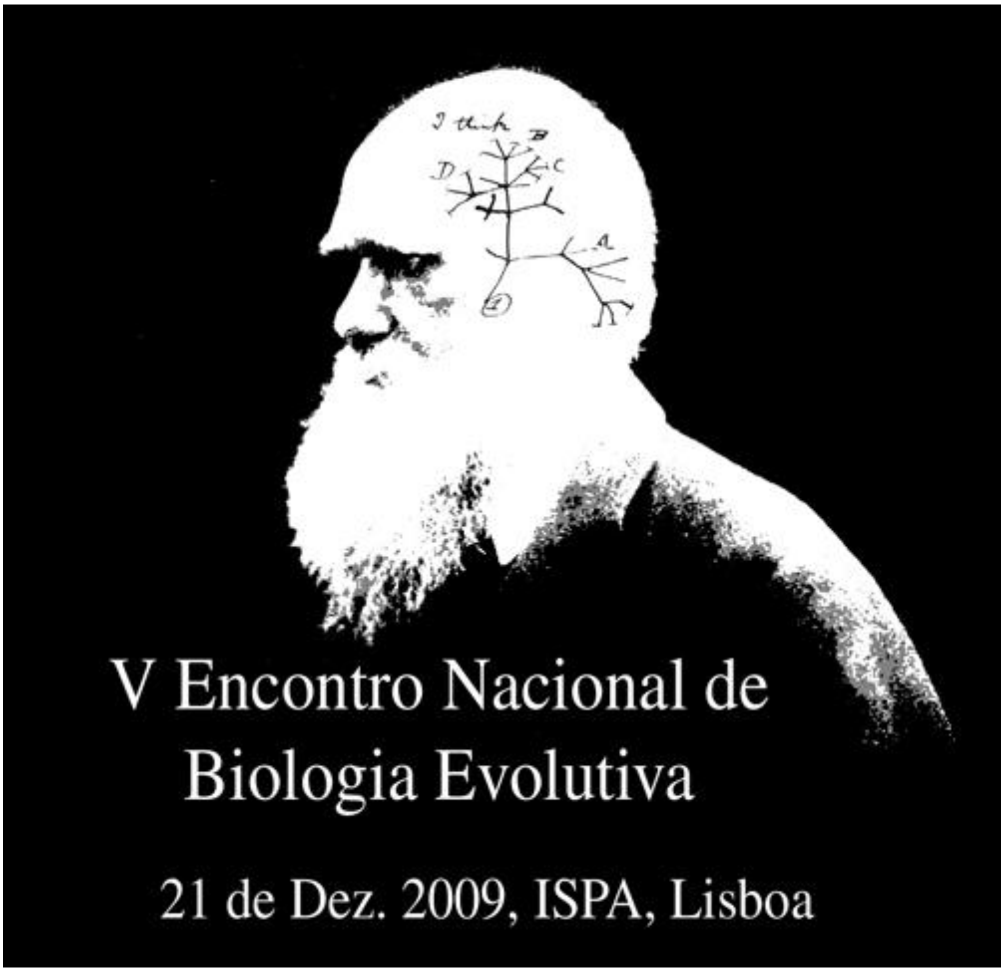

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Centro de Biociências
http://www.ispa.pt/ui/uie
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O quinto «Encontro Nacional de Biologia Evolutiva» vem no seguimento de encontros organizados por e para os biólogos evolutivos portugueses, a trabalhar em Portugal e no estrangeiro, com vista a estes investigadores tomarem conhecimento do trabalho realizado na área e constituirem uma comunidade científica. Tendo este objectivo em mente, existe um sítio da internet e um grupo electrónico para partilha de opiniões e informação sobre palestras, conferências, defesas de tese, workshops e outras actividades de interesse para os biólogos evolutivos portuguêses. Os Encontros têm sido realizados anualmente e hospedado por várias instituições em Portugal. O primeiro teve lugar na Faculdade de Ciências da Universidade de Lisboa (2005), seguidamente no CIBIO/Vairão (2006), IGC/Oeiras (2007) e no IBMC/Porto (2008).

Biologia Evolutiva em Portugal – http://biologia-evolutiva.net/
– http://groups.google.com/group/biologia_evolutiva

Programma

9:30 - 10:00 Registos

10:00 - 10:15 Abertura
10:15 Douglas Futuyma (Stony Brook Univ.): Evolutionary Ecology and Evolutionary Constraints

11:15 - 11:35 Intervalo (20 mins)

11:35 Ana Duarte (Univ. Groningen): Evolution of self-organized division of labour
11:50 Sara Calhim (Queen's Univ. Canada): Postcopulatory sexual selection and evolution of reproductive traits in birds
12:05 Inês Fragata (FCUL): Different patterns of wing size and shape linked to chromosomal inversions in *Drosophila subobscura* populations.
12:20 Bruno Gomes da Silva (CMDT/IHMT): Introgressão assimétrica entre formas biológicas do mosquito *Culex pipiens* (Diptera: Culicidae) na região da Comporta

12:35 - 14:00 Almoço (85 mins)

14:00 Roberto Keller (IGC/AMNH): Evolution of a novel locking mechanism in the mouthparts of ants
14:15 Gilberto Bento (Max Planck para Biologia do Desenvolvimento): Co-option of the endocrine signaling module Dafachronic Acid-DAF-12 in nematode evolution
14:30 Sara Magalhães (FCUL): Reproductive barriers between two sympatric beetle species specialized on different host plants
14:45 Cymon Cox (Univ do Algarve): The application of non-stationary composition models in phylogenetics

15:00 - 15:45 Coffee Break & Poster Session (45 min)

15:45 Josiane Santos (FCUL): Are there confounding effects of sampling in the dynamics of adaptation
16:00 Vera Domingues (Harvard Univ.) Evolution and genetics of adaptive coloration in beach mice
16:15 Ricardo Pereira (UCBerkeley): The continuum of species formation as illustrated by *Ensatina eschscholtzi*i ring species
16:30 Isabel Santos Magalhães (Hull Univ.): Colour polymorphisms as an incipient stage of speciation in cichlid fish of Lake Victoria
16:45 Joana Robalo (UIEE/ISPA): Biodiversidade e relações filogenéticas dos peixes continentais ibéricos: enquadramento paleogeográfico e implicações para a conservação

17:00 - 17:20 Intervalo (20 mins)

17:20 Vitor Sousa (FCUL/IGC): Population divergence with or without admixture: selecting models using an Approximate Bayesian Computation (ABC) approach
17:35 Octávio Mateus (UNL, Museu Lorinhã), Dinosaur eggs and embryos in Portugal: paleobiological implications and paleoenvironmental settings
17:50 Isabel Gordo (IGC): Adaptation of *Escherichia coli* to macrophages

18:05 Discussão aberta

Posteres

Os posteres estão expostos na Galeria do 1º piso, frente à entrada do edifício. Haverá uma sessão de posteres das 15 às 15h45 durante a qual poderão encontrar os autores dos posteres junto aos mesmos.

Ana Margarida Sousa – Rate and effect of compensatory mutations to antibiotic resistance in *Escherichia coli*

Ana Rita Mateus – Coping with changing environments: genetic and physiological mechanisms of adaptive plasticity

Carla Sousa Santos – Double peaks in chromatograms – how to disentangle overlapping nuclear DNA sequences?

Diogo Silva – First insights into the phylogeography of the fungus *Colletotrichum kahawae*, the causal agent of coffee berry disease (CBD)

Ivo M. Chelo – Natural selection dynamics on standing genetic variation of *Drosophila melanogaster* experimental populations

Joana Costa – Filogenia molecular das espécies do género *Dilta* Strand, 1911 (Microcoryphia, Machilidae) e a sua relação com os estudos morfológicos

Joana Micael – Genetic diversity of the strictly protected seastar *Ophidiaster ophidianus* (Echinodermata, Asteroidea)

João Alpedrinha – Demography and soldier function in polyembryonic parasitoid wasps

José Marcelino – Conservation genetics of Collembola bioindicator species in the Azorean archipelago

Lília Perfeito – Efeitos na aptidão de mutações cis-regulatórias no operão lac de Escherichia coli

Marc Gouw – CentrioleDB: a community resource for studying centriolar evolution

Marta Santos – The pace of adaptation: do populations catch up or diverge in the long run?

Patrícia Brito – Mutation Accumulation in *Tetrahymena*

Pedro Belt – Evolution of regulation by phosphorylation

Pedro Branco – Evolution of nutrient uptake reveals a trade-off in the ecological stoichiometry of plant-herbivore interactions

Reeta Sharma – Molecular genetic analysis of Bengal tiger (*Panthera tigris tigris*) populations and its implications in conservation and wildlife forensics

Renato Alves – SporeDB: Searching for the evolutionary origins of endospores

Ricardo Reis Santos – O poder da imagem na persuasão de (pré)conceitos: o caso da evolução

Rita Ponce – The use of a non-LTR retrotransposable element to date the formation of a novel gene cluster

Rita Rasteiro – Y chromosome and mtDNA data support demic diffusion during the European Neolithic

Pérez-Portela R. & Almada V. – Phylogeography of the starfish Marthasterias glacialis in the Atlanto-Mediterranean: is speciation happening into the Mediterranean?

Pérez-Portela R. & Turon X. – Genetic differentiation at small geographical scales: Population genetics and phylogeography of the colonial ascidian Pycnoclavella communis

Rui Castanhinha – Paleo evo-devo: a synthesis

Rui Ramiro – Mating ecology of malaria parasites: insights from multiple-species interactions

Sandra Trindade – Environment shapes mutation effect

Sara Carvalho – Evolution of life-history phenotypes in outcrossing and inbreeding populations during adaptation to a novel environment: insights from an experimental evolution approach

Sara Francisco – Phylogeography and demographic history of *Atherina presbyter* (Pisces: Atherinidae) in the North-eastern Atlantic based on mitochondrial DNA

Sofia Seabra – Adaptation and gene flow in *Philaenus spumarius*, a colour-polymorphic species

Susana Barbosa – Modeling insecticide resistance: measuring selection.

Vera Lúcia Martins Nunes – Ocellated lizard *Lacerta lepida* variation across Iberian Peninsula: patterns of neutral and adaptive divergence and morphology in structured populations

SUMÁRIOS DAS APRESENTAÇÕES

Comunicações Orais

Evolutionary Constraint and Ecological Consequences

Douglas J. Futuyma (futuyma@life.bio.sunysb.edu)
Department of Ecology and Evolution, Stony Brook University

One of the most important shifts in evolutionary biology in the last 50 years is an increased recognition of sluggish evolution and failures to adapt, which seem paradoxical in view of abundant genetic variation and many instances of rapid local adaptation. I review hypotheses of evolutionary constraint (or restraint), and suggest that while constraints on individual characters or character complexes may often reside in the structure or paucity of genetic variation, organism-wide stasis, as described by paleontologists, might better be explained by a hypothesis of Ephemeral Divergence, according to which the spatial or temporal divergence of populations is often short-lived because of interbreeding with nondivergent populations. Among the many consequences of acknowledging evolutionary constraints, community ecology is being transformed as it takes into account phylogenetic niche conservatism and the strong imprint of deep history.

Evolution of self-organized division of labour

Ana Duarte (a.l.f.duarte@rug.nl)
Univ. Groningen

Division of labour is a key feature for the ecological success of social insects. Several theoretical models have been developed to explain how complex patterns of colony organization emerge from interactions of individuals obeying to simple behavioral rules. Fixed response threshold models argue that individuals have internal thresholds for responding to external stimuli associated with certain tasks. Division of labour emerges from individuals having different thresholds for different task-associated stimuli. However, an evolutionary perspective that integrates this mechanistic view is largely lacking. We analyze the fixed threshold model with respect to individual task specialization and worker distribution over tasks. We developed an evolutionary version of the fixed threshold model. Results indicate that evolution of threshold values that promote specialization is possible in the presence of costs of task generalization. We find work distribution to be determined by stimulus dynamics alone, independently of the distribution of thresholds. Our evolutionary analysis deepens our conceptual understanding of the conditions necessary for evolution of division of labor and calls attention to the limitations of the fixed response threshold model.

Postcopulatory sexual selection and evolution of reproductive traits in birds

Sara Calhim (calhims@queensu.ca)
Queen's Univ. Canada

Female promiscuity is associated with several behavioural and anatomical adaptations in males. Being the most variable cell in the animal kingdom and the last step for fertilization success, one can predict that sperm themselves are under strong post-copulatory selection. Using birds as a model system, I will (1) illustrate how sexual and natural selection forces jointly shape the evolution of sperm design, and (2) discuss the consequences of the latter within and across species.

Different patterns of wing size and shape linked to chromosomal inversions in *Drosophila subobscura* populations

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2 Departament de Genètica, Grup de Biologia Evolutiva (GBE), Facultat de Biologia, Universitat de Barcelona Spain
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The *Drosophila subobscura* fly presents a European latitudinal cline in inversion polymorphisms and wing size and shape. Similar inversions and wing size clines have been observed after two different colonizing events in North and South America. In contrast the cline for wing shape presents a different relationship with latitude. Previous work has suggested that wing trait differences among individuals are partially due to the association between chromosomal inversions and particular alleles. More importantly it is known that a few number of effective individuals founded the New World populations, which might have modified the biometrical effect of inversions on quantitative traits. In this work we evaluate the contribution of chromosomal inversion clines in modelling the wing size and shape clines in the three continents. For this we combined information from both inversions polymorphisms and wing patterns, measured for male and female flies from the Adraga (Sintra, Portugal) and Chile (South America) populations. Our results indicate that instead of a contingent, unpredictable evolution, the contrasting patterns observed in the shape clines are due to different inversion-shape associations between continents.

Introgressão assimétrica entre formas biológicas do mosquito *Culex pipiens* (Diptera: Culicidae) na região da Comporta

Bruno Gomes da Silva (bsilva@ihmt.unl.pt)
Centro de Malaria e Outras Doenças Tropicais/Instituto de Higiene e Medicina Tropical

O mosquito *Culex pipiens*, um importante vector de arbovírus, apresenta duas formas biológicas: pipiens e molestus. Estas são morfologicamente indistinguíveis, mas exibem importantes diferenças a nível fisiológico (desenvolvimento dos ovos) e comportamental (cópula e preferência alimentar). No sul da Europa, estas duas formas coexistem à superfície podendo, ocorrer hibridação entre elas. Estudos em insectário e análise de microssatélites foram realizados para caracterizar uma população de *Cx. pipiens* na região da Comporta. Nesta análise verificou-se a existência de dois clusters genéticos distintos na região, associados às características fisiológicas e comportamentais que definem as formas molestus e pipiens. A taxa de hibridação entre as formas variou entre 7% a 10% dependendo do método de estimativa utilizado. Uma maior proporção de genomas híbridos na forma pipiens sugere a ocorrência de introgressão assimétrica entre as duas formas, o que poderá influenciar a capacidade de transmissão de arbovírus por estes mosquitos.

Evolution of a novel locking mechanism in the mouthparts of ants

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Instituto Gulbenkian de Ciência, Oeiras, Portugal

Ants constitute the dominant animal group in terrestrial ecosystems. For the most part, this ecological dominance can be explained by their acquisition of a highly social way of life (i.e., eusociality) early on during the evolution of the group. However, there are other groups of eusocial insects, such as termites and various groups of aculeate wasps and bees, that are not as nearly as speciose or ecologically successful as ants. It has been suggested that the ants' success is due to the conjoin occurrence of eusociality with a suite of morphological novelties that can be traced back to the most recent common ancestor of this clade. Examples of such unique features include the presence of a caste of wingless workers and the presence of an antibiotic-producing gland located in their mesosomas (the metapleural gland). Here I describe a previously unknown mechanical innovation that allows ants to lock their mouthparts shut by interlocking the labrum with both maxillae. This innovation is universally present among ants and has gone through a series of incremental modifications since it first evolved in the common ancestor of the group. The protection that this locking mechanism confers to the soft and otherwise vulnerable head appendages may constitute yet another key innovation responsible for the success of ants.

Co-option of the endocrine signaling module Dafachronic Acid-DAF-12 in nematode evolution

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The nematode *Pristionchus pacificus* has two alternative mouth forms associated with predatory and bacteriovorous feeding strategies. We find that this dimorphism is a polyphenism that is controlled by a co-opted endocrine switch mechanism. Mutations in the nuclear hormone receptor DAF-12 and application of its ligand, the sterol hormone dafachronic acid, strongly influence this switch mechanism. The comparison of dauer formation and mouth morphology switch reveals that different thresholds of the dafachronic acid signal provide specificity. This study identifies dafachronic acid as a key hormone in nematode evolution reminiscent of juvenile hormone and ecdysone in insects.

Reproductive barriers between two sympatric beetle species specialized on different host plants

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Faculdade de Ciências da Universidade de Lisboa

Knowledge on interspecific pre- and post-zygotic isolation mechanisms provides insight into speciation patterns. Using crosses (F1 and backcrosses) of two closely related flea beetles species, *Altica fragariae* and *A. viridicyanea*, specialized on different hosts in sympatry, we measured (a) the type of reproductive isolation and (b) the inheritance mode of preference and host-specific performance, using a joint-scaling test. Each species preferred almost exclusively its host plant, creating strong pre-zygotic isolation between them, and suggesting that speciation may occur at least partly in sympatry. Reproductive isolation was intrinsic between females of *A. fragariae* and either *A. viridicyanea* or F1 males, whereas the other crosses showed ecologically-dependent reproductive isolation, suggesting ecological speciation. The genetic basis of preference and performance was at least partially independent, and several loci coded for preference, which limits the possibility of sympatric speciation. Hence, both ecological and intrinsic factors may contribute to speciation between these species.

The application of non-stationary composition models in phylogenetics

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Univ. Algarve -Centro de Ciencias do Mar (CCMAR)

Non-stationary composition heterogeneity describes the process of change in base composition of lineages through evolutionary time in molecular phylogenetic analyses. Although lineage-specific composition heterogeneity is prevalent in empirical data, substitution models applied in phylogenetic analyses typically assume a time-homogeneous composition process. Here I describe a non-stationary composition model, the Node Discrete Composition Heterogeneity (NDCH) model, and a Bayesian posterior predictive test of model composition adequacy. A case study analyzing the ribosomal RNA "universal" tree of Life is presented.

Are there confounding effects of sampling in the dynamics of adaptation

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Faculdade de Ciências da Universidade de Lisboa

Genetic differentiation between natural populations indicates restricted gene flux that may have important consequences both in evolutionary and conservation terms. Highly polymorphic molecular markers such as microsatellites are frequently used to estimate FST and other measures of differentiation. One main question when analyzing differentiation is to what extent sampling effects involved during collection of the biological material inflate real differences between the target populations. In a previous study, our team has found significant though small differentiation between two recent laboratory foundations from two wild populations of *Drosophila subobscura* (Sintra and Arrábida, Portugal). Part of this difference might have occurred during the founder event, e.g. due to sampling 'error' or small spatial-temporal fluctuations in the populations' composition. Here we present a study in which two samples were collected from each location in order to distinguish between effects of sampling and of geographic origin in the degree of genetic differentiation between populations. We also analyze how much differences in initial genetic variability explain the later evolutionary dynamics of fitness-related traits of the adapting populations.

Evolution and genetics of adaptive coloration in beach mice

Vera Domingues (vdomingues@oeb.harvard.edu)
Harvard University

Understanding the evolutionary origin of adaptive traits is a central question in evolutionary biology. In particular we would like to know which genes (and alleles) underlie adaptive phenotypes, and how interactions with other alleles/genes (epistasis) may influence adaptive change. The oldfield mouse, *Peromyscus polionotus*, is a unique system to study these questions. This species shows extreme variation in color pattern throughout its range in the southeastern United States. In particular, mice inhabiting the coastal dunes and barrier islands of the Gulf Coast of Alabama and Florida exhibit an extremely pale coloration, which has been driven by natural selection for crypsis. Three pigmentation genes (Mc1r, Agouti and Corin) were identified as contributing to color variation in this species. In the case of Mc1r, we identified a derived mutation that contributes to these adaptive color differences. Initial studies suggest that a change in Agouti mRNA expression is highly correlated with pigmentation. Allele-specific assays showed that a cis- regulatory change is responsible for differences in Agouti expression. Fine-scale association mapping studies in natural populations will narrow in on a region in the Agouti cis-regulatory sequence likely to contain the mutation(s) responsible for differences in expression and will ultimately identify the mutation(s). Introgression experiments are being carried on to examine the effects of these genes individually and in combination, both on adult pigmentation pattern and through development. So far, the epistatic interaction of Agouti and Mc1r on adult pigmentation pattern has been shown. Using complementary approaches such as association mapping, classical genetics and developmental biology in natural and laboratory populations, we are reconstructing the evolutionary history of allelic variation at these three loci, providing a model to study the evolution of adaptive phenotypes in natural populations.

The continuum of species formation as illustrated by *Ensatina eschscholtzi*i ring species

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The salamander *Ensatina eschscholtzii* is an example of a ring species in which extant intermediate stages of terminal forms have a nearly continuous range, offering replicated interactions at several stages of divergence. We first employ a greatly expanded allozyme database and individual-based analyses to separate the effects of divergence time and gene flow to evaluate how gradual divergence of populations around the ring contributes to the development of reproductive isolation. Secondly, using a multiple regression approach, we test which of three common speciation models better predicts reproductive isolation in this ring species: divergence by distance, vicariance or ecological gradient. Despite the high degree of genetic ($D \leq 0.39$) and ecomorphological divergence observed in secondary contacts around the ring, reproductive isolation or rare hybridization is observed only at the terminus of the ring. Instead, in the secondary contacts sampled around the ring, hybrids are common and reproductively successful, enabling genetic leakage between parental genomes and the potential for genetic merger. Although the species complex was able to colonize a high diversity of habitats in California, ecological divergence did not result in reproductive isolation, although hybrid zones after ecological divergence tend to be narrow. Instead, reproductive isolation is better predicted by time in geographic isolation. Diversification and consequent genetic interactions in *Ensatina* reveal a continuum between populations, ecological races, and species, where polytypic traits and high genetic differentiation are maintained without reproductive isolation.

Colour polymorphisms as an incipient stage of speciation in cichlid fish of Lake Victoria

Isabel Santos Magalhães (I.Santos-Magalhaes@hull.ac.uk)
Hull University

Colour polymorphisms can sometimes be incipient stages of speciation. We studied two species of Lake Victoria cichlids exhibiting very similar sex-linked colour polymorphisms. The ecology and behaviour of one of these species is well studied, with colour-based mating and aggression preferences. We looked at morph frequencies across 14 years, and analysed morphology and nine microsatellite DNA loci for samples collected in 2005. We ask whether (1) morph frequencies have changed during the 14 year period; and whether (2) mate choice and/or disruptive selection reduces gene flow between the colour morphs, permitting differentiation in traits other than colour. We found that frequencies of colour morphs have oscillated, but not changed directionally, suggesting the colour polymorphism is persistent on an ecological time scale. We found limited evidence of eco-morphological differentiation and no evidence for differentiation at neutral loci between sympatric colour morphs. There is, however, evidence for non-random mating between sympatric colour morphs, manifested in significantly non-random genotypic assignment and in an excess of linkage disequilibrium in one morph. Negative frequency-dependent sexual selection on colour morphs remains the most plausible explanation for the maintenance of these polymorphisms in sympatry, although our data suggests the possibility of ecological character displacement following or parallel to divergence in colouration.

Biodiversidade e relações filogenéticas dos peixes continentais ibéricos: enquadramento paleogeográfico e implicações para a conservação

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A Península Ibérica, no que se refere aos Leuciscinae (Cyprinidae), parece ter sido colonizada por um número muito restrito de linhagens oriundas da Europa Central e/ou da Europa Mediterrânica, que aí chegaram provavelmente em fases muito precoces da orogenia pirenaica, antes da Península Ibérica ter ficado isolada do resto da Europa no que respeita aos cursos de água. Apenas três linhagens de Leuciscinae terão logrado colonizar a península: uma dando origem às espécies do género Squalius, outra às espécies hoje pertencentes aos géneros Achondrostoma, Pseudochondrostotoma, Iberochondrostoma e Parachondrostoma e ainda outra que terá dado origem aos peixes do actual género Anaecypris. Fósseis encontrados na Península Ibérica corroboram esta hipótese. Essas linhagens sofreram depois uma intensa diversificação local, sendo representadas actualmente por um grande número de espécies e uma grande proporção de endemismos, muitos com elevado estatuto de conservação. No entanto, as linhagens que colonizaram a Península Ibérica representam uma fracção muito pequena das linhagens presentes na Europa, o que reforça a ideia de que a colonização da Península Ibérica pelos Leuciscinae se fez através de contactos muito limitados.

Population divergence with or without admixture: selecting models using an Approximate Bayesian Computation (ABC) approach

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[3] University of Reading, UK;
[4] Evolution & Diversité Biologique UMR CNRS, Toulouse, France

Genetic data has been widely used to reconstruct the demographic history of populations, including the estimation of parameters such as migration rates, divergence times and relative admixture contributions from different populations. Recently, increasing interest has been given to the ability of genetic data to identify the most probable among alternative models. Here, we applied an Approximate Bayesian Computation (ABC) approach to select the model that best fits the data among several splitting and admixture models. We performed a simulation study and showed that with reasonably large data sets it is possible to determine with high probability the model that most likely produced the data. This suggests that it is possible to distinguish genetic patterns due to past admixture events from those due to shared polymorphism. We then apply this approach to microsatellite data from an endangered and endemic Iberian freshwater fish species, in which a clustering analysis suggested that a population could be admixed.

Dinosaur eggs and embryos in Portugal: paleobiological implications and paleoenvironmental settings

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Universidade Nova de Lisboa & Museu da Lorinhã

The abundance of dinosaur eggs, embryos, and nests from the Lourinhã Formation (Late Jurassic, Portugal) bears great scientific potential to unravel information on fundamental issues in the biology and ecology of dinosaurs. New discoveries, as well as previous finds, represent several landmarks for vertebrate paleontology: the only embryonic dinosaur remains from Europe, the second oldest known, and the only embryos from primitive theropod dinosaurs. Besides these important characteristics, there are new unstudied Late Jurassic and Early Cretaceous localities with nests, eggshells, and embryos. The study of this fossil heritage is relevant by its own right, but moreover, it can provide important implications on the evolution of dinosaurs. Our research is divided into four different lines: paleobiological characterization, paleoenvironmental characterization, thermoregulation evolution and the role of heterochrony in the evolution of theropods. Therefore, from a geological perspective, the stratigraphy and sedimentology of nest sites provide insights into the paleoenvironmental setting of the discoveries, improving our knowledge of paleoecology and dinosaur reproductive strategies. Moreover, the geology may provide information about diagenetic constraints, geochronology of the localities, and the nesting structures within the paleolandscape. In the other hand from a paleobiological perspective, the anatomy and histology of eggshells and embryos will be decisive to provide essential information for substantiating phylogenetic relationships, evolution, and testing hypotheses regarding ontogenetic growth.

(1) Thermoregulation can be methodologically inferred on the basis of stable-isotope ratios in eggshells, measured using mass spectrometry techniques. Calcite (CaCO3) in eggshell is derived from metabolic carbon dioxide of the egg progenitor. This crucial physiological parameter can be assessed using the Late Jurassic theropods eggshells from Portugal, while the embryonic material allows a correct taxonomical identification. These taxa evolved at key transitional moments between primitive archosaurian ectothermy and more derived avian-grade endothermy.

(2) We hypothesise that heterochrony played an important role in theropod evolution and origin of birds. After a detailed anatomical description, taxonomical classification, and identification of ontogenetical conditions we will study the relevance of heterochrony in the evolution of dinosaurs by comparing the ontogenetic characters of *Lourinhanosaurus* and other undescribed embryos with the more basal and derived clades. Most importantly, ontogenetic information is crucial to validate phylogenetic information. The scarcity of theropod perinates and juveniles for anatomical comparisons is in part resolved by the unique occurrence of embryos of the Portuguese *Lourinhanosaurus*. By exploring the paleobiological foundations (i.e. physiological and evolutionary) of primitive theropods we are giving light to the evolutionary history of their descendants: modern birds.

Adaptation of *Escherichia coli* to macrophages

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Instituto Gulbenkian de Ciência

Experimental evolution with bacteria presents us with the opportunity to directly measure key parameters and to test theoretical predictions about the genetic basis of adaptive evolution in increasingly complex ecosystems. As Dobzansky pointed out "*The greater the diversity of inhabitants in a territory, the more adaptive opportunities exist in it*." Here we study what sort of adaptive strategies a bacterial population evolves when facing one of the sentinels of the innate immune system - the macrophages. We test hypothesis that the rate of adaptation is higher in the presence of such predators than in their absence and test if within and between population diversity is higher in a biotic than in an abiotic environment.

Cancelada

Sexual Selection by Cultural Inheritance in an Invertebrate

Susana Varela (susanaamv@yahoo.fr)
Faculdade de Ciências da Universidade de Lisboa

Organisms require information to make decisions about fitness-affecting resources, such as mates. Animals may extract "personal information" about potential mates by observing their physical characteristics or extract additional "public information" by observing their mating performance. Mate copying by females is a form of public information use that may reduce uncertainty about male quality, allowing more adaptive choices. Experimental studies have produced evidence that female mate copying occurs in several species of fish, birds, and mammals, including humans. We report the first evidence that a female invertebrate can exploit public information to select mates. In a first experiment, Drosophila melanogaster female prospectors increased their time in the attraction zones of poor-condition males, but not of good-condition males, after having observed them with a model female. This suggests that females appraised prospective mates by exploiting public information and did so mainly when it contrasted with personal information. In a second experiment, prospector females preferably mated with males of the color type they had previously observed copulating over males of the rejected color type, suggesting that female Drosophila can generalize socially learned information. The complexity of Drosophila decision-making suggests an unprecedented level of cognition in invertebrates. Our findings have implications for evolution given that socially learned mate preferences may lead to reproductive isolation, setting the stage for speciation.

Posters

Rate and effect of compensatory mutations to antibiotic resistance in *Escherichia coli*

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How does a perfectly adapted genome deals with a single alteration in its code? Here we address this question by studying the distribution of compensatory mutations of a bacterium that carries a single nucleotide substitution that confers antibiotic resistance. Reducing antibiotic therapy to the minimum has long been a main policy to decrease resistance in microbial populations since the fitness cost that chromosomal resistance mutations often confer to the cells makes them less competitive. Counteracting this is selection for a decreased cost of resistance. This can be accomplished by reversion of the resistance mutation or acquisition of a second site compensatory mutation, restoring fitness close or equal to the sensitive strains level. Under most conditions compensation rather than reversion is a more frequent event. Given the importance of compensation in general and in the context of antibiotic resistance prevalence, accurate measurements of the tempo and mode of its evolution is an urgent necessity. We assessed the rate and distribution of compensatory mutations using a powerful technique, based on a neutral marker that enables the quantification of very small effect mutations arising and sweeping to fixation in bacterial populations. Importantly this method is unique in its power of detection at a very small time scale. Our results show that adaptation depends on the starting point on the fitness landscape and that compensatory mutations can be detected in tenths of generations.

Coping with changing environments: genetic and physiological mechanisms of adaptive plasticity

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Organisms are expected to have some intrinsic capacity to respond to changing environmental conditions; in the form of ecological (i.e. physiological and/or behavioral plasticity), dispersal to suitable habitats elsewhere, or evolutionary adaptation. Of special interest in the study of how organisms cope with changing environments is phenotypic plasticity. Adaptive phenotypic plasticity leads to a better phenotype-environment match and can represent a potential solution to the problems posed by fluctuating environments. One of its most compelling examples is seasonal polyphenism in butterfly wing patterns. The adaptive value of such alternative seasonal phenotypes and their relation to hormone cycles has been previously established. However, little is known about how the environmental cues modulate development to produce those phenotypes, and about the evolution of plasticity. In this project will be used laboratory populations of Bicyclus anynana that differ in genetic background and in their wing plasticity in relation to temperature. I plan to investigate how developmental temperature and hormone manipulations affect quantitative levels and spatial patterns of gene expression which produce alternative phenotypes. In the end, I hope to combine information from genes, to development, to physiology, to different phenotypes (wing patterns and life histories), and finally to fitness in natural populations.

First insights into the phylogeography of the fungus *Colletotrichum kahawae*, the causal agent of coffee berry disease (CBD)

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The fungus *Colletotrichum kahawae* is the causal agent of coffee berry disease, one of the most destructive diseases of arabic coffee that only occurs in the African continent, where it can lead to yield losses reaching 80%. In pathogenic fungi, the knowledge of its evolutionary history and of the spatial distribution of genetic variation is vital for the implementation of effective disease control and quarantine measures, specially in countries where coffee represents the bulk of the total exportations revenue. Characterization of the genetic diversity of this fungus has proven to be quite challenging despite several attempts through diverse molecular techniques such as AFLPs, RFLPs, VNTRs and ITS region sequencing, showing the species as a nearly clonal population. This apparent lack of genetic diversity of *C. kahawae* is thought to be due to its presumed recent origin from the closely related pathogenic fungus *C. gloeosporioides*. However, different pathogenic strains are known to occur suggesting the existence of undiscovered molecular variability. To address this issue, in addition to ITS locus, we sequenced 700 b.p. of the β-tubulin 2 gene which is known to be more variable and informative than the ITS region, on a sample comprising populations of several African locations where the disease strikes. Up to now, the results suggest the existence of some level of variability that distinguishing several populations from de Southwest Africa, which may reflect a geographic genetic divergence. These results may start to bring some insights on the evolutionary history and dispersal of *C. kahawae* and help to unravel its origin. This work is the outset of a multi-loci approach aimed at deepening the phylogeographical analysis of *C. kahawae* and the phylogenetical relationshisps between *C. kahawae* and *C. gloeosporioides*.

Natural selection dynamics on standing genetic variation of *Drosophila melanogaster* experimental populations

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In sexual organisms adaptation to different environments can occur by the sorting of favourable alleles present in a population. This independency of new mutations provides a quick way to respond to the demands of changing environmental conditions and may predominate in wild populations. In this study we analyze genotypic changes in *Drosophila melanogaster* experimental populations during adaptation to ancestral conditions, after being selected in several diversifying environments. Genotyping of single nucleotide polymorphisms, mostly located on the 3rd chromosome, provide longitudinal data on allele frequencies and allows us to estimate the contribution of selection and drift for the evolution of these populations. Selection occurs in different loci without general loss or gain of allele diversity and with changes in allele's fitness effects. Adaptive evolution in sexual organisms can be based on the recombination of extant genotypes and contingency in evolution can arise from the non-additive effects of alleles at different loci.

Filogenia molecular das espécies do género *Dilta* Strand , 1911 (Microcoryphia, Machilidae) e a sua relação com os estudos morfológicos

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O género *Dilta* Strand, 1911 (Microcoryphia, Machilidae) é um grupo de insectos estritamente Paleártico, com uma distribuição ao longo da Europa Ocidental, Central e de Leste (com excepção dos Balcãs), e Norte de África. Até hoje são conhecidas cerca de 33 espécies para este género, sendo que a maior diversidade se encontra na Península Ibérica (cerca de 15 espécies). O objectivo deste estudo é tentar inferir, através de marcadores moleculares (12S rRNA e 16S rRNA mitocondriais), as relações filogenéticas para algumas espécies deste género, e comparar com os resultados dos estudos morfológicos. Os primeiros resultados moleculares obtidos indicam uma clara separação entre as espécies, com distâncias genéticas que variam entre 4 e 30%.

Genetic diversity of the strictly protected seastar *Ophidiaster ophidianus* (Echinodermata, Asteroidea)

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Ophidiaster ophidianus is under a strictly protected status in the Mediterranean Sea. To develop a conservation strategy it is fundamental to understand the population's genetic structure. Nevertheless, no genetic studies on *O. ophidianus* populations have been previously carried out. In the present study, population genetic methods were used to characterize patterns of variation of this seastar at mitochondrial loci. Sixty-one sequences of mtDNA (16S and adjacent genes) from 9 locations, spread over ~ 2560 km across the Atlantic and Mediterranean, revealed weak and nonsignificant population structure (overall Fst: 0.06948). However, the pairwise Fst values indicate a slight but significant increase in genetic isolation with geographic distance (Mantel's test P = 0.037), suggesting that populations are not panmictic across the sampled geographic range. Also, it appears to be a unimodal relationship between genetic diversity and longitude, with diversity being lower at both edges of the sampling range and suggesting that historic populations of *O. ophidianus* might have expanded eastward and westward from the centrally located Madeira.

Demography and soldier function in polyembryonic parasitoid wasps

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In parasitoid wasps of the genus *Copidosoma*, adult females lay their eggs into the eggs of other insects, and each wasp egg can proliferate to form ~1000 clonal embryos. Remarkably, a fraction of these embryos develop precociously into sterile "soldier" individuals, which recognize and kill other species of parasitoids growing in the same host, and are also known to kill conspecific larvae (including their siblings) developing in the host. Previous theory relates this behaviour to the extreme female-biased sex ratios among adults wasps emerging from the host, suggesting that the primary function of soldiers is to mediate sex-ratio conflict between siblings. However, this previous theory did not allow for single-sex broods, which are abundant within this genus. Here, we develop a model in which some proportion of hosts contain single-sex broods. We demonstrate that there is always sex-ratio conflict between siblings, and that the observed female-biased soldier production is indicative of their having a sex-ratio conflict function.

Conservation genetics of Collembola bioindicator species in the Azorean archipelago

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Climate and a nutrient rich volcanic soil in the Azores, support an abundant flora with pristine forests covering many islands' hillsides. 14.6% of Azores is protected land. The critical importance of preserving biodiversity is widely recognized. It is an international goal to reduce the loss of biodiversity by 2010, the International Year for Biodiversity. The progressive increase in demand for arable land has drastically altered biotic assemblages in the Azores. Because of their isolation, oceanic islands are particularly sensitive to loss of biodiversity which in turn renders them less resilient to invasion stress among others. Collembola were selected for this study, as model bioindicator organisms, due to their high sensitivity and rapid response to changes in their habitat. Determining and retaining genetic variation among populations of a key bioindicator may be of critical importance for their conservation and persistence at large spatial scales and for the maintenance of species resilience and adaptive responses to environmental changes and/or anthropogenic impacts. Preliminary COI mitochondrial DNA sequences were used to evaluate the phylogeographic structure within and among population assemblages of Collembola (n=50) in 4 islands of the Azores archipelago and Madeira island. Populations were present in thirteen ecosystem types, representing a gradient of anthropogenic impact. Pairwise genetic divergence matrices performed on ca. 1600 COI base pair sequences ranged from 0 to 20%, showing that two of the species (ie, *Pogonognathellus longicornis* and *Lepidocyrtus curvicollis*) appear to be invasive with an ubiquitous presence throughout the gradient. The accumulated differences between populations of *Heteromurus major* indicate a discrete biogeographic pattern and isolation by distance. Discrepancies in individuals of *Ceratophysella* spp. may be related with the presence of three mitochondrial groups which can represent morphologically different species. Maximum genetic distances were observed between artificial production forest (ie, *Cryptomeria japonica*), natural habitats and Madeira island. Our ultimate goal is to combine genetic with ecological data, in order to define critical conservation hotspots and to make recommendations that will reduce the disturbance of anthropogenic activities on the Azorean archipelago.

Efeitos na aptidão de mutações cis-regulatórias no operão lac de *Escherichia coli*

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A distribuição de efeitos de mutações pontuais na aptidão é um parâmetro chave em genética de populações. O tema foi extensivamente explorado do ponto de vista teórico e existem algumas observações empíricas, no entanto, ainda não existe uma descrição precisa do formato desta distribuição. Este projecto está focado em mutações cis-regulatórias, que estão na base de várias adaptações em organismos multi-celulares. O modelo usado é o operão lac de *Escherichia coli*; este foi escolhido porque pode ser facilmente manipulado e os níveis de expressão proteica e a aptidão podem ser facilmente medidos. Os resultados indicam uma grande dependência da aptidão nas condições ambientais e que as diferentes proteínas do operão podem estar sujeitas a pressões selectivas muito diferentes.

The distribution of fitness effects of point mutations is a key parameter in population genetics. The topic was well explored theoretically and some empirical observations were made but we are still lacking an accurate picture of what this distribution looks like. In this work I am focusing on cis-regulatory mutations, which have been shown to underly a number of adaptations. I am using the well described lac operon of Escherichia coli as a model because this system can be easily manipulated and both fitness and protein expression easily measured. I found that fitness effects greatly depend on environmental conditions and that the different proteins coded by the operon may be subject to very different selctive pressures.

CentrioleDB: a community resource for studying centriolar evolution

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Centriole-like structures are present in a wide range of organisms and participate in processes such as cell division and cell motility. There are differences between these structures, whether they are different structures in the same cell or the same structures in different organisms. However, this vast morphological diversity is not properly classified beyond model organisms, and the underlying assembly mechanisms are not fully understood. To address this issue, we created a bioinformatics resource that integrates morphological annotation of centriolar structure and molecular information on proteins involved in centriole assembly. Electron microscopy iimages along with the structural details observed in each image are annotated by means of a controlled vocabulary, a hierarchy of structures and structural attributes. The molecular information consists of proteins known to be involved in centriole assembly in humans, a manually curated list of their orthologs in other species, and homologs identified other species. The unique aspect of CentrioleDB is that, by using a diverse collection of species, it is possible to bridge the gap between morphological details and molecular information using phylogenetic history. Currently, CentrioleDB contains over 300 images from almost 60 species as diverse as Plasmodium falciparum and Chlamydomonas reinhardtii, and molecular information for 180 species. Describing structural and molecular information in an evolutionary context, allows the cell biologist community to view detailed summaries to infer meaningful biological relationships which otherwise could have passed by unnoticed.

The pace of adaptation: do populations catch up or diverge in the long run?

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How much do populations differ in the rate of adaptation to a novel environment? It is expected that adaptation to a common environment will lead to convergence or parallel evolution if natural selection plays the main role, and the genetic background doesn't impose contrasting capacity to respond to the new selective pressures. However differences in the amount of standing genetic variation and in the genetic architecture of life-history traits may lead to variable evolutionary trajectories. Considering that genetic variance for fitness as well as genetic correlations between life-history traits may change during the evolutionary process, disparities between populations may vary between short and long-term evolution. Here we analyze the adaptation to the laboratory environment of Drosophila subobscura populations from several foundations originated from wild populations. By comparing the differences presented in shorter versus longer-term studies, we address the effect of time in the different capacity of populations to adapt to similar environmental challenges as a function of initial and evolving genetic background.

Mutation accumulation in *Tetrahymena*

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Mutation accumulation (MA) is a classical experiment to estimate the rate at which deleterious mutations arise in populations and their effects on fitness. These are important parameters in the study of the evolution of many fundamental processes such as sexual reproduction, aging and polyploidization. In this study we carried out a mutation accumulation study in two closely related species of ciliates: Tetrahymena thermophila and T. pyriformis. We show a correlation between resistance to extinction and the reproductive mode. T. thermophila can reproduce sexually and presents a marked nuclear dimorphism with diploid, micronucleus (Mic) that functions primarily as the germ line, and a large somatic, polyploid, macronucleus (Mac) responsible for all gene expression. The Mac originates from the Mic after site-specific fragmentation of the five chromosomes leading to 200-300 autonomously replicating chromosomal fragments. Each of these fragments undergoes several bouts of duplication and each gene is present at an average level of 45 copies per MAC genome. *T. pyriformis* lack the germinal micronucleus and therefore are unable to reproduce sexually. We evolved 20 lines of T. thermophila (mating type II), under strong bottlenecks of a single individual, all derived from the same founding clonal population. Our results showed that all 20 lines go extinct within a period of 20 bottlenecks, which is characteristic of a mutation meltdown. Natural populations of Tetrahymena thermophila are known to periodically suffer drastic fluctuations in population size and therefore it suggests that this species must undergo sexual reproduction to avoid the deleterious effects seen in our laboratory experiments. The same MA experiment carried out with T. pyriformis,a species that lacks the resetting mechanism of sex, showed a much higher robustness to extinction. Variation in gene copy number was postulated to be a key factor in explaining these results, a conclusion that is supported by mathematical modeling. We test this hypothesis by quantifying the gene copy number in these two species for several important genes. These results suggest that a mechanism of variation in gene copy number can explain how asexual ciliates can be derived from sexual species.

Evolution of regulation by phosphorylation

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Phosphorylation is a key regulatory currency with over 20 thousand phosphosites determined to date in *S. cerevisiae* alone. We have previously studied the evolution of phosphoregulation by comparing the phosphoproteomoes of three yeast species using mass-spectrometry. We estimated that kinase–substrate interactions can change quickly, potentially at similar rates as those of transcription factor–promoter interactions. The functional relevance of most of these phosphorylation sites is however unknown. In order to address this we are developing approaches to dissect the functional role of *S. cerevisiae* phosphosites. Most sites are found in unstructured regions where they tend to cluster with other post-translational modifications participating in phospho-switches. Phosphosites found in globular domains were assigned regulatory roles by mapping them to interface regions of known interactions. We could show that the functional consequence of these phosphorylation events is more likely conserved than the phosphorylation sites themselves pointing to possible routes for neutral evolution of phosphoregulation.

Evolution of nutrient uptake reveals a trade-off in the ecological stoichiometry of plant-herbivore interactions

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Nutrient limitation is a major determinant of the primary production, ecological stoichiometry, and species composition of many ecosystems. Here, we develop a model that combines resource competition theory and ecological stoichiometry to investigate the evolution of nutrient acquisition by primary producers, and its implications for plant-herbivore interactions. The model predicts a trade-off between the competitive ability and grazing susceptibility of primary producers, emerging from changes in their nutrient uptake rates. High nutrient uptake rates enhance the competitiveness of primary producers, but also increase their nutritional quality for herbivores. If herbivores are not selective, evolution favors runaway selection towards primary producers with high nutrient uptake rates. However, if herbivores select nutritious food, primary producers show an evolutionarily stable strategy characterized by intermediate or low nutrient uptake rates. Interestingly, when the model is parameterized for phytoplankton and zooplankton, the evolutionary dynamics may lead to plant-herbivore oscillations at ecological time scales, especially in environments with high nutrient availability and intermediate selectivity of the herbivores. These model predictions show that evolution can drive plant-herbivore communities towards nonequilibrium dynamics, and shed new light on the evolutionary forces that shape the ecological stoichiometry of primary producers.

Molecular genetic analysis of Bengal tiger (*Panthera tigris tigris*) populations and its implications in conservation and wildlife forensics

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The results presented here are from my PhD work and part of the ongoing conservation project on Bengal tiger in India. The Bengal tiger is highly endangered throughout its distribution range therefore, the Project Tiger was initiated by Government of India to provide special protection to this flagship species as well as conservation of other associated species. Using scats we analyzed genetically these isolated populations distributed across Indian subcontinent. Taken together, the results of the first genetic investigation of wild Bengal tiger population ns are important to develop conservation strategies and provides a methodological basis for long term genetic monitoring of wild tiger populations in India. Mitochondrial markers revealed a profound population structure in wild population indicating that the tiger populations from North Western, Western, Central and North East India are significantly differentiated. In the context of recent tiger habitat change in the Teral Arc Region (TAL) of North Western India, I analysed the tiger populations in detail and found signs of genetic isolation in TAL. Using nuclear markers, I found a moderate amount of genetic variability in wild Bengal tiger population in comparison to other tiger subspecies. In conclusion, based on my newly developed markers, I elucidated the genetic status of Bengal tiger populations that will help in routine monitoring, management, and wildlife forensics.

SporeDB - Searching for the evolutionary origins of endospores

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Bacterial endospores (spores) are the most resistant life form known to man. They are produced by a complex developmental program involving hundreds of genes, generating this terminally differentiated cell. Spore-forming bacteria are also the causative agents of a variety of human diseases. They cause botulism, tetanus, anthrax, severe diarrheas, respiratory infections, killing hundreds of thousand of people word-wide every year. On the other hand, their resistance makes many applications of spores in biomedicine or biotechnology possible, being used for example as probiotics. Little is known about the assembly pathways of the endospore at a global, genomic and evolutionary level. Our aim is to identify the understand the evolutionary origins of this cell type and associated developmental program, and in the process to identify the minimal sporulation program, to predict novel molecular components of the spore, and to identify critical points in the spore assembly pathways that are attractive drugable targets. In order to do this, we developed a data integration platform focused on spore-forming bacteria, SporeDB. We integrated information from a variety of publicly available resources, with manually curated information we compiled, such as the regulatory programs that control spore development, protein localization and a novel ontology describing spore structure and diversity. It further contains experimental data produced by us, including microscopy-based descriptions of spore diversity, mutant phenotypes and proteomics data. We aim to turn SporeDB into a community resource. We will show in our poster how we are using of SporeDB to study the evolutionary origins of the endosporulation program. We found that endosporulation is an evolutionary innovation that arose once in a very restricted set of bacterial lineages, even before oxygen levels rose on earth’s atmosphere. It was partly built from the re-use of existing components.

O poder da imagem na persuasão de (pré)conceitos: o caso da evolução

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O primeiro esboço de uma árvore da vida de Darwin tornou-se uma imagem popular. Em quase todos os panfletos e posters a anunciar conferência ou congressos a propósito do Ano Internacional da Biologia lá estava ela devidamente enquadrada. Logo à partida reconhece-se nela um carácter de «imagem de marca». Ela foi posta ali para conotar qualquer coisa a qualquer coisa. Acaso uma imagem de um coral faria sentido? Sim, faria todo o sentido mas não teria a força que esta imagem efectivamente tem. Sobretudo porque esta força advém essencialmente da sua capacidade de sintetizar de uma forma absolutamente eficaz o pensamento de Darwin. Olha-se para a imagem e vê-se Darwin. Ela é, na verdade, uma «imagem de síntese», uma imagem que reflecte de uma forma exemplar aquilo que Darwin pensava sobre a origem e evolução das espécies. No domínio da imagética científica, a imagem é entendida enquanto simples visualizações de fenómenos que nos permitem compreender aquilo que não somos capazes de ver. Muito poucos cientistas reconheceriam numa imagem um conteúdo intrinsecamente ideológico. Para eles, como para Aristóteles, a imagem, entendida aqui como reflexo da natureza, conduz ao conhecimento. Mas a questão é que a imagem, enquanto imitadora, como Platão a considerava, pode desviar da verdade. Reflexo ou sombra, a imagem é efectivamente poderosa. Esse poder está intimamente ligado às noções de expectativa e de conceito. E estas duas noções acabam por condicionar a interpretação da mensagem e completar as de instruções de leitura. Nesta comunicação iremos por em evidência dois aspectos do poder da imagem no domínio da Evolução: a «marcha do progresso», enquanto representação canónica da evolução (Porquê esta imagem? O que representa? Que instruções de leitura?), e a análise comparada das árvores de Darwin e Mereschkowsky (Que diferenças? Que conceitos evolutivos representam?), enquanto operador de uma mudança complexa das ideias.

The use of a non-LTR retrotransposable element to date the formation of a novel gene cluster

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The formation of novel genes involves the formation of a new coding sequence and/or regulatory regions; moreover, the novel gene must spread and be maintained in the population. Recently evolved genes are important to the study of new gene functions, as they may still bear the marks of the events that took place in their formation. The Sdic gene is a novel gene that arose in the lineage of *Drosophila melanogaster* and that encodes a male reproductive protein. There are four tandem copies of Sdic in the X chromosome forming a gene cluster; selection and the possibility of gene conversion between copies difficults the task of determining the age of the cluster. Within the Sdiccluster there are four non- LTR retrotransposons of the RT1C family that were inserted during the early steps of the formation of the cluster and that were duplicated during the duplication events that gave raise to the cluster. As these elements are 5' truncated, they are ''dead-on-arrival'', they lost their ability to transpose upon insertion and evolve neutrally in the site where they were inserted. The above traits make them an excelent marker to date the formation of the cluster. The life history of the RT1C elements in the genome of *D. melanogaster* was used to determine the insertion chronology of the elements in the Sdic cluster and to date the duplication events that originated the cluster. This work illustrates how detailed analysis of transposable elements complemented with phylogenetic analysis may give valuable information on molecular evolution events – dead-on-arrival non-LTR elements are abundant and ubiquitous, and evolve neutrally in the location where they were inserted, making them a useful tool to date molecular events.

Y chromosome and mtDNA data support demic diffusion during the European Neolithic

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There is an ongoing debate regarding the relative contribution of early farmers and hunters-gatherers in the peopling of Europe, during the Neolithic transition. As a first approximation, two alternative demographic scenarios can be considered: (i) Cultural Diffusion, in which the transition to agriculture is essentially regarded as the movement of ideas and practices and (ii) Demic Diffusion, where a movement of people is significantly involved. Both scenarios can be seen as special cases of admixture, between Palaeolithic/Mesolithic European and Near-Eastern Neolithic populations. In a previous study (Chikhi et al., 2002, PNAS, 98: 11007), the analysis of Y-chromosome data provided a strong support for the Demic Diffusion scenario. Here we applied the same approach to new datasets, including a new and large Y-chromosome dataset and mtDNA data. The new results suggest that the contribution from the Near-East is probably large, contrary to an increasingly held view.

Phylogeography of the starfish *Marthasterias glacialis* in the Atlanto-Mediterranean: is speciation happening into the Mediterranean?

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Marine ecosystems, particularly Mediterranean littoral habitats, are subject to both short- and long-term environmental perturbations. The starfish Marthasterias glacialis is a common and emblematic species predator of bivalves and echinoderms with important implications on functional ecology of marine littoral environments which is being affected by anthropogenic activities, such as urbanization along Mediterranean coastline, creating extensive gaps in the distribution of marine natural populations, and littoral water pollution. Despite being an Atlantic-Mediterranean species, abundant at the Atlantic sublittoral habitats, it is not, in general, abundant along the Mediterranean littoral, rarely reaching densities up to 2 ind/50m². In order to understand how historical and contemporaneous events shape the distribution of the genetic diversity of this species, analyses of phylogeography and population genetics were conducted. A fragment of the mitochondrial gene Cytochrome c oxidase subunit I (COI) was sequenced for 215 individuals from nine different localities, including both Atlantic and Mediterranean basins. Pairwise comparisons (Fst) and network analyses did not show population structure as expected for a species with high dispersal capacities but population from South UK was significantly different from others. Moreover, the COI sequences demonstrated the existence of two distant lineages (around 2.5 % of genetic divergence between lineages) within the Mediterranean basin. One the lineage was shared between Atlantic and Mediterranean populations and the another one, only included three haplotypes endemic from the Mediterranean. Allopatric divergence resulting from a vicariance event by basins isolation during glaciation periods more than 500.000 years ago, follows by secondary contact and recolonization from the Atlantic lineage to the Mediterranean seems the most plausible explanation for our findings.

Genetic differentiation at small geographical scales: Population genetics and phylogeography of the colonial ascidian *Pycnoclavella communis*

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Recent studies revealed an unexpected species richness of the genus *Pycnoclavella* in the Atlanto-Mediterranean region. One of those species, Pycnoclavella communis, showed high variability including several colour morphotypes. In order to explore geographical patterns and evolutionary events that can explain the distribution of genetic diversity of *P. communis* we performed a study of population genetics and phylogeography. Variation in the mitochondrial gene cytochrome c oxidase subunit I (COI) was studied for 135 individuals from eight Mediterranean populations of the species. Three haplotypes from Atlantic locations were also included in the study. The study revealed 32 haplotypes, 29 of them grouped within two Mediterranean lineages of P. communis (divergence between lineages 8.55%). Phylogenetic and network analyses suggest the possible existence of cryptic species corresponding to these two lineages. Further population genetic analyses were restricted to the five populations belonging to the main genetic lineage, and for these localities we compared the information gleaned from COI sequence data and from eight microsatellite loci. A high genetic divergence between populations was substantiated using both kinds of markers. There were high numbers of private haplotypes (COI) and alleles (microsatellites) in the populations studied. Microsatellite loci showed a strong incidence of failed amplifications, which we attribute to the marked intraspecies variability that hampered the application of these highly specific markers. Our results show important genetic variability at all levels studied, from within populations to between basins, possibly coupled to speciation processes. This variability is attributable to restricted gene flow among populations due to short-distance dispersal of the larvae.

Mating ecology of malaria parasites: insights from multiple-species interactions

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Malaria parasites are a group of extremely diverse protozoans, infecting a broad range of reptiles, birds and mammals. Despite all the medical and economical relevance of this group of parasites, evolutionary explanations for crucial aspects of their life cycle, such as their transmission biology, are still lacking. In order to transmit to a new host, malaria parasites have to undergo an obligate round of sexual reproduction in a vector. Within 15 minutes of the vector's bloodmeal male and female gametes are produced and fertilisation occurs. Since the same cues trigger sexual reproduction in different Plasmodium species, when a vector feeds on a multiply-infected host, different parasite species will be trying to achieve fertilisation within the same time-window. This raises questions about if, how and why hybridisation between co-transmitting malaria parasites is prevented. In order to test whether hybridization barriers occur and are mediated by sophisticated mating behaviours, we used recently developed genetically-modified rodent malaria parasites that allowed us to distinguish the progenies from different crosses. The gathered data provides insights into the mating biology and behaviour of two Plasmodium species and may be of relevance to the development of medical interventions that block fertilisation and to the spread of drug-resistance genes.

Paleo evo-devo: a synthesis

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It is well known that evolutionary and developmental biology plays a major role in understanding evolution but very few studies have been made in fossil organisms. One evident problem is the very small number of embryo specimens that have been discovered. However, in order to calibrate and support macroevolutionary anatomical modifications in nature, one needs to compare modern embryonic structures with the different variations that are present in the rare embryonic fossil record. Recently, using cutting-edge techniques, various fossil embryos from different taxa have been described, namely: reptiles (e.g. dinosaurs, pterosaurs and choristodera), placodermi, scalidophora, metazoan, cnidarian. All these fossil embryos comprehend different ontogenetic stages and are distributed from the Neoproterozoic until the Cretaceous. Beside all experimental data that can only be obtained by classical Evo-devo research, paleontology can contribute to the study of evolution in a complementary way. The most important contributions that paleontological data can bring to the study of evolutionary and developmental biology are: 1) direct evidences of presence/absence of anatomical traits across millions of years; 2) establish how and when heterochronic processes appeared; 3) compare extinct with extant organisms, testing where the ontogeny of booth groups differ; 4) understand how reproductive biology was shaped along evolution; 5) test hypothesis about ancestral origin of processes/traits. It is proposed that a stronger link should be done between booth disciplines in order to better understand how and when major macroevolutionary steps have been originated.

Environment Shapes Mutation Effects

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Natural populations often face environmental changes. A mutation may be deleterious in one environment but not necessarily deleterious in a new one. Trying to predict the effects of mutations in different environments is an important approach to understand the pattern of adaptation of natural populations. In this work, we studied how the costs of resistance depend on the environment. To do so, we constructed clones resistant to three antibiotics by P1 transduction and measure their fitness by head to head competition assays against the wild type strain both in benign and stressful antibiotic free environments. Surprisingly, some mutations changed from detrimental to beneficial. We found that in a stressful environment some mutations were no longer detrimental even in the absence of the antibiotic to which they confer resistance. This shows that some resistance mutations can be selected for in certain environments even in the absence of antibiotic pressure.

Evolution of life-history phenotypes in dioecious and androdioecious populations during adaptation to a novel environment: insights from an experimental evolution approach

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Extant theory of evolutionary adaptation relies mainly on natural selection in providing a mechanistic explanation for the changes in mean phenotypes with time. Natural selection acts upon the heritable components of phenotypic diversity, namely on the underlying genotypic variation. Genotypes are therefore the ultimate substrate for natural selection. Recombination from standing genetic variation and mutation are two processes by which new genotypes can be created. Breeding systems can strongly influence the rate of effective recombination, and can therefore impose limits to the ability of populations to evolve. To evaluate the extent to which effective recombination can constrain evolutionary adaptation, we generated sets of genetically variable populations of the nematode *Caenorhabditis elegans* differing in system of breeding and therefore differing in levels of outcrossing and selfing: a) androdioecy (hermaphrodites and males) and b) dioecy. These populations were allowed to evolve in the laboratory environment for 100 generations. We measured the reproductive rates of the hermaphrodites and females, the viability of selfed and outcrossed progeny and the mating ability of the males. The observed patterns suggest that low levels of outcrossing are sufficient to allow populations to adapt to novel environments without experiencing the evolutionary costs of obligate outcrossing.

Phylogeography and demographic history of *Atherina presbyter* (Pisces: Atherinidae) in the North-eastern Atlantic based on mitochondrial DNA

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A fragment of the mitochondrial control region was used to assess phylogeographic patterns and historical demography of the sand-smelt *Atherina presbyter* in the North-eastern Atlantic, covering its geographical range. A striking result is the highly marked differentiation between the Canary Islands population and western European ones. A genetic structure among European populations of A. presbyter was revealed, with a pattern of isolation-by-distance or a gradient effect at a scale of hundreds kilometres, an uncommon pattern likely related to the biological and life-history traits of the sand-smelt. The northern European populations present a much lower genetic diversity when compared to southern populations, which is consistent with a recent colonization from southern populations. The results showed signs of Pleistocene signatures, with the population age estimates for the European populations being clearly older than the Last Glacial Maximum (18,000 years bp). Nevertheless, paleotemperature reconstructions show that the sand-smelt could not have inhabited the western European shores during the last glacial phase.

Adaptation and gene flow in *Philaenus spumarius*, a colour-polymorphic species

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The meadow spittlebug, *Philaenus spumarius* (Hemiptera, Cercopidae), has a remarkable dorsal colour/pattern polymorphism mainly controlled by an autosomal locus. This species is a potential highly informative model to test questions about adaptation, particularly about the maintenance of polymorphisms by natural selection. It is the most widely distributed member of a complex of species, some of them sharing the same phenotype types, which suggests an old polymorphism with the persistence of alleles after the splitting of the species. The phylogenetic relationships in this genus are presented. In *P. spumarius* there is differentiation in the proportion of colour morphs among populations and several selective influences have been suggested to explain this variation but need to be tested.

Modeling insecticide resistance: measuring selection

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Insecticide resistance is a major issue in vector borne diseases control programmes and recent scale up of the use of bednets and indoor residual spraying will increase the selection pressure on the restricted set of four different chemical classes of synthetic insecticides. To understand natural selection and for predictive purposes, it is not sufficient to demonstrate that selection occurs: we need to observe its rate in populations under control and its persistence in populations following cessation of control, to enable us to calibrate appropriate genetic models of the process. We describe a general genetic model to estimate selection coefficients, and dominance relationships, key parameters that determine the dynamics of resistance. We use data on pyrethroids resistance from *Aedes aegypti*, to test this approach. The data consists of the frequency of the lle1, 016 mutation, one of the mutations in he voltage-gated sodium channel gene known to confer resistance to pyrethroids, throughout México. The method we developed is similar to that described earlier to estimate selection coefficients. It is a maximum likelihood (ML) procedure using a recursive genetic model. It tracks the changes in the alleles frequencies at a single locus, in a sexually reproducing diploid population, with non-overlapping generations assuming random mating.

Ocellated lizard *Lacerta lepida* variation across Iberian Peninsula: patterns of neutral and adaptive divergence and morphology in structured populations

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Investigating adaptation in natural populations of non-model organisms is an important challenge for Evolutionary Biology. Here we study a lizard exploiting heterogeneous Mediterranean ecosystems, Lacerta lepida, whose distribution ranges almost throughout the Iberian Peninsula. Two subspecies, *L. l. nevadensis* and *L. l. iberica*, are recognized at the extremes of a climatic cline running across Iberia. The former occupies the most arid region in the southeast while the latter is limited to the wetter habitats of northwest Iberia. They differ morphologically in colour pattern and body size. Previous studies with mtDNA revealed strong population structure and corroborated subspecies recognition. Here we genotyped populations along a northwest-southeast transect for 8 microsatellites and 392 AFLP markers. The data obtained partially corroborate previous results on the pattern of spatial structure. Associations between AFLP genotypes and climate variables were investigated with Spatial Analysis Method (Joost et al. 2007). Characterization of colour and body measures is also presented.

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