Comparing the ocelli of temperate and tropical bees with microCT

External observations of bees indicate there is great diversity in the shape and placement of their ocelli, yet no study has examined the visual consequences of such differences. To begin characterizing the ocelli of different bee species, we conducted microCT scans at a synchrotron light source using specimens obtained from Panama, Brazil, and Sweden. The opportunity exists for a pair of motivated students to investigate these exciting results with us. Students will be taught how to analyze volumetric data using specialized software (Amira), and use these techniques to describe our microCT scan data. 3D models of the ocelli will be created, which will allow visual parameters such as the field of view and optical resolution to be calculated. Students will report on the optical specializations found in the eyes of different bee species and relate these findings to our knowledge of their ecology.

Identified as fungus gnat (sopamyg) Department
Optical axes projected onto image

Contact: Emily Baird emily.baird@biol.lu.se
Effects of systemic pesticides on natural pest control in oilseed rape

Background
Insecticides are used to control agricultural pest insects in almost all cropping systems and across various management schemes. As an undesirable side effect, insecticides also impact beneficial insects such as pollinators and parasitoids. The latter can also be an effective control agents against agricultural pests, however without harming other beneficial parts of the environment. This project will analyse to which degree parasitoids are affected by systemic insecticides and if the natural population of parasitoids without pesticide treatments is potentially able to efficiently control distinct pests. In particular it is focussed on the impact of systemic neonicotinoids on pollen beetles and parasitic wasps as their natural enemies, considering abundances and parasitation rates.

Workplan
Altogether 32 samples from oilseed rape fields should be analysed considering the abundance of pollen beetle larvae and their infestation with parasitoid eggs. If possible, pollen beetle larvae should be analysed due to the parasitation rate at untreated and treated fields.

Benefits
The bachelor thesis covers one of the most wanted hot topics in ecology and ecotoxocology – neonicotinoids – within the frame of a large-scale experiment. The possible candidate will also be trained in using the open source statistics program R, which has become a standard in modern ecological analytics. The results of the thesis will probably be published in a scientific journal with the option of a co-authorship.

Contact
Björn K. Klatt: klattbk@googlemail.com
Josef Berger: josef.berger@biol.lu.se
Oilseed rape – a stressor or supporter for solitary bees in agricultural landscapes?

Background
In agricultural landscapes, bees and other pollinators are exposed to various stressors. For some elements it is not clarified whether they should be considered as stressors or beneficial for pollinators. In particular the role of mass-flowering crops has been discussed contrastingly. They can function as important early foraging resources in agricultural landscapes, in particular in complex landscapes where resources are available directly after the flowering of an early mass-flowering crop, but in turn can boost pollinator populations beyond the foraging resources available in simple landscapes.

Aims
This project will focus on the interaction between oilseed rape, as an early mass-flowering crop and wild bee populations, in terms of resource provision and fitness.

Methods
This MSc project will give a deep insight into the fascinating world of solitary wild bees, their lifestyle and potential stressors. The fieldwork has already been done in summer 2017 and task of the thesis is to assess the reproduction success and fitness as well as parasitation of the bee’s offspring in relation to the distance to oilseed rape from trap nests. In Optional, in addition pollen samples will be analysed for the quantity of oilseed rape pollen using a pollen scanner.

Contact
Björn: klattbk@googlemail.com; alternatively, just come to my office and see if I am there for a spontaneous meeting.
What kind of molecular mechanisms do cells use to survive without telomerase?

Telomeres are specialized structures that define the ends of eukaryotic chromosomes and are essential for keeping their integrity and genome stability. The principal mechanism for maintaining long telomeres is dependent on the enzyme telomerase, which synthesizes the specific repeated sequences at the ends of chromosomes. If telomerase is absent, telomeres will shorten and the cells will die. However, intriguingly, a backup mechanism for the elongation of telomeres may be activated, which thus generate survivors.

We are currently studying yeast strains where the telomerase gene has been deleted (knock-out strains). Although the telomeres are drastically shortened in these strains, survivors will frequently appear. We want to understand what kind of molecular mechanism that is activated in these survivors. To elucidate whether DNA recombination is involved, we aim to knock out one of the genes necessary for homologous recombination, *RAD52*, in wild-type strains and in telomerase knock-out strains. In this project you will transform yeast cells with a DNA construct, isolate genomic DNA from the colonies, and then genotype the transformants by PCR amplification and agarose gel electrophoresis. On the positive knock-outs you will perform growth rate analyses and study the cell phenotype and colony morphology.

Contact: Marita Cohn Marita.Cohn@biol.lu.se
Exploring the Molecular Regulation of Plant Stress Responses.

Plants are continuously exposed to changes in environmental conditions that lead to stress and adversely affect growth and reproduction. This is especially relevant where agriculture is threatened by limited water resources, temperature extremes and soil salinity. My research has made a significant contribution to understanding which regulatory networks regulate these signalling events and has identified several novel genes that can improve plant resistance to drought stress and pathogen defence.

The goal of this project will be to further elucidate how these transcription factors are activated to initiate transcription of the downstream stress-response genes, using state-of-the-art molecular biology techniques. The student will have the opportunity to join in on well-established projects that will likely result in exciting new findings to kick-start his/her research career.

In our lab, we have access to state-of-the-art technologies such as next-generation sequencing, CRISPR-Cas9 site-directed mutagenesis, microscopy and phenotypical analysis. The student will be trained at a high level in molecular biology techniques and will have the chance to make a real contribution to world-class research.

Contact: olivier.van_aken@biol.lu.se

A plant’s global response to cope with water deficit, high temperature and salinity is mediated by an intricate network of molecular changes and signalling events.
**Aim**
The aim of this project is to determine if Ferredoxin: NADP$^+$ Reductase-Like (FNRL) is involved in the enigmatic cyclase step of chlorophyll biosynthesis. This will be investigated by cloning the FNRL gene and expressing it in E. coli to produce recombinant FNRL protein, which can then be tested with *in vitro* activity assays for the cyclase reaction.

**Background**
Chlorophyll is the green pigment responsible for the absorption of sunlight to provide energy for photosynthesis in plants, algae, and cyanobacteria. The energy stored in chemical bonds by photosynthesis supports all other life on earth. Although chlorophyll is of great fundamental importance to life on earth, one step of its biosynthesis is not well characterized. This step is the aerobic cyclase reaction that converts Mg-protoporphyrin IX monomethyl ester into protochlorophyllide. We recently identified the *Viridis*-k gene in barley to be a ferredoxin responsible for providing electrons to the cyclase reaction. Ferredoxins can receive these electrons from photosystem I or Ferredoxin: NADP$^+$ Reductase (FNR). Plant genomes also contain a FNR-Like (FNRL) gene which we believe may be responsible for electron transfer to the cyclase reaction via ferredoxin.

**To do:**
1) Clone the FNRL gene into an expression vector and transform into E. coli
2) Express and purify recombinant FNRL
3) Test the effect of recombinant FNRL on our *in vitro* cyclase assay
4) Stability Testing of recombinant FNRL

**Highlight of Techniques Used:**
1) Polymerase Chain Reaction (PCR)
2) Agarose gel electrophoresis
3) Gateway cloning
4) *E. coli* transformation
5) Protein expression in *E. coli*
6) Protein purification by Immobilized Metal Ion Affinity Chromatography (IMAC)
7) SDS-PAGE

**Supervisor:**
Professor Mats Hansson

**Co-Supervisor:**
David Stuart
Population trends of Swedish birds – patterns, causes and consequences

Within the Swedish Bird Survey (Svensk Fågeltaxering) the population development of Swedish breeding and wintering birds are tracked since more than 40 years. Since 18 years we have systematic monitoring data covering the whole of Sweden in a representative way (the Fixed routes, "standardruttena"). From this we produce yearly updated national and regional trends for more than 150 bird species. So far the data has been used to investigate the effect of both climate and land use changes, but much of the data is still unexplored and many questions remain to be answered. For example, how do changing rodent populations such as lemming cycles affect the breeding bird fauna? When and where did the decline of the Greenfinch start, and is it all due to a protozoan parasite? Are the breeding bird-trends similar in Sweden and neighbouring countries, and if not, why? We know that the breeding bird fauna in Sweden has been influenced by a warming climate so that more warm-loving species have increased and cold-loving species have declined in numbers. What does it look like during winter – did milder winters change Swedish winter bird communities? And so on… A project can be shaped after your own interest, in terms of species, questions, analysis methods, and so on.

Please contact Martin Green or Åke Lindström if you are interested.”

martin.green@biol.lu.se; ake.lindstrom@biol.lu.se
Urban pollinering: pollinering i stad och på landsbygd

Jag samlade in massor av spännande data på pollinatörer och pollinering i Malmö i somras, bl.a. frösättning av rödklint. Jag har haft planter i kruka ute i trädgårdar, i olika täta och gröna stadsdelar, samt på landsbygden runt Malmö. Ett kandidatprojekt skulle kunna innebära att räkna frön och jämföra frösättning i stad och på landsbygden: dvs att analysera 7 stadslokaler och 7 från landsbygden, och sedan jämföra dessa.

Contact: Anna Persson anna.persson@cec.lu.se
CRISPR/Cas9 assisted genome editing.

The ability to make precise changes in the genome have broad implications with regards to both basic and applied research. In this project genetic engineering through homologous recombination, known as recombineering, assisted by CRISPR/Cas9 will be applied to engineer *Escherichia coli* for different applications. Marker-free site-specific mutations and gene deletions will be made. The aim is to engineer host strains that are tailored for the production of particular classes of proteins.

Contact: Claes von Wachenfeldt  
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+46 46 222 34 56
2 projects:

1. Investigating genetic variation and potential hybridization in host plant races of *T. conura*

*Tephritis conura* is a tephritid fly species that has formed sub species specializing on different host plants. This project includes investigating which parts of the genome have diverged due to host plant adaptation. It also tests if there is hybridization between sub species as the southern species distribution shift northwards following global warming. Here we will be using RAD-tag data to investigate adaptive divergence between and gene flow introgression. This projec will provide training in both lab skills and bioinformatics skills.

2. Wing adaptations in host plant races of a tephritid fly: shape and color

*Tephritis conura* is a tephritid fly species that has formed sub species specializing on different host plants. This project includes investigating whether wing morphology and coloration diverged due to host plant adaptation and in response to sympatry with the other subspecies to avoid maladaptive hybridization (character displacement). Using geometric morphometrics (statistical analysis of shape) and color analysis we will investigate these questions. The project will provide knowledge of how to use tools for shape and color analysis as well as statistical analysis skills.

Contact: Anna.Runemark@biol.lu.se
Finding partners for a protein

Supervisors: Markus Fröjd and Klas Flärdh

Protein-protein interactions are crucial for many processes in a cell. If you want to understand the function of a specific protein, it is often important to identify other proteins that it interacts with. In this project, you will use a widely useful genetic method called a two-hybrid system to identify and study protein-protein interactions. The specific task is to identify previously unknown interaction partners for a cytoskeletal protein from a bacterium. This protein, FilP in Gram-positive bacteria of the genus *Streptomyces*, is similar to eukaryotic intermediate filament proteins. It is involved in the highly polarised growth that is characteristic of these bacteria (they build their cell walls only at the tips of long filamentous cells), and it is localised in an interesting way just behind the growth zone in the cells. To better understand the function of FilP, we will use a bacterial two-hybrid system to screen a genomic library for interaction partners for FilP. The system builds on classical bacterial genetic tools and methodology in *E. coli* and allows for selection and identification of clones encoding proteins that interact with FilP. Putative partners will be identified by DNA sequencing and further studied to confirm possible interactions. The methods that you will use during the project are generally useful for any molecular biologist.

Reference:

Contact: klas.flardh@biol.lu.se
Investigating the role of phosphorylation of an essential cell polarity determinant in a bacterium

Supervisors: Fanny Passot and Klas Flärdh

Many processes in eukaryotic cells are regulated by phosphorylation of Ser and Thr residues on proteins. For a long time, this type of regulation was believed to be rare in bacteria, but that view has changed and it is now clear that Ser/Thr protein kinases (of the type that is common in eukaryotes) are relatively abundant in many bacterial groups. One example is *Mycobacterium tuberculosis*, where Ser/Thr protein phosphorylation has received a lot of attention. In this project, you will study a case in a related bacterium, *Streptomyces coelicolor*, where Ser/Thr protein phosphorylation is involved in control of growth and morphogenesis. An essential protein that acts as a determinant of cell polarity and cell shape is subject to phosphorylation. In order to determine the role of this phosphorylation, the identified Ser and Thr residues that are phosphorylated have been mutated to Ala to abolish phosphorylation, and to Asp to mimic constitutive phosphorylation. This project will be part of the analysis of these mutants. The effects of mutations on phosphorylation status of the protein will be monitored by protein extractions and Western blotting. You will also determine the effects of activating or deleting the protein kinase and the phosphatase that are involved in the process. Further, the project will include analyses of possible phenotypic effects of manipulating the phosphorylation. The work will include SDS-PAGE and Western blotting, various microbiological methods, and microscopy.

References:

Contact: klas.flardh@biol.lu.se
Sphingosine-1-phosphate (S1P) receptor modulation in cerebrovascular endothelial cell activation

Supervisor: Anja Meissner

Background and project objective
Hypertension negatively affects the macro- and microvasculature of several organs, including the brain. It is the major modifiable risk factor for the development of cerebral small vessel disease and associated cognitive impairment in the elderly. Although blood pressure levels are being thoroughly controlled in patients at high risk for cardiovascular disease, the number of people with mildly but chronically elevated blood pressure often remain untreated. Because recent findings underscored the pathophysiological importance of elevated blood pressure levels for the development of cerebral small vessel disease and vascular dementia later in life, targeting hypertension and associated vascular dysfunction might also evolve as promising therapeutic strategies to treat cognitive phenotypes (e.g., memory loss) emanating from hypertension. Because small arteries and arterioles primarily determine peripheral resistance and tissue perfusion, compromised vascular function and particularly, impaired endothelial function is not only deleterious for our cardiovascular system but also for our brain. Specifically, endothelial impairment that is considered a hallmark of hypertension critically contributes to cerebrovascular inflammation and dysfunction subsequently, altering brain perfusion. Our laboratory recently showed that high levels of the bioactive phospholipid S1P associated to experimental hypertension. S1P signaling is known to play a key role in a number of endothelial functions influencing vascular tone, angiogenesis, permeability, endothelial activation and vascular inflammation. Many of these effects are owing to the activation of S1PR1 receptor. We found that hypertension critically affects vascular S1PR1 expression. Therefore, we aim to test the effect of S1PR1 modulation on cerebrovascular endothelial activation and T-cell adhesion in an in vitro model using cerebral artery endothelial and T-cell cell lines.

Brief overview of the anticipated work plan
Culturing cerebral endothelial cells on an orbital shaker will mimic blood flow-induced shear stress in vitro. The expression of different endothelial activation markers under control conditions and after S1PR modulation will be determined using standard molecular approaches such as, quantitative real-time PCR, Western blotting and immune-fluorescence. The endothelial-dependent generation of S1P, pro-inflammatory cytokines as well as reactive oxygen species will be determined using mass spectrometry or specific enzyme-linked immunosorbent assays, respectively. Co-culture experiments with T-cells will test the effect of S1PR modulation on the adhesion of Sudan Black-labeled human T-cells to the activated endothelial layer.

Work environment
The recently established Vascular Biology group led by Anja Meissner is located at BMC-D12. http://portal.research.lu.se/portal/en/persons/anja-meissner(6a464116-a3b7-4cd2-b418-2206a3f2d1b0).html We work in a newly equipped laboratory and in close collaboration with other laboratories led by experts in the field of vascular physiology.

Contact: anja.meissner@med.lu.se
The role of sphingosine-1-phosphate (S1P) generation in vascular inflammation

Supervisor: Anja Meissner

Background and project objective

Our vasculature plays an important role in the development and progression of cardiovascular disease and majorly contributes to the pathogenesis of hypertension – the main modifiable risk factor for heart failure, coronary heart disease and stroke. Because small arteries majorly determine peripheral resistance, compromised vascular function and particularly, impaired endothelial function is deleterious for our cardiovascular system. Such endothelial impairment critically contributes to the production of reactive oxygen species in the vasculature, the accumulation of activated immune cells (mainly T-cells) within the vessel wall and to the release of pro-inflammatory cytokines. Particularly, the process of T-cell migration into vascular tissue is critically determined by the degree of endothelial activation.

Various stimuli, such as high blood pressure and elevated levels of angiotensin II (AngII) or sphingosine-1-phosphate (S1P) majorly effect endothelial function during hypertension and thus, critically determine T-cell accumulation and vascular inflammation with implications for vascular structure and function. Our laboratory recently described a fundamental contribution of the bioactive phospholipid S1P to the pathogenesis of experimental hypertension, whereby its generating enzyme SphK2 evolves as key player in S1P-directed T-cell trafficking and vascular dysfunction contributing to hypertension. The inhibition of SphK2 drastically lowered blood pressure levels and lessened vascular inflammation in mice.

We now, aim to test the effect of SphK2 inhibition on endothelial activation and T-cell adhesion in an in vitro model using primary human endothelial and T-lymphocyte cell lines.

Brief overview of the anticipated work plan

Culturing human endothelial cells on an orbital shaker will mimic blood flow-induced shear stress in vitro. The expression of different endothelial activation markers under control conditions and after SphK2 inhibition will be determined using standard molecular approaches, such as quantitative real-time PCR, Western blotting and immune-fluorescence. The endothelial-dependent generation of S1P, pro-inflammatory cytokines as well as reactive oxygen species will be determined using mass spectrometry or specific enzyme-linked immunosorbent assays, respectively. Co-culture experiments with T-cells will test the effect of SphK2-inhibition on the adhesion of Sudan Black-labeled human T-cells to the activated endothelial layer.

Work environment

The recently established Vascular Biology group led by Anja Meissner is located at BMC-D12. http://portal.research.lu.se/portal/en/persons/anja-meissner(6a464116-a3b7-4cd2-b418-2206a3f2d1b0).html We work in a newly equipped laboratory and in close collaboration with other laboratories led by experts in the field of vascular physiology.

Reference:


Contact: anja.meissner@med.lu.se
Community level analysis of spore dispersal phenology in bryophytes

Colonization of bryophytes on bare soil takes place by spores (or sometimes vegetative propagules). Seasonal timing of spore release differs between species. Spore release timing of individual species may depend on temporal availability of bare ground, climatic parameters (availability of water) and the seasonal degree of competition. Spores that are dispersed at the same time will compete for space during colonization of bare ground. We have undertaken experiments which show that this interaction between spores during germination, subsequent protonema formation and budding of gametophytes involves both exploitation and interference competition.

The approach of this project is to use lists of species which occur together in the same habitat. Such lists have been compiled by Torbjörn Tyler for Scania and are included in the Scanian bryophyte key, which is use in the Scanian bryophyte inventory ("Projekt Skånes mossor"). The timing of spore release will be extracted from literature (mostly in Swedish or German) and/or from inspection of herbarium samples. The overall idea is to check whether different species in the same habitat have different periods of spore release or not and maybe if they have a long or short spore dispersal period. Several different habitats could be compared.

Nils Cronberg
nils.cronberg@biol.lu.se
Follow the Daphnia and discover how they respond in natural populations and under stress.

In the context of an on-going research project at the Aquatic Ecology Unit, Lund University, we propose an internship that can develop into a BSc or MSc thesis, to begin as soon as possible.

The research project aims at evaluating the genetic structure and swimming behaviour of Daphnia magna (a zooplankton species) in natural populations and at investigating how individual Daphniids cope with environmental stressors, such as UV and Predation, over generations.

During the BSc/MSc thesis, the student will learn and apply diverse genetic techniques and will have the opportunity to approach microorganism tracking techniques within the team. The length and focus of the student project can be adapted to his/her interest.

For more information on one or several aspects of this project, please contact: Sylvie Tesson (sylvie.tesson@biol.lu.se).

Glimpses in our world:
http://canmovefieldblog.blogspot.se/2017/05/all-you-want-no-know-about-daphniass.html
http://www.biology.lu.se/research/research-groups/aquatic-ecology/research-projects/migration-in-small-aquatic-animals

Key words: asexual reproduction, population genetic structure, inheritance, fitness, transgenerational acclimation and adaptation to environmental stressors, natural populations.

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Potential impacts of genetically modified maize on the abundance of non-target insects

**Background:**

Maize is a relatively new and small crop in Sweden, without much prior knowledge about which organisms may colonize it. Genetically modified maize has been designed primarily to prevent infestations by the European Corn Borer *Ostrinia nubilalis*, but an important question is how this affects non-target organisms such as other herbivores and particularly their natural enemies but also pollinators. In order to assess how to adjust sampling effort to achieve protection goals, insect samples were collected during a European Union project called AMIGA (Assessing and Monitoring Impacts of Genetically modified plants on Agro-ecosystems).

**Workplan:**

Insect samples from maize fields need to be sorted into major groups (no prior entomological knowledge necessary, as the supervisors will provide assistance with this task). The relative abundances of these groups will then be analysed for differences between GMO maize and conventional maize.

Since we have data from both window traps and pitfall traps, and also abundance data on aphids which have been hand-plucked from the leaves, there is an option for several students to work in parallel on material from these different collection methods. A further option is to suggest your own ideas if you are interested.

**Benefits:**

You will learn common methods in biodiversity analysis by processing material from raw field samples to statistical analysis and presentation of scientific data. By sorting insect material into major groups during a couple of weeks, you will gain experience in agricultural entomology that goes far beyond what you may remember from the basic faunistics course. You will also be trained in the most commonly used statistical software, which is a valuable skill for all future ecological contexts.

If the results of the project will be included into a larger scientific publication within the AMIGA framework, then you will of course be offered coauthorship.

**Contact:**

Tina D’Hertefeldt, Biodiversity Unit: tina.dhertefeldt@biol.lu.se
Josef Berger, Biodiversity Unit: josef.berger@biol.lu.se
Intraspecific versus interspecific variation in morphology: Is it one species or several species?

Background:
*Euderus albitarsis* is a small parasitoid wasp which is poorly known yet widespread over the entire Holarctic and parts of the Oriental region. It has a large host record which spans 5 different insect orders and includes some important agricultural pests (such as the cabbage seedpod weevil). Traditional species delimitation in the genus *Euderus* has previously been based on subjective interpretations, and molecular information on species level is lacking, with most material available exclusively as museum specimens. The big question is whether this actually is one species, or whether several species are hidden under the simple species description "three hairlines in the forewing".

Work plan:
This project consists of taking digital images of a large sample size of available specimens (provided by the supervisor), measuring several morphological characters in the images, and performing a morphometric analysis in order to answer the question whether this is one species or several species.
If overlapping morphological patterns are found among the available specimens and if these are not correlated with any particular habitat/host, then this may support the null hypothesis of one single species that is a broad generalist.
If distinct morphological clusters can be found among the available material, and if these happen to be correlated with habitat/host, then this may support the alternative hypothesis of multiple species.

Benefits:
You will be trained in working with a binocular microscope and in digital imaging analysis. In case of interest, we can also involve scanning electron microscopy. You will learn several morphometric methods which enable objective species discrimination based on sophisticated statistics. You will also be trained in R, an open-source statistics software which is becoming the standard in biological analysis. In addition, you will gain knowledge of insect morphology (which is becoming rare nowadays since the young generation of entomologists is becoming obsessed with genetics).

The results of this project will probably be included into a larger scientific publication (a taxonomic revision of the genus *Euderus*) with the option of a coauthorship.

Contact:
Josef Berger, Biodiversity Unit: josef.berger@biol.lu.se