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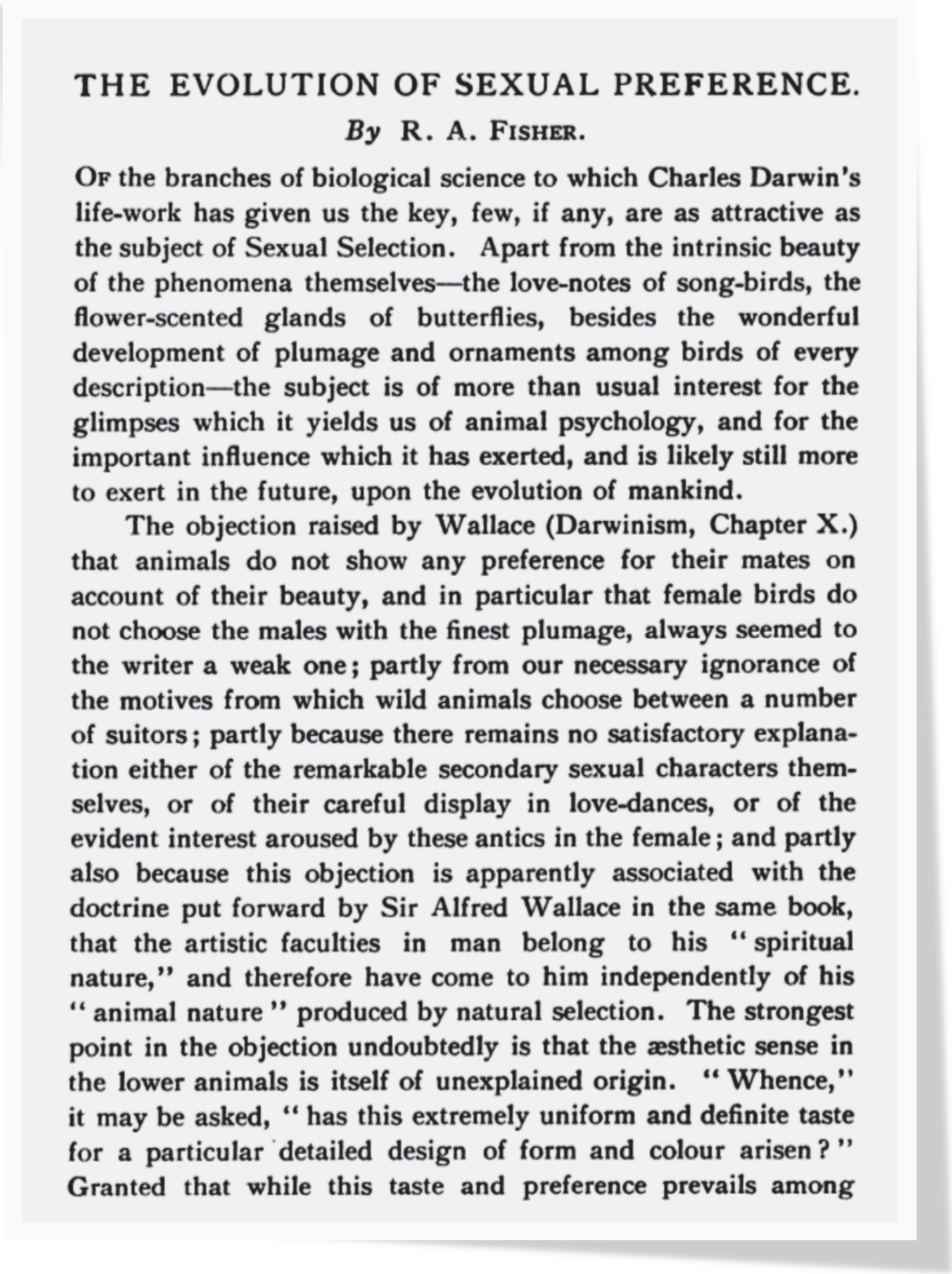
Celebrating the 100th anniversary of R. A. Fisher's paper on the Evolution of Sexual Preference



THE EVOLUTION OF SEXUAL PREFERENCE.

By R. A. FISHER.

OF the branches of biological science to which Charles Darwin's life-work has given us the key, few, if any, are as attractive as the subject of Sexual Selection. Apart from the intrinsic beauty of the phenomena themselves—the love-notes of song-birds, the flower-scented glands of butterflies, besides the wonderful development of plumage and ornaments among birds of every description—the subject is of more than usual interest for the glimpses which it yields us of animal psychology, and for the important influence which it has exerted, and is likely still more to exert in the future, upon the evolution of mankind.

The objection raised by Wallace (Darwinism, Chapter X.) that animals do not show any preference for their mates on account of their beauty, and in particular that female birds do not choose the males with the finest plumage, always seemed to the writer a weak one; partly from our necessary ignorance of the motives from which wild animals choose between a number of suitors; partly because there remains no satisfactory explanation either of the remarkable secondary sexual characters themselves, or of their careful display in love-dances, or of the evident interest aroused by these antics in the female; and partly also because this objection is apparently associated with the doctrine put forward by Sir Alfred Wallace in the same book, that the artistic faculties in man belong to his "spiritual nature," and therefore have come to him independently of his "animal nature" produced by natural selection. The strongest point in the objection undoubtedly is that the æsthetic sense in the lower animals is itself of unexplained origin. "Whence," it may be asked, "has this extremely uniform and definite taste for a particular detailed design of form and colour arisen?" Granted that while this taste and preference prevails among

Fisher, R.A. (1915) The evolution of sexual preference. Eugenics Review (7) 184:192

Schedule

08:30	–	09:15	Registration
09:15	–	09:30	Welcoming Reception
09:30	–	10:15	PL1 - Plenary Talk 1 - ISABEL GORDO
10:15	–	10:30	**O1 | Daniel Pereira** Y-chr and mtDNA diversity in the context of Eurasian language diversity
10:30	–	11:00	Coffee Break
11:00	–	11:15	**O2 | Francisco Pina-Martins** Uncorking the evolutionary history of cork oak populations. From past fragmentation to present unification – and future uncertainty
11:15	–	11:30	**O3 | Joana Costa** Changes to the mating system during invasion: an experimental test of Baker's Law
11:30	–	11:45	**O4 | Inês Fragata** Phenotypic and genetic levels tell different tales. Convergence (or not so much…) during adaptation to a new environment
11:45	–	12:00	**O5 | Gilberto Bento** Genetics and Evolution of Host Resistance in *Daphnia magna*
12:00	–	13:30	Lunch Break
13:30	–	13:45	NEDE presentation
13:45	–	14:30	PL2 - Plenary Talk 2 - TOMMASO PIZZARI
14:30	–	14:45	**O6 | Carla Gonçalves** Functional evolution in a fungal sugar transporter family
14:45	–	15:00	**O7 | Simone F. Delgado** The impact of chromosome rearrangements on the evolutionary path of populations
15:00	–	15:15	**O8 | Elvira Lafuente** Genetic basis of variation in thermal plasticity for body pigmentation
15:15	–	16:45	POSTER SESSION (& Coffee Break at 16:00)
16:45	–	17:00	**O9 | Flore Zélé** The interplay between *Wolbachia* and haplotype-associated reproductive barriers among populations of *Tetranychus urticae*
17:00	–	17:15	**O10 | Tânia F. Paulo** Testing endosymbiont-mediated immune protection in a novel host species
17:15	–	17:30	Closing Session & Awards
17:30			Happy Hour
18:30	–	19:30	APBE Plenary

Plenary Talks and Invited Speakers

PL1
09:30h

Evolution of *Escherichia coli* in the Mouse Gut

Isabel Gordo

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Gut commensal bacteria play important roles in mammalian nutrition/digestion, tissue maturation, development of the immune system and protection against pathogens, yet their evolution and adaptation is still poorly understood. Bacterial adaptation typically involves the accumulation of beneficial mutations, which allow acquisition of phenotypes that best fit the present environment. In the case of the gut the environment is likely to fluctuate over time. Many important questions about the adaptive process remain unanswered, especially in a complex environment such as the gut. I will present a summary of the main patterns of adaptation observed during *E. coli* evolution in the gut and will compare these patterns with those observed in very simple laboratory environments. Using the streptomycin-treated mouse model of colonization we have followed the evolution of *E. coli* in the gut and determined the rate and effects of beneficial mutations, as well as their genetic basis, through whole genome sequencing.

Isabel Gordo did a PhD in Evolutionary Genetics at the University of Edinburgh. As Principal Investigator, she currently leads the group of Evolutionary Biology at the Instituto Gulbenkian de Ciência pursuing research that combines theoretical and empirical work with the aim at understanding the major forces that shape variation in microbial populations. The main topics of current work in her group are: evolution of antibiotic resistance, adaptation of bacteria to cells of the innate immune system, transition of commensalism to pathogenesis and evolution of bacteria in the mammalian intestine. A research study on the latter topic and been recently recognized with the PLOS Genetics Research Prize 2015 for its scientific excellence and high community impact.

PL2
13:45h

Beyond sexual selection: sexual dynamics in structured populations

Tommaso Pizzari

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Sexual selection has largely been studied under rather simplistic assumptions, namely that it operates in panmictic populations through either pre- or post-mating episodes in isolation from each other. In this talk I present a synopsis of studies of sexual selection in populations of fowl, *Gallus gallus*. This system is characterised by strong population structuring and high levels of female promiscuity which creates opportunity for both pre- and post-mating sexual selection. I show how studying sexual selection under these characteristics is revealing a much more complex picture of sexual dynamics than one would expect based on the assumptions of classic sexual selection theory.

Tommaso Pizzari is an evolutionary biologist interested in sexual behaviour and its evolutionary and ecological implications. His lab focuses on resolving different aspects of sexual selection, sexual conflict and promiscuity using a strongly experimental approach. He studied Zoology at the University of Aberdeen, did his PhD at Sheffield, and has held postdoctoral positions at Sheffield and in Sweden. He was appointed Lecturer at Leeds in 2003, University Lecturer at Oxford in 2005, and became Professor of Evolutionary Biology in 2014. He was awarded the ASAB Outstanding Young Investigator Award in 2005, the Philip Leverhulme Prize in 2008, and the ZSL scientific medal in 2014.

Selected Oral Communications

01| Y-chr and mtDNA diversity in the context of Eurasian language diversity
Daniel Pereira

02| Uncorking the evolutionary history of cork oak populations. From past fragmentation to present unification – and future uncertainty
Francisco Pina-Martins

03| Changes to the mating system during invasion: an experimental test of Baker's Law
Joana Costa

04| Phenotypic and genetic levels tell different tales. Convergence (or not so much…) during adaptation to a new environment
Inês Fragata

05| Genetics and Evolution of Host Resistance in *Daphnia magna*
Gilberto Bento

06| Functional evolution in a fungal sugar transporter family
Carla Gonçalves

07| The impact of chromosome rearrangements on the evolutionary path of populations
Simone F. Delgado

08| Genetic basis of variation in thermal plasticity for body pigmentation
Elvira Lafuente

09| The interplay between *Wolbachia* and haplotype-associated reproductive barriers among populations of *Tetranychus urticae*
Flore Zélé

010| Testing endosymbiont-mediated immune protection in a novel host species
Tânia F. Paulo

The XI ENBE Scientific Committee


Rui Faria
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(IGC)

01 | Y-chr and mtDNA diversity in the context of Eurasian language diversity

Daniel Pereira

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Taking in mind the hypothesis first stated by Darwin [1] over the possibility of genomic and linguistic phylogenetic trees sharing the trace of human demographic history, the LanGeLin [2] project is focused on uncover how much of this is true. As part of this interdisciplinary project and making use of new approaches in linguistic classifications, such as the use of syntax and the PCM methodology [3], and the vast availability of genomic information for our species, such as HVR 1 sequence data, SNPs and STRs markers, this study focused on uncovering the relationship between genomic and linguistic diversity for paternal and maternal lineages within the context of Eurasian languages. The results of the analysis performed here showed statistically significant correlation between genomic and linguistic diversity with the geographical distance, demonstrating that a clear geographical structure is evident and both genomes and languages tend to be closer to their geographical neighbours. A clear correlation between both genomic and linguistic traits of populations was observed for both parental lineages, in special for the paternal line. The results also showed a higher diversity on the male line than on the female, which is indicative of a higher dispersal rate on females. Both of these results were visible at different time scales, even though a comparison of strength between both time-related analyses could not be performed do to constrain on the genomic dataset. These results are in agreement with previous results, even when using different data for the linguistic or genomic variables [4,5].

[1] Darwin C (1859) *The origin of species by means of natural selection.* Oxford, U.K.: Oxford University Press.
[2] LanGeLin (2015) in https://www.york.ac.uk/language/research/projects/langelin/
[3] Guardiano C, Longobardi G (2005). *Parametric Comparison and Language Taxonomy*. in M. Batllori, M.-L. Hernanz, C. Picallo, & F. Roca, *Grammaticalization and Parametric Variation* (pp. 149-174). Oxford, UK: Oxford University Press.
[4] Barbujani G, Sokal R (1990) Proc Natl Acad Sci U S A 87: 1816-1819.
[5] Creanza N, Ruhlen M, Pemberton T, Rosenberg N, Feldman M, Ramachadran S (2015) Proc Natl Acad Sci U S A 112: 1265-1272.

02 | Uncorking the evolutionary history of cork oak populations. From past fragmentation to present unification – and future uncertainty

Francisco Pina-Martins

Francisco Pina-Martins[1,2], Dora Batista[1,3], Georgios J. Pappas Jr[4], Octávio S. Paulo[1]

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Quercus suber L., the cork oak, is a species of great economic and ecological importance. With a West Mediterranean distribution, ranging from Portugal and Morocco in the West, to Bulgaria in the East, *Q. suber* populations endure in a large range of environmental conditions. Cork oak evolutionary history has been previously studied, resorting to plastidial DNA markers, which have revealed up to four distinct lineages clearly split by region. However, new data based on our research, with more than 1000 nuclear SNP markers seems to disagree with this established pattern as they do not reflect the assumed geographic splits and indicate instead genetically unstructured populations. Based on data mined from EST 454 sequences and GBS assembled SNPs, we look at the evolutionary history of the species from another, disruptive, perspective. Resorting to methods such as outlier detection, environmental association, and cluster analysis, we craft new hypotheses to explain cork oak evolutionary history where local adaptation takes central role.

03

Changes to the mating system during invasion: an experimental test of Baker's Law

Joana Costa

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Establishment and spread of plant species after long-distance dispersal usually involves changes to the mating system. Thus, comparative studies of reproductive biology including both native and invasive populations offer an outstanding opportunity to investigate contemporary shifts in the mating system during colonization. *Oxalis pes-caprae* L. is a South African tristylous species that was introduced to regions of the World with Mediterranean climate, where it became a widespread invasive. Here, we use *O. pes-caprae* as a model system to investigate evolutionary transitions in the mating system under mate limitation after long-distance dispersal (Baker's Law). We investigated variations in the expression of the incompatibility system in plants from native and invasive populations by performing controlled legitimate (among morphs) and illegitimate (self- and within morph) pollinations. We detected differences in fruit and seed production among pollination treatments and between areas. Native plants had higher fitness after cross-pollinations than plants from the invaded range. The opposite pattern was found after illegitimate pollinations, with invasive plants having higher fitness than native ones. Morph-specific differences in the weakening of the incompatibility system were also observed among invasive plants. Our results show an evolutionary transition from strong trimorphic incompatibility to partial compatibility during the invasion of the Mediterranean region by *O. pes-caprae*, thus supporting Baker's Law. Selective pressures in the new range as the lack of compatible mates might have contributed for the observed weakening in the incompatibility system.

04

Phenotypic and genetic levels tell different tales. Convergence (or not so much…) during adaptation to a new environment

Inês Fragata

Inês Fragata[1], Pedro Simões[1], Margarida Bárbaro[1], Bárbara Kellen[2], Josiane Santos[1], Marta A. Santos[1], Gonçalo S. Faria[1], Sofia G. Seabra[1], Mauro Santos[3], Margarida Matos[1]

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The ability to adapt to environmental changes is of utmost importance for species survival. Insights on the mechanisms and forces underlying this ability can be obtained from studying species that present a wide geographical distribution. However, few studies have examined how history affects the adaptive dynamics of such species, at several levels of organization. In order to test the impact of historical differentiation during adaptation, we followed the real-time evolutionary dynamics of several phenotypic traits, thermal plasticity and chromosomal inversion frequencies in replicated *Drosophila subobscura* populations. These populations were derived from the 3 locations along the European latitudinal cline and introduced in a new (laboratorial) common environment. Initially populations were highly differentiated for all traits and presented differential thermal plasticity in several of those traits. However, fast convergence was observed for both adult phenotypic traits and plastic response to non-optimal temperatures. A different story was told at the karyotypic level, with selection shaping the evolutionary dynamics of inversion frequencies, but doing so within the constraints imposed by previous history. The signature of history and its impact on the evolutionary dynamics may thus have different outcomes depending on the level of observation. Here we show that adaptation to a stable environment does not hamper later response to novel environmental challenges. We also show that history does not constrain phenotypic adaptive evolution, or the plastic thermal response. Finally, our results suggest that adaptation to a new environment can be attained through different genetic mechanisms.

05 Genetics and Evolution of Host Resistance in *Daphnia magna*

Gilberto Bento

Gilberto Bento[1], Peter Fields[1], Jarkko Routtu[1], Yann Bourgeois[1], Dieter Ebert[1]

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Daphnia magna is a model organism for host-pathogen coevolution [1]. Genotype-to-genotype interactions between *D. magna* and its bacterial pathogen *Pasteuria ramosa* have been shown [2] and one QTL was found to underlie natural variation in *D. magna* resistance to *P. ramosa* C19 genotype [3]. Here we first reduce the mapping interval of the putative resistance locus by breakpoint mapping. We use a whole genome sequencing approach to obtain parental haplotypes and find extreme structural variation between haplotypes with significant differences in length and sequence that include a large non-homologous region. We characterize the resistance locus and find that it lays within a non-recombining region that is a mutational hotspot in the manner of vertebrate MHC complex, supporting a role for balancing selection in the maintenance of diversity in the resistance locus. Next, we use an independently generated transcriptome analysis of both parental clones. We find that differences in expression patterns due to treatment with pathogenic bacteria did not map to the resistance locus. In contrast, multiple transcripts mapping to the resistance locus are differentially expressed in a constitutive manner between the *D. magna* parental clones. Interestingly, we identify a cluster of glycosyltransferases that are consistently downregulated in the resistant clone and speculate that glycosyltransferases are prime candidates to underlie natural variation in *D. magna* to attachment by *P. ramosa* infective spores to *D. magna* foregut.

[1] Ebert D (2008) Curr Opinion Microb, 11: 290-301.
[2] Luijckx P *et al.* (2011) Ecol Letters 14: 125-31.
[3] Routtu *et al.* (2015) Heredity 2: 241-8.

06 Functional evolution in a fungal sugar transporter family

Carla Gonçalves

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Sugars are favorite carbon and energy sources in all domains of life, making sugar transport a biological process of vital importance. In fungi, specifically in ascomycetous yeasts, glucose is usually the preferred carbon source being accordingly more efficiently transported than other hexoses [1]. In contrast, in fructophilic *Zygosaccharomyces* yeasts, transport and consumption of fructose is more efficient than other hexoses including glucose and this seems to be due to the presence of a recently described high capacity fructose facilitator named Ffz1 [2,3]. Interestingly, while most sugar transporters from all kingdoms of life belong to the Sugar Porter Family, the Ffz facilitators share a common ancestor with a functionally distinct family, the drug antiporter family 1 (DHA1) [3], suggesting an independent evolutionary course. In this work, we focused on understanding the evolutionary trajectory of this peculiar family of transporters while also trying to uncover the origin of fructose preference, named fructophily, in yeasts. To understand that, we exploited the wealth of genomic data publicly available to delimit the Ffz-like transporter family, and showed that they are exclusive of the fungal kingdom, more specifically of the sub-kingdom Dikarya. *In vivo* characterization of Ffz homologues brought to light a variety of biochemical properties among extant transporters from different lineages, suggestive of a stepwise fructose transport specialization. Subsequent phylogenetic analyses revealed a patchy distribution of the gene, driven both by complex patterns of gene losses and duplications, and by horizontal gene transfer (HGT) events. One such HGT event seems to have set the stage for the onset of fructophilic metabolism in yeasts, a trait that according to our results may be the metabolic hallmark of around 100 yeast species dwelling in sugar rich environments.

[1] Reifenberger E, Boles E, Ciriacy M (1997) Eur J Biochem. 245: 324-333
[2] Pina C, Goncalves P, Prista C, Loureiro-Dias MC (2004) Microbiology 150: 2429-2433
[3] Leandro MJ, Cabral S, Prista C, Loureiro-Dias MC, Sychrova H, Eukaryot Cell (2014) 13: 1371-1379

07

The impact of chromosome rearrangements on the evolutionary path of populations

Simone F. Delgado

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Forecasting evolution requires a deep understanding of the fitness landscape and the trajectories available to genetic variants (short-term effects), as well as, the effect of new mutations (long-term effects). Despite having short-term deleterious effects in sexual species, genomic rearrangements are highly frequent and pervasive in natural populations. Moreover, the genetic background and architecture is known to have an effect in fitness and is, therefore, subject to natural selection. Here we measure the impact of chromosomal rearrangements in the long-term success of populations under asexual reproduction. We used fission yeast as a model for experimental evolution, and tracked the evolutionary path of a set of populations from different starting genetic backgrounds and karyotypes. We found that the genetic background affects the rate of adaptation of populations in a predictable manner. All the populations converged to similar fitness levels, despite having very different starting points. Moreover, whole genome sequencing showed that this fitness convergence is done through the accumulation of very different mutations. These results suggest that the potential for adaptation is not very sensitive to the genetic details of the founder genotypes but rather depends strongly on their initial fitness. We show that this is true even when the genomic differences are caused by large chromosome rearrangements.

08

Genetic basis of variation in thermal plasticity for body pigmentation

Elvira Lafuente

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External environmental cues can influence developmental rates and trajectories and lead to the production of different phenotypes from the same genotype. This developmental plasticity sometimes results in a better match between adult phenotype and its environment, and thus helps organisms to cope with environmental heterogeneity. Plasticity is a complex trait that is heritable, subject to selection, and, therefore, can evolve. However, little is known about the specific loci contributing to natural variation in plasticity. We focus on thermal plasticity in body pigmentation in *Drosophila melanogaster* to explore the genetic basis of inter-genotype variation in reaction norms. We reared flies of over 200 different genotypes at different temperatures, quantified adult color and color pattern, and unraveled genetic differences in the height and slope of reaction norms. These data allow us to characterize genetic correlations between pigmentation traits and plasticity therein, and to identify the loci contributing to variation in those. These loci provide the raw material for the evolution of pigmentation and pigmentation plasticity under different thermal environments.

09 | The interplay between *Wolbachia* and haplotype-associated reproductive barriers among populations of *Tetranychus urticae*

Flore Zélé

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In spider mites, both host (nuclear and/or cytoplasmic) factors and bacterial reproductive manipulators can lead to reproductive isolation among populations within a single species. However, the study of their interaction was still lacking so far. Here, we carried out a first experiment in which reciprocal crosses were performed between *Tetranychus urticae* haplotypes harboring the endosymbiotic bacteria *Wolbachia*. Our results show that both *Wolbachia* and host-associated incompatibilities lead to partial and asymmetric reproductive isolation among populations. However, these barriers are expressed in a different manner: while *Wolbachia* leads to an increase of female mortality in the brood, haplotype-associated incompatibilities induce an overproduction of males. In addition, we found a reduced level of *Wolbachia*-induced incompatibility when associated to incompatibility between haplotypes. Next, we investigated whether this interaction is expressed (i) during premating behavior, (ii) during prezygotic, postmating sperm transfer or fertilization, or (iii) postzygotically (i.e. mechanisms behind the ability of *Wolbachia* to induce cytoplasmic incompatibility). Our results show that haplotype-associated incompatibilities are also due to postcopulatory mechanisms (partial failure of fertilization and/or haploidization of the eggs after fertilization). This contributes to our understanding of ongoing differentiation process potentially leading to speciation, as well as their consequences for both spider mites population dynamics and *Wolbachia* spread among populations.

010 | Testing endosymbiont-mediated immune protection in a novel host species

Tânia F. Paulo

Tânia F. Paulo[1], Vítor G. Faria[1], Alexandre B. Leitão[1], Élio Sucena[1,2]

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Wolbachia is one of the most widespread endosymbionts described to date. These maternally transmitted bacteria naturally infect arthropods and nematodes and induce reproductive manipulations in arthropods that promote infected female's fitness. Another well-described phenotype they induce is protection against viral infections in *Drosophila melanogaster* [1,2]. Being vertically transmitted, *Wolbachia* phylogeny should recapitulate that of its hosts, although phylogenetic studies show that host and symbiont phylogenies are not concordant. This disparity points to the occurrence of horizontal transfers across evolutionary time. Some of these horizontal transmission cases have been described to occur between parasitoid wasps and their hosts [3,4]. Here, we aimed at uncovering at which rate horizontal transmission of *Wolbachia* occurs between *D. melanogaster* and its parasitoid *Leptopilina boulardi*, as well as test if the viral protection phenotype induced in *Drosophila* would be passed onto the novel host, after horizontal transfer. Simultaneously, we screened a wild-caught population of *Leptopilina heterotoma* for *Wolbachia* presence, established an infected isofemale line and derived *Wolbachia*-negative counterparts using antibiotic treatment. Using both lines we characterized the effects of *Wolbachia* infection in parasitoid wasps upon viral systemic infection. We have shown that horizontal transmission happens between *L. boulardi* and its host, but the infection is not stably maintained. Moreover, these wasps do not appear to be susceptible to viruses that are pathogenic in *Drosophila*. The same viruses seem mildly detrimental to *Wolbachia*-infected *L. heterotoma*. Finally, we verified that a natural *Wolbachia* infection delays development time in *L. heterotoma*, but did not detect an effect on longevity.

[1] Werren JH, Baldo L, Clark ME (2008) Nat Rev Microbiol 6: 741–751.
[2] Teixeira L, Ferreira Á, Ashburner M (2008) PLoS Biol 6: 2753–2763.
[3] Vavre F, Fleury F, Lepetit D, Fouillet P, Boulétreau M (1999) Mol Biol Evol 16: 1711–1723.
[4] Heath BD, Butcher RDJ, Whitfield WGF, Hubbard SF (1999) Curr Biol 9: 313–316.

Poster Session

(Ordered alphabetically by first author's name)

P1 | How to find a virgin in a haystack of mated females
Alexandre Figueiredo

P2 | Searching for genome-wide patterns of convergent evolution between cephalopods and vertebrates
Alvarina Couto

P3 | Molecular evolution and structure of the GPCR signalling network explains their role in disease
Ana Barradas

P4 | Can evolution of gut microbiota alter *C. elegans* longevity?
Ana C. Laranjeira

P5 | Experimental Evolution of a Molecular Weapon
Ana P. Marques

P6 | Assessing genotype-phenotype associations between RADseq loci and three dorsal colour morphs in spittlebug *Philaenus spumarius*
Ana S. B. Rodrigues

P7 | Association between Transposable Element Expression and Number of Insertions
Ana T. Eugénio

P8 | Chronological age estimation *versus* biological maturation: Impact on hominini evolutionary biology
Andreia Mendes & Sónia Soares

P9 | Older mothers know best? Maternal age and the evolution of nongenetic inheritance
Bram Kuijper

P10 | Genetics of diversification: a hotspot locus for pigmentation evolution
Carolina Peralta

P11 | Bats (Chiroptera: Noctilionoidea) challenge recent origin of extant Neotropical diversity
Danny Rojas

P12 | Within-plant distribution and performance of herbivorous mites affected by differences in plant quality
Diogo P. Godinho

P13 | Predicting the evolution of fitness-related traits
Diogo Santos

P14 | Learning to tell the differences: When can mate-choice copying facilitate hybridization?
Gonçalo S. Faria

P15 | Differences in mutation accumulation in *S. pombe* due to the presence of chromosomal rearrangements
Gustavo Eduardo

P16 | Can male mating decisions be explained by the Marginal Value Theorem?
Inês Órfão

P17 | *Wolbachia* infection in males does not affect female choice, despite clear costs
Inês Santos

P18 | Searching for putative/alternative origins of replication (OL-like) structures in mitochondrial genomes of birds and crocodiles using an *in silico* approach
Joana C. O. Martins

P19 | Evidence for disassortative pollination in the absence of reciprocal herkogamy in natural populations of heteromorphic species of Plumbaginaceae
Joana Costa

P20 | Good Heavens, What flower can this insect suck?
João Gameiro

P21 | The reciprocal interaction between *Wolbachia* and host-plant specialization in spider mites
Joaquim Santos

P22 | Integrating competition for food, hosts or mates via experimental evolution
Leonor R. Rodrigues

P23 | The evolution of haploid chromosome numbers in Asteraceae does not support the existence of a paleoploidization event on the family's origin
Lucie Mota

P24 | Predicting Convergent Evolution? A Multi-level Experiment in *Drosophila subobscura*
Margarida Matos

P25 | *Rhipicephalus sanguineus* (Acari: Ixodidae) species complex: new insights in its variability
Maria João Dores

P26 | Metagenomic mining of pathogenicity and antibiotic resistance traits across human populations worldwide
Pedro Escudeiro

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P1 | How to find a virgin in a haystack of mated females

Alexandre Figueiredo

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In spider mites *Tetranychus urticae*, the first male fertilizes most of the offspring of their partner (1, 2). In line with this, males prefer to mate with virgins relative to mated females (3). However, the cues underlying such distinction remain unknown, being chemical cues the most likely candidate. To test this, males were placed in the centre of a bridge connected to two patches with a virgin or a mated female, under different treatments: (a) Females were removed from a patch where they had left chemical trails during 24h, (b) females were dead, hence not displaying mating behaviour, and (c) patches with females were not connected to the arena, thus males could perceive volatile cues only. Alive females in connected patches and dead females in unconnected patches were, respectively, positive and negative controls.
Males preferred virgin to mated females, in both alive connected and unconnected patches and when females were removed from the patches before the test. In treatments where females were dead, the preference was lost. Our results suggest that volatile cues or chemical trails are sufficient to trigger male preference for virgins. Female behaviour, although not necessary, may also contribute to this choice. Future studies should address cue composition.

[1] Helle W (1967) Entomol Exp Appl 10: 103-110.
[2] Potter DA, Wrensch DL (1978) Ann Entomol Soc Am 71: 882-885.
[3] Oku K (2010) Exp Appl Acarol 50: 107-113.

P2 | Searching for Genome-Wide Patterns of Convergent Evolution Between Cephalopods and Vertebrates

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The giant squid, *Architeuthis dux*, is one of the world's largest invertebrates and remarkably little is known about their biology, distribution and taxonomy. They are deep-ocean animals characterized by rapid growth (reaching 14 m!), short life spans and early maturity. They belong to Cephalopoda, one of the most complex classes amongst invertebrate phyla. Cephalopods are believed to be the most "advanced" invertebrates [1] due their large, highly differentiated, brains and a set of sensory organs. This highly sophisticated nervous system appears to be associated with their complex behavioral and learning capabilities [2] and their brains are comparable both in size and complexity with the ones of vertebrates. The genome of *Architeuthis dux* is currently being assembled and annotated. Using 25 genomes, comprising cephalopods, vertebrates and other of lophotrochozoans, ecdysozoans and chordates, ortholog sets were estimated and filtered in order to include at least one cephalopod, one vertebrate plus another taxa. The resulting 8,573 orthologs clusters are being used to search for signatures of convergent evolution at protein function level among cephalopods and vertebrates, in particularly in genes related to the continuous growth (apoptosis) and the nervous system. Several approaches are being employed [3,4,5]. Design and preliminary results will be presented.

[1] Zullo L and Hochner B (2011) Commun Integr Biol 4: 26–29.
[2] Nixon M and Young JZ (2003) Oxford University Press.
[3] Foote AD, Liu Y, Thomas GW, *et al.* (2015) Nat Genet 47: 272-275.
[4] Zou Z and Zhang J (2015) Mol Biol Evol 32: 1237–1241.
[5] Parker J, Tsagkogeorga G, Cotton JA, *et al.* (2013) Nature 502: 228-231.

P3 | Molecular evolution and structure of the GPCR signalling network explains their role in disease

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G protein-coupled receptors (GPCRs) are an important group of paralogous signaling molecules that play a central role in physiology. They are at the core of a signaling network that, when disrupted, frequently results in pathological outcomes. While GPCR dysfunction can be very broadly divided into gain-of-function or loss-of-function mechanisms, the molecular basis for malfunction is very diverse and may have their origins in defective network components other than the receptors. When compared to singletons, genes that have retained paralogues from their duplication history tend to be associated with human heritable disorders, especially if they have arisen by whole-genome duplication (WGD), and diseases caused by mutations in WGD genes have a tendency to be autosomal dominant. In order to assess the contribution of the GPCR network components to the emergence of disease, we determined the duplication status of the groups of genes in each component of the signalling network: GPCR, ligand, downstream signaling proteins, and GPCR-interacting proteins, and quantified their association to disease. We find that WGD genes have been retained in distinct proportions for the different components, and that all disease categories are enriched in WGD genes, with the exception of the ligands, suggesting that the evolution history for disease within this particular group is WGD-independent. The majority of the GPCR-associated diseases are autosomal dominant, confirming the tolerance of WGD genes for variation and disease pervasiveness.

P4 | Can evolution of gut microbiota alter *C. elegans* longevity?

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Interactions between species are very common in nature and they determine eco- evolutionary feedbacks that can influence many processes, such as the evolution of species. One of the more prevalent interactions in nature is the relationship between a host and its gut microbiota. This kind of interaction can be studied in model organisms such as Caenorhabditis elegans. Previous studies have shown that specific strains or mutants of bacteria can influence and alter the longevity of its host. In this project, we aim to take advantage of this interaction and indirectly select and evolve gut microbiota, namely Escherichia coli OP50, through selection of a trait in C. elegans – longevity. We will also analyze the level at which selection acts, if the evolution of the gut microbiota is mainly driven by individual or group selection. We expect this to be one of the first studies that alter a host trait through evolution of its gut microbiota and one of the first that tests the impact of group selection on evolutionary dynamics between host and its gut microbiota. Preliminary findings of survival rates from two different *C. elegans* (wild-type N2 and a longevity mutant – *hsf-1*) indicate that when fed on different strains of bacteria (such as pathogenic bacteria like *Serratia marcescens* or highly beneficial bacteria like *E. coli* OP50), *C. elegans* have different lifespans, emphasizing the impact of different bacteria strains on *C. elegans* longevity. Additionally, our results suggest that *C. elegans* fed on *E. coli* OP50 have lower mortality rates.

[1] Kasada M, Yamamichi M, Yoshida T (2014) Proc Natl Acad Sci U S A 111: 16035-16040.
[2] Portal-Celhay C, Blaser MJ (2012) Infect Immun 80: 1288-1299.
[3] Cabreiro F, Gems D (2013) EMBO Mol Med 5: 1300-1310.
[4] Portal-Celhay C, Bradley ER, Blaser MJ (2012) BMC Microbiol 12: 49.
[5] Hsu AL, Murphy CT, Kenyon C (2003) Science 300: 1142-1145.

P5 Experimental evolution of a molecular weapon

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Biological improvement has been an intrinsic part of human culture. The main objective remains the same: to shape the biological world to improve quality of life. However, due to the exponential increase in human population size and life span, we can no longer rely on proteins and processes that have come about by natural evolution. We need methods which are more directed to our needs. In order to solve this problem, we want to use experimental evolution to improve biological molecules for agriculture, biotechnology and clinic applications. We also expect to illuminate the more fundamental question of how biological molecules evolve in a fitness landscape. One group of proteins that is an interesting target for experimental evolution is the Cry family of toxins, because of their activity against insects and nematodes. Nematodes in specific are important threats to many plants of economic importance and are also relevant animal pathogens. We will improve a Cry protein using several rounds of mutagenesis to generate diversity, which will be selected by letting *Caenorhabditis elegans* feed on *Escherichia coli* expressing the mutant molecules. Our experiment requires that the proteins most effective in killing *C. elegans* are also the ones that provide a higher fitness to *E. coli* in the presence of the nematode. We are able to show this holds true for three toxins of the Cry21 family (Cry21Fa, Cry21Ga and Cry21Ha). Our results indicate that Cry21Fa is the most efficient of these toxins at killing *C. elegans* and that bacteria expressing it are less predated than bacteria not expressing the toxin. These preliminary results demonstrate that we are able to couple natural selection in the lab with increased toxicity for *C. elegans*.

[1] Bornscheuer UT, Pohl M (2001) Curr Opin Chem Biol 5: 137-43.
[2] Iatsenko I, Boichenko I, Sommer RJ (2014) Appl Environ Microbiol 80: 3266-75.
[3] Schenk MF, Szendro IG, Krug J, de Visser JA (2012) PLoS Genet 8: e1002783.
[4] Bornscheuer UT, Altenbuchner J, Meyer HH (1999) Bioorg Med Chem 7: 2169-73.
[5] Elvin M, Snoek LB, Frejno M, Klemstein U, Kammenga JE, Poulin GB (2011) BMC Genomics 12: 510.

P6 Assessing genotype-phenotype associations between RADseq loci and three dorsal colour morphs in spittlebug *Philaenus spumarius*

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Colour polymorphisms are common across animals and when combined with genetic and ecological data, can be extraordinary models to understand the process of adaptation and the molecular change underlying phenotypic evolution. The meadow spittlebug, *Philaenus spumarius*, a widespread insect species in the Holarctic region, shows a dorsal colour/pattern balanced polymorphism making it a potential good model to test hypotheses about adaptation and maintenance of polymorphisms in natural populations. Although crossing experiments have revealed the Mendelian inheritance of this trait, its genetic basis remains unknown. In this study we attempted for the first time to identify candidate genomic regions that could be associated with the polymorphism in this species. By using restriction site-associated DNA (RAD) sequencing we were able to obtain a set of 1012 markers across 34 individuals to test for associations with three dorsal colour phenotypes (*typicus*, *marginellus* and *trilineatus*). Single-SNP association analyses using Fisher's exact test and a Bayesian regression approach identified a total of 44 loci possibly associated with dorsal colour morphs, 21 being detected by both tests. In Multi-SNP analysis, 29 loci revealed a colour morph association. From those, 24 were also significant in single analyses. Loci of interest were "blasted" against NCBI databases but no match with colour candidate genes sequences was found. These are preliminary results and screening not only more individuals and populations but also the remaining morphotypes described in *P. spumarius* are crucial. Nevertheless, this study provided a basis for future research on the genetic architecture of this trait.

P7 | Association between Transposable Element expression and number of insertions

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Transposable elements (TEs) are repetitive DNA sequences capable of changing their position within the genome, thereby causing mutations. TEs have been implicated in adaptive evolution of natural and experimental populations, as well as in the evolution of novel gene regulation and novel traits. However, TE mobilization often harms the host, by disrupting protein-coding genes, altering transcriptional regulatory networks or causing chromosomal breakage and genomic rearrangements. Great advances have been made in the characterization of TEs and of the mechanisms that repress their activity. TE expression is frequently used as a proxy for activity. However, little is known about which genetic and environmental factors regulate TE expression and how this expression correlates with transposition. We used a panel of wild- derived and fully sequenced *Drosophila melanogaster* genomes to characterize inter-genotype variation in TE expression levels. Specifically, we aimed at testing the hypothesis that TE expression levels are positively correlated with TE copy number. We observed clear effects of genetic background on TE expression. However, we did not find that inter-genotype differences in copy number were correlated with TE expression. It remains to be investigated what inter-genotype differences explain differential regulation of TE transcription and to what extent this transcription is, indeed, a good proxy of TE jumping.

P8 | Chronological age estimation *versus* biological maturation: Impact on hominini evolutionary biology

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Various methods are used to establish age-at-death of hominin. These have been primarily developed in human skeletonized remains (HSR). Despite their significant accuracy limitations related with the translation of the biological, age-at-death assessment into a chronological age-at-death conclusion exist. This paper explores the delicate relationship between chronological age and biological maturation highlighting the implications it may have in hominin evolutionary history. It is based on the appraisal of the methods used to estimate age-at-death of several well-known hominin, e.g. Lucy (AL 288-1), Taung Child, Dikika baby (DIK-1-1) and Nariokotome Boy (KNM WT 15000). Data is presented by hominin according to date of publication of the age estimations, with identification of the methods used and age-estimation. Publications were selected based on Google Scholar/ ScienceDirect/ Wiley search between November 1 and 10, 2015. A total of 47 publications were consulted, ranging from 1991-2015 year of publication. The majority of information was related with the Taung Child and Nariokotome Boy fossils. The results showed that scientific knowledge on hominin evolutionary patterns have identify that hominin growth and development differ from humans. Hominin possess more ape-like features when compared to humans, consequently the methods used conveyed such specificities. However, age-assessment methods based on osteological maturation have known limitations highlighted by bioarchaeological research, such as third molar agenesis, individuals' variability and complexity of cranial sutures obliteration. Such limitations need to be considered when aiming to chronologically categorize hominin otherwise biased age estimations may be presented with significant implications on the interpretation of hominin evolutionary biology.

[1] Buckberry JL, Chamberlain AT (2002) Am J Phys Anthropol 119: 231–239.
[2] Šešelj M (2013) Am J Phys Anthropol 150: 38-47.
[3] Harrub B, Thompson B (2003) The truth about human origins. Montgomery: Apologetics Press, Inc.
[4] Smith BH, Tompkins RL (1995) Annu Rev Anthropol 24: 257-279.
[5] Kimbel WH, Delezene LK (2009) Am J Phys Anthropol 140: 2-48.

P9 Older mothers know best? Maternal age and the evolution of nongenetic inheritance

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Parental information transmitted via nongenetic effects (e.g., epimutations, small RNAs or maternal hormones) can inform offspring about their future environment. Indeed, recent models predict that the strength of nongenetic inheritance should vary strongly with the rate of environmental change. Yet, these models assume that all parents have the same life history, whereas it is well known that variation in parental age has fitness effects to offspring. Here we therefore model how parental age affects the evolution of nongenetic inheritance. We find that offspring born from young parents are selected to never inherit the parental phenotype; rather, these offspring should always produce the same phenotype that matches to the most frequent environment. By contrast, offspring born from older parents are selected to inherit their parental phenotype. The reason for these age differences in inheritance is that an older parent's phenotype is likely to the match the local environment, otherwise the parent wouldn't have survived to old age. Hence offspring are selectively favored to copy the older parent's phenotype. By contrast, offspring have no such information about the younger parent's phenotype, as it still has to survive to old age. Overall, our model suggests that the strength of nongenetic inheritance should strongly increase over a parent's lifespan.

P10 Genetics of diversification: a hotspot locus for pigmentation evolution

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Unravelling the nature and effects of the loci underlying adaptive evolution is a key challenge in evolutionary biology, now made easier by increasingly accessible tools and methods. To derive general principles regarding the genetic basis of adaptive evolution it is crucial to gather knowledge from diverse species groups and different types of traits. Here, we focus on pigmentation patterns on butterfly wings which are an ecologically relevant, evolutionarily diverse and developmentally tractable trait. In *Bicyclus anynana*, a genomic region was found to be implicated in different morphological aspects of the eyespot, in a manner that resembles existing phenotypes in other species of the genus. This region includes the BFS locus, which carries allelic variation implicated in variation in eyespot size and colour, as well as in embryonic development. Previous work had suggested two candidate genes in and around this region that we proposed to study further: the genes *washout* and *domeless*. We explored to what extend these genes are implicated in development and variation in eyespot morphology and embryonic development by analysing variation in coding sequence, spatial patterns of expression during embryonic and wing development, and potential function of these genes in wing pattern formation. We will discuss these results that underscore how this type of integrative analysis can contribute towards a deeper understanding of the loci of morphological evolution.

P11 | Bats (Chiroptera: Noctilionoidea) challenge recent origin of extant Neotropical diversity

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The mechanisms underlying the high extant biodiversity in the Neotropics have been controversial since the 19th century. Support for the influence of period-specific changes on diversification often rests on detecting more speciation events during a particular period. The timing of speciation events may reflect the influence of incomplete taxon sampling, protracted speciation, and null processes of lineage accumulation. Here we assess the influence of these factors on the timing of speciation with new multi-locus data for New World noctilionoid bats (Chiroptera: Noctilionoidea). Biogeographic analyses revealed the importance of the Neotropics in noctilionoid diversification, and the critical role of dispersal. We detected no shift in speciation rate associated with the Quaternary or pre-Quaternary periods, and instead found an increase in speciation linked to the evolution of the subfamily Stenodermatinae (~18 Ma). Simulations modeling constant speciation and extinction rates for the phylogeny systematically showed more speciation events in the Quaternary. Since recording more divergence events in the Quaternary can result from lineage accumulation, the age of extant sister species cannot be interpreted as supporting higher speciation rates during this period. Instead, analyzing the factors that influence speciation requires modeling lineage-specific traits and environmental, spatial and ecological drivers of speciation.

P12 | Within-plant distribution and performance of herbivorous mites affected by differences in plant quality

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Differences in plant quality, caused by plant nutrition or herbivory, are known to affect herbivore distribution. However, how these factors interact to determine within-plant distribution of herbivores is unknown. We addressed this using two spider-mite species, *Tetranychus evansi* and *T. urticae*, known to down-regulate and up-regulate tomato plant defences, respectively. These interactions translate into different effects on plant quality. Additionally, we grew plants with high and low N fertilization (i.e., different C/N ratios) and for both regimes we assessed the distribution of these spider mites within uninfested plants or plants infested with heterospecifics. On uninfested plants, both species preferred young leaves, and lost this preference when nitrogen fertilization was higher. This choice correlates with the C/N ratio on those leaves, and reinforces the potential for competition between these species. On heterospecifically-infested plants, mite distribution did not correlate with their performance. Indeed, independently of plant fertilization, *T. urticae* avoided infested leaves, although their performance was higher on those leaves than that on uninfested leaves. *Tetranychus evansi* distributed evenly on infested plants while performing better on older leaves, independently of the position of the competitor and of plant fertilization. These differences in behaviour may be explained by the long-term performance of mites, as *T. evansi* out-competes *T. urticae* on tomato. In conclusion, correlation between performance and preference is found for differences in quality due to plant nutrition, but not for herbivore damage.

P13 | Predicting the evolution of fitness-related traits

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In order to understand and predict the evolutionary fate of any population, we must understand how natural selection acts upon that population. The quantification of that action is called fitness.
A large body of knowledge exists to explain how changes in fitness due to mutations affect population dynamics, but little is known about the biological constraints that generate the distribution of fitness effects of mutations. Our objective is to derive general rules based on biological processes and features that can explain and predict fitness. We modeled fission yeast growth and extracted the specific growth parameters for several strains both before and after adaptation. Our objective is to understand: 1) how growth characteristics are converted to competitive fitness; 2) how these growth phenotypes change during adaptive evolution; 3) what constrains them. With this approach we expect to derive general rules about the fitness of new mutations and how it changes with the genetic background. Moreover, we also want to make clear predictions about how these growth phenotypes evolve.

P14 | Learning to tell the differences: When can mate-choice copying facilitate hybridisation?

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Mate-choice copying (MCC) by females occurs when they obtain information about the performance of a male, increasing or decreasing their preference for that male, accordingly. MCC has been suggested to cause reproductive isolation between populations with different mate preference traditions. However, the opposite scenario can also occur, if invader individuals copy the choices of natives, leading to hybridization events. We studied the hybridization hypothesis using different populations of *Drosophila subobscura*, originated from the extremes of the species European latitudinal cline: Portugal (PT) and the Netherlands (NL). Half of the females received positive social information about a male from their own population and the other half about a male from a control (lab) population. At generation six, we saw that females had an innate preference for the males of their own population, and that they did not copy. Only after four more generations of convergent adaptation in the lab, PT females, but not NL, started to copy. We made an additional assay ten generations later. Interestingly in this generation PT females again did not copy, presenting similar patterns to the first assayed generation. We hypothesize that this pattern may have been caused by later divergence between body size of PT and control males. All told, our data suggests that MCC does not facilitate hybridization at an early phase after invasion, and that it may be selected in nature only under specific ecological and social contexts, supporting the hypothesis that MCC is most advantageous when males are phenotypically similar.

P15 Differences in mutation accumulation in *S. pombe* due to the presence of chromosomal rearrangements

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Large chromosomal rearrangements are common in natural populations and thought to be involved in speciation events. In this project, we used experimental evolution to determine how the speed of evolution and the type of accumulated mutations depend on the ancestral chromosomal structure and genotype. We utilized two Wild Type strains and a set of genetically engineered *Schizosaccharomyces pombe* strains, different solely in the presence of a certain type of chromosomal variant (one inversion and four translocations), along with respective controls. Previous research has shown that these chromosomal variants have different fitness levels in several environments, probably due to changes in the gene expression along the genome. These strains were subjected to a Mutation Accumulation experiment, propagated in the laboratory at very low population sizes, in which we expect natural selection to be less efficient at purging deleterious mutations. We then measured these strains' changes in fitness throughout this accumulation of deleterious mutations, comparing the evolutionary trajectories in the different rearrangements to understand if the chromosomal structure affected the speed of evolution.

P16 Can male mating decisions be explained by the Marginal Value Theorem?

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Research on optimal behaviour theory has traditionally focused on foraging behaviour. Marginal Value Theorem (MVT) [1] suggests that the optimal foraging time within a patch is related with success in that patch in terms of cumulative energy intake (constrained by resource depletion) and with the time spent travelling between patches. Choices made during sexual contexts provide an analogous situation. Females represent a resource to males that can deplete over time due to a decrease of female interest or male sperm availability. Accordingly, the optimal time that a male spends with a female (or a group of females) should increase when it takes longer to find a female. The frequency of mating attempts (a proxy of cumulative fertilization success) should increase as well. To test these hypotheses, we conducted experiments with male guppies (*Poecilia reticulata*) assigned to one of two treatments: isolation from females for a 20 hours period (to simulate longer intervals spent searching for females) and no isolation period. Males were individually observed with a group of three females. We recorded the time males spent following females, as well as the frequency of courtship displays and forced mating attempts. Males that had been isolated spent more time following the females and performed more forced attempts, but not more courtship. Our results thus provide evidence that investment time with females is related to the time searching for this sexual resource, in agreement with the MVT. Certainty of fertilization success is probably more related with forced attempts than with courtship displays.

[1] Charnov EL (1976) Theor Popul Biol 9: 129–136.

P17 | *Wolbachia* infection in males does not affect female choice, despite clear costs

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Wolbachia is a widespread endosymbiotic bacterium, commonly found in populations of the two-spotted spider mite *Tetranychus urticae*. In such populations, *Wolbachia* often induces cytoplasmic incompatibility, whereby a cross between an uninfected female and an infected male yields no fertilized offspring. Hence, uninfected females should prefer uninfected males to infected ones. Indeed, this has been shown in a laboratory population of spider mites. Here, we investigate whether this result can be generalized to other populations of spider mites. We used five naturally-infected populations of *T. urticae* and maintained them in the lab for some generations prior to testing. Populations were either kept infected or treated with an antibiotic to generate *Wolbachia*-free mite populations. Female mate choice tests were performed and duration and latency to copulation recorded. Latency to copulation was not different, although in one of the populations copulation duration was longer when crosses involved infected males. Uninfected females did not show any preference in any of the populations. Therefore, *T. urticae* females did not avoid cytoplasmic incompatibility via mate choice, despite clear benefits of preventing the embryonic death of fertilized offspring.

P18 | Searching for putative/alternative origins of replication (OL-like) structures in mitochondrial genomes of birds and crocodiles using an *in silico* approach

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For decades, mitochondrial DNA (mtDNA) replication was thought to occur through strand-displacement where both strands use strand-specific origins of replication. However, in the last decade, alternative models of mtDNA replication were proposed that challenge the strand-displacement model. One argument used against the original replication model is the fact that some vertebrate groups, especially all birds and crocodiles, lack the typical origin of replication used by the lagging-strand (OriL) according to the strand-displacement model. One possibility is that these species might use the same mtDNA replication origin for both strands. Another possibility, as suggested in previous studies, is that replication could use alternative mtDNA origins of replication. The aim of this work was to search for putative OriL in the mtDNA of the species that lack this structure in its typical location. To do that, we first characterized "real" OriL found in 3117 mitochondrial genomes of vertebrates. Then, using some of its typical characteristics such as entropy, nucleotide composition, stem and loop sizes, we screened the mtDNA of birds and crocodiles for OriL-like structures. Our results show that both birds and crocodiles mitochondrial genomes have hairpins with OL-like characteristics. A detailed analysis of these structures may help us understand how the replication mechanism occurs in the mtDNA of these species.

P19 | Evidence for disassortative pollination in the absence of reciprocal herkogamy in natural populations of heteromorphic species of Plumbaginaceae

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Most heterostylous species possess a reciprocal arrangement of stigmas and anthers (reciprocal herkogamy), diallelic self-incompatibility and ancillary polymorphisms of pollen and stigma. Plumbaginaceae is unique in possessing typical distyly (e.g., *Limonium*), but also species lacking reciprocal herkogamy (*Armeria* spp.) despite possessing diallelic incompatibility and ancillary characters. This variation in heteromorphic characters provides an outstanding opportunity to examine the extent to which ancillary characters alone work to promote disassortative (legitimate) pollination. Here, we investigate patterns of pollen dispersal in 11 natural populations of *Armeria maritima*, *A. pubigera*, and *Limonium vulgare*. In each population, we compared legitimate and illegitimate stigmatic pollen loads and calculated pollen transfer proficiencies for each mating type. Pollen dispersal in all but two populations of *Armeria* was largely disassortative, regardless of the absence of reciprocal herkogamy. This result arises because illegitimate pollen commonly fails to adhere to own-form stigmas and falls from the stigmatic papillae. Legitimate pollen transfer proficiency was similar for the two mating types across all populations for the three species, but cob stigmas were more likely to receive illegitimate pollen than papillate stigmas. Our results provide the first evidence for Dulberger's (1975) topographical complementarity hypothesis [1] and demonstrate that pollen-stigma dimorphisms can function to promote disassortative pollen transfer in the absence of reciprocal herkogamy.

[1] Dulberger R (1975) Proc R Soc Lond B 188: 257-274.

P20 | Good heavens, what flower can this insect suck?

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One of the most remarkable examples of Darwin's deductive reasoning was his ability to predict the existence and coevolution, by natural selection, of an organism with a snout long enough to pollinize an epiphytic orchid, *Angraecum sesquipedale*, endemic to Madagascar and known for its very elongated spur. The pollinator, a hawkmoth, was discovered in Madagascar in 1903, 43 years after Darwin predicted its existence. It is a subpescies of *Xanthopan morganii*, and was given the name of *X. morganii predicta*, in Darwin's honor.

The same species of moth was found in Kibale forest, Uganda, in July 2014. The specimen found had a shorter snout than the ones found in Madagascar. Using Darwin's deductive reasoning, one could predict the existence of a plant whose flowers had a spur that would match the length of this moth's proboscis.

A plant from the Rubiaceae family (*Rothmannia stanleyana*) was, indeed, found several days later, having flowers with a very long spur. One of these flowers was collected and compared with the specimen of *X. morganii*, whose match between the length of the flower's spur and the length of the moth's proboscis was remarkable.

The present discovery, although not providing direct evidence of the pollinator-plant interaction between these two species, shows how powerful the scientific method is and how discoveries similar to those of Darwin still have the ability to amaze us. This example may be use to motivate young scientists to join the scientific career and be part of exciting investigations projects.

P21 The reciprocal interaction between Wolbachia and host-plant specialization in spider mites

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Bacterial endosymbionts of phytophagous arthropods may affect their relationship with host plants, and, in turn, plants can affect host-symbiont interactions. However, studies addressing both these interactions simultaneously are still scarce. Here, we studied the tripartite relationship between the spider mite *Tetranychus urticae*, a polyphagous agricultural pest, five of its natural host plants and its endosymbionts *Wolbachia*, *Rickettsia* and *Cardinium*, which can be reproductive manipulators, and/or mutualists towards their host. The prevalence of these endosymbionts is highly variable (from 0 to 100%) in natural populations of *T. urticae*. The factors affecting their distribution are still largely unknown. We first investigated whether *Wolbachia* affects the performance of *T. urticae* on different host plants. *Wolbachia* infection was found to be detrimental, beneficial, or neutral on eggs hatching rate depending on the host plant. These results were unaffected by the mites' rearing history (i.e. laboratory maintenance on different plants). All other life history traits were affected only by the plant species, or by *Wolbachia* infection. Subsequently, we evaluated the effect of the same plants on endosymbiont prevalence in natural populations of *T. urticae* in Portugal (5 replicates per host plant). The prevalence of *Wolbachia* and *Rickettsia* varied with the host plants, but not that of *Cardinium.* Interestingly, the plants leading to the lower prevalence of *Wolbachia* are also those in which *Wolbachia* infection results in lower eggs hatchability. These results suggest that host plants may play an important role in endosymbionts spread in *T. urticae* populations. Conversely, *T. urticae* host-plant colonization may hinge on endosymbiont presence.

P22 Integrating competition for food, hosts or mates via experimental evolution

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Competitive interactions shape the evolution of organisms. However, often it is not clear whether competition is the driving force behind the patterns observed. The recent use of experimental evolution in competitive environments may help establish such causality. Unfortunately, this literature is scattered, as competition for food, mates and hosts are subjects belonging to different research fields. Here, we group these bodies of literature, extract common processes and patterns concerning the role of competition in shaping evolutionary trajectories, and suggest perspectives stemming from an integrative view of competition across these research fields. Our review reinstates the power of experimental evolution in addressing the evolutionary consequences of competition, but highlights potential pitfalls in the design of such experiments.

P23 | The evolution of haploid chromosome numbers in Asteraceae does not support the existence of a paleoploidization event on the family's origin

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Changes of chromosome number during the evolution of angiosperms are likely to have played a major role in speciation [1], being their study of utmost importance, especially now, when a probabilistic model is available to study chromosome evolution within a phylogenetic framework [2]. In the present study, likelihood models of chromosome number evolution were fitted to the largest family of flowering plants, the Asteraceae family [3]. Specifically, a phylogenetic supertree of this family was used to reconstruct the ancestral chromosome number and infer genomic events. Our results strongly evidenced that $n = 9$ was the most probable ancestral chromosome number of the family. Also, our models supported that genomic duplications and descending dysploidy were common genomic events in the evolution of Asteraceae. The increase in the number of chromosomes through polyploidy events was related with a high frequency of chromosome losses, the most frequent event in the chromosome numbers evolution. The best-fitted model inferred more than one hundred WGD events; nevertheless, it did not support the proposed paleopolyploidization events at the origin of the family nor at the time of divergence of the main lineages of this family, as it has been hypothesized previously, using a limited sampling effort [4]. Therefore, our study besides casting doubts about the position of those paleopolyploidization events, further supports the use of macroevolutionary inferences of chromosome number changes. Further intensive and expensive genomic analyses, focused in disentangling genomic processes and gene neofunctionalization will strongly benefit from a more accurate choice of target taxa, provided by this study.

[1] Lysák MA, Schubert I (2013) Plant Genome Diversity: Physical Structure, Behavior and Evolution of Plant Genomes. Springer-Verlag, 2: 137-147.
[2] Glick L, Mayrose I (2014) Mol Biol Evol 31: 1914–22.
[3] Funk VA, Susanna A, Stuessy TF, Bayer RJ, editors (2009) Systematics, Evolution, and Biogeography of Compositae. Vienna (Austria).
[4] Barker MS, Kane NC, Matvienko M, *et al.* (2008) Mol Biol Evol 25: 2445–2455.

P24 | Predicting Convergent Evolution? A Multi-level Experiment in Drosophila subobscura

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How capable are populations to adapt to environmental changes? Will populations of contrasting histories converge, at the phenotypic and genomic level, tracking a smooth fitness landscape? In spite of the importance of this issue, few studies have addressed it. Taking advantage of their natural differentiation, we followed the real-time evolutionary dynamics of *Drosophila subobscura* populations, analyzing phenotypic traits, chromosomal inversion frequencies and genome-wide data. Our populations were founded from contrasting latitudes in Europe and introduced in a laboratorial common environment. Initially, the populations were highly differentiated for all traits. However, pervasive phenotypic convergence occurred after only a few generations in the laboratory. Interestingly, history played an important role in the evolutionary dynamics of chromosomal inversions: despite the role of selection, after 40 generations of lab evolution, populations remained differentiated at the karyotypic level. Ongoing genomic analyses indicates so far that convergence is not occurring at the genome-wide level. A new experiment, using additional collections made 3 years later is testing for repeatability of evolutionary patterns across years of sampling. While fecundity-related traits showed repeatability of convergent evolution across locations and years, traits more loosely related to fitness (starvation resistance) revealed more contingent evolution upon time of sampling. Our overall data from the earlier foundations indicate hitherto that similar phenotypic optima were reached through different genetic routes, suggesting that history plays an important role but does not constrain adaptive evolution. The signature of history and its impact on the evolutionary dynamics may have different outcomes depending on the level of observation.

P25 | *Rhipicephalus sanguineus* (Acari: Ixodidae) species complex: new insights in its variability

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Rhipicephalus sanguineus is a three-host tick that parasitizes vertebrates, including occasional human hosts. It is worldwide distributed, although is more common in areas with a relatively warm climate, and is a vector of some zoonosis with public health importance. A relation between increasing temperatures and augmented *R. sanguineus* tick activity has been suggested in recent European studies, and it's probably a consequence of climate change [1]. However, there is much speculation and disagreement around *R. sanguineus* taxonomic classification, and further studies must be conducted to clarify this question. Explaining further, many authors suggest the existence of a species group so-called "*R. sanguineus* complex", which includes at least 11 species with close morphologic/ecologic resemblances to *R. sanguineus sensu stricto* and that are easily misidentified [2,3]. In order to clarify taxonomic relationships within this complex, a phylogeographic study of *R. sanguineus spp.* complex across Iberian Peninsula using COI and 16S mitochondrial DNA markers is being conducted. Our main goal is to explore which *R. sanguineus* like species are present in the Iberian Peninsula and if it is possible to genetically clarify the "*R. sanguineus* complex" elements. Some preliminary results seem to support the huge morphological and genetic variation among these populations, suggesting that *R. sanguineus* is a term used to mistakenly identify different species. Furthermore, given some evidences (unpublished data) that different ticks morphotypes of this complex can cause diseases with variable severity degrees, therefore its importance in public health.

[1] Beugnet F, Kolasinski M, Michelangeli PA, *et al.* (2011) Geospat. Health 5: 255–263.
[2] Camicas JL, Hervy *et al.* (1998) The Ticks of the World: Nomenclature, described stages, hosts, distribution. Orstom Éditions, Paris.
[3] Gray J, Dantas-Torres F, Estrada-Peña A, Levin M (2013). Ticks Tick Borne Dis 4: 171–180.

P26 | Metagenomic mining of pathogenicity and antibiotic resistance traits across human populations worldwide

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Genes contributing to the pathogenicity of a particular bacterial species are often grouped in pathogenicity islands, and encoded on mobile genetic elements such as plasmids or phages, as happens with some genes coding for resistance to antibiotics. Pathogenic bacteria have gradually become resistant to antibiotics as a result of intense selective pressure they are subjected to. Through means of metagenome mining, we ask whether there is a relationship between the presence of genes coding for virulence factors and genes coding for antibiotic resistance. The dataset chosen to carry out such study encompasses human gut metagenomes issuing from different individuals as well as different human populations across the world, having contrastive cultural, dietary and sanitary lifestyles, as well as different medical access to antibiotics. Our findings show that the presence of some virulence factors is in fact correlated with that of antimicrobial resistance in bacterial communities naturally occurring in the human gut microbiome, reinforcing our hypothesis that under the antibiotics selective pressure, resistance and virulence traits are co-selected amongst bacterial communities.

P27 | Is evolution predictable? Studying temporal and spatial effects at the phenotypic and karyotypic levels

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Environmental changes across space and time as well as stochastic events can shape genetic backgrounds affecting evolutionary responses and potential. To some extent this might limit predictions concerning the initial stages of adaptation and the subsequent evolutionary patterns during evolution in new environments. Here we address experimentally these effects on the initial performance of populations and their evolutionary changes in fecundity, physiological traits and inversion polymorphisms during short-term adaptation to a new (laboratorial) common environment. We use two sets of two laboratory foundations of *Drosophila subobscura*, sampled 3 years apart (2010 and 2013), from the same contrasting European locations (Portugal *vs.* Netherlands). We found initial differentiation between foundations from different locations for most traits. Initial differences between years were found only for age of first reproduction and male starvation resistance. Age of first reproduction also showed significant variation across years in the evolutionary rates. As for chromosomal inversion frequencies, these differed initially across locations (as predicted from the cline). Its mode of evolution was somewhat different between years, particularly in the Groningen foundations. Also, the evolutionary pace differed between years. Altogether, our findings indicate that spatial rather than temporal variation in source natural populations is more likely to produce disparate starting points for evolution. Evolutionary patterns were generally predictable at the phenotypic level - with convergence occurring, mostly for fecundity-related traits - but less likely so at the genetic level (chromosomal inversion frequencies).

P28 | Size does matter: diversification of bee hummingbirds (Aves: Trochilidae)

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The concurrent increase in speciation and phenotypic diversity is a central feature of the ecological theory of adaptive radiation that not always finds support by empirical research. We examined this pattern in hummingbirds, one of the largest radiations of Neotropical birds. We estimated the dynamics of species diversification and evolution of body mass using a Bayesian framework, and tested the evolutionary relationship between path-wise rates of speciation and phenotypic evolution. This relationship was significantly positive in all major hummingbird clades. However, bee hummingbirds showed the highest slope in this relationship, which suggests that the concerted burst in taxonomic and phenotypic diversification occurred at the highest pace in this group than in any other clade of hummingbirds. This coupling was probably linked to occupying a particular region of body mass morphospace. These results support the hypothesis that macroevolutionary lability of phenotype is linked to the dynamics of speciation through time. Moreover, our results demonstrate this link not only operates on larger macroevolutionary scales or on island or island-like ecosystems, but also in smaller phylogenetic scenarios and over broad geographic ranges.

P29 The buff-tailed bumblebees in Iberian Peninsula: how are populations genetically structured and how do they cope with the introduction of commercial lineages?

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Bombus terrestris, the buff-tailed bumblebee, is a West Paleartic native species of recognised importance in crop pollination. It has been deliberately introduced worldwide for over 200 years, with increased efficiency since it started to be reared artificially by commercial companies for greenhouse crop pollination in the 1980's. When non-native these bumblebees could eventually compete with other bees for nest sites and flower resources, and cause spread of new parasites and pathogens, profoundly impacting native ecosystems. Also, introgressive hybridisation between introduced and native Bombus species / subspecies may alter their genetic composition with unforeseen consequences. In Portugal, *Bombus terrestris dalmatinus* (from Greece and Turkey) and *B. t. terrestris* (from central / northern Europe) are used for commercial purposes, and its ecological and genetic impact on the native *B. t. lusitanicus* should be assessed. A preliminary phylogeographic study of *B. terrestris* across Iberian Peninsula conducted with mitochondrial DNA demonstrated a lack of population genetic structure. Furthermore, in greenhouse areas, the presence of one shared haplotype between native and commercial lineages was detected. This could indicate occasional escape of commercial bees, or even mating between lineages, causing genetic admixture. Thousands of single nucleotide polymorphisms (SNPs), already obtained in this study through Restriction-Site Associated DNA (RAD) sequencing, are expected to allow a more detailed phylogeographic analysis of native Iberian Peninsula populations and a more powerful assessment of signatures of introgression between commercial and native bumblebees.

P30 Phylogeographical patterns and glacial refugia on the Atlantic-Mediterranean transition: the example of the rusty blenny (*Parablennius sanguinolentus*, Blenniidae)

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Phylogeography of *Parablennius sanguinolentus* from the Northeastern Atlantic and Mediterranean was assessed using sequences from the mitochondrial control region (CR) and the first intron of the S7 ribosomal protein gene (S7). Our data showed high genetic diversity for the eastern Mediterranean populations and very low values for the Atlantic ones and the westernmost Mediterranean population of Cabo de Gata. The CR mismatch analysis and neutrality tests values provide clear evidence of demographic and spatial expansion for the Atlantic and western Mediterranean populations. The relationship between genetic and geographic distance supported isolation by distance for the S7, but not for CR, suggesting a complex scenario for the history of the rusty blenny in the Mediterranean Sea. The pattern of genetic structure displayed by *P. sanguinolentus* supports a post-glacial colonization of the Atlantic coast of Europe from Mediterranean Sea glacial refuges, some of which were probably located along the coast of the Italian peninsula. Our results confirm that fishes of tropical and temperate affinities differ from the cool-water species in their response to the glacial changes that affected the Atlantic–Mediterranean area.

P31 Genomic changes during adaptation to a common environment in initially differentiated Drosophila subobscura populations

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Fast phenotypic convergence has been observed in real-time evolution studies of laboratory populations of *Drosophila subobscura* derived from contrasting latitudes in Europe (Portugal and Netherlands) and put in a new common environment. Chromosomal inversion frequencies of these populations also suffered significant changes across generations but the populations remained differentiated. We are now performing genome-wide analysis in these populations (each three-fold replicated), in order to characterize the initial genomic differentiation, as well as the genomic temporal changes during laboratory adaptation. Genome resequencing was done for 24 samples, each being a pool of individuals from one of the replicated populations and generations (founders, generation 6, 25 and 50), and including a long-established laboratory population. Allele frequency variation in genome-wide SNPs, as well as in SNPs with signal of selection, revealed that initially differentiated populations followed different genetic routes during laboratory adaptation, with no genetic convergence detected between these populations. However, there was a trend for convergence of the Portuguese population to the long-established population collected from the same geographical origin. To find SNPs associated with chromosomal inversions and to compare the genetic content of chromosomal inversions between populations and generations, we used restriction site associated DNA (RAD) sequencing of individual larvae with known karyotype. Preliminary analysis detected genetic differentiation between types of inversions of chromosome O. Further investigation of patterns of SNP variation will allow us to address the impact of history, chance and selection in genomic variation and evolution, and further the knowledge of the genomic impact of chromosomal inversions.

P32 Negative public information in mate-choice copying helps the spread of a novel trait

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Numerous field and laboratory experiments have shown that many species have the capacity for social learning, including mate-choice decisions that can be influenced by witnessing the mating decisions of others. This phenomenon, known as mate-choice copying, is a type of non-genetic information than can increase behavioural plasticity and cause genetic changes across generations. Here we develop a numerical model of mate-choice copying that follows the population genetics tradition, consisting in tracking allele frequencies in a population over time under scenarios with and without copying. In contrast to previous evolutionary models, we consider both positive and negative social information because many mating systems are driven by males in pursuit of a mate, and female refusal of copulation may provide negative social information. The inclusion of negative social information to mate-choice copying helps the spread of a novel trait, even if female innate mate-choice preference is biased towards the common male-type. We argue that the presence or absence of copying might simply mirror the associated cost-benefit relationship of the mating system of a given species, and suggest how to test this prediction.

P33 May the Selection be with you: the interplay of evolutionary forces in the speciation of *Timon lepidus*

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In this very galaxy, on the Iberian Peninsula, the lizard *Timon lepidus* has been evolving for millions of generations, enduring true evolutionary challenges such as the glaciations, demographic fluctuations, and the constant need to adapt, or perish. Understanding speciation requires the integration of ecology, evolution and the role of history in shaping the diversification or decline of lineages. We must understand both how variation in phenotype may affect the fitness of individuals in their local environment, and how natural selection is shaping the genome of those organisms. Focused on two, of the three described, subspecies inhabiting continental Iberian Peninsula, we set to investigate the speciation continuum phase in which these populations stand, looking for patterns of adaptation and natural selection signatures across the genome of this lizard. Recurring to NGS technology (RAD-seq), together with phenotype and environmental data, we uncover the interplay of evolutionary forces, neutral and non-neutral, shaping the adaptation of these populations, and discover an unexpected strong pattern of local adaptation, which does not follow the currently described taxonomy. Furthermore, cues for repeated adaptive evolution arise, opening exciting perspectives to the research on how populations adapt to their environment.

Timon lepidus is under selective pressure, and the force is strong in this one.

P34 Evolution in Portugal: what Portuguese people know, do not know and are convinced to know, but do not

Xana Sá-Pinto

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Understanding evolution is fundamental for people to understand the natural world and make informed choices concerning issues with strong social impacts. Public understanding of the implications and applications of biological evolution is also important to increase public support for this research field. With this study we aim to characterize the awareness and understanding of the Portuguese population regarding evolution and its daily life implications, and use these results to identify priority areas to address in future curricula changes and outreach events. We applied a questionnaire to samples of general public, public attending science outreach events and students entering the biology course. To assess the content validity of the questionnaire, it was further applied to researchers attending the IX ENBE. Our results suggest high levels of acceptance of evolution, with less than 8% of inquired people agreeing with creationist statements. However, this high acceptance does not translate into evolution understanding: misconceptions are frequent and there is a pervasive lack of knowledge about the processes promoting evolution and daily life applications of evolutionary biology. These results highlight the weaknesses of the Portuguese education system, supporting the claims for an earlier introduction of evolutionary biology contents in school curricula and also for the importance of implementing evolution education and outreach actions. These actions should be based on practical examples, exploring evolution in contexts that are familiar and important to the various publics segments, further promoting the recognition of the social, economic and cultural importance of evolutionary biology research.

The XI ENBE Organizing Committee

Members of UCIBIO and Departamento de Ciências da Vida, FCT/UNL

Marco A. Coelho

Paula Gonçalves

Márcia Palma

Carla Gonçalves

Ana Pontes

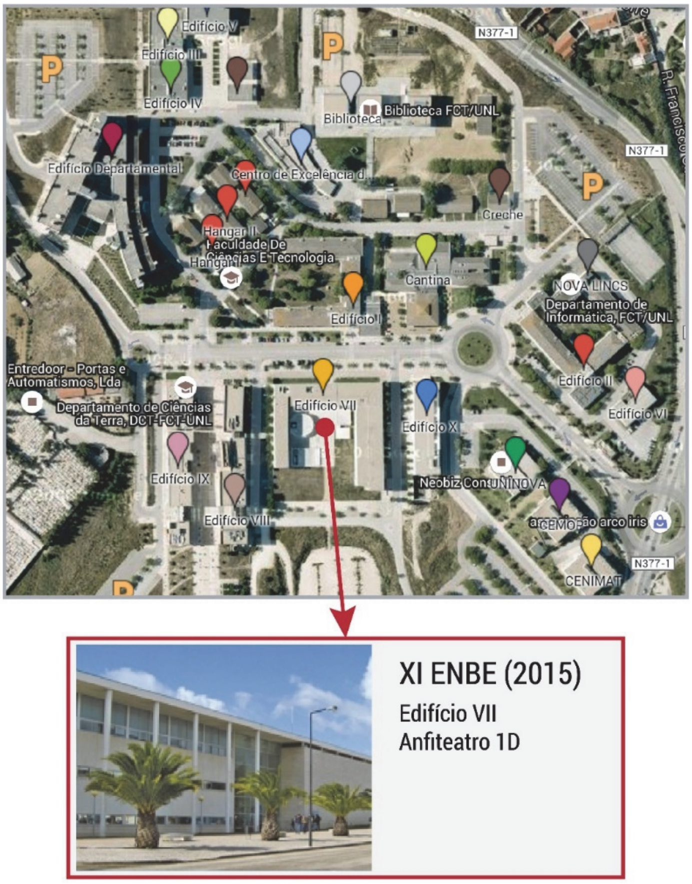
Meeting location and contact information

The XI Encontro Nacional de Biologia Evolutiva (ENBE) will take place in Campus de Caparica, at the Faculdade de Ciências e Tecnologia, Universidade NOVA de Lisboa, on December 21st , 2015.

Address:
Faculdade de Ciências e Tecnologia
2829-516 Caparica
Portugal

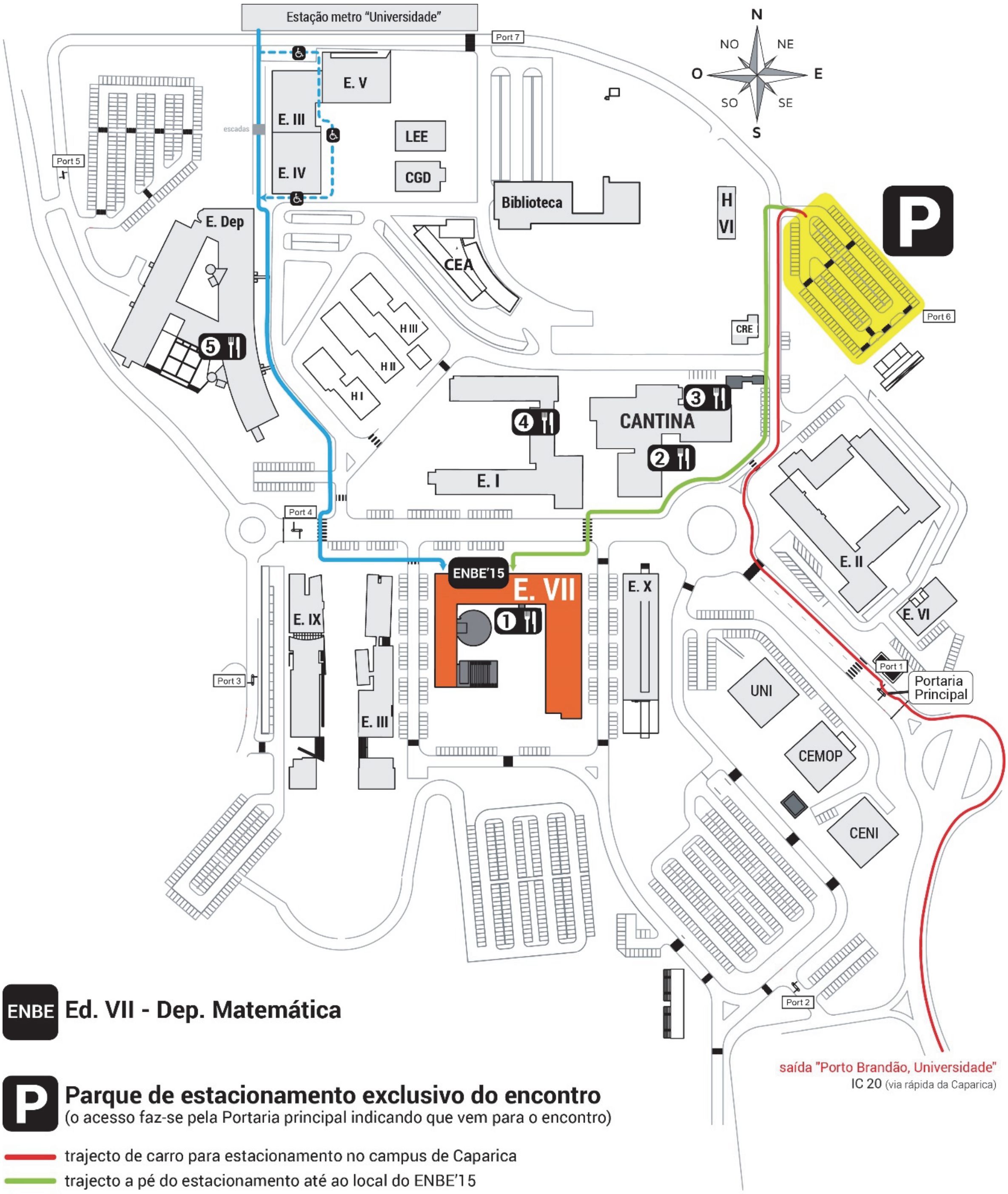
GPS Coordinates:
Latitude: 38°39’36.42”N
Longitude: 9°12’11.45”W

Contact email:
enbe2015@campus.fct.unl.pt



XI ENBE (2015)
Edifício VII
Anfiteatro 1D

Guide map of the campus and useful information



ENBE Ed. VII - Dep. Matemática

P **Parque de estacionamento exclusivo do encontro**
(o acesso faz-se pela Portaria principal indicando que vem para o encontro)

🟥 trajecto de carro para estacionamento no campus de Caparica
🟩 trajecto a pé do estacionamento até ao local do ENBE'15
🟦 trajecto a pé desde a estação de metro "Universidade" até ao local do ENBE'15

Espaços de refeição aconselhados:

① Bar "Espaço Mais" - Edifício VII
② Cantina
③ Bar "My Spot" (entrada por baixo)
④ Casa do Pessoal
⑤ Bar "Espaço Mais" - Ed. Departamental

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