00 | lunch                           |
| 14:00-15:15 | workshop session 1              |
| 15:15-15:45 | tea break                       |
| 15:45-17:00 | workshop session 2              |
| 17:00-18:00 | break                           |
| 18:00-19:00 | invited speaker: Laurent Keller |
| 19:00       | dinner                          |
| 22:00       | coach to Penryn                 |

## WORKSHOPS AT THE EDEN PROJECT

We'll be at the Eden Project for the workshops, but there'll be time during the day to explore Eden's breathtaking biomes. One is the world's largest indoor rainforest, the other a Mediterranean paradise. Each is filled with thousands of plant species (and a few cheeky birds!), and realistically replicates their respective climates as you follow long and meandering paths through the greenery.

### **Open Access Publishing - Sponsored by BMC Ecology**

As the attitudes of funding councils, research institutions and journal publishers are shifting towards "Open Access", postgraduates and early career researchers need to fully understand its implications for their research, data storage and future career progression. This interactive workshop brings together the EMPSEB19 delegates, plenary speakers and expertise from the Open Exeter initiative in order to explore the costs and benefits of a fully "open" research community.

### **Public engagement - Sponsored by University of Exeter Catalyst Project**

Public engagement is becoming an increasingly important part of being a scientist. It is essential to be able to communicate your findings to a wide audience to educate and inspire people, as well as to secure funding for your future research. This event will involve an interactive workshop at the inspirational Eden Project, where delegates will develop and practice their skills of public engagement. In addition, on the Friday evening we have organised a public engagement event to be held at the National Maritime Museum in Falmouth. All delegates are invited. Many top scientists from the University of Exeter will be giving short, fascinating talks on science and evolution aimed at the general public. Excitingly, some of you will have the opportunity of putting what you've learnt at the workshop into practice by presenting a poster at this event and chatting to the public about your research.

**GROUP A***Open Access first, Public Engagement second*

|                      |                      |                     |
|----------------------|----------------------|---------------------|
| Akash Sharma         | Diamanto Mamuneas    | Merel Breedveld     |
| Alexis Sullivan      | Eduard Solà          | Naga Apoorva Kasala |
| Alson Cotton         | Elizabeth Duxbury    | Paul Saunders       |
| Anasuya Chakrabarty  | Eryn McFarlane       | Pepijn Kamminga     |
| Ann Kathrin Huylmans | François Renoz       | Richa Joag          |
| Anni Hämäläinen      | Gwennaël Bataille    | Robert Griffin      |
| Antoine Stier        | Ilka Vosteen         | Roslyn Henry        |
| Ben Ashby            | Isabel Mück          | Sarah Bouchemousse  |
| Benja Fallenstein    | Isabel Salome Keller | Simon Uphill        |
| Charlotte Récapet    | Jana Wolf            | Sophie Reichert     |
| Chen Hou             | Katrine Lund-Hansen  | Uttaran Maiti       |
| Christine Tansey     | Maarit Mäenpää       | Valentina Botto     |
| Christopher Culbert  | Małgorzata Grzesiuk  | Virginie Thuillier  |

**GROUP B***Public Engagement first, Open Access second*

|                       |                     |                     |
|-----------------------|---------------------|---------------------|
| Anna Campbell         | Julien Amouret      | Pascal Milesi       |
| Anne Winters          | Kati Saarinen       | Raïssa de Boer      |
| Charlie Ellis         | Konstanze Schiessl  | Ramith Nair         |
| Christopher Quickfall | Lien Reyserhove     | Rebecca Jones       |
| Dimitri Stucki        | Louise Christensen  | Rebecca Watson      |
| Gaëlle Pontarotti     | Lucas Marie-Orleach | Saskia Wutke        |
| Georgina Brennan      | Marie Rescan        | Silvio Waschina     |
| Isabel Winney         | Marine Pouget       | Stefania Meconcelli |
| Iwona Giska           | Mark Harrison       | Tanya Pennell       |
| Jenni Pavalala        | Martin Vallon       | Tess Driessens      |
| Joanna Sudyka         | Nina Wale           | Timothée Bonnet     |
| Jonathan Henshaw      | Nolwenn Fresneau    | Wolfgang Reschka    |
| Juan Ramirez          | Pablo Valverde      | Yun Huang           |

---

'The alternative to thinking in evolutionary terms is not to think at all.'

Peter B. Medawar

---

Friday



## Evolutionary trajectories in multivariate space

Adaptive evolution is influenced by the fitness landscape and by the amount of heritable variation. But traits do not occur in isolation, since they are often genetically correlated by pleiotropy or linkage disequilibrium. This causes non-independent inheritance that influences the response to selection. The additive genetic variance-covariance matrix  $G$  efficiently summarizes the intricate genetic structure and dependencies among trait and the general structure of  $G$  can be analyzed by spectral decomposition into eigenvectors. Adaptation will be facilitated if the leading eigenvector of  $G$  ( $g_{max}$ ) is aligned with the vector of selection, but when these vectors are not aligned then the response to selection will follow a curved trajectory towards the optimum. Our major interest lies in understanding by how much  $G$  influences evolutionary trajectories. There is a fairly large body of literature estimating  $G$  in a variety of different organisms. We here review the published studies on the alignment of the  $g_{max}$  with vectors of selection or divergence among closely related species with the aim to identify the general underlying patterns. We will also highlight and discuss persistent issues that arise from specific choice of traits in evolutionary analyses of  $G$  matrices and we will propose solutions to some of these issues.



**Anasuya Chakrabarty**

University of Bielefeld

1st year PhD student

## Expression of tissue-specific genes on the X-chromosome of *Drosophila*

Even though males and females of the same species often show large phenotypical and behavioural differences, they have almost the same genetic makeup. Most of these differences can thus be attributed to differential gene expression rather than difference in gene content. *Drosophila*, like mammals, has a XY sex determination system where females have two X-chromosomes and males have one X and one Y-chromosome. Sex chromosomes experience very different selective pressures compared to autosomes due to their unequal distributions among the sexes. In *Drosophila melanogaster*, genes with a male-biased expression are underrepresented on the X-chromosome. There are multiple hypotheses that try to explain this phenomenon but different experimental studies have produced contradictory results. One of them is the inactivation of the X-chromosome in the male germ-line. However, a recent study indicated that all tissue-biased genes might be underrepresented on the X-chromosome and thus, the phenomenon might not be explained by the sex-bias. I want to study the expression of tissue-specific genes according to their location in the genome. In order to do this, I use tissue-specific promoters that drive the expression of a reporter gene. These constructs are inserted into multiple places in the genome of *D. melanogaster*. This allows to compare the expression of the same construct on the X-chromosome and the autosomes. With this approach, I hope to clarify whether we can see lower expression on the X-chromosome compared to autosomes only for testis-biased genes or if the same phenomenon is observed for all tissue-biased genes.

**Ann Kathrin Huylmans**

Ludwig Maximilians University of Munich  
1st year PhD student



## STIs, mate inspection and the evolution of virulence

Our knowledge of the mechanisms that govern the evolution of pathogen virulence has greatly improved over the last 30 years, but much of the literature has taken virulence to be synonymous with host mortality, neglecting alternative disease outcomes. In particular, our understanding of the processes that shape the evolution of sterilising pathogens is poor. Non-sterilising pathogens may exhibit a trade-off between transmission rate and longevity, preventing the emergence of highly virulent strains, but this interaction will not apply to pathogens that target reproductive rather than vital organs. This leads to the conclusion that pathogens should evolve to castrate their hosts, making the relative scarcity of this disease outcome something of an enigma. To date, only three mechanisms have been proposed that can limit the evolution of virulence among sterilising pathogens: vertical transmission, spatial-structure and host investment in tolerance rather than resistance. Here I shall present another possibility in the context of sexually transmitted infections (STIs), namely mate inspection. Evidence suggests that STIs are more commonly associated with sterilisation and have lower mortality rates than infections transmitted via alternative routes, which makes sexual transmission a good target for this study. In addition, hosts should be under considerable pressure to avoid virulent STIs, which sets up the intriguing prospect of coevolution between STIs and mating behaviour.



**Ben Ashby**

Oxford University

3rd year PhD student

## Is hyperbolic discounting an adaptation for rate maximization?

In laboratory experiments, animals typically choose a small food reward delivered after a short delay over a larger reward delivered after a longer delay, but will reverse this preference when both delays are increased by equal amounts. This and related phenomena suggest that animals value delayed rewards according to what is called hyperbolic discounting. In the experimental setting such behavior is suboptimal, but it might be produced by a decision rule that is well adapted to natural environments. For example, Alex Kacelnik has proposed that hyperbolic discounting may lead a foraging animal to maximize its rate of energy intake. Kacelnik's proposal can be analyzed mathematically by making a very simple modification to a well-known model from optimal foraging theory. Under this model, it can be optimal to reverse preferences when both delays are increased by the same amount or when both rewards are multiplied by the same factor, both of which have been observed in experiments. However, it has also been observed that animals may change their mind after an initial delay if given an opportunity to do so, a feature which this model can not account for. In addition to this problem, I will discuss several other, well-known discrepancies between the empirical data on intertemporal choice and the adaptive explanation based on rate maximization.

**Benja Fallenstein**

University of Bristol  
1st year PhD student



## Predicting community dynamics

Studies of evolutionary responses to novel environments typically focus on a single species in isolation or pairs of interacting species. Although these studies generate vital information with regard to genetic mechanisms, all organisms co-occur with many other species, resulting in evolutionary dynamics that might not match those predicted using single species approaches. Using environmental communities of between five and seven bacterial species I will explore the effects of interspecific resource competition on species fitness and extinction risk in the laboratory using natural resources. By deconstructing each community down into monocultures, systematically testing each on separated parts of their environmental liquid matrices and then gradually reconstructing each community in stepwise fashion, I intend to test whether the dynamics of the whole community can be predicted through modelling pairwise interactions of all the communities' species. These experiments should provide novel results that contribute effectively towards our understanding of community dynamics. The ultimate goal is to formulate accurate predictive models, capable of anticipating community structure shifts with relation to environmental fluctuations.



**Christopher Culbert**

Imperial College London

1st year PhD student

## Fish sex & personality: Why do males make better decisions?

Variation is the fodder on which natural selection depends in order to shape evolutionary change. In many animals, individual differences in personality types have been observed and, further, been found to influence social behaviour. In the three-spined stickleback (*Gasterosteus aculeatus*), personality and sex were both found to influence decision-making speed and accuracy. Bolder fish made faster decisions than shyer fish and males were found to be both faster and more accurate than females. In this talk I will present these results and explore possible explanations for the selective maintenance of this variation in wild populations of fish.

**Diamanto Mamuneas**

The Royal Veterinary College  
2nd year PhD student



## **Influence of genetic relationship on the evolution of life history traits in different environments on *Tetrahymena thermophila***

In the context of global change, the individual has to cope to a fast variation of their environment. It could be achieved in some case by the association of life history traits conferring a benefit on their fitness. This talk aims to present the evolution of traits in different environments and the influence of genetic relationship on *Tetrahymena thermophila*. This presentation is divided in two parts. On one hand, the characterization of the phenotypic plasticity for several traits is shown on 44 genotypes through a gradient of temperature. This aims to know if the plasticity is similar between genotypes and between different traits. We could also determine if genotypes present different life styles, association of life history traits. On another hand, the life style is compared to the genetic distance between genotypes measured by molecular markers. It could offer the possibility to visualize if there is an influence of genetic relationship on life style and on the phenotypic plasticity.



**Virginie Thuillier**

Catholic University of Louvain

2nd year PhD student

## Male eyespan size is associated with meiotic drive in wild stalk-eyed flies (*Teleopsis dalmanni*)

This study provides the first direct evidence from wild populations of stalk-eyed flies to support the hypothesis that male eyespan is a signal of meiotic drive. Several stalk-eyed fly species are known to exhibit X-linked meiotic drive. A recent QTL analysis in *Teleopsis dalmanni*, found a potential link between variation in male eyespan, a sexually selected ornamental trait, and the presence of meiotic drive. This was based on laboratory populations subject to artificial selection for male eyespan. In this study we examined the association between microsatellite markers and levels of sex ratio bias (meiotic drive) in 12 wild *T. dalmanni* populations. We collected three data sets: a) brood sex ratios of wild-caught males mated to standard laboratory females, b) brood sex ratios of wild-caught females, and c) variation in a range of phenotypic traits associated with reproductive success of wild-caught males and females. In each case, we typed individuals for 8 X-linked microsatellite markers, including several that previously were shown to be associated with male eyespan and meiotic drive. We established that one microsatellite marker was strongly associated with meiotic drive. We also found that this microsatellite marker was strongly associated with male eyespan, with smaller eyespan males being associated with more female-biased broods. These results suggest that mate preference for exaggerated male eyespan allows females to avoid mating with males carrying the meiotic drive gene and is thus a potential mechanism for the maintenance and evolution of female mate preference.

**Alison Cotton**

University College London  
2nd year PhD student





## Metabolic rate as a proximate mechanism underlying life history strategies in flycatchers

Competitive exclusion can occur when closely related species inhabit the same geographic area, unless there is some type of niche differentiation. Collared and pied flycatchers are closely related sympatric passerine species that compete for nesting sites and other resources. These species have previously been shown to have a life history trade off between competitive interference in collared flycatchers and robustness to poor environments in pied flycatchers. These different life history strategies may promote regional coexistence, but proximate mechanisms underlying these strategies are unknown. We will test if the differences between pied and collared life history strategies are associated with differences in metabolic rate. Higher metabolic rate has previously been associated with higher competitive ability, faster growth rate and more resource use, traits that differ between collared flycatchers and pied flycatchers. Resting metabolic rate (RMR) of collared, pied and hybrid flycatchers, both chicks and adults, will be measured using respirometry during the breeding season on the Swedish island of Öland. We will test if metabolic rate is significantly different between species, specifically whether collared flycatchers have higher metabolic rates than pied flycatchers. We will also determine if metabolic rate is associated with growth rate and territory quality within and between species. Understanding the metabolic rate of closely related, hybridizing species could give insight into proximate mechanisms that facilitate life history strategies and regional coexistence.



**Eryn McFarlane**

Uppsala University

1st year PhD student

## Infection monitoring, tissue tropism and transmission dynamic of a free-living *Serratia symbiotica* strain in the pea aphid

Symbiosis with microorganisms is a common feature in insects. Among insects, bacterial symbionts of aphids are perhaps the best described. They typically host an obligate symbiont, *Buchnera aphidicola*, required for host survival. In addition, aphids may also harbor a wide range of facultative symbionts involved in interaction of a more recent origin and often described as an intermediary state in an evolutionary transition from free-living to obligate intracellular life-style. These bacteria are associated with various phenotypes such as protection against heat stress and natural enemies. Findings of closely related bacteria in distantly related insect hosts suggest that, unlike *Buchnera*, which is exclusively vertically transmitted from mother to offspring, facultative symbionts experience horizontal transfers and seem to have retained their ability to colonize and persist in novel hosts. Facultative bacterial partners show irregular distributions among host tissues: they can reside in specific cells as well as extracellularly in the hemolymph. Despite studies relative to the localization of facultative symbionts and their interaction with *Buchnera* in stable infection, it remains unclear how facultative symbionts are welcomed at the early stages of infection. Furthermore, the oral opening has been poorly explored in symbiont transmission. Here, using two infection routes, ingestion and injection, we have described the infection dynamic of a free-living form of *Serratia symbiotica* strain in a novel host. Survival rate of infected aphids was examined. Evolution of the cellular tropism and the interaction between *S. symbiotica* and *Buchnera* are described using qPCR and fluorescence techniques.

**François Renoz**

Catholic University of Louvain  
2nd year PhD student



## How is sexual selection affected by its environmental context?

Many studies on sexual selection focus on inter- and/or intra-sexual selection. Thereby, research on sexual selection is often done ignoring the social and population ecological context. Therefore, I aim to integrate and especially address the question how sexual selection and its natural context interact. This approach has an evolutionary view on both behavioural and population ecological studies. A suitable target species for experimental work in the field is a small marine fish, the common goby (*Pomatoschistus microps*) which occurs throughout the Baltic Sea. Coastal areas of the Baltic Sea provide a natural arena with steep environmental gradients in terms of biotic, abiotic, structural, and community ecological factors. Gradients like water temperature, salinity, natural nest availability, individual density and predation risk are factors that vary greatly between the West and the East of the Baltic Sea. I compare common goby populations along these geographic clines and hence study adaptations of mating systems, phenotypic plasticity and plasticity in sex-roles. In standardized field experiments I compare nest occupation success, courtship and agonistic behaviour as well as mating and reproductive success, of five different common goby populations throughout the Baltic Sea. Preliminary results show highest reproductive success as well as greatest body size and weight of both sexes, in the population facing the most moderate environmental conditions.



**Isabel Mück**

University of Tübingen  
2nd year PhD student

## Evolution of immune genes in the Argentine ant

Ants are among the most abundant and influential social insects in terrestrial ecosystems. Most ant populations are kin structured meaning that the nestmates are highly related to each other. High relatedness between the nestmates assures that natural selection is working efficiently. Some ant species, however, possess an unusual form of social organization called uniclonality. The nests of uniclonal populations contain many queens which together with the exchange of individuals between the nests lead to extremely low relatedness between the nestmates. The introduced populations of Argentine ant (*Linepithema humile*) represent one of the most extreme examples of uniclonality. The species has invaded all the continents in the world except Antarctica. In contrast native populations are characterized by a pattern of genetic isolation by distance. Nestmates in the native range are more closely related, and local genetic differentiation is evident. Relatedness within nests and colonies is markedly lower in the introduced range than in the native range. Introduced populations have a competitive advantage regarding the native ants, but at the same time the high population densities combined to a new pathogen fauna and reduced genetic diversity is a threat to the survival of Argentine ants creating a potential selection pressure on the immune genes. The specific aim of this study is to investigate whether the evolution rate of immune genes is higher in introduced than in native populations of the Argentine ant. The genetic variation of selected immune genes will be compared between the native and introduced populations of *L. humile*.

**Jenni Paviala**

University of Helsinki  
2nd year PhD student



## Parent-gamete proximity and the evolution of sex roles

Why do some female marine animals release their eggs into the water to be fertilised, while others retain them on, or inside, their bodies? Why do terrestrial plants disperse pollen but not ovules, and why do most terrestrial animals hold onto both sperm and eggs until they find a mate? Research on sex roles has largely overlooked the significance of where gametes are located when fertilisation occurs. Parent-gamete proximity during fertilisation is not only a basic difference between the sexes in many species; it is also essential to the evolution of parental care and most forms of mate choice. I explore the evolutionary logic behind gamete release and retention using mathematical models. I focus particularly on marine invertebrates, in which evolutionary changes in these behaviours are common. Along the way, I provide a new explanation for why egg retention, small body size, and large egg size are correlated in sessile marine invertebrates. I also explain why there are no species in which males retain their gametes while females release them.



**Jonathan Henshaw**

Australian National University

1st year PhD student

## Fishing with a cut line: Why is siderophore secretion a successful iron uptake strategy for bacteria?

Bacteria face iron scarcity in many environments, no matter whether they live in oceans, soil or a host. The need for efficient iron acquisition led to the evolution of strong chelators called siderophores. These molecules are secreted and bind iron outside the cell. Bacteria take up the resulting iron-siderophore complexes. This strategy has major drawbacks, though. Secreting a molecule a cell invested energy and resources in is risky. Once released, there is no guarantee the molecule will return benefits to the producer. From an evolutionary perspective, the maintenance of siderophore secretion can only be explained within certain conditions like spatially structured environments. This does not reflect the universal occurrence of siderophores, however – thus, how is the strategy of siderophore secretion stably maintained in environments as different as the host or the ocean? I am investigating this question using modeling and fluorescence time-lapse microscopy. Microscopy allows to monitor bacterial behavior and its consequences on fitness at the single-cell level. I use genetically modified strains to manipulate and measure investment in siderophore secretion, and try to understand what consequences of this investment I observe. Finally, I hope to transfer my results to the environment bacteria experience ‘in the real world’ outside the lab.

**Konstanze Schiessl**

ETH Zurich & Eawag  
2nd year PhD student



## Does reproductive effort influence telomere length in blue tit?

Ageing constitutes a hot topic among researchers in evolutionary biology. This interest is not only due to observed variation between organisms but also due to the fact that this issue can be directly related to humans. There is accumulating evidence that telomeres, protective caps at the ends of chromosomes shorten with age and this may potentially explain some of the observed variation in longevity. Somatic deterioration reflected in telomere decay in ageing animals may arise from allocation of resources in reproduction at the expense of repair and maintenance. Such presumption is based on the idea of trade-offs, which is essential to understand the evolution of life histories and ageing as a part of it. However, the link between telomere length and reproductive performance received surprisingly little attention. Main question is whether increased reproductive effort causes greater telomere loss. We will employ an experimental manipulation of reproductive effort to study its potential effect on telomere loss in wild blue tit (*Cyanistes caeruleus*). Brood size manipulation will be applied: some broods will be enlarged after clutch completion while others will remain unaltered. We will sample adults at the time of nest building and then at the expected fledging to examine change of telomere length. We expect larger telomere loss among parents experiencing experimentally elevated reproductive effort.



**Joanna Sudyka**

Jagiellonian University  
2nd year PhD student

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

In ecological stoichiometry, ecological interactions are depicted as a flow of essential elements from one level to another. One principle is that *Daphnia* suffer reduced growth and survival when fed on P-deprived algae. This response of *Daphnia* depends on its genetic signature, a result of local adaptation. A few points of criticism arise. First, little is known about the genetic variation towards historical changes in N:P ratio within the same pond. Furthermore, other stressors such as parasites can act as an extra source of variation. Moreover, it remains unknown how this G x E interaction applies to other life history traits. Our goal was 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 used two sets of *Daphnia* clones. Both sets were hatched from the same sediment core, differing in their depth of isolation. The selected depth range corresponds to a time span of about 40 years. Therefore, we expected these sets to differ genetically as a result of historical adaptation towards differences in P-availability. Our results show a significant three-way GxGxE 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.

**Lien Reyserhove**

K.U.Leuven Campus KULAK  
2nd year PhD student





## Evolution of life cycles

Sexual organisms alternate between a haploid phase following meiosis, and a diploid phase following gamete union. In addition to haploid (ascomycetes) and diploid (animals) life cycles, one observes a great diversity of biphasic life cycles (with cell divisions both in the haploid and diploid phases), particularly in the marine environment. Genetic models showed that diploidy benefits from the immediate advantage of masking deleterious mutations, whereas haploidy benefits from more efficient selection. This second effect can overcome the first only when genetic exchanges are restricted (weak recombination, rare sex or high inbreeding). However, these previous models do not consider differential, or even antagonist effects of selection in the two ploidy phases; furthermore, they assume that haploids and diploids occupy the same ecological niche and compete against each other. Here we analyze the effects of differential selection among phases and niche differentiation using a two-locus model: a modifier locus controls the timing of meiosis, while mutations occur at a viability locus under direct selection. We show that both the masking and purging effect depend on the relative strength of selection in both ploidy phases, and that niche separation tends to eliminate the benefit of masking: Without direct competition, haploidy can be favored despite high recombination rates. We also find that increasing the variance of mutational effects across loci increases the purging advantage, and should generally tend to favor haploidy. Multilocus, individual-based simulations confirm these analytical results and show that these genetical models do not allow the maintenance of stable biphasic life-cycles.



**Marie Rescan**

CNRS-UPMC

1st year PhD student

## Endemic species: can it restrain the biodiversity crisis? A discussion of between-species altruism

Biodiversity conservation mainly focuses on species diversity and rarity. But several recent studies have shown that species and genetic diversity structures are not geographically correlated. This leads to a simple question: Which spatial areas and biodiversity indicators should be focused to protect all aspect of biodiversity as well as the evolutionary processes sustaining it? By applying phylogeographic, ecological and phylogenetic methods at a sub-regional scale, we are wondering if the protection of within-species genetic structure is in favor of the maintenance a high level of biodiversity. On the contrary we can also question if protection of high level of biodiversity will favor the conservation of the genetic diversity of species, fuel of evolution. *Arenaria provincialis*, an endemic plant species and its community located in the south-east of France will be the focus system of this talk. What knowledge the evolutionary history and the spatial pattern of genetic diversity of this rare plant can furnish for a biodiversity conservation? Various geographical patterns dealing with the history and the evolution of this rare plant will be compared to the species and phylogenetic diversity of its associated plant community.

**Marine Pouget**

University of Aix-Marseille  
2nd year PhD student



## Dulling the double-edged sword: manipulating within-host ecology to prevent the evolution of drug-resistant pathogens.

The creation of strategies to combat the evolution of drug resistance, which threatens our ability to manage infectious diseases worldwide, is a major challenge for evolutionary biologists. Aggressive, high-dose drug treatment has been advocated as a resistance management strategy because it dramatically reduces the population size of parasites and thus the probability that a *de novo* resistance mutation will emerge. However, aggressive treatment is a doubleedged sword: in mixed genotype infections it confers a great selective advantage to any pre-existing resistant parasites and enables their growth by releasing them from competition with drug-susceptible parasites. We attempted to resolve this tension by mimicking the suppressive presence of susceptible competitors within-host. Mice infected with both susceptible and resistant strains of the rodent malaria *Plasmodium chabaudi* were either provided with or deprived of a nutrient necessary for parasite growth. Following aggressive antimalarial treatment, resistant parasites in nutrient-supplemented mice grew to high densities, causing a concurrent bout of anaemia. In contrast, no resistant parasites were observed in nutrient-deprived mice, which remained healthy. The dramatic reduction in the fitness of resistant parasites was mediated by the combination of competition and nutrient deprivation, as resistant parasites grew well in single infections irrespective of nutrient treatment. Manipulation of the within-host environment represents a novel, potentially ‘evolution proof’ approach to slowing the emergence of resistant pathogens. Moreover, environment-manipulating compounds, which may have gone undetected in screens for lethal drugs, could represent a much-needed new class of drugs.



**Nina Wale**

The Pennsylvania State University  
2nd year PhD student

## In search of underlying mechanisms of begging behaviour: Physiological and genetics covariances

Begging behaviour, the solicitation of food from parents, is one of the first coordinated behaviours performed by nestlings of altricial bird species. Begging has significant positive effects on growth and survival. However, begging also entails cost for the offspring such as in terms of energy consumption or enhanced predation risk, and is therefore subject to trade-offs. It typically precedes parental feeding and is thought to elicit additional resources from parents. It thus exerts a selective pressure on parental behaviour, further flavoured by an evolutionary conflict over parental investment. Offspring indeed tend to demand greater resources than the parents are willing to give. Being agent of selection on parents, begging is also target of selection, because it is influenced by the parental response. It requires, therefore, detailed information on both selection and inheritance of begging in order to understand its evolutionary potential. However, controlling mechanisms and potential physiological constraints shaping the evolution of begging remain as yet largely unclear. By creating two lines of selection according to begging score (low begging and high begging line), I will measure (a) the heritability and response to selection (b) several physiological characteristics as testosterone level, corticosterone level, immunocompetence and digestive efficiency in order to investigate underlying mechanisms and potential covariances.

**Nolwenn Fresneau**

University of Antwerp  
1st year PhD student



## Does faster developmental speed explain competitiveness in *Myxobacterial* development?

*Myxococcus xanthus* is a soil dwelling delta-proteobacterium known for its cooperative behaviors throughout its lifecycle. In response to starvation, *Myxococcus* makes multicellular fruiting bodies and spores through a process of aggregative development. Spores aid *Myxococcus* survival and propagation in nature. Studies have established that natural isolates of *Myxococcus* that make similar numbers of spores in pure culture show great variation in spore production when competing against each other in mixed groups. The reasons for this competitive asymmetry, however, remain unclear. We hypothesize that the speed at which individual strains develop intrinsically in pure culture may be an important component of developmental fitness in competitive mixes. Our project will test this hypothesis by screening *Myxococcus* strains for different intrinsic rates of development and competing faster developers against slower developers. We will use isolates from a large set of experimentally evolved *Myxococcus* populations that have been classified with respect to the time at which they first produce mature fruiting bodies upon starvation. Faster developing isolates will be mixed with slower developers and spotted on a starvation medium at different frequencies and relative developmental fitness (in terms of relative spore representation in subsequently developed fruiting bodies) will be quantified and we will test for the existence or non-existence of a correlation between intrinsic speed of development and developmental competitiveness in mixed groups.



**Ramith Nair**

ETH Zurich

1st year PhD student

## The effect of genetic condition on song expression and mate choice behaviour in canaries (*Serinus canaria*)

The existence of conspicuous traits in nature, such as bird song, is explained by the theory of sexual selection. This theory assumes that females are picky when it comes to choosing males, while males need to compete over the access to females. This causes males to evolve traits that help them become either more dominant than other males or more attractive to females in order to successfully reproduce. Under both scenarios it is expected that the expression of these traits provides honest information on the quality of the male. The quality of the male in turn is a result of genetic condition, environmental conditions, and an interaction between both. Yet, the effects of genetic condition and a possible gene-environment interaction on the expression of sexually selected traits have only rarely been studied. Here, we use inbreeding in a songbird (*Serinus canaria*), a currently un(der)explored approach to directly manipulate genetic condition. This will give us the opportunity to study the condition-dependence of bird song. We also investigate the effects of a reduction in genetic condition on the ability to compete over females through male-male competition and their attractiveness to females. In addition, we test the effect of inbreeding on female mate choice, since female choosiness may also be a condition-dependent trait, which is rarely considered. In this talk, I will present the experiments I will perform in the first year of the PhD project.

**Raïssa de Boer**

University of Antwerp  
1st year PhD student



# For the love of science!



A public engagement event at Falmouth's National Maritime Museum to which everyone is invited and some of you will be presenting posters and putting into practice what you learnt on Thursday's workshop.

|             |                                                                             |
|-------------|-----------------------------------------------------------------------------|
| 19:30       | Doors open                                                                  |
| 20:00-20:05 | Welcome                                                                     |
| 20:05-20:15 | Professor Tom Tregenza<br>"Grand unified theory of life"                    |
| 20:15-20:25 | Professor David Hosken<br>"Why sex, why sexes"                              |
| 20:25-20:35 | Professor Stuart Bearhop<br>"Avian migration: literally a wild goose chase" |
| 8:35-9:30   | Poster Q&A and Wine Reception                                               |
| 9:30-9:40   | Dr Britt Koskella<br>"How evolution might save your life"                   |
| 9:40-9:50   | Prize giving and wrap up                                                    |
| 09:50-10:00 | Finish                                                                      |

Coaches have been arranged to take us there and bring us back. Details will be confirmed at the conference.

---

Saturday



## A discussion of between-species altruism

Can altruism evolve between species? This is an important theoretical question, which remains ambiguous in the literature. I shall use a simple model of between-species altruism, in which two populations, representing species, interact with one another in pairwise interactions. Individuals act either altruistically or not at all. The evolution of both altruism and altruism-suppression shall be considered. Using several variations of this simple model of between-species altruism, I shall consider whether or not altruism can evolve under assumptions of varying strengths. Results are found using three methods; firstly, analytically, emphasising the importance of Hamilton's rule. Secondly, I shall use a deterministic algorithm, and finally, a genetic algorithm which introduces stochasticity to the two populations.



**Christopher Quickfall**

University of Sheffield

1st year PhD student

## The evolution of chemical defence and visual warning signals in nudibranchs

Aposematic animals use vibrant patterns as visual signals to warn potential predators of their defences. This evolutionary strategy is beneficial to both predator and prey. The predator learns to avoid inefficient or harmful food items, and the prey profits from less frequent attacks. Nudibranchs are a charismatic clade of opisthobranch molluscs with an astounding array of colours and patterns coupled with toxic chemicals and stinging nematocysts. Some nudibranchs have conspicuous patterns, while others are well camouflaged against their natural backgrounds. This variation in predator avoidance strategies makes nudibranchs an ideal model system to test theories about the evolution of aposematism. Recent advances in underwater spectral measurements and vision models allow us to essentially 'see through the eyes of a fish,' making it possible to measure nudibranch colour patterns as they appear to marine predators. This state of the art technique coupled with chemical analyses allows me to test aposematic theories in the marine environment. In this study, nudibranchs were photographed on the reef and transported to the lab for processing. Spectral reflectance of colour patches were measured using a spectrophotometer and analyzed using the Vorobyev Osorio predator vision model. Brightness contrast and spatial frequency of the pattern and natural background were analysed using 1st and 2nd order image statistics. Next, secondary metabolites were extracted from nudibranch tissue to determine the chemical content, molecular structure, and relative deterrence using analytical tools such as  $^1\text{H}$  NMR, HPLC, and predator deterrence assays. Aposematic theories were tested using these measures of conspicuousness and defence.

**Anne Winters**

University of Queensland  
2nd year PhD student



## Nine bacterial species can't be wrong: Fluctuating temperature leads to asymmetric changes in thermal tolerance

Fluctuating temperature is predicted to select for generalist genotypes that are capable of performing well across a wide range of temperatures. Although theories particularly predict fast fluctuations in selecting for thermal generalists, such experiments are scarce. Our aim was to find out whether fluctuating temperature selects for temperature generalists and test how uniform the temperature induced evolutionary changes are across different bacterial species. We set up a factorial experiment where ten replicate populations of nine different bacterial species were propagated separately either in a constant temperature (30 °C) or in a rapidly fluctuating temperature (2 h 20 °C - 2 h 30 °C - 2 h 40 °C, mean 30 °C). After 2.5 months we isolated altogether 720 bacterial clones from experimental populations and measured growth rate and yield (growth efficiency) in three constant temperatures (20, 30 and 40 °C). Meta-analysis of all of the species over all of the temperatures indicated that clones from the fluctuating temperature treatment had higher overall growth efficiency compared to clones from the constant environment. Moreover, the selection was found to be asymmetric, selecting more profoundly the tolerance of hottest temperatures. Generality of the results across studied species gives a strong support for the theories of evolution of thermal generalism but also indicates that evolutionary consequence of fluctuating temperature is especially strong in hot temperatures where the fitness consequences of increased or decreased heat are much more profound than in cold temperatures.



**Kati Saarinen**

University of Jyväskylä  
2nd year PhD student

## Genetic markers as a tool for monitoring lobster populations and the impact of stock enhancement

Lobster stock enhancement programmes are run at a variety of locations around Europe as a fisheries conservation or restoration technique but, due to the financial and practical constraints of physical tagging technologies, few projects are currently able to undertake routine monitoring of their success. Additionally, appropriate fisheries management of these valuable crustaceans is inhibited by a lack of fundamental understanding of their population dynamics. The development of a suitable marker is required to identify individuals in order to undertake mark-recapture analyses and generate data relevant to the regulation of populations. The difficulty of tagging small, moulting crustaceans is discussed, and the use of microsatellite DNA markers is proposed to provide a method of assigning parentage and tracking individuals in the wild. While only in preliminary stages, the aim of this study is to provide lobster hatcheries with a tested method to undertake quantitative impact assessments of their stocking work, so they can create informed release strategies and maximise their contribution to fishery sustainability.

**Charlie Ellis**

University of Exeter  
1st year PhD student



## Seasonal changes in immune defense in the ant *Formica exsecta*

Eusocial insects are favorable targets for parasites due to high relatedness within a colony and a large amount of interacting individuals. Consequently, eusocial insects evolved a strong defense against parasites on an individual, as well as a social level. When resources are scarce, individuals and colonies are weakened and opportunistic pathogens might be able to infect the hosts, which face a trade-off between energy saving and immune defense. Different demands for energy use during the active season and hibernation are likely to influence this trade-off. This possible trade-off might even be stronger when resource availability is low and starvation imposes additional stress on the individual. Here we investigate seasonal differences in regulation of immune defenses under starvation in the ant *Formica exsecta*. We used bioassays coupled with gene expression analysis of immune, stress and storage protein. In order to estimate the organism's capability to fight off infections, depending on seasonal and nutritional status, entomopathogenic bacteria *Serratia marcescens* and *Pseudomonas entomophila* were used.



**Dimitri Stucki**

University of Helsinki  
2nd year PhD student

## Free spawned sperm in a changing marine environment

The majority of marine taxa reproduce via free spawning their sperm directly into the water column. This strategy is thought to be the ancestral reproductive mode and remains highly prevalent. Sperm perform the same basic function; to fertilise an egg, yet exhibit dramatic evolutionary divergence in form. Given this morphological diversity, and the strong selective pressures acting on sperm to maintain an individuals' fitness, it is surprising that we still have such limited understanding of the adaptive significance of morphological sperm traits and sperm diversity. The need to address this knowledge gap is becoming increasingly urgent given the rapid rate of change currently being recorded in the world's oceans, as a result of climate change. One unanswered question is whether some of this morphological and physiological diversity observed in sperm is related to the diverse fertilisation environments encountered by free spawned sperm in the marine environment and the resultant selective pressures generated by each set of ecological conditions? Can some of the variation in sperm morphology explain the individual-, population- or species-specific level of response of sperm performance to stressors such as ocean acidification and exposure to metal contaminants and therefore help us to predict population level responses to these stressors? A more complete understanding of the selective pressures that have driven the sperm traits of current broadcast spawners may aid predictions of how the new and intensifying selective pressures, as a result of a rapidly changing marine environment, may impact upon future populations of broadcast spawners.

**Anna Campbell**  
University of Exeter  
1st year PhD student



## Tracking the foraging behavior of a parasitoid wasp at a landscape scale

The specialist wasp *Hyposoter horticola* is a parasitoid of the Glanville fritillary butterfly (*Melitaea cinxia*), which lives as a typical metapopulation in a fragmented landscape in the Åland Islands in Finland. Adult females parasitize the larvae of *M. cinxia* in the short time period while the host is still in the egg shortly before hatching. There is strong competition among female wasps for host egg clusters. The foraging female wasps learn the location of host egg clusters and monitor them until they become susceptible to parasitism. This is a very time- and energy-consuming process, therefore a huge evolutionary investment. It is not yet known how *H. horticola*, or any insect other than social bees and ants, navigates through the landscape, which navigational system is used, and what spatial learning occurs. Ants, social bees and nesting bees have a nest as a fixed starting point for navigation, whereas solitary non-nesting insects such as *H. horticola* don't. Yet both function in a complex navigational context. In my research I study which navigational system is used by *H. horticola*, a cognitive map or path integration in order to compare this to closely related social insects. I am using an array of RFID systems positioned at host egg clusters to track the foraging path of wasps equipped with laser-activated RFID chips. I am presenting the results of the research of my first field season.



**Wolfgang Reschka**

University of Helsinki  
2nd year PhD student

## Associations between genomic and transcriptomic variation in three-spined sticklebacks from five parapatric lake-river population pairs

The three-spined stickleback (*Gasterosteus aculeatus*) has repeatedly colonized and adapted to different freshwater habitats since the last ice age and thus provides promising opportunities to study the genetic basis of adaptive radiations. We sampled individuals from 5 parapatric lake-river population pairs, 3 pairs from Europe and 2 pairs from North America. Because the parapatric pairs are adapted to their local environment, our sampling allows us to investigate the underlying genetic variations contributing to ecological speciation. Recent advances in genomics, such as high throughput DNA and RNA sequencing, enable us to identify genomic regions that are divergent between the ecotypes as well as to detect patterns of habitat-specific gene expression. We aim to study the genomic landscape of divergence and identify islands of differentiation between river and lake ecotypes. Through transcriptomic analysis we want to reveal the consequence of identified genomic features, in terms of gene expression levels and the presence of transcriptional isoforms. Integrating the genomic and transcriptomic analysis of geographically distinct lake-river ecotype pairs provides us insight into the role of genetic variations in ecological adaptation.

**Yun Huang**

Max Planck Institute for Evolutionary Biology  
1st year PhD student





## How do pluralistic models of inheritance change our conceptions about inheritance and evolutionary processes?

Inheritance refers both to the permanence of forms throughout generations (Jacob, 1970) and to the processes involved in the reliable recurrence of features within lineages (Mameli, 2005). Although the science of heredity has been dominated by the genetic paradigm for decades, several critics recently asserted the replication and transmission of DNA, which appeared to be the support of heritable characters, are not the sole responsible for intergenerational resemblances, and claim for the integration of pluralistic or inclusive models of inheritance in biology (Jablonka & Lamb, 2005; Danchin et al., 2011). I will argue the multiplication of resemblance channels may bring about a drastic conceptual reform regarding inheritance and change our way of conceiving evolutionary processes. After a brief presentation of non-genetic inheritance (ecological, epigenetic, cultural, etc.), I will show that pluralistic models betray the obsolescence of the replication of traits rhetoric and urge scientists to adopt that of maintenance. Given the mosaic nature of evolving entities, made up of elements not necessarily able to beget offspring and following unsynchronized recurrence cycles, I will then suggest an inclusive concept of inheritance should be coupled to the notion of persistence of entities and thought, consequently, without reproduction or generations. Finally, I will hold the fickleness of non-genetic variants may sign the return, after the stable Mendelian inheritance, of a highly dynamic phenomenon. Inheritance being one of the major concepts in the Darwinian theory, I will sketch the potential impacts of a conceptual reform on evolutionary thinking.



**Gaëlle Pontarotti**

IHPST - Paris 1 Panthéon Sorbonne

1st year PhD student

## What is the cost of environmental environmental complexity?

Environmental change is complex. For example, ocean acidification involves not only changes in pH, but also changes in temperature, water column stratification, irradiation, nutrient availability, and interactions between organisms. However, most experimental evolution aiming to explain how organisms adapt to changes in their environments investigates evolution in response to one or two environmental changes. My PhD work uses experimental microbial evolution with the model alga *Chlamydomonas* to investigate how adaptation to a single environmental change differs system-atically from adaptation in the face of many simultaneous environmental changes. Existing evolutionary theory, suggests that increasing organism complexity increases the cost during adaptation (Fisher, 1930; Orr, 2000). We want to identify if this theory can be used to assess the cost of increasingly complex environments on adaptation or if they must be treated separately, in which case an alternative evolutionary theory would be required in order to understand evolutionary adaptation to many simultaneous environmental changes. I will present how and why our experimental design is able to answer this question, and discuss data from early on in the experiment. The data collected at the very beginning of this selection experiment allows us to assess the initial drops in fitness and the difference in selection pressure between the different combinations of environmental changes. Using flow cytometry methods, we are able to measure the physiological responses of *C. reinhardtii* to many different regimes (different complex and simple environmental changes). I will discuss how I expect these early differences to affect microevolution.

**Georgina Brennan**

University of Edinburgh  
2nd year PhD student



## Fitness consequences of cross fostering in a wild passerine

Researchers cross foster to pull apart environmental and genetic effects on traits. Often, cross fostering involves swapping offspring between two or more broods or litters so that offspring are cared for by foster parents. This separates the influence of the genetic parents from the rearing environment provided by the foster parents, dividing nature from nurture. Cross fostering is however an experimental manipulation, and may have unforeseen fitness consequences outside the scope of the study. Here we show how cross fostering affects fitness estimates at different life history stages, and point out the difficulties associated with using cross fostering data. We use twelve years of data from a long term study of a population of wild house sparrows, *Passer domesticus*, based on Lundy Island, UK.



**Isabel Winney**

University of Sheffield  
2nd year PhD student

## Searching for local adaptations to metal pollution in populations of the earthworm *Lumbricus rubellus*: genome scan with RAD tag sequencing approach

Multigenerational exposure to metal pollution may lead to evolution of resistance to metals. In my project I test whether the tolerance to high heavy metal contamination in natural populations of the earthworm *Lumbricus rubellus* inhabiting polluted environments results from physiological acclimation or adaptation. I study several populations of earthworms living along a metal pollution gradient in southern Poland. Metal concentrations in soils at the most contaminated sites reach up to (in dry soil): Zn - 4000 mg/kg, Pb - 2000 mg/kg, Cd - 50 mg/kg, Cu - 58 mg/kg. The key point of the study is the genome scan with the high-throughput SNP genotyping by RAD tags sequencing. To generate RAD tags I have performed digestion of genomic DNA with two restriction enzymes, followed by library preparation and Illumina sequencing. Aiming at finding genetic regions putatively under selection I will associate allele frequency across the genome with metal concentrations in the soils and earthworms. Furthermore, by annotation of these regions to partially available *L. rubellus* genome, I will check functions of genes present there. I predict that, if metal contamination acts as the selective force, the signatures of such selection are present in genes controlling the response of organisms to metals.

**Iwona Giska**

Jagiellonian University  
3rd year PhD student



## Evolution through Bayesian inference in a two-outcome random experiment

Animal survival depends on its ability to react appropriately to their surrounding conditions to exploit resources than might be beneficial or to evade danger. Natural environments generally pose a level of uncertainty and being able to infer its actual circumstances can be a key factor for an animal before determining the right course of action. This inference ability could offer an evolutionary advantage, even though the information acquired is not communicated to the genotype. We examine learning-based evolution with a computational model where a population of agents attempt to determine the probability that one event (a particular outcome of an observable experiment) occurs. The probability of that event changes periodically with values being sampled randomly from a beta distribution whose hyperparameters are themselves attributes of the environment the agents live in. Individuals are able to make independent observations of the experiment and their fitness is measured in terms of their ability to estimate quickly and accurately the current probability of the event. Agents can be of two types: those who always use bayesian inference when new evidence is gained and those who use frequentist inference instead. Results show that bayesians seem to make accurate estimates about the event and infer some information about the background parameters of the distribution that dictate the changes in the environment. Repeated competition against frequentists shows in what conditions natural selection favours individuals who act as if they were using bayesian reasoning when making such estimates.



**Juan Ramirez**

University of Sheffield  
2nd year PhD student

## Evolutionary status of the redpoll subspecies *Carduelis flammea islandica* (Aves: Passeriformes: Fringillidae)

The Icelandic redpoll *Carduelis flammea islandica* is one of three subspecies of *Carduelis flammea*. The other two are *C. f. rostrata*, breeding in Greenland, and *C. f. flammea*, widely distributed at high latitudes in both N-America and Eurasia. Recent studies on variation of the mtDNA control region and in microsatellites among redpolls mainly from Scandinavia and including comparison with different species (*C. hornemanni*, *C. cabaret*) didn't reveal clear genetic differentiation. The lack of differentiation could result from introgression (hybridization has been supported also by direct observations) and/or incomplete lineage assortment following recent diversification. Here we add result of the Icelandic subspecies *C. f. islandica* to previous analysis of the species complex to evaluate its reproductive isolation. This includes comparison of different genetic markers: mitochondrial; control region and Col, nuclear introns; TGFβ2 and Fib7. All markers are highly variable. Significant differences in haplotype frequencies of the mtDNA control region are observed between the Icelandic subspecies and the common redpoll. The Col reflects more a geographical barrier, which describes two lineages: one "mainland" and the other "atlantic". First results of introns in nuclear genes (Fib7 and TGFβ2) have shown high variation. The nuclear marker TGFβ2 and the mitochondrial control region support the lesser redpoll species (*Carduelis cabaret*).

**Julien Amouret**  
University of Iceland  
2nd year PhD student



## Oxidative damage, life history and ageing

The average expected lifespan of humans continues to increase, and research devoted to unravelling the mechanisms underlying ageing and age-related diseases (cardiovascular disease, osteoporosis, type 2 diabetes, Alzheimer's etc) is becoming increasingly important. The aim of my research project is to determine whether there is a connection between oxidative damage, life history and ageing in a population of wild mammals. To supplement this, I will also undertake a more in-depth investigation of the metabolic signature of individual animals across a range of age-classes. This is done to assess whether the metabolic fingerprint changes with age- and if so, to identify potential biomarkers of longevity/ 'biological age'. I hope to present the first data from both the oxidative stress analysis and from the metabolomic analysis and to tie this together with data on life histories of the study population.



**Louise Christensen**

University of Aberdeen

1st year PhD student

## Quantifying pre- and post-copulatory episodes of sexual selection in a simultaneous hermaphrodite

Classical sex roles are often assumed to apply to all sexually reproducing organisms with males being typically more eager to mate whereas females being more choosy. For simultaneous hermaphrodites this implies that mating should be more beneficial for the male than for the female sex function, but empirical tests are scarce. Specifically, a high mating activity (mating success) is expected to lead to the successful transfer of numerous sperm cells (insemination success) and thus to the fertilization of numerous eggs (fertilization success), jointly leading to a high male reproductive success. These consecutive episodes of sexual selection are often challenging to quantify separately especially given the generally cryptic nature of post-copulatory processes. A recently established transgenic line in the transparent flatworm *Macostomum lignano* expresses green fluorescent protein (GFP) in all cell types, including the spermatozoa, which enables to observe the mating interactions, the number of sperm received from a GFP-expressing mating partner and the resulting offspring produced. We created groups of 5 individuals, including one focal GFP-expressing individual, and assessed the mating success, the insemination success and the male and female reproductive success of these focals, of which we also measured a suite of morphological traits. We aim to quantify (1) how mating success affects male and female reproductive success, (2) how mating success, insemination success and fertilization success contribute to male reproductive success, and (3) how these episodes of selection are affected by specific morphological traits.

**Lucas Marie-Orleach**

University of Basel  
4th year PhD student





## Is the bumblebee genome 'lumpy'?

Background selection - selection that purges deleterious mutations - is an important mechanism shaping genomic variation. The efficacy of background selection, however, depends on mutations being 'visible' to selection. For example, recessive deleterious mutations can be purged when homozygous because they express the deleterious phenotype, but ineffectively purged when heterozygous because the deleterious allele is sheltered by the expressed allele. I am investigating the effect of gene expression and ploidy on the visibility of genetic variation to selection and the resultant genome-wide genetic load. Hymenoptera are haplodiploid: males haploid and females diploid, and these ploidy differences, coupled with sex-specific expression, will alter the relative visibility of genes to selection. The male-only expressed genes are continuously exposed to selection because of haploidy. Conversely, female-only expressed deleterious genes will be sheltered from selection when heterozygous. I wish to test two explicit predictions of this reasoning. First, that the distribution of molecular variation across the buff-tailed bumblebee genome (*Bombus terrestris*) should be 'lumpy' with lower genetic load at male-only expressed genes compared to female-only expressed genes. Second, that, on average, overall load is lower than that found in diplo-diploid species. In a first step, gender-specific genes will be identified by sequencing transcriptomes of male and female bees and measuring the respective, relative abundances of mRNA molecules at each locus. Subsequently, molecular variation between individuals from several populations will be quantified. In a final step I will attempt to explain the variation pattern observed in the bumblebee genome with the information on gender-specific expression.



**Mark Harrison**

University of Leicester  
1st year PhD student

## Context-dependent plasticity of reproduction in the common goby, *Pomatoschistus microps*

Reproduction in animals can be highly variable with characters like reproductive rates and reproductive success being affected by numerous abiotic and biotic factors. Different populations of one species usually experience different kinds of such external influences. Likewise, there are often temporal changes in the environment, e.g. in the course of the progressing breeding season. By differentially affecting reproduction in males and females this social and population ecological context can also determine the direction and strength of sexual selection. While most research on sexual selection thus far has ignored this background, this study is specifically addressing the interactions between reproduction, sexual selection and its natural context, using the common goby (*Pomatoschistus microps*) as a model species. This small marine fish has exclusive paternal care, a resource-based mating system and plastic sex roles. Additionally, it occurs throughout the Baltic Sea and its distribution thus naturally stretches over steep environmental gradients. In this study, we investigated how different seawater temperatures and adult sex ratios affect reproduction, the operational sex ratio and intra- and intersexual competition in a controlled laboratory experiment. We found that warmer water led to higher reproductive rates in both sexes. However, this increase was much higher in males. Other preliminary results show larger clutches and higher reproductive rates under female-biased conditions. This study thus helps to further our understanding of the context-dependency of reproduction and ultimately sexual selection.

**Martin Vallon**

University of Tübingen  
2nd year PhD student



## Condition dependent expression: Effects of an immune & a genetic challenge on sexual and non-sexual traits

The expression of sexually selected traits has for long been argued to be dependent on an individual's condition. Condition dependence will ensure honesty of a sexual signal as a quality indicator, because it reflects the ability of an individual to maintain good condition in the current environment. Condition dependence also offers an explanation for how genetic variation in sexual ornaments is maintained, if ornament expression 'captures' the sum of a large number of loci influencing condition ('genic capture hypothesis'). Genic capture makes a sexual ornament relevant for signaling indirect genetic benefits, which is particularly relevant in systems without parental care. Here we assess the effect of an environmental (immune) challenge and a genetic challenge (achieved by inbreeding) on the expression of a dimorphic trait on males of the club-legged grasshopper *Gomphocerus sibiricus*. Traits that have evolved to capture overall condition should be particularly strongly affected by these challenges and we therefore predict stronger effects on putative sexual signals as compared to non-sexual traits. The data serves to understand the evolution of striking, sexually dimorphic ornament that makes the Alpine dwelling club-legged grasshopper unique among Acridids: the swollen front legs that are presented to the female during courtship and are thus a particularly strong candidate for signaling individual quality.



**Pablo Valverde**

University of Bielefeld

1st year PhD student

## Role of gene duplications in resistance to insecticides in the mosquito *Culex pipiens*

Evolutionary potential is limited by the number of genes present, and so can be enlarged by gene duplications. Gene duplications have been considered for long just as raw genetic material for long- term evolution. However recent work shows that adaptative duplications could play a major role in micro-evolution. Insecticide resistance in the mosquito *Culex pipiens* provides one of the few examples of contemporary duplications. The *ace-1* gene encodes the target of organo-phosphate insecticides. A mutation causes high resistance levels in many mosquito species, albeit associated with a decreased enzymatic activity. Recently, we identified in *Cx. pipiens* new *ace-1* alleles that carry one susceptible and one resistant copy in tandem. These different duplicated alleles show different dynamics in the field. We propose that duplications are selected because they improve enzymatic activity while maintaining resistance. I will present our recent work investigating 1) the molecular origin of the duplications and 2) the complex gene-dosage/fitness relations and their impact in the resistance dynamics. Our work stresses the role of duplications as adaptive features, and the threat they represent for vector control.

**Pascal Milesi**

University of Montpellier II  
1st year PhD student



## Infectious spread of aposematism in wax worms

Many nematode species are currently used for biocontrol for agricultural pests to great effect. Recent study of the soil-dwelling nematode *Heterorhabditis bacteriophora* which has an obligate symbiosis with the bacteria *Photorhabdus luminescens* has shown that infection by this bacto-helminthic complex causes the insect host to turn red. It has recently been proposed that there is a defensive warning colouration aspect to this behaviour although there are a number of hypotheses which could explain this. These alternate hypotheses suggest that the change in host colouration could simply be a by-product of metabolism by the bacteria or an attractant signal for other potential host species. My talk will cover some theory and results of field experiments looking at these hypotheses, discovering what processes are underlying this remarkable colour change.



**Rebecca Jones**

University of Liverpool

1st year PhD student

---

## **Increasing number of coat color variants and decreasing number of paternal lineages in the domestic horse – What ancient DNA tells us about artificial selection**

Although modern domestic horses show a huge diversity in their maternally inherited mitochondrial DNA they have nearly no variation at their paternally inherited Y chromosome. In contrast pre-domestic stallions displayed a formidable number of paternal lineages. The decline and disappearance of these lineages is addressed by screening a recently discovered set of SNPs located at the Y chromosome in a broad set of samples ranging from pre-domesticated via early domesticated up to medieval stallions from different Eurasian regions. Using the same sample set, I also investigate a set of coat color-associated genes considering the fact that the occurrence and the number of coat color phenotypes are valuable indicators for domestication and breed formation.

**Saskia Wutke**

Leibniz Institute for Zoo and Wildlife Research  
1st year PhD student



## Immune ageing in a wild mammal population

The evolutionary and ecological context of age-related decline in the immune system has been little studied in free-living animals, and yet could offer great insight into the interactions between the immune phenotype and the natural environment. Research in this area has predominantly focused on human ageing and laboratory work with mice, with few studies of natural populations. The study of a free-living population in which the individuals are subject to natural selection, experience the challenges of a harsh environment and often face multiple infections, can give an insight into the factors affecting the ability of an individual to respond to a pathogen. The study species for this data is a free-living population of Soay sheep living on the archipelago of St.Kilda. This large longitudinal data set makes it possible to follow the phenotypic changes throughout an individual's lifespan and determine how these contribute to variation at the population-level. The results show changes and variation in the proportions of various T cell subsets with age across the population. We use this data to show potential trade-offs between immune function and other fitness functions such as reproduction, parasite burden, growth and repair in relation to the environment and ecology of the individual and ultimately the population as a whole.



**Rebecca Watson**

University of Edinburgh

1st year PhD student

## Differences in metabolic profiles promote cross-feeding in microbial communities

Overflow metabolism, for example in *Escherichia coli*, is an energy-spilling metabolic state where a high amount of energy-rich organic compounds are released. These released metabolites are freely available as public goods to neighboring cells. It has been hypothesized, that some individuals in the community may simply take up these metabolites from environment and thereby save the biosynthetic cost. The evolutionary potential for such by-product cross-feeding is especially high between strains with differences in the metabolic profile. For instance, one strain may have high overflow of an amino acid, which is growth rate-promoting for another strain. We showed, that *E. coli* exhibits distinct differences in the profile of released amino acids when utilizing different single carbon sources. There was a significant influence of the type of carbon source on the total- and individual amount of amino acids that were produced. This observation implies that in a natural population where multiple carbon sources are present a diversity of strains specialised in using specific carbon source can lead to emergence of cross-feeding interactions. This is because the overflow of one amino acid by one strain might be beneficial for another strain, which can save biosynthesis costs by taking up this amino acid. We argue, that the release of by-products of the cellular metabolism can shape complex metabolic interactions and dependencies between actors in microbial communities.

**Silvio Waschina**

Max Planck Institute for Chemical Ecology  
1st year PhD student





## What determines dewlap diversity in the brown anole, *Anolis sagrei*?

Animal signals often exhibit substantial variation both within and among species. In theory, this variation may reflect differences in the relative contribution of sexual selection, species recognition and predation risk, or may echo variation in broadcasting conditions. Empirical support for explaining signal diversity is however scant, especially at the intraspecific level. Within my project, I aim to identify the causes of intraspecific variation in a complex signaling system, the anoline dewlap, using *Anolis sagrei* as model species. Specifically, I attempt to elucidate the various selective forces explaining the diversity in dewlap size, colour and pattern among several *A. sagrei* populations from different islands in the Caribbean. The islands differ in the surface area, number and kind of predators, sexual size dimorphism and *Anolis* species composition. In addition, I investigate whether selective pressures acting on dewlap design differ between male and female brown anole lizards. To fully appreciate the complexity of the dewlap signaling system, a set of morphological, behavioural, performance, and physiological measurements were taken on captive *A. sagrei* individuals, under controlled laboratory conditions.



**Tess Driessens**

University of Antwerp  
2nd year PhD student

## Exploring the genetic basis of Intralocus sexual conflict in *Drosophila melanogaster*

As the evolutionary interests of males and females are frequently divergent, a trait value that is optimal for one sex is often not optimal for the other. A shared genome also means the same genes may underlie the same trait in both sexes. When sex-specific gene regulation cannot be achieved, this can give rise to a form of sexual antagonism, known as intralocus sexual conflict (IASC). Here, a tug of war over allelic expression can occur, maintaining alleles in a population that have opposite fitness effects in the sexes. We hope to identify specific alleles that may be mediating IASC (evidence of which is almost entirely lacking) in a model organism, *Drosophila melanogaster*. This involves creating 200 hemiclinal lines, where flies within each line have one identical haplotype that is expressed in a random genetic background from an outbred lab population. We will then be assaying sex-specific fitness within each line and using whole-genome sequencing to identify the target haplotype. This will allow us to conduct a genome-wide association study, testing how interactions between genes and sex affect fitness.

**Tanya Pennell**

University of Sussex  
2nd year PhD student



## Sexual lability in *Ophryotrocha* worms (Polychaeta: Dorvilleidae)

Regarding plasticity during the development from larvae to adulthood in the gonochorist species within the genus *Ophryotrocha*, in the literature two different types of plasticity are reported: 1) the development of intersexes (or pseudohermaphrodites): sexually mature animals capable of producing gametes of the opposite sex, even if non-functional. 2) sex inducibility: when young specimen are reared with an adult conspecific they are inclined to differentiate so as to form an heterosexual pair condition. Considering that phenotypes are the results of the interactions between genes and environments throughout the development of an organism, in this experiment we tried to verify what is the role of these two factors (genes and environment) in determining the sexual phenotype in three gonochorist species of the genus *Ophryotrocha*. The experiment consisted of two successive stages: 1) growth of a young specimen from hatching to sexual maturity in pair with and adult conspecific (male or female) or isolated. 2) rearing of these same individuals, now sexually differentiated, with an adult conspecific of the opposite sex or of the same sex. Preliminary results show a highly significant effect of the social environment in which the animal are reared in determining the sex of young specimen of at least one of the three species. Only during the juvenile phase the social environment can affect the sexual phenotype of the animals, after which the phenotype is strictly determined. For all of the three species the presence of intersexes does not depend on environmental condition, but seems to be genetically determined.



**Stefania Meconcelli**

University of Turin

2nd year PhD student

## Causes and consequences of body-mass and fitness variations: linking evolution and demography in a snow vole population

Variation in fitness and its maintenance is a relevant concept both at an individual level where it allows selection, under the interaction of genes and the environment, and at the population level where it shapes demography and the distribution of traits and genes. Thus fitness can be seen as a link between micro-evolution and ecology. On both levels, fitness is influenced by genes and environment, making the understanding of their relationship complex. Recently methodological advances have opened the possibility of new insights into the genes and environment interplay which shape evolutionary-ecological dynamics. However very few studies have applied them on natural population whereas this is crucial in the context of unprecedented global environmental changes. Here, to address this question we take advantage of the monitoring of a snow vole (*Chionomys nivalis*) population located in the Swiss Alps. It already consists of 8 years of mark-recapture, body measurements and DNA sampling. Mark-recapture analysis give us insights into demographic parameters while DNA is used for pedigree inference and further, combined with measurements, for estimation of heritabilities. Both methods give selection gradients, on survival or reproduction respectively. We hypothesize winter temperatures and snow cover are here strong environmental forces while body-mass should be a major target of selection. Contrasting pattern of selection across seasons or years might account for the maintenance of variation on body-mass and fitness and at the same time for demography and trait-distribution shifts at the population level.

**Timothée Bonnet**

University of Zürich  
1st year PhD student



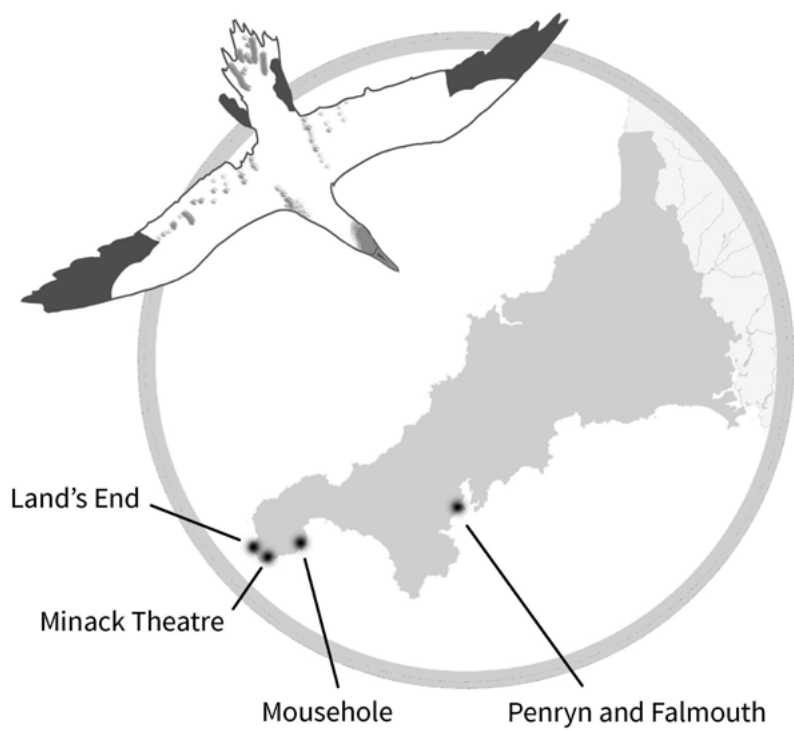
---

'There are animals we haven't stopped by.  
Don't think they're harmless. Life will defend  
itself no matter how small it is.'

Yann Martel

---

Sunday



## the excursion

The excursion will be a day trip to Cornwall's scenic west coast. In the morning you will be able to choose between a walk exploring the South-West coast path near Lands End, a route that takes in beautiful beaches and dramatic cliff top scenery, or something more adventurous – hopefully a surfing lesson with one of Cornwall's best known surf schools. We will then go to the world-famous Minack Theatre to enjoy a picnic lunch in this spectacular open-air space. The Minack sits on the cliffs above one of Cornwall's finest beaches, and we will take time to stop for some fun and games here too. In the afternoon we will head to the picturesque old fishing village of Mousehole to learn more about Cornwall's history and culture. All this will be followed by a big barbeque once we have arrived back in Falmouth. A day of non-stop excitement!





---

BMC Evolutionary Biology  
Information and selected abstracts



This abstract book has been funded by  
BMC Evolutionary Biology

## **Journal Information**

BMC Evolutionary Biology, published by BioMed Central, is an open access, peer-reviewed journal that considers articles on all aspects of molecular and non-molecular evolution of all organisms, as well as phylogenetics and palaeontology.

It is journal policy to publish work deemed by peer reviewers to be a coherent and sound addition to scientific knowledge and to put less emphasis on interest levels, provided that the research constitutes a useful contribution to the field.

## Section Information

The journal is split into the following editorial sections, each headed by world renowned Section Editors:

Evolutionary developmental biology and morphology - Section Editor Sylvie Mazan

This section considers studies in the evolution of development and developmental processes, and into morphological evolution.

Evolutionary ecology and behaviour – Section Editor Tom Pizzari

This section considers studies in the areas of evolutionary behavior and ecology including sexual conflict and selection.

Experimental evolution – Section Editor Michael Brokhurst

This section considers studies in testing evolutionary theories by the use of controlled experiments.

Genome evolution and evolutionary systems biology – Section Editors David Liberles and Arndt von Haeseler

This section considers studies on genome evolution and systems biology approaches to determining evolutionary processes.

Phylogenetics and phylogeography – Section Editors Jim Provan and Hervé Philippe

This section considers studies in the phylogeny and phylogeography of organisms.

Speciation and evolutionary genetics – Section Editor Walter Salzburger

This section considers studies into speciation and the role of inheritance and variation in individuals and among populations in evolution.

Theories and models - Section Editor Susanna Manrubia

This section considers studies in mathematical modeling of evolutionary processes and research into theoretical areas.

## State-of the art methodologies dictate new standards for phylogenetic analysis

Maria Anisimova, David A Liberles, Hervé Philippe, Jim Provan, Tal Pupko and Arndt von Haeseler

The intention of this editorial is to steer researchers through methodological choices in molecular evolution, drawing on the combined expertise of the authors. Our aim is not to review the most advanced methods for a specific task. Rather, we define several general guidelines to help with methodology choices at different stages of a typical phylogenetic 'pipeline'. We are not able to provide exhaustive citation of a literature that is vast and plentiful, but we point the reader to a set of classical textbooks that reflect the state-of-the-art. We do not wish to appear overly critical of outdated methodology but rather provide some practical guidance on the sort of issues which should be considered. We stress that a reported study should be well-motivated and evaluate a specific hypothesis or scientific question. However, a publishable study should not be merely a compilation of available sequences for a protein family of interest followed by some standard analyses, unless it specifically addresses a scientific hypothesis or question. The rapid pace at which sequence data accumulate quickly outdates such publications. Although clearly, discoveries stemming from data mining, reports of new tools and databases and review papers are also desirable.

# The cost of antibiotic resistance depends on evolutionary history in *Escherichia coli*

Daniel C Angst and Alex R Hall

## Background

The persistence of antibiotic resistance depends on the fitness effects of resistance elements in the absence of antibiotics. Recent work shows that the fitness effect of a given resistance mutation is influenced by other resistance mutations on the same genome. However, resistant bacteria acquire additional beneficial mutations during evolution in the absence of antibiotics that do not alter resistance directly but may modify the fitness effects of new resistance mutations.

## Results

We experimentally evolved rifampicin-resistant and sensitive *Escherichia coli* in a drug-free environment, before measuring the effects of new resistance elements on fitness in antibiotic-free conditions. Streptomycin-resistance mutations had small fitness effects in rifampicin-resistant genotypes that had adapted to antibiotic-free growth medium, compared to the same genotypes without adaptation. We observed a similar effect when resistance was encoded by a different mechanism and carried on a plasmid. Antibiotic-sensitive bacteria that adapted to the same conditions showed the same pattern for some resistance elements but not others.

## Conclusions

Epistatic variation of costs of resistance can result from evolution in the absence of antibiotics, as well as the presence of other resistance mutations.

## Serotonin-immunoreactive neurons in the ventral nerve cord of Remipedia (Crustacea): support for a sister group relationship of Remipedia and Hexapoda?

Torben Stemme, Thomas M Iliffe, Björn M von Reumont, Stefan Koenemann, Steffen Harzsch and Gerd Bicker

### Background

Remipedia were initially seen as a primitive taxon within Pancrustacea based on characters considered ancestral, such as the homonomously segmented trunk. Meanwhile, several morphological and molecular studies proposed a more derived position of Remipedia within Pancrustacea, including a sister group relationship to Hexapoda. Because of these conflicting hypotheses, fresh data are crucial to contribute new insights into euarthropod phylogeny. The architecture of individually identifiable serotonin-immunoreactive neurons has successfully been used for phylogenetic considerations in Euarthropoda. Here, we identified neurons in three species of Remipedia with an antiserum against serotonin and compared our findings to reconstructed ground patterns in other euarthropod taxa. Additionally, we traced neurite connectivity and neuropil outlines using antisera against acetylated  $\alpha$ -tubulin and synapsin.

### Results

The ventral nerve cord of Remipedia displays a typical rope-ladder-like arrangement of separate metameric ganglia linked by paired longitudinally projecting connectives. The peripheral projections comprise an intersegmental nerve, consisting of two branches that fuse shortly after exiting the connectives, and the segmental anterior and posterior nerve. The distribution and morphology of serotonin-immunoreactive interneurons in the trunk segments is highly conserved within the remipede species we analyzed, which allows for the reconstruction of a ground pattern: two posterior and one anterior pair of serotonin-immunoreactive neurons that possess a single contralateral projection. Additionally, three pairs of immunoreactive neurons are found in the medial part of each hemiganglion. In one species (*Cryptocorynetes haptodiscus*), the anterior pair of immunoreactive neurons is missing.

## Conclusions

The anatomy of the remipede ventral nerve cord with its separate metameric ganglia mirrors the external morphology of the animal's trunk. The rope-ladder-like structure and principal architecture of the segmental ganglia in *Remipedia* corresponds closely to that of other Euarthropoda. A comparison of the serotonin-immunoreactive cell arrangement of *Remipedia* to reconstructed ground patterns of major euarthropod taxa supports a homology of the anterior and posterior neurons in Pancrustacea. These neurons in *Remipedia* possess unbranched projections across the midline, pointing towards similarities to the hexapod pattern. Our findings are in line with a growing number of phylogenetic investigations proposing *Remipedia* to be a rather derived crustacean lineage that perhaps has close affinities to Hexapoda.

## Keywords:

Euarthropoda; Homology; Comparative neuroanatomy; Ground pattern; Phylogeny; Immunocytochemistry; Speleonectes; Godzillioognomus; Cryptocorynetes



## Forelimb preferences in quadrupedal marsupials and their implications for laterality evolution in mammals

Andrey Giljov, Karina Karenina and Yegor Malashichev

### Background

Acquisition of upright posture in evolution has been argued to facilitate manual laterality in primates. Owing to the high variety of postural habits marsupials can serve as a suitable model to test whether the species-typical body posture shapes forelimb preferences in non-primates or this phenomenon emerged only in the course of primate evolution. In the present study we aimed to explore manual laterality in marsupial quadrupeds and compare them with the results in the previously studied bipedal species. Forelimb preferences were assessed in captive grey short-tailed opossum (*Monodelphis domestica*) and sugar glider (*Petaurus breviceps*) in four different types of unimanual behaviour per species, which was not artificially evoked. We examined the possible effects of sex, age and task, because these factors have been reported to affect motor laterality in placental mammals.

### Results

In both species the direction of forelimb preferences was strongly sex-related. Male grey short-tailed opossums showed right-forelimb preference in most of the observed unimanual behaviours, while male sugar gliders displayed only a slight, not significant rightward tendency. In contrast, females in both species exhibited consistent group-level preference of the left forelimb. We failed to reveal significant differences in manual preferences between tasks of potentially differing complexity: reaching a stable food item and catching live insects, as well as between the body support and food manipulation. No influence of subjects' age on limb preferences was found.

### Conclusions

The direction of sex-related differences in the manual preferences found in quadrupedal marsupials seems to be not typical for placental mammals. We suggest that the alternative way of interhemispheric connection in absence of corpus callosum may result in a fundamentally distinct mechanism of sex effect on limb preferences in marsupials compared to placentals. Our data confirm the idea that non-primate mammals differ from primates in sensitivity to task complexity. Comparison of marsupial species studied to date indicate that the vertical body orientation and the bipedalism favor the expression of individual- and population-level forelimb preferences in marsupials much like it does in primates. Our findings give the first evidence for the effect of species-typical posture on the manual laterality in non-primate mammals.

## Parasitic plants have increased rates of molecular evolution across all three genomes

Lindell Bromham, Peter F Cowman and Robert Lanfear

### Background

Theoretical models and experimental evidence suggest that rates of molecular evolution could be raised in parasitic organisms compared to non-parasitic taxa. Parasitic plants provide an ideal test for these predictions, as there are at least a dozen independent origins of the parasitic lifestyle in angiosperms. Studies of a number of parasitic plant lineages have suggested faster rates of molecular evolution, but the results of some studies have been mixed. Comparative analysis of all parasitic plant lineages, including sequences from all three genomes, is needed to examine the generality of the relationship between rates of molecular evolution and parasitism in plants.

### Results

We analysed DNA sequence data from the mitochondrial, nuclear and chloroplast genomes for 12 independent evolutionary origins of parasitism in angiosperms. We demonstrated that parasitic lineages have a faster rate of molecular evolution than their non-parasitic relatives in sequences for all three genomes, for both synonymous and nonsynonymous substitutions.

### Conclusions

Our results prove that raised rates of molecular evolution are a general feature of parasitic plants, not confined to a few taxa or specific genes. We discuss possible causes for this relationship, including increased positive selection associated with host-parasite arms races, relaxed selection, reduced population size or repeated bottlenecks, increased mutation rates, and indirect causal links with generation time and body size. We find no evidence that faster rates are due to smaller effective populations sizes or changes in selection pressure. Instead, our results suggest that parasitic plants have a higher mutation rate than their close non-parasitic relatives. This may be due to a direct connection, where some aspect of the parasitic lifestyle drives the evolution of raised mutation rates. Alternatively, this pattern may be driven by an indirect connection between rates and parasitism: for example, parasitic plants tend to be smaller than their non-parasitic relatives, which may result in more cell generations per year, thus a higher rate of mutations arising from DNA copy errors per unit time. Demonstration that adoption of a parasitic lifestyle influences the rate of genomic evolution is relevant to attempts to infer molecular phylogenies of parasitic plants and to estimate their evolutionary divergence times using sequence data.

## *Wolbachia* association with the tsetse fly, *Glossina fuscipes fuscipes*, reveals high levels of genetic diversity and complex evolutionary dynamics

Rebecca E Symula, Uzma Alam, Corey Brelsfoard, Yineng Wu, Richard Echodu, Loyce M Okedi, Serap Aksoy and Adalgisa Caccone

### Background

*Wolbachia pipientis*, a diverse group of  $\alpha$ -proteobacteria, can alter arthropod host reproduction and confer a reproductive advantage to *Wolbachia*-infected females (cytoplasmic incompatibility (CI)). This advantage can alter host population genetics because *Wolbachia*-infected females produce more offspring with their own mitochondrial DNA (mtDNA) haplotypes than uninfected females. Thus, these host haplotypes become common or fixed (selective sweep). Although simulations suggest that for a CI-mediated sweep to occur, there must be a transient phase with repeated initial infections of multiple individual hosts by different *Wolbachia* strains, this has not been observed empirically. *Wolbachia* has been found in the tsetse fly, *Glossina fuscipes fuscipes*, but it is not limited to a single host haplotype, suggesting that CI did not impact its population structure. However, host population genetic differentiation could have been generated if multiple *Wolbachia* strains interacted in some populations. Here, we investigated *Wolbachia* genetic variation in *G. f. fuscipes* populations of known host genetic composition in Uganda. We tested for the presence of multiple *Wolbachia* strains using Multi-Locus Sequence Typing (MLST) and for an association between geographic region and host mtDNA haplotype using *Wolbachia* DNA sequence from a variable locus, groEL (heat shock protein 60).

### Results

MLST demonstrated that some *G. f. fuscipes* carry *Wolbachia* strains from two lineages. GroEL revealed high levels of sequence diversity within and between individuals (Haplotype diversity = 0.945). We found *Wolbachia* associated with 26 host mtDNA haplotypes, an unprecedented result. We observed a geographical association of one *Wolbachia* lineage with southern host mtDNA haplotypes, but it was non-significant ( $p=0.16$ ). Though most *Wolbachia*-infected host haplotypes were those found in the contact region between host mtDNA groups, this association was non-significant ( $p = 0.17$ ).

### Conclusions

High *Wolbachia* sequence diversity and the association of *Wolbachia* with multiple host haplotypes suggest that different *Wolbachia* strains infected *G. f. fuscipes* multiple times independently. We suggest that these observations reflect a transient phase in *Wolbachia* evolution that is influenced by the long gestation and low reproductive output of tsetse. Although *G. f. fuscipes* is superinfected with *Wolbachia*, our data does not support that bidirectional CI has influenced host genetic diversity in Uganda.

## Simulating gene trees under the multispecies coalescent and time-dependent migration

Joseph Heled, David Bryant and Alexei J Drummond

### Background

The multispecies coalescent model has become popular in recent years as a framework to infer a species phylogeny from multilocus genetic data collected from multiple individuals. The model assumes that speciation occurs at a specific point in time, after which the two sub-species evolve in total isolation. However in reality speciation may occur over an extended period of time, during which sister lineages remain in partial contact. Inference of multispecies phylogenies under those conditions is difficult. Indeed even designing simulators which correctly sample gene histories under these conditions is non-trivial.

### Results

In this paper we present a method and software which simulates gene trees under both the multispecies coalescent and migration. Our approach allows for both population sizes and migration rates to change over the species lifetime. Also, migration rates are specified in units of fraction of emigrants per time unit, which makes them easier to interpret. Overall this setup covers a wide range of migration scenarios. The software can be used to investigate properties of gene trees under different migration settings and to generate test cases for programs which infer species trees and/or migration from sequence data. Using simulated data we investigate the effect of migrations between sister lineages on the inference of multispecies phylogenies and on post analysis detection.

### Conclusions

Our results indicate that while estimation of species tree topology can be quite robust to the presence of gene flow, the inference and detection of migration is problematic, even with methods based on full likelihood models.

| Time        | Tues 03/09       | Wed 04/09            | Thurs 05/09                     | Fri 06/09                | Sat 07/09             | Sun 08/09           |
|-------------|------------------|----------------------|---------------------------------|--------------------------|-----------------------|---------------------|
| 08:00-09:00 |                  | Breakfast            | Breakfast                       | Breakfast                | Breakfast             |                     |
| 09:00-10:00 |                  | Tom Currie *         | Coach to Eden Project           | Judith Mank *            | Paula Stockley *      |                     |
|             |                  | GREEN                |                                 | GREEN                    | GREEN                 |                     |
| 10:10-10:30 |                  | Akash Sharma         |                                 | RED                      | RED                   |                     |
| 10:30-10:50 |                  | Antoine Stier        | Geoff Parker                    | Ansuja Chakrabarty       | Christopher Quickfall | Anne Winters        |
| 10:50-11:10 |                  | Anni Härmäläinen     |                                 | Ben Ashby                | Kati Saarinen         | Charlie Ellis       |
| 11:10-11:30 |                  | Valentina Botto      |                                 | Christopher Culbert      | Dimitri Stucki        | Anna Campbell       |
| 11:30-12:00 |                  | Uttaran Maiti        |                                 | Virginie Thuillier       | Wolfgang Reschka      | Yun Huang           |
|             |                  | Coffee break         |                                 | Alison Cotton            |                       |                     |
| 12:00-12:20 |                  | Elizabeth Duxbury    | Discussion groups/<br>free time | Coffee break             |                       |                     |
| 12:20-12:40 |                  | Eduard Solà          |                                 | Eryn McFarlane           | Gaelle Pontarotti     | Georgina Brennan    |
| 12:40-13:00 |                  | Isabel Salome Keller |                                 | Isabel Mück              | Isabel Winney         | Iwona Giska         |
|             |                  | Jana Wolf            |                                 | Jonathan Henshaw         | Juan Ramirez          | Julien Amouret      |
| 13:00-14:00 |                  | Lunch                | Lunch                           | Lunch                    | Lunch                 |                     |
| 14:00-15:00 |                  | Johanna Mappes *     |                                 | Troy Day *               | Britt Koskella *      |                     |
| 15:10-15:30 |                  | Naga Apoorva Kasala  |                                 | Joanna Sudyka            | Lien Reyserhove       | Lucas Marie-Orléach |
| 15:30-15:50 |                  | Merel Breechveld     | Workshops                       | Marie Rescan             | Marine Pouget         | Martin Vallon       |
| 15:50-16:10 |                  | Malgorzata Grzesluk  |                                 | Nina Wale                | Pablo Valverde        | Pascal Milesi       |
| 16:10-16:30 |                  | Katrine Lund-Hansen  |                                 | Ramith Nair              | Rebecca Jones         | Saskia Wutke        |
| 16:30-17:00 |                  | Christine Tansey     |                                 |                          | Raissa de Boer        | Coffee break        |
|             |                  | Paul Saunders        |                                 |                          |                       | Rebecca Watson      |
| 17:00-17:20 |                  | Peipin Kamminga      |                                 |                          |                       | Silvio Waschina     |
| 17:20-17:50 | Check in         | Richa Joag           | Free time                       | free time                |                       | Tess Driessens      |
| 17:50-18:10 |                  | Roslyn Henry         |                                 |                          |                       | Tanya Pennell       |
|             |                  | Robert Griffin       |                                 |                          |                       | Stefania Meconcelli |
|             |                  | Sarah Bouchemousse   |                                 |                          |                       | Timothée Bonnet     |
| 18:10-19:00 | Andy Gardner *   | Sophie Reichert      | Laurent Keller                  | Dinner (17:30)           | Free time             |                     |
|             |                  | Simon Uphill         |                                 |                          |                       |                     |
| 19:00       | Dinner & welcome | Activities           | Dinner at Eden                  | For the Love of Science! | Dinner/ PARTY!        |                     |
|             |                  | Dinner               |                                 |                          |                       |                     |

\*These talks will be held in the chapel

