



4th EES conference



October 12th and 13th 2010
Ludwig-Maximilians-Universität
Biozentrum, Planegg-Martinsried

LMU

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MUNICH GRADUATE SCHOOL FOR
EVOLUTION, ECOLOGY AND SYSTEMATICS

EES LMU



About the EES conference 2010

The EES Conference 2010 offers our second-year master students and last-year PhD students an opportunity to present their research to the EES community. We also aim at giving a “scientific” welcome to the new generation of master students, coming from different parts of the world. We hope our selection of talks will inspire the new EES generation to formulate questions that will guide their own evolutionary research. Finally, we congratulate the graduating master class of 2010 and wish them all the best in their future careers.

Welcome to the 4th EES Conference!

The organising team:

Fernanda Antunes C., PhD student Systematic Botany

Juliana Chacón, PhD student Systematic Botany

Pablo Duchén B., PhD student Evolutionary Biology

Lars Nauheimer, PhD student Systematic Botany

Francesco Paparazzo, PhD student Evolutionary Biology

Ricardo Wilches, PhD student Evolutionary Biology

Dr. Winfried Hense, Evolutionary Biology

Dr. Alice Edler, EES program coordinator

Prof. Dr. John Parsch, Speaker of the EES program



PROGRAM

Tuesday October 12th

Morning session

10:00 **Opening words**

John Parsch

Keynote Talk

10:15 Colin Hughes

Multiple continental radiations and ecological correlates of diversification in *Lupinus* (Leguminosae).

11:15 **Coffee break**

EES Master talks

11:30 Xenia Schleuning

Responsiveness as an animal personality trait: Individual differences in behavioural plasticity within and across contexts.

11:45 Catalina Olano

Molecular phylogeny, biogeography and character evolution in the tribe Rhinanthaeae (family Orobanchaceae).

12:00 **Lunch**

Afternoon session

13:30 Katharina Böldel

The evolutionary history of a plant resistance gene: Balancing selection and introgression between species.

13:45 Lotte Schlicht

Fledging behaviour in the blue tit (*Cyanistes caeruleus*).

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14:00 Ana Catalán

Evolution of CO₂ avoidance behavior response in the *Drosophila* genus.

14:15 **Coffee break**

14:30 Anne-Kathrin Graber

The effect of diversity on the lipid content of micro-algae.

14:45 Meike Wittmann

Can *Daphnia lumholtzi* invade European lakes?

15:00 Philipp Rausch

The influence of blood group antigens on the human intestinal microbiota.

15:15 **Coffee break**

15:30 Annamarie Gabrenya

Growth and organic matter release by two common coral reef organisms in response to inorganic nutrient addition: effects on planktonic microbial activity.

15:45 Hannes Imhof & Robert Sigl

Acanthaster planci - plasticity in morphology and behaviour?

16:00 *Graduation ceremony*

EES Master class 2010

-End of day 1-

Wednesday, October 13th

Morning session

Keynote talk

10:00 Andrea Manica

The long march of human genes.

11:00 **Coffee break**

11:15 3rd semester EES Master students

Poster session announcements

12:00 **Lunch**

Afternoon session

13:00 **Poster session (Faculty meeting)**

EES PhD talks

14:30 Patrizia Sebastian

Finding the wild relatives of melon, cucumber, and chayote: molecular phylogenetics and biogeography of Cucurbitaceae.

14:50 Andreas Fleischmann

Phylogeny, genome evolution, taxonomy and biogeography of *Genlisea* (Lentibulariaceae).

15:10 Claus Kemkemer

The silent X: Functional analysis of male germline X-inactivation in *Drosophila*.

15:30 **Coffee break**

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15:50 Anja Hörger

Evolution of a resistance gene family in wild tomatoes: relating nucleotide diversity to functional consequences.

16:10 Sonja Grath

Molecular evolution of sex-biased genes in the *Drosophila ananassae* subgroup.

16:30 Christoph von Beeren

Differential host defense against multiple parasites in ants.

16:50 **Coffee break**

17:10 *EES prizes award*

Farewells

-End of day 2-

Abstracts

Keynote talks

MULTIPLE CONTINENTAL RADIATIONS AND ECOLOGICAL CORRELATES OF DIVERSIFICATION IN *LUPINUS* (LEGUMINOSAE).

Colin Hughes

Institute of Systematic Botany, University of Zurich, Zollikerstrasse 107, 8008 Zurich, Switzerland. colin.hughes@systbot.uzh.ch

Ever since Darwin's seminal observations of Galapagos finches, adaptive radiations have offered some of the most spectacular examples of diversification, providing uniquely powerful insights into how and why diversification occurs. However, aside from a few well explored model systems, the dynamics and mechanisms of diversification remain poorly understood, especially for species-rich continental lineages, for which surprisingly little is known about geotemporal patterns of diversification. Nonetheless, with recent advances in comparative phylogenetic methods and rapidly emerging opportunities to generate bigger and better phylogenies, there is tremendous scope to investigate the dynamics of species diversification more precisely and objectively than ever before. This is important if we are going to be able to discover why some lineages diversify and others do not, and the extent to which this is attributable to synchrony – or lack of it – between intrinsic trait evolution and extrinsic opportunity. I will explore these questions using new phylogenies alongside life history and ecological data for the species-rich legume genus *Lupinus*, using Bayesian relaxed clock analyses and likelihood models of diversification. These analyses reveal a series of multiple lineage diversification rate shifts corresponding to an array of nested and parallel radiations. Ancestral state reconstruction and likelihood analyses of correlated diversification suggest that increased rates of diversification are significantly associated with the derived evolution of perennial life history and invasion of montane ecosystems. This evidence is consistent with the hypothesis that iteroparity functioned as a key innovation, providing an ecological mechanism for range expansion and rapid divergence in upper elevation regions throughout the western New World. The results are discussed in relation to issues surrounding incomplete taxon sampling and the often conflicting demands of quality vs quantity in studies of diversification rate shifts.

THE LONG MARCH OF HUMAN GENES.

Andrea Manica

Evolutionary Ecology Group Department of Zoology. University of Cambridge,
Downing Street, Cambridge, CB2 3EJ, UK. am315@cam.ac.uk

In this talk, I will discuss how we can use worldwide patterns in genetic diversity to reconstruct human movements and selection. Anatomically modern humans have been argued to have migrated out of Africa 50-70k years ago to colonise the whole world. The rapid spread into new, previously uninhabited lands was characterised by a series of bottlenecks (founder effects), which led to a gradual loss of genetic and phenotypic diversity the further one moves away from the African origin. Using the genetic signatures left by these movements, we can reconstruct the historical demography of human migrations. Such reconstructions are also fundamental in removing confounding patterns that prevent the meaningful comparison of the effect of selection in different populations. After taking into account the historical demography of humans, I will look at how selection has shaped genetic diversity at the Major Histocompatibility Complex (MHC, the main genes governing the innate immune response) and mitochondria.

EES Master talks

RESPONSIVENESS AS AN ANIMAL PERSONALITY TRAIT: INDIVIDUAL DIFFERENCES IN BEHAVIOURAL PLASTICITY WITHIN AND ACROSS CONTEXTS.

Xenia Schleuning

EES master student. Behavioural Ecology and Evolutionary Genetics groups. MPI for Ornithology. Seewiesen.

Supervisors: Dr. N. Dingemanse and Prof. Dr. B. Kempenaers.

Animal personalities (consistent individual differences in the average level of behaviour across time and contexts) have been shown to exist in a wide variety of animal taxa. Progressively this field has moved from studying behaviours within single contexts to using a more holistic approach across time and contexts. Nevertheless certain facets, central for the evolution and maintenance of personalities, have not been satisfyingly addressed yet. Only recently are correlations of whole suites of behaviours ('behavioural syndromes') or individual variation in behavioural plasticity being addressed. This study formally tests whether individuals differ in their levels of behavioural plasticity. Moreover I investigated if plasticity is correlated across contexts (i.e. are there 'plasticity syndromes?') and whether behavioural and plasticity syndromes are associated suites of traits. Wild great tits were repeatedly tested in the wild for three behaviours: male aggression towards conspecifics (in two contexts: egg laying and incubation), exploration of a novel environment (in two contexts: nest building and chick provisioning stage), and provisioning behaviour along the gradient of begging intensity. The variation in each behavioural trait was analysed using a reaction norm approach. Differences in the degree of behavioural plasticity were found in aggressive behaviour, as there was less variation in aggression during incubation than during laying with a lowered mean. But this may have been due to an autocorrelation between the mean and variance. For exploration behaviour, females were more plastic than males, whereas I could not detect any individual differences in plasticity for provisioning behaviour. Individual plasticity in exploration was correlated to plasticity in provisioning behaviour (aggression could not be added to this analysis due to a low sample size). The present data suggest that there is a 'plasticity syndrome' in that individuals are consistently plastic across contexts. I propose that variation in behavioural plasticity can be an important factor when studying the evolution of personality, as fluctuating selection pressures can act on different types and thereby maintain the variation of behaviour found in different animal personalities.

MOLECULAR PHYLOGENY, BIOGEOGRAPHY AND CHARACTER EVOLUTION IN THE TRIBE RHINANTHEAE (FAMILY OROBANCHACEAE).

Catalina Olano

EES Master student. Botanical Garden Munich.

Supervisor: Prof. Dr. G. Heubl

A molecular systematic approach using DNA sequences of three plastid genes (trnK, trnH-psbA and rps16) and the nuclear marker ITS was applied to reconstruct the phylogenetic relationships within the tribe Rhinanthaeae, family Orobanchaceae (the largest parasitic family of flowering plants). This tribe includes approximately 19 genera, which occur predominantly in the Old World. An exception is the genus *Bartsia* with a remarkable radiation (45 species) in the Andes and only one species (*Bartsia alpina*) distributed in central Europe. Rhinanthaeae represents a good study case due to unclear phylogenetic relationships between the taxa, obscure taxonomic circumscription of the genera and mainly, because it has been neglected in previous molecular studies. In both the nuclear and plastid datasets, the monophyly of the Rhinanthaeae tribe is strongly supported and it is revealed to be divided in four major clades. Despite topological conflicts in relationships between terminal groups, both the congruence of crown groups and the broad sampling of this study allow some taxonomic conclusions, especially regarding the generic delimitations of the polyphyletic genus *Bartsia* and the *Odontites* s.l group, the latter comprising several monotypic independent genera. The insights on infrageneric relationships within Orobanchaceae tribe Rhinanthaeae gained from these studies could help to achieve a much more comprehensive understanding of the generic relationships and phylogeny within the tribe Rhinanthaeae.

THE EVOLUTIONARY HISTORY OF A PLANT RESISTANCE GENE: BALANCING SELECTION AND INTROGRESSION BETWEEN SPECIES.

Katharina Böndel

Diplom student. Evolutionary Biology group. Biozentrum LMU, Planegg-
Martinsried campus.

Supervisors: Dr. L. Rose and Prof. Dr. W. Stephan.

Plants are able to recognize and defend themselves against many different pathogens. Most pathogens deliver effector molecules into the plant cell to enhance microbial fitness. Plant immune defense is based upon specific recognition of these effector molecules by so called resistance genes. Recognition triggers a defense response stopping the infection. Such specific interactions between pathogen effector and host resistance gene lead to coevolution, i.e. a never-ending struggle between evasion of recognition by the pathogen and maintenance of recognition by the plant. These coevolutionary dynamics between host and pathogen favour balancing selection, by which several host and pathogen alleles are maintained in populations over long periods of time. Over speciation times, trans-species polymorphisms can occur either due to ancient polymorphism pre-dating the divergence of the sister species, or to adaptive introgression of beneficial alleles from one species to the other. In this project I analyze nucleotide variation at the resistance gene *Pto*, which confers resistance to a bacterial pathogen *Pseudomonas syringae* in two closely related wild tomato species (*Solanum peruvianum* and *S. chilense*). I aim to test the existence of: 1) balancing selection in each species, 2) trans-species polymorphisms between these species, 3) higher rates of introgression between species in *Pto* compared to the genome average.

Analyses of species wide sequence data reveal elevated levels of nonsynonymous nucleotide variation and an excess of polymorphism in intermediate frequency at this locus in the two species. This suggests that balancing selection acts within each species. Interestingly, I detect alleles shared between the species, as well as a low level of private polymorphism accumulated in these alleles. This indicates that the observed trans-species polymorphism is most likely due to recent introgression of a potentially beneficial allele from one species to the other, confirming the strong selection imposed by *Pseudomonas* populations on these wild tomato species.

FLEDGING BEHAVIOUR IN THE BLUE TIT (*CYANISTES CAERULEUS*)

Lotte Schlicht

Diplom student. Behavioural Ecology, MPI for Ornithology. Seewiesen.

Supervisor: Prof. Dr. B. Kempenaers

The trial of leaving the nest and flying for the first time is a unique feature in the development of young birds. Optimizing the time of fledging potentially has important consequences for immediate and long-term survival and leads to a trade-off between costs and benefits of staying in versus leaving the nest. Thus, based on existing literature, we developed a cost-benefit framework of fledging behaviour depending on individual (body size and mass, sex and paternity) as well as brood parameters (level of inequality/competition among young and food availability). We then tested this framework in a wild population of blue tits (*Cyanistes caeruleus*) using a transponder-based automated recording system. Our results indicate that the fledging time of individual young depends both on reaching a threshold size and on the energetic reserves they carry. These relationships were most pronounced for large broods, possibly as a consequence of an increased risk of abandonment for later fledging young. Thus, apart from developmental and nutritional state, the behaviour of siblings appears to be the most important determinant of fledging patterns.

EVOLUTION OF CO₂ AVOIDANCE BEHAVIOR RESPONSE IN THE *DROSOPHILA* GENUS

Ana Catalán

EES Master student. MPI for Neurobiology and Evolutionary Biology group,
Biozentrum LMU. Planegg-Martinsried campus.
Supervisors: Dr. I. Kadow and Prof. Dr. J. Parsch

CO₂ can elicit different behavioral responses in insects. In mosquito CO₂ is a cue to find a host whereas in *Drosophila melanogaster* it triggers a strong avoidance response. In *Drosophila*, the chemosensory neurons that respond to CO₂ are located in the antenna and co-express two chemosensory receptors Gr21a and Gr63a. In CO₂ behavioral response experiments I found that CO₂ response is a polymorphic behavior across the *Drosophila* genus where *D. simulans*, *D. pseudoobscura* and *D. virilis* show a weak avoidance response. Significant differences in the strength of CO₂ avoidance response were also found between populations of *D. melanogaster* and *D. ananassae*. A weak avoidance response is suggested to be the ancestral state of this behavior shifting to a strong avoidance response in most of the *Drosophila* group and having a weak response evolved independently in the *D. simulans* lineage. Using *D. melanogaster* x *D. simulans* hybrids I found that CO₂ is a polygenic heritable trait where it seems that dominant alleles code for a weak avoidance response. The results presented here suggest that the difference in CO₂ avoidance response may lay in a fine tuning pathway in the olfactory system circuitry of *Drosophila* and that CO₂ avoidance strength might be a trait that is evolving under specific selective forces.

THE EFFECT OF DIVERSITY ON THE LIPID CONTENT OF MICRO-ALGAE.

Anne-Kathrin Graber

EES Master student. Aquatic Ecology. Biozentrum LMU, Planegg-Martinsried campus.

Supervisor: Prof. Dr. H. Stibor

It is part of the EU's energy program to increase the fraction of biofuel to 10% of the total fuel consumption by 2020. To reach this target, biofuel is currently being produced using terrestrial plants, which may lead to a negative impact on global food supply. An alternative to this could be algae, since they can double their biomass several times a day and their cultivation does not compete with food production. Additionally, the lipid content of planktonic algae is considerably higher than that of terrestrial plants. The two current methods of cultivating algae are using either expensive closed photo-bioreactors with highly controlled algal monocultures or open pond systems with less controlled and more diverse algal communities. At present, closed photo-bioreactors are preferred over open pond systems, because most research focuses on identifying the most productive algal species. However, this study shows that diverse communities have a higher resource use efficiency, assimilate more carbon and produce more neutral lipids than the respective monocultures. This is most probably due to complementary and synergistic cooperation among the different species and not to the effect of one single, highly productive species.

CAN *DAPHNIA LUMHOLTZI* INVADE EUROPEAN LAKES?

Meike Wittmann

EES master student. Evolutionary ecology group. Biozentrum LMU, Planegg-Martinsried campus.

Supervisors: Prof. Dr. W. Gabriel, Dr. C. Laforsch and Dr. J. Jeschke

Daphnia lumholtzi is a water flea native to the Paleotropics that has been introduced to North America, where it is continuously expanding its range. This invasive species is protected against fish predation by inducible or permanent morphological defenses. To investigate whether *D. lumholtzi* could potentially invade a native European *Daphnia* assemblage, I developed an individual-based simulation model, conducted an invasion experiment in the laboratory, and finally compared the results of both approaches. The individual-based model describes the dynamics of native and introduced *Daphnia* and takes into account individual variation and stochasticity in life-history events, phenotypic plasticity and predation. Since life-history strategies in the model are heritable and cause differential reproductive success, evolution of *Daphnia* life histories can emerge from the model and influence the outcome of the introduction. The model was parameterized with information from the literature as well as an experiment on the encounter rate between a fish predator and *Daphnia* individuals. In the laboratory, an inducibly defended or a permanently defended *D. lumholtzi* clone were introduced into mesocosms containing native European *Daphnia* clones from Klostersee, Germany, under two different temperatures (20 °C or 24 °C) and in the absence or presence of fish predation. The densities of native and introduced *Daphnia* were monitored for five weeks following the introduction of *D. lumholtzi*. In the model simulations, *D. lumholtzi* was able to invade a European *Daphnia* community and eventually outcompete native *Daphnia* species. The invasion proceeded faster at higher temperatures and in the presence of fish predation. Evolutionary processes and the inducibility of morphological defenses in the introduced clone did not have an effect on the density of *D. lumholtzi* five weeks after its introduction. In the experiment, on the other hand, *D. lumholtzi* was only able to invade in the absence of predation and reached higher densities at 20 °C than at 24 °C. The inducibly defended clone invaded more successfully than the permanently defended clone. The contrasting results of simulations and experiment point to potential problems in the experimental design and to the need to reevaluate the temperature-dependency of life-history processes in *D. lumholtzi*. Overall, this study predicts that *D. lumholtzi* would be able to successfully establish in a European lake.

THE INFLUENCE OF BLOOD GROUP ANTIGENS ON THE HUMAN INTESTINAL MICROBIOTA.

Philipp Rausch

EES Master student, Biozentrum, Planegg-Martinsried campus & MPI for Evolutionary Biology, Plön.

Supervisors: Prof. Dr. J. Baines, Dr. S. Hutter and Prof. Dr. J. Parsch.

With the introduction of high throughput sequencing, the uncountable diversity of microbial life became apparent and made studies comparing microbial ecosystems in their depth possible. Of special interest are human associated bacterial assemblies such as that inhabiting the human gut. In this study, we describe the impact of the strongly selected glycosyltransferase gene FUT2 on the human intestinal microbiota. We observed patterns of increased diversity and evenness among the communities inhabiting individuals with no functional copy of FUT2 (the “nonsecretor” phenotype). In addition to a greater variability of communities among individuals expression FUT2 (the “secretor” phenotype), we observe a significant effect of FUT2 on the distance of mucosa bound bacterial aggregates and identify taxa which are highly associated with the secretor phenotype, such as the Spirochaetes and members of the Actinobacteria. Overall, the gut community of nonsecretors appear to consist of a subset of the communities of secretors, which might help explain why individuals with nonsecretors are more susceptible to developing Crohn’s disease.

GROWTH AND ORGANIC MATTER RELEASE BY TWO COMMON CORAL REEF ORGANISMS IN RESPONSE TO INORGANIC NUTRIENT ADDITION: EFFECTS ON PLANKTONIC MICROBIAL ACTIVITY

Annamarie Gabrenya

EES Master student. Geobiozentrum, Munich

Supervisor: Prof. Dr. C. Wild

The import of inorganic nutrients from land has many far-reaching effects on coastal marine ecosystems. Among those, oligotrophic coral reefs are especially sensitive to nutrient inputs, and such addition could affect reef ecosystem functioning by influencing processes such as organic matter release and cycling as well as interactions between reef organisms. Only one previous study has recently investigated the effects of inorganic nutrient input on organic matter release by one species of coral. This combined field and laboratory study therefore aims to extend our knowledge by evaluating the effect of inorganic nutrient addition (phosphate and ammonium) on the growth and particulate (POM) and dissolved organic matter (DOM) release by two other common and competing benthic reef-associated organisms (the scleractinian coral *Euphyllia* spec. and the green algae *Caulerpa serrulata*) and ensuing mineralization of this organic matter by planktonic microbes. Four treatments were applied (phosphate, ammonium, mix of both and no nutrient control) over a total of four weeks. Measurements were conducted once per week including an initial incubation without nutrient addition. Findings revealed that during combined addition of ammonium and phosphate, nutrients were taken up faster by both investigated species compared to single nutrient addition, and nutrient uptake in general was lower after four weeks of exposure compared to the first week. Nutrient addition significantly decreased growth of *Caulerpa* fragments, while only ammonium addition reduced the growth rate of *Euphyllia* polyps. However, release or uptake of organic matter was not affected by inorganic nutrient enrichment, although a lower C:N ratio of suspended POM in the mixed nutrient treatment hinted at induced compositional changes. *Euphyllia* significantly stimulated microbial activity in the phosphate treatments, while there was no such effect visible for *Caulerpa*. These results suggest that inorganic nutrient availability has different effects on the growth of the two investigated reef organisms and influences the quality rather than the quantity of their organic matter release. This may have implications for interactions with microbes and resulting organic matter recycling.

ACANTHASTER PLANCI - PLASTICITY IN MORPHOLOGY AND BEHAVIOUR?

Robert Sigl & Hannes Imhof

Diplom students, Evolutionary ecology group. Biozentrum LMU, Planegg-Martinsried campus.

Supervisor: Dr. C. Laforsch

The aim of our Diploma-thesis was to prove morphological plasticity and investigate migration behaviour in the coral predator starfish *Acanthaster planci* (crown-of-thorns) under food limitation.

The ability to starve over a long period of time while using their own body mass as energy storage may allow *A. planci* to migrate in groups over large distances from one coral reef patch to another and therefore might be an additional explanation for the poorly understood outbreaks of this starfish, which are dramatically destructive for tropical coral reef ecosystems. We applied state of the art techniques in computed tomography (CT), ultrasound scanning as well as magnetic resonance imaging (MRI) to analyze morphological plasticity in *A. planci*. Out of these findings we established a non-invasive method using MRI followed by 3D modelling to show inner structures and organs of *A. planci* and to make an accurate estimate of the volume of pyloric ceace and the gonads in vivo. Concerning morphological plasticity of *A. planci* our research at the Marine Laboratory of the University of Guam found that the starfish is able to starve over a time period of at least 100 days while significantly reducing its size, volume and weight.

Concerning migration behaviour of *A. planci* under food limitation we figured out that the animals are still able to travel over large distances although being in a bad nutritional state. The walking distances were not as high as distances travelled by animals in a good food condition supposing that the starfish would leave a coral reef patch before it is totally exploited. Although they are not migrating in tight groups we found that the starfish have an overall common direction in which they travel and therefore might use chemical signals to trigger migration. These abilities could make *A. planci* able to move in huge amounts from one coral reef patch to the other and therefore explain the often observed sudden appearance and disappearance of huge numbers of starfish before, respectively after an outbreak.

PhD talks

FINDING THE WILD RELATIVES OF MELON, CUCUMBER, AND CHAYOTE: MOLECULAR PHYLOGENETICS AND BIOGEOGRAPHY OF CUCURBITACEAE.

Patrizia Sebastian

Department of Biology I - Systematic Botany and Mycology. LMU, Munich
Supervisor: Prof. Dr. S. Renner

The gourd family, Cucurbitaceae, is among the economically most important families of plants, with many of the crop species forming the basis of multi-million dollar industries. Knowledge of these species' geographic origin, closest wild relatives and region of domestication is fundamental to breeding efforts, genetic improvement and conservation. Surprisingly, these aspects have been unknown or misunderstood for some of the most important Cucurbitaceae crops, partly due to lack of comprehensive molecular phylogenetic study of plant material that has long been available in herbaria across the world. I am applying molecular phylogenetic methods to solve questions regarding the evolution of three domesticated plants of Cucurbitaceae, namely the Latin American chayote or vegetable pear (*Sechium edule*) and two crops of the genus *Cucumis*, cucumber (*C. sativus*) and honey melon (*C. melo*). Until recently, only two species of *Cucumis*, namely cucumber and its closest relative *C. hystrix*, were thought to be of Asian origin, and honey melon was thought to have originated in Africa, from where 30 species were known. Using DNA sequences from plastid and nuclear markers for some 100 *Cucumis* accessions from Africa, Australia and Asia, I have shown that melon and cucumber are of Asian origin and form a clade with 25 previously overlooked species-level relatives in Asia, Australia and around the Indian Ocean, some of them new to science. My fieldwork in Thailand and Australia has contributed new knowledge about the life forms and habitats of some of these understudied species. Both, cucumber and melon have their wild progenitors in the Eastern Himalayas, but my study has also revealed that the sister species of melon is the re-discovered *C. picrocarpus* from Australia. Future breeding efforts and investigations of wild species related to melon and cucumber should now concentrate on Asia and Australia, instead of Africa.

PHYLOGENY, GENOME EVOLUTION, TAXONOMY AND BIOGEOGRAPHY OF *GENLISEA* (LENTIBULARIACEAE).

Andreas Fleischmann

Department of Biology I - Systematic Botany and Mycology. LMU, Munich
Supervisor: Prof. Dr. G. Heubl

The carnivorous plant genus *Genlisea* (Order Lamiales, Lentibulariaceae: Bladderwort family) currently comprises 22 species, which are distributed in South to Central America and Africa. *Genlisea*, since its discovery over 200 years ago, remained the most understudied and poorly known genus of carnivorous plants, and it has only recently been shown to be a true carnivore, specialized in trapping protozoa and other small soil organisms. The exact functioning of the traps is still not revealed in full detail, but ongoing studies on living plants indicate that the complex traps of the plants actively produce a constant water-current to inhaul small soil invertebrates. This elusive genus gained the interest of science with the discovery in 2006, that some species possess ultra-small nuclear genomes, the smallest known in angiosperms. Moreover, the chromosomes of some members of that genus are diminutive in size, reaching those of bacteria, a reason why karyotypes are not known for the majority of species of the genus. However not all *Genlisea* species show ultra-small genome sizes, nor do related genera. Therefore one focus of my work was to study the evolution of genome sizes and chromosome numbers in phylogenetic context. Only one advanced lineage of South American taxa shows a strong tendency for genome miniaturization, which correlates with diminutive chromosome sizes and an increase in chromosome number. A statistically highly supported comprehensive molecular phylogeny of *Genlisea* was retrieved for all taxa studied, based on three chloroplast loci (*trnK/matK*, *rps16* and *trnQ-rps16*). Ancestral state reconstruction and analyses of phylogeographical data showed that the most recent common ancestor of *Genlisea* was of Neotropical origin. The further evolution of various characters during the diversification of the genus was discussed in phylogenetic context. The clades based on molecular data can be clearly distinguished by a set of morphological characters and on biogeographic patterns, which led to a new sectional taxonomic classification for the genus. Field and herbarium studies revealed new taxa of both subgenera from Venezuela and Brazil, which are currently described as new to science. The comprehensive taxonomical results of my studies are presented in the first monograph of the genus *Genlisea*.

THE SILENT X: FUNCTIONAL ANALYSIS OF MALE GERMLINE X-INACTIVATION IN *DROSOPHILA*

Claus Kemkemer

Evolutionary Biology group, Biozentrum LMU, Planegg-Martinsried campus.

Supervisor: Prof. Dr. J. Parsch

Like mammals, *Drosophila* has XY sex determination with the X chromosome hemizygous in males. This difference between the sexes may cause the X chromosome to evolve differently than the autosomes. For example, there is a significant excess of retroposed genes, many of which are expressed in testis, that have moved from the X chromosome to the autosomes. Additionally, transcriptomic studies have shown that genes with male-biased expression are underrepresented on the X chromosome. A possible explanation for these observations is the X-inactivation hypothesis, which proposes that genes with functions late in spermatogenesis benefit from “escaping” the X chromosome, because otherwise their expression would be limited by male germline X-inactivation. To test for X-inactivation in *Drosophila*, we used the promoter of the autosomal testis-specific gene *ocnus* to drive expression of the *lacZ* gene. This reporter construct was inserted into a transposable element vector and inserted randomly into the *D. melanogaster* genome. Reporter gene expression was significantly higher for autosomal inserts than for X-linked inserts, which is consistent with X chromosome inactivation in the male germline. To date, we have mapped over 100 independent reporter gene insertions on the X chromosome, all of which show very low levels of expression. This suggests that the silencing of gene expression is a global property of the X chromosome and that no regions escape inactivation.

The above approach was also used to test reporter gene expression driven by the promoters of three different X-linked testis-expressed genes (*CG10920*, *CG12681*, *CG1314*). In all cases, autosomal inserts showed significantly higher expression than X-linked inserts. This demonstrates that escape from the X chromosome can provide a direct advantage with respect to gene expression levels in testis and is consistent with the predictions of the X-inactivation hypothesis to explain the observed excess of duplicate genes that have moved from the X to the autosomes.

EVOLUTION OF A RESISTANCE GENE FAMILY IN WILD TOMATOES: RELATING NUCLEOTIDE DIVERSITY TO FUNCTIONAL CONSEQUENCES

Anja Hörger

Evolutionary Biology group. Biozentrum LMU, Planegg-Martinsried campus.
Supervisor: Dr. L. Rose and Prof. Dr. W. Stephan

Parasites have a negative fitness impact on their hosts and can be responsible for drastic epidemics in human, animal and plant populations. Following the “arms race” analogy, coevolution between hosts and parasites is often seen as a recurrent struggle for increased resistance in hosts and evasion of recognition by pathogens. This evolutionary process can maintain considerable allelic diversity at parasite-recognition loci and can also shape the genome architecture of host and parasite species via gene duplication, transposition and deletion of disease resistance and virulence genes. In plants, the molecular mechanisms of disease resistance are well understood and provide a perfect basis to study evolutionary processes shaping host and parasite molecules. In the tomato genus, the *Rcr3*-gene is involved in recognition of the fungal pathogen *Cladosporium fulvum*. I analyzed nucleotide polymorphism at the *Rcr3*-locus in wild tomato species to understand the evolution of pathogen resistance genes in plants. Interestingly, I show evidence that this gene harbors a high level of sequence variation and has undergone recent duplication events in at least one species. In follow-up studies, I investigated the functional consequences of the observed nucleotide variation on expression of host defenses. Functional assays with 50 *Rcr3* protein variants *in vitro* and *in vivo* were performed. The observed natural variation within and between the gene duplicates reflects indeed variation at the functional level. Some variation caused altered perception of pathogen virulence factors and resulted in modified defense responses. At least one of the gene duplicates seems to have undergone pseudogenization. This duplicate may serve as a reservoir of genetic variation, facilitating the maintenance of polymorphism or creation of functional novelty through mechanisms such as gene conversion. These results at the level of nucleotide and functional diversity provide empirical support following the birth and death hypothesis of resistance gene evolution.

MOLECULAR EVOLUTION OF SEX-BIASED GENES IN THE *DROSOPHILA ANANASSAE* SUBGROUP.

Sonja Grath

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Genes with sex-biased expression often show rapid molecular evolution between species. Previous population genetic and comparative genomic studies of *Drosophila melanogaster* and *D. Simulans* revealed that male-biased genes have especially high rates of adaptive evolution. To test if this is also the case for other lineages within the *melanogaster* group, we investigated gene expression in *D. ananassae*, a species that occurs in structured populations in tropical and subtropical regions. We used custom-made microarrays and published microarray data to characterize the sex-biased expression of 129 *D. ananassae* genes whose *D. melanogaster* orthologs had been classified previously as male-biased, female-biased, or unbiased in their expression and had been studied extensively at the population-genetic level. For 43 of these genes we surveyed DNA sequence polymorphism in a natural population of *D. ananassae* and determined divergence to the sister species *D. atripex* and *D. phaeopleura*. We found, that sex-biased expression is generally conserved between *D. melanogaster* and *D. ananassae*, with the majority of genes exhibiting the same bias in the two species. However, about one-third of the genes have either gained or lost sex-biased expression in one of the species and a small proportion of genes (~4%) have changed bias from one sex to the other. The male-biased genes of *D. ananassae* show evidence of positive selection acting at the protein level. However, the signal of adaptive protein evolution for male-biased genes is not as strong in *D. ananassae* as it is in *D. melanogaster* and is limited to genes with conserved male-biased expression in both species. Within *D. ananassae*, a significant signal of adaptive evolution is also detected for female-biased and unbiased genes. To conclude, our findings extend previous observations of widespread adaptive protein evolution to an independent *Drosophila* lineage, the *D. ananassae* subgroup. However, the rate of adaptive evolution is not greater for male-biased genes than for female-biased or unbiased genes, which suggests that there are differences in sex-biased gene evolution between the two lineages.

DIFFERENTIAL HOST DEFENSE AGAINST MULTIPLE PARASITES IN ANTS.

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Host-parasite interactions are ideal systems for the study of coevolutionary processes. Although infection with multiple parasite species is presumably common in nature, most studies focus on the interactions of a single host and a single parasite. To the best of our knowledge, we present here the first study on the dependency of parasite virulence and host resistance in a multiple parasite system. We evaluated whether the strength of host defense depends on the potential fitness cost of parasites in a system of two Southeast Asian army ant hosts and five parasitic staphylinid beetle species. The potential fitness costs of the parasites were evaluated by their predation behavior on host larvae in isolation experiments. The host defense was assessed by the ants' aggressiveness towards parasitic beetle species in behavioral studies. We found clear differences among the beetle species in both host-parasite interactions. Particular beetle species attacked and killed the host larvae, while others did not. Importantly, the ants' aggressiveness was significantly elevated against predatory beetle species, while non-predatory beetle species received almost no aggression. As a consequence of this defensive behavior, only the less costly parasites are able to achieve a high level of integration in the ant society. We conclude that the selection pressure on the host to evolve counter-defenses is higher for costly parasites and, thus, a hierarchical host defense strategy has evolved that depends on the parasites' impact.

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