research group:

Evolutionary & Population Biology

Research Projects

The role of ants as pollinators and seed dispersers in the rare *Thesium humifusum*

Supervisors: Gerard Oostermeijer & Sheila Luijten (Science4Nature)
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Project outline

Even though ants are very common members of nearly every biological community, they are remarkably scarce as pollinators, in particular in temperate regions. Even though they regularly visit flowers of various species, ants are generally considered poor pollinators because of their small size, low action radius and frequent grooming. Recently, the fact that ants secrete antibiotic compounds has also been associated with their limited role as pollinators. Nevertheless, specialized pollination relations occur between orchids and ants, and in harsh systems that favour low growth forms, ant pollination also occurs, albeit rarely.

Ant dispersal (myrmecochory) is much more frequent in our flora, and many species have seeds bearing food bodies, or elaiosomes, that cause ants to carry them (in)to their nest. Because ants are small, and have a limited foraging range, the function of this dispersal is not so much attaining a distance from the mother plant, but more about being deposited in a safe site for germination and survival (directional dispersal).

We study the demography and genetics of the extremely rare plant *Thesium humifusum* (Santalaceae), which occurs at only a single locality in The Netherlands. Stems of this species lay flat on the vegetation, and we have observed that the small, open flowers are visited by ants for nectar. It is not known to what extent ants actually function as pollinators, transferring (cross) pollen from one flower to the next. In addition, *T. humifusum* has seeds bearing an elaiosome, and we have also observed that ants readily (attempt to) carry them to their nest sites.

The main question of this research project is: How important are ants for the pollination and dispersal of this species?

Techniques:

- Designing and carrying out pollinator exclusion experiments;
- Determining the extent of pollen transport by ants using e.g. cubes of sticky gel
- Counting fruit and seed set
- Performing (cafetaria) experiments to demonstrate (directional) seed dispersal by ants

Background reading:

Beattie AJ (2006) The evolution of ant pollination systems. Bot. Jahrb. Syst. 127, 43–55.

Oostermeijer J.G.B. (1989) Myrmecochory in *Polygala vulgaris* L., *Luzula campestris* (L.) DC. and *Viola curtisii* Forster in a Dutch dune area. Oecologia 78, 302-311.

How do genetic processes drive individual fitness in reintroduced populations of endangered plants?

Supervisors: Gerard Oostermeijer, Sheila Luijten (Science4Nature), Patrick Meirmans
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Project outline

Many plant and animal populations are threatened with extinction by extensive habitat fragmentation, which reduces population sizes and increases isolation. Inbreeding depression is an important mechanism lowering individual fitness and subsequently population viability. We are trying to alleviate inbreeding depression by genetic rescue, i.e. adding genetic diversity from one or more other (preferably large) populations. When we reintroduce new populations in ecologically restored habitat, we increase genetic diversity by mixing gene pools in a breeding program in the greenhouse or common garden. Although it is quite likely that this reduces inbreeding depression, there is a risk that the mixing of gene pools disrupts local adaptations, resulting in outbreeding depression.

We are conducting recovery programs on several endangered plant species, such as *Primula vulgaris*, *Antennaria dioica*, *Scorzonera humilis*, *Phyteuma nigrum* and *Lathyrus linifolius*. In the context of these programs, there are many opportunities for Master research projects in which the role of genetic processes like heterosis, inbreeding depression and outbreeding depression can be studied. The detailed backgrounds of each recovery project differ, so that it is best to talk to one of the abovementioned supervisors and discuss a specific research project that best suits your particular interests and time schedule.

Techniques:

- Plant breeding systems: crossing experiments in the greenhouse and/or in the field
- Plant fitness: measuring plant performance traits (fitness components) in the greenhouse and/or in the field
- Genetic diversity: sampling plant leaf tissue in the field or greenhouse and determining genotypes using microsatellites (and in the near future also RADseq/SNPs) in the IBED molecular lab.
- Statistical analysis of reproductive success, variation in fitness components and genetic diversity, and relationships between them.

Background reading:

Barmentlo SH, Meirmans PG, Sheila H. Luijten SH, Triest L, Oostermeijer JGB (2017) Outbreeding depression and breeding system evolution in small, remnant populations of *Primula vulgaris*: consequences for genetic rescue. Conservation Genetics, in press.

Oostermeijer JGB, Luijten SH, den Nijs JCM (2003) Integrating demographic and genetic approaches in plant conservation. Biological Conservation 113, 389-398.

Pierson JC, Beissinger SR, Bragg JG, Coates DJ, Oostermeijer JGB, Sunnucks P, Schumaker NH, Trotter MV, Young AG (2015) Incorporating evolutionary processes into population viability models. Conservation Biology 29, 755-764.

Ecotypic differentiation between heathland and hay meadow populations of Gentiana pneumonanthe

Supervisors: Gerard Oostermeijer, Sheila Luijten (Science4Nature), Patrick Meirmans
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Project outline

Ecotypic differentiation reflects the first stages of speciation, in which populations are adapting to the environmental conditions characterising different habitats. Such differences are very important for conservation biology of endangered species, because mixing ecotypes during genetic rescue, or using the wrong ecotype for reintroduction attempts, will almost certainly decrease the success rate. This is because (a) the genotypes used are less likely to match the environmental conditions and (b) mixing differentially adapted gene pools might result in outbreeding depression by disrupting coadapted (epistatic) gene complexes.

In *Gentiana pneumonanthe*, two putative ecotypes occur, one adapted to wet heathlands and grass heaths and the other to wet hay meadows. In the former, nutrient-poor habitat, demography is driven by episodic recruitment in patches of bare soil created by sod removal, grazing/trampling and/or fire. In this habitat, individual plants need to grow, flower and set seed rapidly, before the vegetation closes by succession. In the more mesotrophic hay meadows, annual mowing and haymaking keeps vegetation succession at bay, and populations are demographically more stable by high survival of established adults, and only occasional recruitment in gaps in the vegetation. The hypothesis is that these two very different types of demographic behaviour are the result of different genetic adaptations.

The project entails a comparative study of adaptive traits in heathland and hay meadow populations of *G. pneumonanthe* in a common garden. In a later stage also a reciprocal transplant experiment will be carried out in the field. Using molecular markers, genetic differentation will also be compared among the studied populations, searching for markers indicating adaptive selection.

Techniques:

- Plant fitness: measuring plant performance traits (fitness components) in a comparative growth experiment in the greenhouse;
- Genetic diversity: sampling plant leaf tissue in the field or greenhouse and determining genotypes using microsatellites (and in the near future also RADseq/SNPs) in the IBED molecular lab.
- Statistical analysis of variation in fitness traits and genetic diversity, and relationships between them.

Background reading:

Oostermeijer JGB, Luijten SH, den Nijs JCM (2003) Integrating demographic and genetic approaches in plant conservation. Biological Conservation 113, 389-398.

Hufford KM, Mazer SJ (2003) Plant ecotypes: genetic differentiation in the age of ecological restoration. Trends in Ecology and Evolution 18, 147-155.

Pierson JC, Beissinger SR, Bragg JG, Coates DJ, Oostermeijer JGB, Sunnucks P, Schumaker NH, Trotter MV, Young AG (2015) Incorporating evolutionary processes into population viability models. Conservation Biology 29, 755-764.

Regeneration niches and the restoration biology of endangered plants

Supervisors: Gerard Oostermeijer, Sheila Luijten (Science4Nature), Patrick Meirmans
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Project outline

In many cases, recovery projects for endangered plant species involve relatively haphazard reintroduction in what is believed to be good habitat. The definition of good habitat is at best based on old vegetation relevés or descriptions in papers, but rarely includes experimental study of the regeneration niche. The latter is defined as the (micro)habitat in which a species can successfully germinate, establish and grow up to become a flowering adult that can eventually produce new offspring. Management, soil conditions, hydrology, vegetation structure, the timing of sowing (or seed release) and seed viability are all important variables determining a species' regeneration niche.

In many reintroduction projects, conservation biologists do not introduce seeds, but plant out pregrown adult plants. The main drawbacks of this approach are that (a) all genetic-environmental filters are circumvented, so that there is no selection for the fittest, best-adapted genotypes, (b) survival of the adults provides no information about the suitability of the reintroduction site for completion of the species' entire life cycle, and (c) there is no guarantee that the established "population" will show long-term viability (hence there is a false idea of restoration success).

Science4Nature is currently working on restoration projects for a large number of endangered plant species, i.e. *Primula vulgaris*, *Antennaria dioica*, *Scorzonera humilis*, *Phyteuma nigrum*, *Thymus serpyllum*, *Cirsium dissectum* and *Lathyrus linifolius*. One of the main problems is that other parties involved in these projects are often in a hurry to get a "population" established, without being interested in ecological site suitability and long-term population viability. We always have to argue extensively that we want to use seeds for reintroductions instead of greenhouse-grown adult plants (of which we often have many). For many species there is no good experimental data on the regeneration niche, however, which makes choosing suitable locations for reintroduction more difficult. We therefore urgently need such data!

Techniques:

- Lab and field experiments on seed germination and seedling establishment in relation to relevant environmental variables.
- Statistical analysis of variation in germination and survival, and the relationships with the environmental parameters.

Background reading:

Young TP, Petersen DA, Clary JJ (2005) The ecology of restoration: historical links, emerging issues and unexplored realms. Ecology Letters 8, 662-673.

Silvertown J (2004) Plant coexistence and the niche. Trends in Ecology and Evolution 19, 605-611.

Isselstein J, Tallowin JRB, Smith REN (2002) Factors affecting seed germination and seedling establishment of fen-meadow species. Restoration Ecology 10, 173-184.

Testing the effectiveness of fauna overpasses (“ecoducts”)

Supervisors: Gerard Oostermeijer, Patrick Meirmans, Hans Breeuwer
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Project outline

The Netherlands is spending a lot of (tax) money on mitigating habitat fragmentation by constructing faunal overpasses (ecoducts). However, there are hardly any good studies that test (a) whether or not the ecoduct was necessary to connect fragmented populations suffering from a lack of gene flow, and (b) the effectiveness of the ecoduct in terms of re-establishing “normal” rates of gene flow. Most research involving ecoducts focuses on the use of overpasses by several organisms. This, however, only demonstrates that individuals can potentially migrate among formerly separated populations, but not that they do and realize gene flow in the process.

The dune area between Zandvoort and IJmuiden is managed as a single National Park Zuid-Kennemerland. Three main barriers, two roads and one railroad, fragment the park into four subareas. The province of North-Holland has funded the construction of three overpasses to mitigate possible effects of habitat fragmentation on population viability of typical dune species. However, the subareas are all still quite large, which diminishes the risk of subpopulations experiencing negative (demographic-genetic) consequences of small population size and isolation.

In a pilot project, we plan to study the population genetic structure of several animal species in the four National Park subareas, to create baseline data on possible fragmentation effects on genetic diversity and gene flow. We have started with work on Carabid beetles, but intend to expand this to rare butterflies (e.g. *Argynnis niobe*, *Pyrgus malvae*), which are more likely to suffer from fragmentation but are also relatively mobile and thus less likely to experience the roads as barriers. Another interesting group are reptiles, for which *Lacerta agilis* (mobile) and *Anguis fragilis* (less mobile) are good study objects. The reptile species are also studied in relation to overpasses in the Veluwe area.

Techniques:

- Sampling tissue from animal populations in National Park Zuid-Kennemerland.
- DNA extraction and molecular analysis of genetic variation in the IBED molecular lab.
- Statistical analysis of genetic diversity and structure and assessing gene exchange among populations in different subareas in the national park.

Background reading:

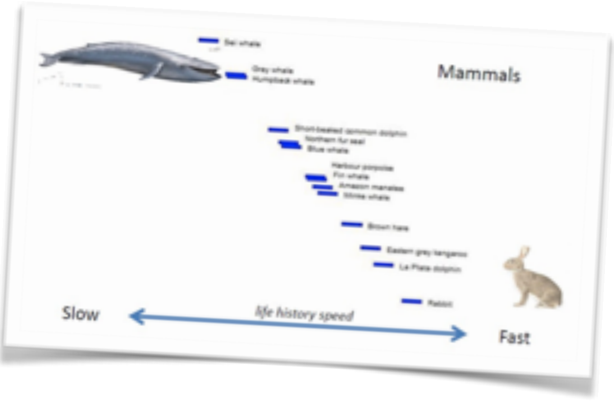
VandenBroeck A., Maes D, Kelager A, Wynhoff I, Wallis de Vries MF, Nash DR, Oostermeijer JGB, Van Dyck H, Mergeay J (2017) Gene flow and effective population sizes of the butterfly *Maculinea alcon* in a highly fragmented, anthropogenic landscape. Biological Conservation 209, 89-97.

Spikmans, F., M. Schiphouwer, J. Kranenbarg & H. Breeuwer, 2013. Naar duurzame populaties beekprik in Noord-Brabant. Voorbereidingsstudie herintroductie. Stichting RAVON, Nijmegen & IBED – Universiteit van Amsterdam.

Predicting life history patterns across the fast-slow life history continuum

Supervisors: Isabel Smallegange
Contact: i.smallegange@uva.nl.

Project outline



Responses to environmental change tend to match with life history characteristics. For example, slow organisms are less sensitive to increases in environmental variability than fast organisms and lifetime reproductive success can serve as an indicator of average fitness and life-history speed across stochastic environments . For this project, you will use a recently developed population model to describe life histories and population dynamics of species across a range that covers the spectrum of metabolic organisation from supply (flexible growth and metabolism [starvation resistant], low behavioural flexibility) to demand (constrained growth and metabolism, high behavioural flexibility) systems. This spectrum is comparable to the life history speed spectrum from a slow-living to a fast-living organism. Resulting patterns will provide mechanistic insights, based on individual energy budgets, in how climate change can influence populations and how populations may persist or decline in the future because of it.

Techniques:

- Demography
- Literature review
- Data management
- MatLab-programming
- Statistical analysis in R

Background reading:

Gaillard, J.-M., D. Pontier, D. Allaine, J. D. Lebreton, J. Trouvilliez, and J. Clobert. 1989. An analysis of demographic tactics in birds and mammals. Oikos 56:59–76.

Kooijman, S.A.L.M. (2000) Dynamic Energy and Mass Budgets in Biological Systems, 2nd edn. Cambridge University Press, Cambridge, UK.

Morris, W.F., Pfister, C.A., Tuljapurkar, S., Haridas, C.V., Boggs, C.L., Boyce, M.S., Bruna, E.M. et al. (2008) Longevity can buffer plant and animal populations against changing climatic variability. Ecology, 89, 19–25.

Smallegange, I.M., Deere, J.A. & Coulson, T. (2014). Correlative changes in life-history variables in response to environmental change in a model organism. American Naturalist, 183, 784-797.

Smallegange IM, Caswell H, Toorians, MEM, de Roos, AM. (2017). Mechanistic description of population dynamics using dynamic energy budget theory incorporated into integral projection models. Methods in Ecology and Evolution 8: 146-154.

The bacteriome of chironomid flies and their role in host tolerance toward pollution in fresh water systems

Supervisors: Hans Breeuwer, Michiel Kraak
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Project outline

Insects of the fly family Chironomidae, also known as chironomids, are distributed worldwide in a variety of water habitats. These insects display a wide range of tolerance toward metals and organic pollutions. Recently, bacterial species were identified that have the ability to degrade toxicants in chironomid egg masses, leading to the hypothesis that bacteria may contribute to the survival of chironomids in polluted environments. They transferred these bacteria to uninfected chironomids and showed that these flies were more tolerant against toxic heavy metals. They concluded that chironomids, which are considered pollution tolerant, are inhabited by stable endogenous bacterial communities that have a role in protecting their hosts from toxicants. Chironomids have been in modelsystem in toxicity bioassays of aquatic pollutants. Chironomids can adapt rapidly to toxic compounds in a laboratory experiments, but he underlying mechanism is not clear but hinted to a genetic component. The finding of metal tolerant bacteria in gut of chironomid larvae provides an exciting alternative mechanism.

Obvious questions are:

- Do chironomids from polluted and unpolluted streams harbour different bacterial communities?
- How are bacterial communities affected by different pollutants, such as heavy metals, pesticides, and herbicides.
- What role do they have in tolerance levels and plasticity of their host?
- Does the bacteriome explain phenotypic plasticity and repaid response to the host to environmental pollution?

Techniques:

- Next generation sequencing
- Bioinformatics
- Field sampling
- Microbial culturing
- Ecological experimentation in the laboratory

Background reading

Dillon, R J and Dillon, V M (2004). The gut bacteria of insects: nonpathogenic interactions. Annual review of entomology 49: 71-92.

Senderovich, Yigal; Halpern, Malka (2012). Bacterial community composition associated with chironomid egg masses. Journal of Insect Science 12: 149.

Senderovich, Y. and Halpern, M. (2013). The protective role of endogenous bacterial communities in chironomid egg masses and larvae. The ISME Journal 7, 2147–2158.

The mycobiome of chironomid flies and their role in host tolerance toward pollution in fresh water systems

Supervisors:	Hans Breeuwer, Michiel Kraak, Teun Boekhout
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Project outline

Insects of the fly family Chironomidae, also known as chironomids, are distributed worldwide in a variety of water habitats. These insects display a wide range of tolerance toward metals and organic pollutions. Recently, bacterial species were identified that have the ability to degrade toxicants in chironomid egg masses, leading to the hypothesis that bacteria may contribute to the survival of chironomids in polluted environments. They transferred these bacteria to uninfected chironomids and showed that these flies were more tolerant against toxic heavy metals. They concluded that chironomids, which are considered pollution tolerant, are inhabited by stable endogenous bacterial communities that have a role in protecting their hosts from toxicants. However, bacteria are not the only inhabitants of guts, also fungi are found in the digestive system. Fungi, like bacteria, have been ignored as gut organisms that can provide their host with novel traits. The gut mycobiome of chironomids has not been identified, nor has its role in tolerance of chironomids towards pollution been determined. A first survey by bachelor students has shown that the mycobiome of chironomid midges is diverse.

Obvious questions are:

- Do chironomids from polluted and unpolluted streams harbour different fungal communities?
- Is the mycobiome affected by different pollutants, such as heavy metals, pesticides, and herbicides.
- What role do they have in tolerance levels and plasticity of their host?
- Does the mycobiome explain phenotypic plasticity and repaid response to the host to environmental pollution?

Techniques:

- Next generation sequencing
- Bioinformatics
- Field sampling
- Microbial culturing
- Ecological experimentation in the laboratory

Background reading

Dillon, R J and Dillon, V M (2004). The gut bacteria of insects: nonpathogenic interactions. Annual review of entomology 49: 71-92.

Senderovich, Yigal; Halpern, Malka (2012). Bacterial community composition associated with chironomid egg masses. Journal of Insect Science 12: 149.

Senderovich, Y. and Halpern, M. (2013). The protective role of endogenous bacterial communities in chironomid egg masses and larvae. The ISME Journal 7, 2147–2158.

History or demography? Determining the drivers of genetic variation in plants

Supervisors: Patrick Meirmans
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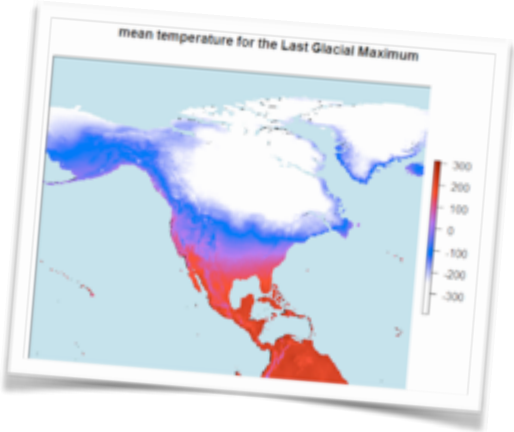
Project outline



Historical climate fluctuations are known to have had drastic impacts on the distribution of genetic variation across species' distribution ranges. Besides such historical processes, the level and distribution of genetic variation is also largely dependent on demographic processes taking place within populations. In this project you will compile a database of genetic data of plant species from throughout the world. You will use state-of-the-art GIS-techniques to create a Species Distribution Model for each species, to model the distribution of the species during the last glacial maximum. With these distributions, you will test the importance of historical and demographical processes on the genetic variation within species, and –more specifically– the central-marginal hypothesis and the pleistocene recolonisation hypothesis.

Techniques

- Genetic Data Analysis
- Species Distribution Modeling
- Data management
- R-programming

Background reading:

Nadeau, S., Meirmans, P.G., Aitken, S.N., Ritland, K. & Isabel, N. 2016. The challenge of separating signatures of local adaptation from those of isolation by distance and colonization history: The case of two white pines. Ecol Evol 6: 8649–8664.

Meirmans, P.G. 2012. The trouble with isolation by distance. Molecular Ecology 21: 2839–2846.

Meirmans, P.G. 2015. Seven common mistakes in population genetics and how to avoid them. Molecular Ecology 24: 3223–3231.

Can ecological niche differentiation explain the maintenance of sexual reproduction?

Supervisors: Patrick Meirmans, Gerard Oostermeijer
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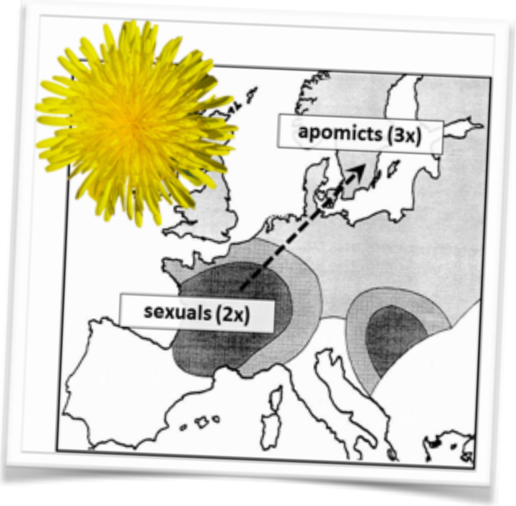
Project outline

One of the major unsolved problems in evolutionary biology is why so many species reproduce sexually, even though asexual reproduction is in theory much more advantageous. In fact, this question has been dubbed "the queen of problem in evolutionary biology". The problem of the maintenance of sex can probably best be studied using species in which both sexual and asexual reproduction exists. In many of these species there are striking patterns in the geographical distribution of the two modes of reproduction; a pattern that is called "geographical parthenogenesis". Several hypotheses have been put forward to explain these patterns, most importantly that asexuals are better adapted to extreme climatic conditions, especially cold temperatures. Other hypotheses involve an increased recolonization speed of asexuals after the pleistocene ice-ages.

Though there have been many studies on the distribution of sexuals and asexuals, to date there are no large-scale meta-analyses that have tested overall differences in ecology between the two modes of reproduction. In this project, you will mine the literature for datasets –across a wide variety of plant and animal species– concerning the geographical distribution of sexuals and asexuals. For every species, you will create a separate environmental niche model for each mode of reproduction, using a set of GIS layers related to past and current climatic conditions. This dataset will allow testing which climatic variables best explain the differences in distribution of the sexuals and asexuals.



Techniques:

- Ecological Niche Modeling
- Data management
- R-programming

Background reading:

Glennon, K.L., Ritchie, M.E. & Segraves, K.A. 2014. Evidence for shared broad-scale climatic niches of diploid and polyploid plants. Ecol Lett 17: 574–582.

Meirmans, S., Meirmans, P.G. & Kirkendall, L.R. 2012. The costs of sex: Facing real-world complexities. Q Rev Biol 87: 19–40.

Neiman, M., Meirmans, S. & Meirmans, P.G. 2009. What can asexual lineage age tell us about the maintenance of sex? Annals of the New York Academy of Sciences 1168: 185–200.

Population genomics of shelled pteropods

Supervisors: Katja Peijnenburg, Le Qin Choo, Patrick Meirmans
Contact: l.q.choo@uva.nl

Project outline

Pteropods are planktonic gastropods that live in the water column across the world's oceans. They have large population sizes and relatively short lifespans (1 to a few years) so are expected to be able to respond quickly to selection pressures, such as changing ocean conditions. They are also found across broad spatial scales with differences in environmental parameters. Therefore, pteropods are useful study organisms to investigate genetic variation across spatial (by comparing different populations) and temporal scales (based on signals of evolution within populations).
By looking at single nucleotide polymorphisms (SNPs) across various coding and non-coding regions, we can observe the genetic variation across adaptive and neutral loci. From this, we can assess their population structure and the nature of dispersal barriers and identify putative adaptive loci that correlate with environmental parameters.

Techniques:

This research internship will be primarily based at Naturalis Biodiversity Center in Leiden. You will be able to use bioinformatic skills to analyse a Next Generation Sequencing (NGS) DNA dataset, including alignment and variant calling. Unix shell experience will come in useful, but can also be learnt during the project. Depending on the project question and interest, some geometric morphometric analyses or wet lab components can also be included.

Background reading:

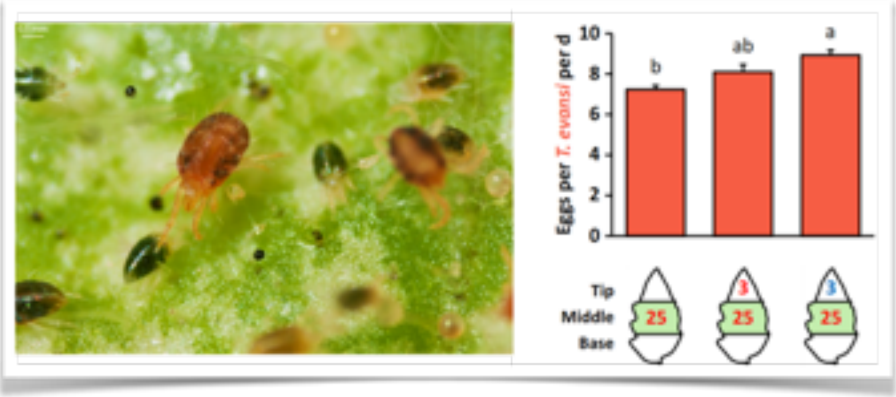
- Peijnenburg, K.T.C.A. and Goetze, E., 2013. High evolutionary potential of marine zooplankton. Ecology and Evolution, 3(8), pp.2765-2781.
- https://nico-expeditie.nl/blogs/life-sea-during-leg-8

Ecological consequences of hypersuppression

Supervisors: Juan Alba, Merijn Kant
Contact: J.M.Albacano@uva.nl or M.Kant@uva.nl

Project outline

Tetranychus evansi is an invasive herbivore specialized in Solanaceae plants. This species has the ability to suppress plant defenses (Alba et al. 2015). We have recently describe that *T. evansi* can modulate the oviposition in the presence of conspecific of heterospecific competitors (Schimmel et al. 2017). The increase in number of eggs is correlated with higher expression of a salivary protein that interfere with plant defenses (Villarroel et al. 2016), this phenomena is called hypersuppression (Schimmel et al. 2017). The left part of the figure below shows several individuals of the spider mite *T. evansi* in developmental stages (green forms) and adult females (red forms). The right part of the figure shows the increase in oviposition in the presence of conspecific competitors (bar in the middle) and heterospecific competitors (right bar).



The fact that *T. evansi* can modulate the oviposition raises several ecological questions:

1) Why do *T. evansi* not oviposit at its maximum performance?
2) How does *T. evansi* perceive the presence of competitors?

Techniques:

The student/s responsible for this project will have to study these two questions by describing the population structure in control conditions (isolated) and in the presence of competitors (con- and heterospecific). Student will try to find if higher performance carry a trade-off for *T. evansi* females in competitive conditions. To study the second question the student will explore if there is any plan-mediated signal perceived by *T. evansi* that announces the presence of competitors in the same or different plant.

Background reading:

Alba et al. 2015. Spider mites suppress tomato defenses downstream of jasmonate and salicylate independently of hormonal crosstalk. New Phytologist 205: 828-840.

Schimmel et al. 2017. Overcompensation of herbivore reproduction through hyper-suppression of plant defenses in response to competition. New Phytologist 214: 1688-1701.

Villarroel et al. 2016. Salivary proteins of spidermites suppress defenses in *Nicotiana benthamiana* and promote mite reproduction. Plant Journal 86: 119-131.

Predicting the outcome of experimental evolution in the nematode *C. elegans*

Supervisors: Ken Kraaijeveld & Meike Wortel
Contact: k.kraaijeveld@uva.nl & m.t.wortel@uva.nl

Project outline:

We use experimental evolution with the nematode *C. elegans* to study to what extent evolution can be predictable. Within this topic we offer several projects:

1 Repeatability of evolution in replicated evolutionary lines

As part of a nationwide project (www.originscenter.nl), different labs across the Netherlands and Belgium have evolved a sexual *C elegans* line on a new food source (*Bacillus megaterium*). Previous experiments suggest that this affects their food choice behaviour, but how repeatable is that across different labs and treatments? And can we select for food preference and predict a priori how much adaptation we expect?

2 Predictability of compensatory evolution in mutant strains

Strains growing poorly due to a deleterious mutation can increase in fitness through compensatory mutations in an evolution experiment. From mutagen screens we know effective compensatory mutations, but does that knowledge allow us to predict evolution? Previous experiments have given some indications that stains do evolve, but this project aims to find the underlying mechanisms that caused that change.

3 Repeatability of co-evolution between nematode and its bacterial food source

A co-evolution experiment between a nematode predator and it's bacterial prey *E coli* is ongoing. With competition assays we will estimate the extent and repeatability of co-evolution. Additionally, genome sequencing will allow us to identify the acquired mutations in the bacteria and change in allele frequencies in the nematodes.This project can also be done as a theoretical project, using simulated evolution in the computer with The Virtual Microbe platform.

Techniques:

- Culturing nematodes and fitness assays
- Data analysis in R
- Behavioural assays
- Taking part in cross university collaborative project
- DNA sequencing / analysis
- Experimental evolution
- Microscopy or flow cytometry
- Competition experiments
- DNA sequencing / analysis

Background reading:

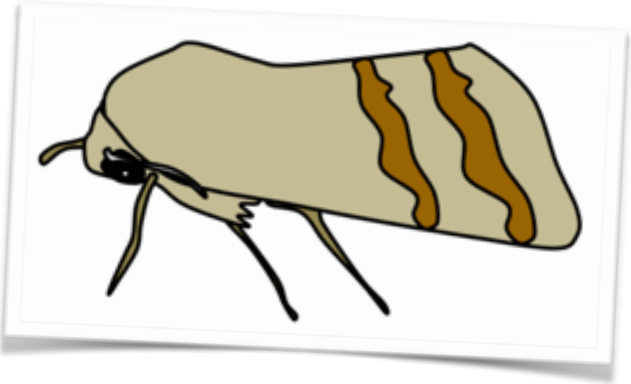
Kraaijeveld K, Oostra V, Liefting M, Wertheim B, de Meijer E, Ellers J 2018 Regulatory and sequence evolution in response to selection for improved associative learning ability in Nasonia vitripennis. BMC Genomics 19:892

How costly it is to be sexy? Trade-offs between sexual attractiveness and life history traits in a noctuid moth

Supervisors: Elise Fruitet, Thomas Blankers, Emily Burdfield-Steel, Astrid Groot
Contact: e.c.e.fruitet@uva.nl

Project outline:

For species that reproduce sexually, it is important to find a mate and even better to find a good one. Sexual communication allows individuals from the same species to recognize each other and to avoid hybridization with individuals from different species, but also to discriminate the more attractive individuals. For example, male birds often have brightly-colored feathers which are used to attract females. However, coloration is costly so resources invested in these sexual ornaments cannot be used for other foraging, metabolism, etc. This is called a trade-off. The project will focus on *Heliothis subflexa*, a Noctuid moth, which emit long-range sex pheromones to attract males. Females produce a particular set of compounds in their pheromone blend, acetates, that attract males from the same species and repel males from others. As *H. subflexa* females produce high amounts of acetate in presence of interfering species and low amounts in their absence, we hypothesize that production of acetates may be costly. Thus, there may be trade-offs between production of high rates of acetates and female fitness. The project aims to determine if producing more acetates will impact life history traits such as growth and fertility using previously-established selection lines for high and low acetate production.



Techniques:

- Chemical analyses (sex pheromone extraction)
- Behavioral experiments
- Life history experiments
- Data analysis in R

Background reading:

Stearns, S.C. 1989. Trade-offs in life-history evolution. Functional Ecology 3: 259-268

Groot, A. T., Inglis, O., Bowdridge, S., Santangelo, R. G., Blanco, C., López, J. D., … Schal, C. (2009). Geographic and temporal variation in moth chemical communication. Evolution, 63(8), 1987–2003.

Co-evolution of sex-specific behaviors: genetic correlations between sex pheromones and sex pheromone preferences in a noctuid moth

Supervisors: Thomas Blankers, Astrid Groot
Contact: t.blankers@uva.nl

Project outline:

Traits used in mate communication are often unique to one sex or take different optimal values between the sexes; that is, these traits are sexually dimorphic. However, males and females of the same species share a genome and it is important that the traits used in mate communication change in a coordinated fashion within species. This results in conflict at the genetic level which can have strong implications for the way sexually dimorphic traits respond to selection. Ultimately, these conflicts constrain the potential diversity of animal mating displays and the rate at which new species arise. Thus, to understand how sex-specific traits evolve, we have to analyze the genetic architecture of male and female traits. Are male and female traits genetically correlated and how do they change in response to sexual selection?

The aim of this project is to illuminate the genetic architecture of sex pheromone signals and preferences in the noctuid moth, *Heliothis subflexa*. *Heliothis subflexa* is closely related to major global crop pests and the bidirectional communication behavior (both male and female moths produce pheromones) make it an exciting model to explore the genetic connections among sexually dimorphic traits. There are selection lines available that have diverged our lab populations based on characteristics of the female sex pheromone. These selection lines are an ideal basis for experiments aimed at understanding the genetic architecture and co-evolution of sex-specific phenotypes.

Techniques:

- Chemical analyses (sex pheromone extraction)
- Behavioral experiments (wind tunnel preference assays)
- Quantitative genetics
- Programming, data management, and data analysis in R

Background reading

Bonduriansky. R, Chenoweth, S.F. Intralocus sexual conflict. 2009. Trends in Ecology and Evolution 24: 280-288

Groot, A.T., Horovitz, J.L., Hamilton, J., Santangelo, R.G., Schal, C., Gould, F. 2006. Experimental evidence for interspecific directional selection on moth pheromone communication. Proceedings of the National Academy of Sciences 103: 5858-5863.

Discover new antimicrobial peptides by analysing the antimicrobial properties of moth pupae

Supervisors:	Teun Boekhout, Naomi Zweerus, Astrid Groot
Contact:	t.boekhout@westerdijkinstitute.nl, n.l.zweerus@uva.nl, a.t.groot@uva.nl

Project outline

Many night-active butterflies (i.e., moths) feed as caterpillars on various host plants, then pupate in the soil, and after ~ 10 days they emerge as adult butterflies. In rearing moths in the lab on artificial diet, last instar caterpillars dig into the diet to pupate. It is striking how the artificial diet can be very moldy, while the direct environment around the pupal case seems to be completely clean. This raises the question whether pupae excrete antibiotics and/or natural fungicides. This project will determine whether the pupae are indeed as clean as they look by conducting several bioassays (e.g. inhibition zone assays with different media and substrates) with the different life stages of the moths. If these experiments show that pupae are indeed clean, chemical analyses will be done on pupal extracts to characterize the (possible) antibiotics and/or natural fungicides. This project will be conducted in collaboration with the Westerdijk Institute.

Techniques

- Inhibition-zone assays
- Chemical analyses

Background reading

Wu, Q., Patočka, J., & Kuča, K. 2018. Insect antimicrobial peptides, a mini review. Toxins, 10(11): 461.

Ecological immunology: do immunity and sexual attraction trade-off through a desaturase?

Supervisors: Ke Gao, Peter Kuperus, Astrid Groot
Contact: k.gao@uva.nl, p.kuperus@uva.nl , a.t.groot@uva.nl

Project outline

The immunocompetence handicap hypothesis (ICHH) states that immunocompetence should trade off with sexual attraction. This basic idea stems from vertebrate research, where testosterone seems to be involved in both immunosuppression and in the brightness of sexual signals. In invertebrates such a direct link has not been found yet. However, our research so far has found that infected moths produce less sex pheromone and the sex pheromone composition shifts towards more saturated compounds instead of the attractive unsaturated pheromone components. These results has led to the following hypothesis that should be tested: Desaturases have a dual role in immune function and in the quality of the sexual signal. In the laboratory, we selected for High vs Low unsaturated sex pheromone compounds, in which the production of unsaturated compounds is almost completely suppressed and now have stable High and Low lines, where the Low line represents a functional knock-out of the desaturase. These lines thus forms the perfect starting point to test this hypothesis. Experiments to conduct will include infection assays in the High and Low lines to determine whether the Low line is more or less immunocompetent than the High line, chemical analyses to determine the effect of infections on the pheromone composition in both lines, and possibly qPCR experiments to assess differential gene expression levels of the desaturases.

Techniques

- Infection assays
- Chemical analyses
- qPCR experiments

Background reading

Barthel A, Staudacher H, Schmaltz A, Heckel DG, Groot AT. 2015. Sex-specific consequences of an induced immune response on reproduction in a moth. BMC Evolutionary Biology 15: 282

Groot AT, Schöfl G, Inglis O, Donnerhacke S, Classen A, Schmalz A, Santangelo RG, Emerson J, Gould F, Schal C, Heckel DG. 2014. Within-population variability in a moth sex pheromone blend: genetic basis and behavioural consequences. Proceedings of the Royal Society B 281: 20133054

Optimizing *Galleria mellonella* as a new model for biomedical research: lessons to learn from the moth

Supervisors: Teun Boekhout, Ferry Hagen, Dennis van Veldhuizen, Astrid Groot
Contact: a.t.groot@uva.nl

Project outline

In recent years, the greater waxmoth *Galleria mellonella* has been increasingly used as a model system to replace mice as clinical models to study human infectious diseases. Using larvae of this moth has a number of advantages, such as its ability to sustain 37° C, short life span, small size, and possibility to administer precise doses of pathogens. In the past decade, *G. mellonella* has been used to test the pathogenicity of bacteria, fungi, viruses and the effectiveness of antimicrobial compounds.

However, many labs find different results, depending on how, at what stage and what dose infections are performed. To begin resolving these discrepancies we need a more thorough understanding of the life history of this moth in its natural environment. Specifically, responses to infections may vary due to larval health, rearing history, and/or whether previous generations have been infected (immune priming). Since the wax moth is also a pest in beehives, a better understanding of its life cycle may also help in finding sustainable solutions to minimize or control this species as pest in nature. For example, its sex pheromone could potentially be used for mating disruption to minimize population growth, or the bee alarm pheromone could be used to inhibit attraction of the moths to beehives in the first place. These responses are likely also dependent on the health and infection history of the insects.

This project mainly aims to determine the causes and consequences of variable infection responses in *G. mellonella* larvae. The focus will be on how fungal infections affect its life history, as this project is in close collaboration with the Westerdijk Institute and University Medical Center Utrecht

Techniques:

- Infection experiments
- Behavioral experiments in lab and field
- Chemical analyses (sex pheromone extractions of adult males)
- Developing optimal rearing protocols

Background reading:

Andrea A, Krogfelt KA, Jenssen H. 2019. Methods and challenges of using the greater wax moth (*Galleria mellonella*) as a model organism in antimicrobial compound discovery. Microorganisms 7: 85.

Svensson GP, Gündüz EA, Sjöberg N, Hedenström, Lassance JM, Wang H-L, Löfstedt C, Allebrant O. 2014. Identification, synthesis, and behavioral activity of 5,11-dimethylpentacosane, a novel sex pheromone component of the greater waxmoth, *Galleria mellonella* (L.). Journal of Chemical Ecology 40: 387-395.

Li Y, Jiang X, Wang Z, Zhang J, Klett K, Mehmood S, Qu Y, Tan K. 2019. Losing the arms race: greater wax moths sense but ignore bee alarm pheromones. Insects 10: 81. doi:10.3390/insects10030081

De Jong AW, Hagen F. 2019. Attack, defend and persist: How the fungal pathogen *Candida auris* was able to emerge globally in healthcare environments. Mycopathologia 184: 353-365.

Simulation models of primate foraging behaviour to gain insight in the evolution of cognitive skills

Supervisors: Emiel van Loon; Karline Janmaat
Contact: e.e.vanloon@uva.nl

Project outline

It is a challenge to test the use of cognitive abilities in free-ranging animals: the senses, memory and planning skills need to be inferred from the animals' behaviour, while alternative mechanisms can easily lead to similar behaviours. It is even more challenging to gain an understanding of the evolutionary value of cognitive strategies. Under which socio-ecological conditions does the use of certain cognitive strategies, such as planning for the next day or the use of an Euclidean map lead e.g. to an advantage for a forager?

The aim of this project is to build and apply an agent based model (ABM) that will help to understand the food finding strategy by two sympatric primate species: the chimpanzee and the sooty mangabey in the Taï National Park (Côte d'Ivoire). Based on the field knowledge of these species, an existing spatio-temporal map of fruit tree availability and existing models for food-finding by rainforest primates, we will make an ABM that is appropriate for investigating theoretical questions about chimpanzees and mangabeys foraging behaviour.

After initial building and testing, the model can be extended and applied to investigate a range of ecological and behavioural questions, such as:

- What are the energetic implications of having short- or long-term memory for fruit location or availability?
- Which form(s) of competition and predation between chimpanzees and mangabeys result in niche segregation?
- Which aspects of trajectory shape are most informative to test memory or sensory cues for food-finding?
- How sensitive are relevant system variables (trajectory shape, repeat-visits) to different regimes of fruit-availability?

Techniques:

- Simulation modelling
- Summarizing and exploring model output (basic statistics and visualization)
- Statistical analysis of model-output by linear models (multiple regression; optional)
- Data management (storing & documenting output of simulation runs)
- R programming (The required programming skills are easily acquired within a month)

Background reading:

Bonnell TR, Campennì M, Chapman CA, Gogarten JF, Reyna-Hurtado RA, Teichroeb JA, et al. (2013) Emergent Group Level Navigation: An Agent-Based Evaluation of Movement Patterns in a Folivorous Primate. PLoS ONE 8(10): e78264.

Ban SD, Boesch C, N'Guessan A, N'Goran EK, Tako A, Janmaat KRL (2016) Taï chimpanzees change their travel direction for rare feeding trees providing fatty fruits. Animal Behaviour 118: 135-147,

Janmaat KRL, Ban SD, Boesch C (2013) Chimpanzees use long-term spatial memory to monitor large fruit trees and remember feeding experiences across seasons. Animal Behaviour 86: 1183-1205.

Exploring and modeling the spatio-temporal distribution of fruit production in the wet tropics, based on an extensive field data set

Supervisors: Emiel van Loon; Karline Janmaat
Contact: e.e.vanloon@uva.nl

Project outline

Properly describing the spatio-temporal distribution of organisms (as well as their properties and behaviours) is a key step in ecological research. It allows us to effectively use raw observations for testing ecological theories (e.g. about organism-environment relations, dispersion, reproduction, settlement, competition and predation, resource availability).

In this study, we focus on making an accurate description of the distribution of flowers and fruits in the wet tropics for a range of imporant species. While the nature of fruit-bearing tree distribution is interesting for its own sake and for studying plant ecological processes (e.g. how are seeds being dispersed, and how can a given distribution of a species inform about this), our main interest is to learn more about resource availability for primates living in these environments.

During a long-term monitoring program in the Taï National Park (Côte d'Ivoire) an extensive data set on the spatial distribution and phenology of important fruit-bearing tree species has been collected. Our aim is to explore the spatial distribution of the trees as well as the spatio-temporal patterns of fruit production, based on this data. Next, a stochastic model is made which describes the spatio-temporal distribution (and variability) in fruit availability.

Techniques:

- Data summary, visualization and exploration
- Statistical modeling
- Data management (storing & documenting output of simulation runs)
- R programming

Background reading:

Janmaat, K. R.L., Boesch, C., Byrne, R., Chapman, C. A., Goné Bi, Z. B., Head, J. S., Robbins, M. M., Wrangham, R. W. and Polansky, L. (2016), Spatio-temporal complexity of chimpanzee food: How cognitive adaptations can counteract the ephemeral nature of ripe fruit. Am. J. Primatol., 78: 626–645.

Lan G, Getzin S, Wiegand T, Hu Y, Xie G, Zhu H, et al. (2012) Spatial Distribution and Interspecific Associations of Tree Species in a Tropical Seasonal Rain Forest of China. PLoS ONE 7(9): e46074.

Seidler TG, Plotkin JB (2006) Seed Dispersal and Spatial Pattern in Tropical Trees. PLoS Biol 4(11): e344.

Male cannibalism in a predatory mite

Supervisors: Arne Janssen, Martijn Egas
Contact: arne.janssen@uva.nl; egas@uva.nl

Project outline

Predatory mites are small (max. 0.5 mm) arthropods that feed on small insects and mites. The best studied species is undoubtedly *Phytoseiulus persimilis*, natural enemy of the spider mite *Tetranychus urticae*, which is an important pest of many different crops worldwide. This spider mite forms colonies consisting of several generations on host plants, which expand rapidly, covering the plants with a fine silken web and damaging leaf cells until the plant finally dies. Alternatively, if the predatory mites arrive in time on a plant with spider mites, they can also form a local population, eventually exterminating the spider mite population, after which they need to disperse to find new prey.

It is known that the predatory mites can cannibalize on smaller conspecifics, especially in the absence of other food, i.e. spider mites. This implies that cannibalism mainly occurs towards the end of the interaction, when spider mites are (nearly) exterminated by the predatory mites. These predators then have the choice to stay and cannibalize or to disperse. Recent experiments showed that especially adult males engage in cannibalism, whereas adult females disperse more. This may be because females, after having mated, need plenty of food to reproduce, whereas males may mainly look for females to mate with. While waiting for females to mature, the males will frequently encounter juvenile conspecifics. Their best option would be to cannibalize juvenile males, thus reducing future competition for matings, and not to cannibalize juvenile females so as not to kill future mates. The current project aims at testing this new idea

Techniques:

- Behavioural experimentation
- Binocular microscopy
- Mite rearing
- Statistical analysis ®

Background reading:

Pels B, Sabelis MW (1999). Local dynamics of overexploitation and predator dispersal in an acarine predator-prey system. Oikos 86:573–583.

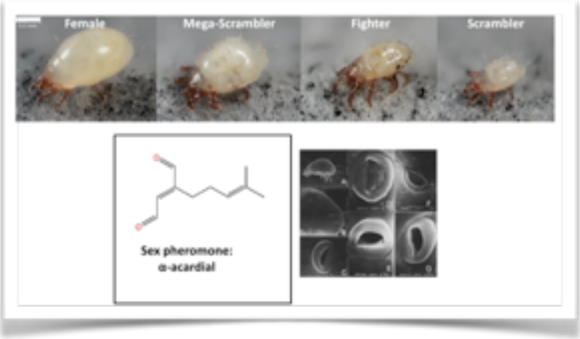
Revynthi, A. M., Janssen, A., & Egas, M. (2018). Gender-specific differences in cannibalism between a laboratory strain and a field strain of a predatory mite. Experimental and Applied Acarology, 74(3), 239-247.

Schausberger, P., & Croft, B. A. (2001). Kin recognition and larval cannibalism by adult females in specialist predaceous mites. Animal Behaviour, 61(2), 459-464.

The Smell Report A: Pheromone signals of male alternative mating tactics

Supervisors: Kat Stewart, Isabel Smallegange
Contact: K.Stewart@uva.nl

Project outline



What makes males and females behave differently, and how do different types of reproducing males within the same species, or even population, coexist?

It has long been accepted that males and females emit sex-specific odor compounds that function as pheromones to promote stereotypic behavior, such as mate attraction, territoriality, warning or bonding. In the blind bulb mite (*Rhizoglyphus robini*), females emit more than twice the quantity of sex pheromone than males do, but females are also nearly twice as large as their male counterparts, which has led to speculation that perhaps pheromone production is associated with body size or nutritional resources. These microscopic mites however, also demonstrate a unique life-history phenomenon – males demonstrate three alternative mating tactics that differ in size and weaponry (Fighters with weapons, Scramblers without weapons, and a possible female mimic the Megascrambler), dictated predominately by how much food they acquire as juveniles. What is unknown to date is whether pheromone production is merely a linear relationship to body size, or whether sex and male alternative mating tactics demonstrate unique quantities and patterns of sex pheromones. For example, do male Megascramblers that look like females (large body size and no weapons) emit pheromones similar to females to reduce combat with other male competitors? What about small scrambler males? By assessing the pheromonal profile of all three alternative male mating tactics in the bulb mite, your research aims to answer how these males coexist within populations while competing for females. *The student on this project will work in conjunction with another student involved in the project "The Smell Report B: Are nutritionally mediated pheromone signals heritable?".

Techniques:

- Animal Rearing
- Life-history & sexual selection theory
- Pheromone assays, including Gas-Chromatograph (GS) analysis
- Data Management
- R programming

Background reading:

Henneken J, et al. 2017. Diet-Mediated Pheromones and Signature Mixtures Can Enforce Signal Reliability. Frontiers in Ecology and Evolution 4: 145

Stewart KA, Draaijer R, Kolasa MR, Smallegange IM. 2019. The role of genetic diversity in the evolution and maintenance of environmentally-cued, male alternative reproductive tactics. BMC Evolutionary Biology. 19:58.

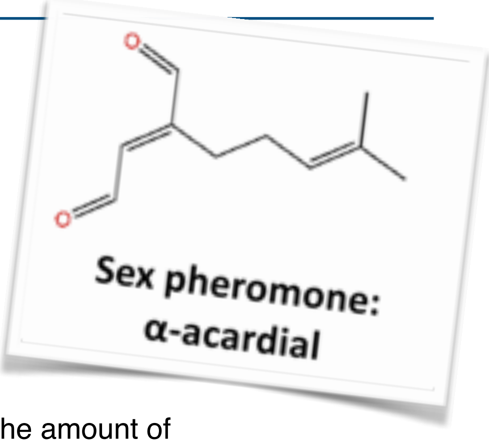
Stewart KA, Van den Beuken TPG, Rhebergen FT, Deere JA, Smallegange IM. 2018. Evidence for a third male type in a male-dimorphic model species. Ecology. 99(7):1685-1687

Smallegange IM. Complex environmental effects on the expression of alternative reproductive phenotypes in the bulb mite. Evol Ecol. 2011;25:857–73. .

The Smell Report B: Are nutritionally mediated pheromone signals heritable?

Supervisors: Kat Stewart, Isabel Smallegange
Contact: K.Stewart@uva.nl

Project outline



Nature vs nurture is a question as old as Greek philosophy. Traits often thought to be dictated by one or the other are now known to often encompass a bit of both. But can we tease their relative contribution apart?

The blind bulb mite (*Rhizoglyphus robini*), is an interesting microscopic invertebrate – males of the species encompass one of three mating morphologies (or Alternative Mating Tactics) that differ in body size, weaponry, and behavior. These morphologies have been demonstrated to be mediated mostly by environmental factors such as nutrition during juvenile stages, but they are also somewhat heritable and affiliated with different levels of genetic diversity. We know that bulb mite sexes differ in the amount of sex pheromone they emit, with females producing more than twice the quantity compared to the males. Still, male pheromone production is quite variable in male bulb mites, either due to their underlying morphologies (Alternative Mating Tactics), or due to their heritability (or both). In this project, your aim will be to take isoline populations of bulb mites (inbred until little to no genetic variation exists) and see if nutrition and mating tactics show dissimilar patterns of pheromone production. In this way, you may be able to definitively demonstrate that diverged pheromone production between males is due to nurture rather than nature.

*The student on this project will work in conjunction with another student involved in the project "The Smell Report A: pheromone signals of alternative reproductive tactics".

Techniques:

- Animal Rearing
- Life-history & sexual selection theory
- Pheromone assays, including Gas-Chromatograph (GS) analysis
- Data Management
- R programming

Background reading:

Henneken J, et al. 2017. Diet-Mediated Pheromones and Signature Mixtures Can Enforce Signal Reliability. Frontiers in Ecology and Evolution 4: 145

Stewart KA, Draaijer R, Kolasa MR, Smallegange IM. 2019. The role of genetic diversity in the evolution and maintenance of environmentally-cued, male alternative reproductive tactics. BMC Evolutionary Biology. 19:58.

Stewart KA, Van den Beuken TPG, Rhebergen FT, Deere JA, Smallegange IM. 2018. Evidence for a third male type in a male-dimorphic model species. Ecology. 99(7):1685-1687

Smallegange IM. Complex environmental effects on the expression of alternative reproductive phenotypes in the bulb mite. Evol Ecol. 2011;25:857–73.

Developing an insect-based nose to detect fungal infections in humans

Supervisors: Peter Roessingh, Astrid Groot, Teun Boekhout
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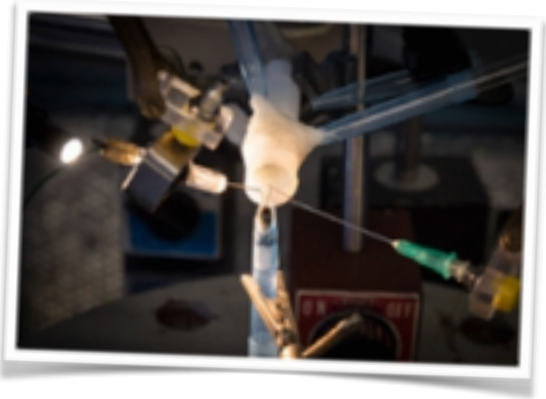
Project outline



Fungal infections in humans are in the majority of the cases caused by at most five pathogenic yeast species. Diagnostic tools to determine which of the pathogen species cause the infection are tedious and not straightforward. As these yeast species likely differ in their chemical profiles, it may be possible to distinguish the pathogens based on the volatiles they produce. Insects are known to be much more sensitive in detecting chemical compounds than chemical detection devices, which is the reason that several attempts have been made to develop an 'insect detection device' (Leitch et al. 2013; Strauch et al. 2014). This project aims to determine whether it will be feasible to develop a 'bionose' to distinguish the main pathogenic yeast species. Preliminary results indicate that this should be possible (Goedhard and Benning, 2018 BSc report UvA; de Jong and Peek, 2019 BSc repor UvA).

Techniques:

- Chemical analyses
- GC-EAD
- Portable electroantennogram

Background reading:

Leitch O, Anderson A, Kirkbride KP, Lennard C. 2013. Biological organisms as volatile compound detectors: A review. Forensic Science International 232: 92–103.

Strauch M, Luedke A, Muench D. Laudes T, Galizia, CG, Martinelli E, Lavra L, Paolesse R, Ulivieri A, Catini A, Capauano R, Di Natale C. 2014. More than apples and oranges - Detecting cancer with a fruit fly's antenna. Scientific Reports 4: 3576 I DOI: 10.1038/srep03576

Immunity versus sexual selection: how does sexual attraction in moths trade off with infections of different pathogens?

Supervisors: Ke Gao, Elise Fruitet, Thomas Blankers, Astrid Groot
Contact: k.gao@uva.nl, e.c.e.fruitet@uva.nl, t.blankers@uva.nl, a.t.groot@uva.nl

Project outline

Immune response induction benefits insects in combatting infection by pathogens. However, organisms have a limited amount of resources available and face the dilemma of partitioning resources between immunity and other life-history traits. Since males and females differ in their life histories, sex-specific resource investment strategies to achieve an optimal immune response following an infection can be expected. So far we have found in moths that the female sex pheromone quantity and quality is reduced in infected females, and that the mating success of infected females is negatively affected, which is not the case in males. Recently, we also found indications for a trade-off between attractiveness and immunity; attractive females were more infectious than unattractive females (BSc thesis S. Nichols, D. Muijderman 2018). However, we do not know whether infections affect female and male responses to potential mating partners, although we have preliminary data showing that infected females choose healthy males (MSc thesis Q. Dangh 2018). Since in moths sexual attraction includes female sex pheromones to attract males from a distance and male sex pheromones that are likely used at close range for female choice, we are also interested whether and how infections may affect the male sex pheromone and/or female choice

Techniques:

- Infection experiments
- Behavioural analyses (mate choice assays)
- Chemical (pheromone) analyses

Background reading:

Barthel A, Staudacher H, Schmaltz A, Heckel DG, Groot AT. 2015. Sex-specific consequences of an induced immune response on reproduction in a moth. BMC Evolutionary Biology 15: 282

Hosseini SA, van Wijk M, Gao K, Goldansaz SH, Schal C, Groot AT. 2016. Experimental evidence for chemical mate guarding in a moth. Scientific Reports 6: 38567

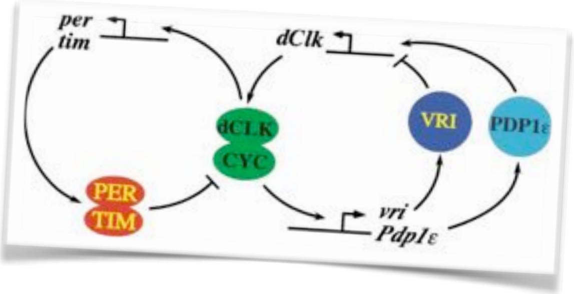
Circadian rhythm differences between butterflies and moths due to SNPs in clock genes?

Supervisors: Sabine Haenniger, Peter Kuperus, Astrid Groot
Contact: shaenniger@ice.mpg.de, p.kuperus@uva.nl, a.t.groot@uva.nl

Project outline

The circadian rhythm of behavior has interested many researchers in the past decades, yet amazingly little is known on the evolution of natural variation in circadian rhythms of behavior. Most butterfly species are active during the day, while most moth species show specific activity rhythms in their sexual activities at night, some species being sexually active early at night, while others are sexually active late at night. This differentiation has been suggested to have arisen to minimize communication interference between closely related species, as co-occurring and closely related species with overlapping sex pheromone blends show a temporal differentiation in their daily sexual activities. For example, *Spodoptera frugiperda* (Lepidoptera: Noctuidae) consists of two naturally occurring morphologically identical strains that exhibit strain-specific timing of mating in the night: the so-called corn-strain calls, mates and oviposits early at night, while the rice-strain mates late at night. The main candidate gene underlying this genetic differentiation of this allochronic separation is vrille, which shows butterfly- and moth-specific SNPs (BSc thesis M. Hulswit 2017). The open question is whether this differentiation is vrille-specific or whether other clock genes show a similar pattern. This project is to assess possible genetic variation in identified clock genes in day-active and night-active Lepidoptera in comparison to genes that are unrelated to circadian rhythm.

Requirements: Students need to have some molecular background for this project.



Techniques

- PCR and sequencing genes
- SNP analysis

Background reading

Niepoth N, Gao K, De Roode JC, Groot AT. 2017. Comparing behavior and circadian gene expression between caterpillars, butterflies and moths. Journal of Biological Rhythms 33: 54-64 doi: 10.1177/0748730417746458

Groot AT. 2014. Circadian rhythms of sexual activities in moths: a review. Frontiers in Ecology and Evolution, section Chemical Ecology 2: 43

Haenniger S, Dumas P, Schöfl G, Gebauer-Jung S, Vogel H, Unbehend M, Heckel DG, Groot AT. 2017. Genetic basis of allochronic differentiation in the fall armyworm. BMC Evolutionary Biology 17: 68 (DOI: 10.1186/s12862-017-0911-5)

How predatory hoverflies differ in their preferences for flowers

Supervisors: Paul van Rijn
Contact: p.c.j.vanrijn@uva.nl

Project outline

Conservation biological control, improving the performance of native predators and parasitoids of pests, is a serious alternative for chemical pest control in arable crops. Many of these natural enemies require floral resources in their adult stage whereas the juveniles require insect hosts or prey. Providing flower strips in the margins of crop fields is therefore considered an effective way to support these natural enemies, especially predatory hoverflies. These hoverflies have only small proboscis, strongly limiting the range of flowers they can feed on. Flower preferences have been studied well for one species, but in the field many other species are considered equally important. The question therefore is how these species differ in their flower visitation preferences, and can these differences be understood from differences in proboscis length? The results can help to improve the selection of flower species used in the field margin strips.

Techniques

- Field work (in June or July): Systematically observe the visitation of various flower patches within field margin strips.
- Lab choice experiments in cages: Provide individuals with different flowers to choose from and record their behavior.
- Statistical analysis in R.

Background reading

Van Rijn, P.C.J., M. Klompe, S. Elzerman, M.E.T. Vlaswinkel & H. Huiting. 2019. The role of flower-rich field margin strips for pollinators, natural enemies and pest control in arable fields. IOBC-WPRS Bulletin 143: 56-60.

Van Rijn, P.C.J. & F.L. Wäckers. 2016. Nectar accessibility determines fitness, flower choice and abundance of hoverflies that provide natural pest control. Journal of Applied Ecology, 53(3): 925-933.

Van Rijn, P.C.J., J. Kooijman & F.L. Wäckers. 2013. The contribution of floral resources and honeydew to the performance of predatory hoverflies (Diptera: Syrphidae). Biological Control 67: 32–38.

Wäckers, F.L., P.C.J. van Rijn & J. Bruin (Eds.) 2005. Plant-provided Food for Carnivorous Insects: A Protective Mutualism and its Applications. Cambridge University Press, Cambridge, UK, 356 pp.

The effect of ploidy level on the ecological niche: a meta-analysis

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Project outline

Polyploidy is an important aspect of the evolution of plants; most plant species have gone through one or several rounds of whole-genome duplication during their evolutionary history. In addition, there are many species where multiple ploidy levels (cytotypes) co-occur; in such cases there are often striking patterns in the geographical distribution of the different cytotypes. Several hypotheses have been put forward to explain these patterns, most importantly that higher ploidy levels are better adapted to extreme climatic conditions, especially cold temperatures. Other hypotheses involve survival of different cytotypes in different refugia during the pleistocene ice-ages.

Though there have been many studies on the distribution of cytotypes, to date there are no large-scale meta-analyses that have tested overall differences in ecology between ploidy levels. In this project, you will mine the literature for datasets –across a wide variety of plant species– concerning the geographical distribution of cyotypes. For every species, you will create a separate environmental niche model for each cytotype present, using a set of GIS layers related to past and current climatic conditions. This dataset will allow testing which climatic variables best explain the differences in distribution of the different cytotypes.

Techniques:

- Ecological Niche Modeling
- Data management
- R-programming

Background reading:

Glennon, K.L., Ritchie, M.E. & Segraves, K.A. 2014. Evidence for shared broad-scale climatic niches of diploid and polyploid plants. Ecol Lett 17: 574–582.

Kolář, F., Čertner, M., Suda, J., Schönswetter, P. &, Husband, 2017 Mixed-Ploidy Species: Progress and Opportunities in Polyploid Research. Trend in Plant Science.

Meirmans, P.G. & Van Tienderen, P.H. 2013. The effects of inheritance in tetraploids on genetic diversity and population divergence. Heredity 110: 131–137. Nature Publishing Group.

Parisod, C. & Broennimann, O. 2016. Towards unified hypotheses of the impact of polyploidy on ecological niches. New Phytol 212: 540–542.

What flowers can support green lacewings as predators of crop pests?

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Project outline

Conservation biological control, improving the performance of native predators and parasitoids of pests, is a serious alternative for chemical pest control in arable crops. Many of these natural enemies, such as green lacewings, require floral resources in their adult stage whereas the juveniles require insect hosts or prey. Providing flower strips in the margins of crop fields is therefore considered an effective way to support these natural enemies. Lacewings have only small mouthparts, limiting the range of flowers they can feed on. The question therefore is which flowers allow the lacewings to survive long enough and to reproduce? And can differences in flower suitability be understood from flower morphology.

Techniques

- Cage studies: Provide pairs of adult lacewings in cages with one type of flowers and record their (bi)daily survival and reproduction rates.
- Make scans of dissected flowers to measure nectar accessibility.
- Statistical analysis in R.

Background reading

Van Rijn, P.C.J., M. Klompe, S. Elzerman, M.E.T. Vlaswinkel & H. Huiting. 2019. The role of flower-rich field margin strips for pollinators, natural enemies and pest control in arable fields. IOBC-WPRS Bulletin 143: 56-60.

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Van Rijn, P.C.J. 2012. The suitability of field margin flowers as food source for Chrysoperla lacewings. IOBC-WPRS Bulletin 75: 213-216.

Wäckers, F.L., P.C.J. van Rijn & J. Bruin (Eds.) 2005. Plant-provided Food for Carnivorous Insects: A Protective Mutualism and its Applications. Cambridge University Press, Cambridge, UK, 356 pp.

Effect of hoverfly foraging behaviour on its distribution in crop fields using Individual Based Modelling (IBM)

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Project outline

Conservation biological control, improving the performance of native predators and parasitoids of pests, is a serious alternative for chemical pest control in arable crops. Many of these natural enemies, such as hoverflies, require floral resources in their adult stage whereas the juveniles require insect hosts or prey. Providing flower strips in the margins of crop fields is therefore considered an effective way to support these natural enemies. The question is how these insects cope with the spatial segregation of the two essential resources. And how far into the fields will the insect reproduce and thereby affect the control of the pest.

In addition field observations modelling the spatial behavior of the adult predator can help us to understand the distribution pattern and how it will be affected by environmental conditions. Individual-Based Modelling (IBM) tools, such as NetLogo, allow us to study the distribution and impact of organisms in an artificial landscape by defining simple behavioral rules.

Techniques

- Individual-Based Modelling (IBM)
- Data management

Background reading

Van Rijn, P.C.J. 2017. Natural pest control requires a complete landscape. IOBC-WPRS Bulletin 122: 107-111.

Van Rijn, P.C.J. & F.L. Wäckers. 2016. Nectar accessibility determines fitness, flower choice and abundance of hoverflies that provide natural pest control. Journal of Applied Ecology, 53(3): 925-933..

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Wäckers, F.L., P.C.J. van Rijn & J. Bruin (Eds.) 2005. Plant-provided Food for Carnivorous Insects: A Protective Mutualism and its Applications. Cambridge University Press, Cambridge, UK, 356 pp.