



XVII ENBE Annual Meeting of the Portuguese Association for Evolutionary Biology

16-17 December 2021

Online meeting

hosted by Ciências, University of Lisbon, Lisboa, Portugal



<https://enbe2021.rd.ciencias.ulisboa.pt/>

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About the ENBE

The international meeting of Portuguese Association for Evolutionary Biology (ENBE) is an annual meeting that aims to bring together Evolutionary Biologists working in Portugal and abroad to promote scientific cohesion and excellence. This meeting is a forum for scientists of all academic levels (from master students to principal investigators), to present their work and discuss, fostering new ideas and collaborations. We invite researchers from all over the world to participate and submit their work.

This year the meeting takes place **online**, between **Thursday and Friday afternoon, the 16th and 17th of December**. It includes a public round table to discuss evolution and pandemics.

Students (MSc, PhD) presenting their work are eligible for the [APBE awards](#) for the best oral and poster presentation.

The open session on the evolution of SARS-CoV-2 and pandemics gathers Isabel Gordo (IGC), Manuel Carmo Gomes (FCUL), and Thiago Carvalho (EMBO) in a debate on what is already known about the SARS-CoV-2 virus and how it is evolving, chaired by Filipa Vala (PlanAPP, cE3c). Also, with a discussion around the educational book "[Animal and human coronaviruses](#)" and the game "Beat Corona", presented by Margarida Duarte (INIAV). This session, [AskmeCOVIDevolution](#), was held in Portuguese.

Organizing and Scientific Committees

APBE

ENBE is an annual meeting promoted by the Portuguese Association for Evolutionary Biology (“Associação Portuguesa de Biologia Evolutiva” – APBE) in collaboration with universities and research centres in Portugal.

XVII ENBE Organizing committee

Vítor Sousa, cE3c-U.Lisboa (chair of the Organizing Committee)

Bárbara Parreira, IGC

Filipa Borges, NOVA-FCSH and IGC

Inês Fragata, cE3c-U.Lisboa

João Alpedrinha, cE3c-U.Lisboa

Teresa Nogueira, INIAV,I.P. and cE3c-U.Lisboa



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XVII ENBE Evaluation committee

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Catarina Pinho, CIBIO-U.Porto

Erik van Bergen, U.Zurich

Rémi Tournebize, IGC

Ricardo Pereira, LMU-Munich

Contact

You can contact the organizing committee by e-mail: enbe2021@fc.ul.pt

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Support



Acknowledgments

We are very grateful to the sponsorship of SARSTEDT, and institutional support from APBE, FCUL, IGC and FCT, as mentioned in the previous pages.

Furthermore, we thank the following persons for their support towards the XVII ENBE meeting:

Dr. Patrícia Tiago, cE3c communication office

Ana Fragata for the graphical design of the ENBE XVII logo

We also thank the following persons for their support towards the AskmeCOVID evolution session:

Dr. Mónica Bettencourt-Dias, Director of the Instituto Gulbenkian de Ciência.

Regina Fernandes, Instituto Gulbenkian de Ciência Science Events.

Cristina Monteiro, Fundação Calouste Gulbenkian technical support.

Program

Day 1 Thursday, 16th December

13:00

Opening session

13:10-14:35	Session 1 – chair Bárbara Parreira	
13:10-13:50	Plenary: Life Through the Hologenome Window	Tom Gilbert, Univ. Copenhagen, Denmark
13:50-14:05	A genomic study of Iberian cattle from the Medieval Islamic and post-Medieval Christian periods	Cindy Sarmento, Univ. Porto, Portugal
14:05-14:20	Isolation-by-distance and time in the context of habitat loss and fragmentation	Gabriele Maria Sgarlata, IGC, Portugal
14:20-14:35	Relentless Selection: Polygenic selection within a single generation creates subtle divergence among ecological niches	Moritz Ehrlich, RSMAS, USA
14:35-14:40	Break!	
14:40-15:25	Poster Session 1	
15:25-15:30	Break!	
15:30-16:55	Session 2 – chair Teresa Nogueira	
15:30-16:10	Plenary: The tempo of virus evolution	Katrina Lythgoe, Univ. Oxford, UK
16:10-16:25	Virulence constrains transmission even in the absence of a genetic trade-off	Diogo Godinho, Univ. Lisbon, Portugal
16:25-16:40	Mutation rate of SARS-CoV-2 and emergence of mutators during experimental evolution	Massimo Amicone, IGC, Portugal
16:40-16:55	Wolbachia effects on Transposable Element mobilization	Ana Eugénio, IGC, Portugal

Day 2 Friday, 17th December

13:00	Opening session	
10:00-11:30	Public Session: AskmeCOVID evolution	
13:15	Announcements	
13:20-14:45	Session 3 - chair Inês Fragata	
13:20-14:00	Plenary: Population-scale sequencing of <i>Drosophila melanogaster</i> and <i>Anopheles coluzzi</i> uncovers transposable element contribution to gene expression variation and adaptive evolution	Josefa Gonzalez, Institute of Evolutionary Biology, Spain
14:00-14:15	Longevity associated microbial and evolutionary signatures in the gut of old mice resemble youthful profiles	Rita Melo-Miranda, Univ. Lisboa, Portugal
14:15-14:30	Can evolutionary change keep us with the fast-paced global warming? <i>Drosophila</i> says no	Marta Alexandra Santos, Univ. Lisboa, Portugal
14:30-14:45	Functional specialization of social and asocial learnings in <i>Drosophila melanogaster</i>	Carla Simões-Henriques, IGC, Portugal
14:45-14:50	Break!	
14:50-15:25	Poster Session 2	
15:25-15:30	Break!	
15:30-16:15	Session 4 – chair Vítor Sousa	
15:30-15:45	Population structure of Brittany provides new insights on the introduction of steppe ancestry in Western Europe	Isabel Alves, Univ. Nantes, France
15:45-16:00	Phylogenetic relationships and selective constraints in the visual pigments of the <i>Astyanax mexicanus</i> (Characiformes, Characidae) cavefish and surface populations	Silvia Perea, UNAM, Mexico
16:00-16:15	evALLution: translating evolution into touch, making evolution accessible for people with blindness	Telma Laurentino, ESPM, USA
16:15-16:20	Break!	
16:20-16:30	Closing session	
16:30-17:30	APBE Assembly	

Plenary speakers



Tom Gilbert

Center for Evolutionary Hologenomics, GLOBE Institute, University of Copenhagen.

Tom Gilbert's group studies a range of different questions on speciation, adaptation, conservation and domestication of different species, using a combination of hologenomics, ancient DNA and metabarcoding technologies. For that they have been developing new methods to extract and analyse ancient DNA and metabarcoding data. Part of this work is also be applied to food industry to identify microbial interactions during the fermentation process. Tom Gilbert is the group leader of the Hologenomics group at the GLOBE Institute and Director of the Danish National Research Foundation Center for Evolutionary Hologenomics.

If you want to know more about the work they do, check their [website](#).



Katrina Lythgoe

Big Data Institute, University of Oxford

Katrina Lythgoe is a group leader at the Big Data Institute and her group focus on evolutionary epidemiology of viral infections. They use a combination of population genetics, modelling and genomic data analyses to study how evolutionary and ecological processes operate at different biological scales.

If you want to know more about the work they do, check their [website](#).

Josefa González

Institute of Evolutionary Biology, CSIC-UPF



Josefa González is a CSIC Scientist at IBE and her group focuses on understanding how organisms adapt to the environment. They use a broad range of omics approaches, including DNA-seq, RNA-seq, ATAC-seq, CHIP-seq and HiC, to identify adaptive mutations that they further characterized using molecular and functional analyses. Josefa is the co-leader of the European *Drosophila* population genomics consortium (DrosEU) and she is currently a council member of the ESEB and the SMBE. Josefa's group is involved in science outreach, sharing their work with the general public and co-leading a citizen science initiative.

If you want to know more about the work they do, check their [website](#)

Awards

Every year at the ENBE meeting, the APBE gives two awards for the best oral and poster presentations. Eligible talk and poster presentations were evaluated by members of the scientific committee (evaluation committee), according to scientific quality, originality, impact, audience engagement and presentation quality. Eligible candidates for the best talk and poster awards must be MSc or PhD students.

We are delighted to announce the following 2021 APBE Prize Winners.

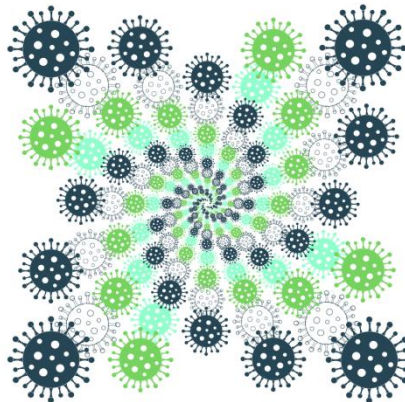
2021 Best Talk Award Winner:

Ana Eugénio, Instituto Gulbenkian de Ciência, Portugal, for her talk “Wolbachia effects on Transposable Element mobilization”. The prize consists of free registration in the [Congress of the European Society for Evolutionary Biology 2022](#) (14-19 August, Prague, Czech Republic).

2021 Best Poster Award Winner:

Hugo Barreto, Instituto Gulbenkian de Ciência, Portugal, for his poster “Gut mélange à trois: fluctuating selection modulated by microbiota, host immune system and antibiotics”. The prize consists of free registration to ENBE 2022.

Open session: AskmeCOVID evolution



Quais os processos evolutivos que tornam os vírus mais resistentes? Seremos capazes de prever a sua evolução? Como conseguimos excluir certas doenças no passado? Conseguiremos eliminar o SARS-CoV-2?

Este é um espaço aberto a perguntas sobre evolução, COVID-19 e a pandemia onde algumas perguntas do público foram discutidas por especialistas.

No dia 17 de dezembro, juntamos Isabel Gordo (IGC), Manuel Carmo Gomes(FCUL), o Thiago Carvalho (EMBO) com moderação de Filipa Vala (PlanAPP, cE3c) para debater o que já se sabe sobre este vírus e de que forma este está a evoluir. Nesta sessão irão ser esclarecidos alguns conceitos e dúvidas acerca da evolução do SARS-CoV-2 através de um debate e da divulgação do livro '[Coronavírus dos animais e do Homem](#)' e do jogo de sociedade '[Beat Corona](#)', pela editora Margarida Duarte (INIAV).

Quando? 17 de dezembro de 2021 das 10h00-11h30.

Onde? Esta sessão decorreu presencialmente na sala 1 da Fundação Calouste Gulbenkian, em Lisboa, e foi também transmitida em *streaming*.

Sobre o debate:

Os vírus em circulação numa população de alta densidade, como a população humana, têm mais possibilidades de se transmitir, replicar, e, portanto, de sofrer alterações. Mas mesmo sem sofrerem alterações, quando organismos patogénicos escapam ao seu hospedeiro natural (por exemplo, morcego) e conseguem infectar outro hospedeiro, como os humanos, podem ter efeitos devastadores.

A intervenção na saúde pública, através do desenvolvimento de vacinas e antibióticos, foi um dos maiores avanços científicos do século XX, sendo responsável pelo controle e mesmo erradicação de doenças (como por exemplo, a varíola). Ainda assim, nos últimos 50 anos a humanidade tem-se debatido com novos agentes patogénicos (por exemplo, SARS, MERS, Ébola, gripe A). O aparecimento do SARS-CoV-2 mostrou que as doenças infecciosas estão a voltar a ter o papel que já outrora tiveram na humanidade, tendo o poder de afetar e alterar o curso da sua história. A seguir aos rinovírus, os coronavírus são a principal causa de constipações, mas, até às últimas décadas, raramente causavam doença grave em humanos. Os vírus continuam a evoluir constantemente, e podem mesmo tornar-se mais resistentes aos tratamentos como resposta às intervenções humanas.

Oradores da Sessão Aberta



Filipa Vala (Moderadora). Comunicadora de ciência. Doutorada em Evolução e Ecologia (University of Amsterdam, 2001) é membro externo do [Centro de Ecologia, Evolução e Alterações Ambientais \(cE3c\)](#). Em 2006 fez uma mudança de carreira para a comunicação científica, motivada por um estágio de 3 meses no jornal diário nacional Público. Desde aí, escreveu para exposições de ficção científica, incluindo *The Evolution of Darwin and Brain - Wider than the sky* (produzida pela Fundação Calouste Gulbenkian em 2009 e 2019), e *Variações Naturais* (produzida pela Câmara Municipal de Lisboa, ICNF e Universidade de Lisboa). Desde dezembro de 2021, trabalha como mediadora de conhecimento no PlanAPP (Centro de Competências da Administração Pública para o Planeamento, Política e Prospectiva) como líder da equipa dedicada a encontrar e conectar parceiros relevantes na academia para planeamento específico e projetos prospectivos (o Planeamento, Prospectiva e equipe da Rede de Parceiros).



Isabel Gordo. Bióloga evolutiva. Lidera o grupo de [Biologia evolutiva no Instituto Gulbenkian de Ciência](#), sendo uma referência na área em Portugal. Combina trabalho teórico e experimental para compreender as principais forças evolutivas por detrás da variação genética em bactérias e no microbioma. Publicou diversos trabalhos científicos, nomeadamente na resistência a antibióticos e na diversidade genética do SARS-CoV-2 que causa a covid-19.



Manuel Carmo Gomes. Professor, investigador e epidemiologista de doenças transmissíveis na [Faculdade de Ciências da Universidade de Lisboa](#). Aplica técnicas de matemática aplicada para estudar a dinâmica de doenças infecciosas em humanos com o objetivo de informar as decisões de saúde pública. Faz parte da comissão técnica de vacinação portuguesa e esteve envolvido na equipa de aconselhamento para as medidas de combate à Covid19. Ao longo do último ano escreveu diversos artigos e relatórios sobre a pandemia.



Thiago Carvalho. ‘Senior writer’ para a educação e comunicação da [Organização Europeia de Biologia Molecular](#) (EMBO) tendo larga experiência na comunicação de ciência para a cidadania. Foi curador assistente para a exposição "A Evolução de Darwin", na Fundação Calouste Gulbenkian em 2009. Tem um doutoramento em Imunologia e foi investigador pós-doutorado no Departamento de Microbiologia da Universidade do Alabama (USA) e no grupo de Fisiologia dos Linfócitos no Instituto Gulbenkian de Ciência, tendo publicado diversos trabalhos sobre o sistema imunitário. Foi diretor do programa de doutoramento do IGC, coordenador da pós-graduação na Fundação Champalimaud, e editor científico da revista *Journal of Experimental Medicine*.



Margarida Duarte. Investigadora do Instituto Nacional de Investigação Veterinária (INIAV) desde janeiro de 1990. Licenciou-se em Medicina Veterinária em 1986 em Lisboa, obteve o grau de Mestre em Biotecnologia/Biologia Molecular em 1991 e o Doutoramento em Biologia em 2000. Os seus interesses científicos têm-se centrado nas doenças infecciosas virais dos animais, nomeadamente na patogénese, epidemiologia, filogenética, evolução e desenvolvimento de vacinas. Possui vasta experiência em diagnóstico clássico e molecular, tendo desenvolvido e validado diversos métodos de diagnóstico, alguns recomendados pelos manuais da OIE (*World organisation for animal health*). Atualmente é Chefe do Laboratório de Virologia da Unidade de Saúde Animal do INIAV. Desde o surgimento do SARS-CoV-2, o Laboratório de Virologia do INIAV tem apoiado o Sistema Nacional de Saúde Português no diagnóstico do COVID-19.

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Abstracts of Plenary talks

Life Through the Hologenome Window

Tom Gilbert

Center for Evolutionary Hologenomics, GLOBE Institute, University of Copenhagen.
Copenhagen, Denmark

It is increasingly clear that symbiotic microbes not only benefit their eukaryotic hosts through food conversion and nutrient uptake, but they can also have broader effects on their hosts' morphology, health, and even behavior. They are no longer considered passive passengers but active crew, who can affect and even condition phenotypes in complex organisms, whether plants, invertebrates, or vertebrates. The extent of these effects is so great, that although the two parties have traditionally been studied independently, a new “hologenomic” approach is now being embraced by the genomics community, that jointly analyzes the interconnection between host genomes and microbial metagenomes, and their combined functions. This is now feasible because the genomic revolution enables the generation of multi omics-scale data sets and analysis using novel data-mining methods. Indeed, recent research has showcased the feasibility of applying hologenomics to questions of ecological and evolutionary relevance. Therefore, there is a pressing need to understand how the evolution of complex host organisms is shaped by their associated microbes. Furthermore, now is the time to explore their broader implications in the context of fundamental ecological and evolutionary processes, grand transitions of life, and the history of humans – all topics that are typically attributed to other host-centric features such as genomic variation.

The Tempo of Virus Evolution

Katrina Lythgoe

Big Data Institute, University of Oxford. Oxford, UK

Viruses replicate and evolve within the hosts that they infect, but sooner or later they need to transmit if they are going to survive in the long term. This can create evolutionary trade-offs, because what makes a virus fit within a given individual does not necessarily make it good at transmitting. On the other hand, within-host evolution might facilitate evolutionary ‘leaps’ that make the virus even fitter at the between-host level. I will explore how these processes can affect the tempo of viral evolution in human viruses, including HIV and SARS-CoV-2.

Population-scale sequencing of *Drosophila melanogaster* and *Anopheles coluzzii* uncovers transposable element contribution to gene expression variation and adaptive evolution

Josefa González

Evolutionary and Functional Genomics Laboratory, Institute of Evolutionary Biology, CSIC-UPF. Barcelona, Spain.

How organisms adapt to the environment is still an open question in Biology. Short read genome sequencing has allowed to explore the role of single nucleotide polymorphisms (SNPs) in environmental adaptation. However, SNPs alone can only explain a fraction of the existing ecologically relevant phenotypic variation. Among the structural variants that can now be studied thanks to the availability of long-read sequencing, transposable elements are likely to play a major role in adaptation due to their capacity to generate mutations that often have phenotypic effects of a complexity that is not achievable by point mutations. In our lab, we are studying the role of transposable elements in adaptation in the fruitfly *Drosophila melanogaster* and in the malaria vector *Anopheles coluzzii*. *D. melanogaster* is an excellent model species to quantify the role of transposable elements in environmental adaptation as it has recently colonized very distinct environments. We have generated 32 new *D. melanogaster* reference genomes using long-read sequencing of natural populations collected in arid, cold and temperate environments. We have discovered thousands of new transposable element insertions including copies from three new families. We have also generated transcriptomic data for 18 of these genomes, which is allowing us to elucidate the role of transposable elements in expression quantitative trait loci (eQTL) variation. In *Anopheles* species we are focusing on the potential role of transposable elements in urban adaptation. Based on the long-read sequencing of six larvae collected in urban breeding sites, we have generated the most comprehensive transposable element annotation in this species to date. This annotation has allowed us to identify several insertions that could potentially impact both genome architecture and the regulation of vectorial capacity genes. Overall, our results show that transposable elements contribute to gene expression variation and adaptive evolution.

Abstracts of oral presentations

A genomic study of Iberian cattle from the Medieval Islamic and post-Medieval Christian periods

Sarmiento, C (1); Guimarães, S (2,3); Davis, SJM (4); Detry, C (5); Arruda, A (5); Viegas, C (5); Martins, A (5); Kilinç, GM (6); Götherström, A (7); Fonseca, NA (2); Pires, AE (2,8); Ginja, C (2,3)

(1) FCUP - Faculdade de Ciências, Universidade do Porto, Porto, Portugal; (2) CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal; (3) BIOPOLIS - Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, Vairão, Portugal; (4) LARC/DGPC - Laboratório de Arqueociências, Direcção Geral do Património Cultural, Lisboa, Portugal; (5) Uniarq, Faculdade de Letras, Universidade de Lisboa, Lisboa, Portugal; (6) Department of Bioinformatics, Graduate School of Health Sciences, Hacettepe University, Ankara, Turkey; (7) Archaeological Research Laboratory, Stockholm University, Stockholm, Sweden; (8) Faculdade de Medicina Veterinária, Universidade Lusófona de Humanidades e Tecnologias, Lisboa, Portugal

Iberian cattle represent an important pool of genetic diversity with a distinct evolutionary history. Local breeds display diverse mitochondrial and Y-chromosome lineages, besides the well-established African taurine ancestry also observed in their autosomes. They are considered to have high potential to reveal how trading and breeding practices shaped the genomes of cattle. However, complementary archaeogenomic data, which would allow a direct view into these past evolutionary events, are still lacking. In this study we describe newly obtained genome sequences of southern Portuguese cattle from the Medieval Islamic and post-Medieval Christian periods. A size increase of cattle was documented to have occurred along with this cultural transition. Our data also includes specimens from the Iron Age and the Roman period for broader comparisons. The amount of endogenous DNA we were able to retrieve ranged from 0.17 to 43.57% and samples were sequenced to an average of 0.38× depth of coverage. The biological sex was determined for all specimens. The population genetics analyses presented here provided further evidence of an early African influence, preceding the Moslem occupation of this territory. We also observed some level of genetic continuity between these past cattle and the extant Mertolenga native breed.

Isolation-by-distance and time in the context of habitat loss and fragmentation

Sgarlata, GM (1); Maié, T (1); Zoeten, T (1); Rasteiro, R (1); Chikhi, L (1,2)

(1) IGC - Instituto Gulbenkian de Ciência, Oeiras, Portugal; (2) 2 Laboratoire Évolution & Diversité Biologique (EDB UMR 5174), Université de Toulouse Midi-Pyrénées, CNRS, IRD, UPS, Toulouse, France

Throughout Earth's natural history, habitats have undergone drastic changes in quality and extent, influencing the distribution of species. In the last few hundred years, human activities have destroyed natural habitats at an unprecedented rate, converting continuous habitat into fragmented and isolated patches. Recent global meta-analyses suggest that habitat loss and fragmentation (HL&F) has negatively impacted the genetic diversity of many taxa across the world. These conclusions have been drawn by comparing present-day genetic patterns from populations occurring in continuous and fragmented landscapes. In this work, we attempted to go beyond 'pattern' and propose a theoretical framework that could help describe the temporal 'processes' that influence genetic variation in the context of HL&F. Since most species worldwide have a geographically restricted dispersal (known as "isolation-by-distance"), the proposed theoretical framework considers both the effect of space and time in shaping population genetic variation. In particular, we modify the original theoretical results on isolation-by-distance (Slatkin, 1991; Slatkin, 1993) and apply them to a toroidal stepping-stone model in the context of HL&F.

Relentless Selection: Polygenic selection within a single generation creates subtle divergence among ecological niches

Ehrlich, MA (1); DeLiberto, AN (1); Drown, MK (1); Wagner, DN (2); Oleksiak, MF (1); Crawford, DL (1)

(1) RSMAS - Rosenstiel School of Marine and Atmospheric Science, University of Miami, Miami FL, USA; (2) EBIO - Ecology and Evolutionary Biology, University of Colorado, Boulder CO, USA

Selection constantly reshapes the genetic and phenotypic composition of populations, yet often adaptive changes are not propagated due to e.g. prohibitively high drift or gene flow. Nevertheless, selection may still induce temporary phenotypic divergence at extremely small spatial and short temporal scales. These changes may ultimately be of higher ecological importance than long-term evolutionary trends. Selection on polygenic traits specifically may allow for repeated divergence every generation without significant reduction in standing genetic variation. The teleost *Fundulus heteroclitus* inhabits salt marsh estuaries that are characterized by high environmental heterogeneity (tidal ponds, creeks, coastal bays). Populations are large (>10K) and panmictic breeding results in negligible genetic structure. However, individuals demonstrate high site fidelity to microhabitats with distinct temperature and oxygen regimes. We tagged/recaptured 2000/200 individuals and confirmed residency in two disparate microhabitats: a cooler, oxygenated coastal basin and hotter, anoxic tidal ponds. After common-gardening basin and pond residents we measured fitness-related traits such as critical thermal maximum, resting metabolic rate, cardiac metabolic rate and aquatic surface respiration latency. We found significant phenotypic divergence of 5% ($p=0.02$) and 9% ($p=0.004$) among basin and pond residents in resting metabolic rate and cardiac metabolic rate respectively, suggestive of selection in microhabitats. We also identified >10,000 genome-wide single nucleotide polymorphisms using a genotyping-by-sequencing (GBS) approach. By sampling each microhabitat at two time points within a single generation we determined allele frequency change over time. Only few SNPs individually displayed significant allele frequency changes beyond that expected by random mortality. However, the proportion of SNPs showing i) non-zero allele frequency changes over time and ii) divergence among microhabitats, is significantly elevated over the neutral expectation. This pattern is consistent with selection on polygenic traits where minor allele frequency changes at multiple loci of small-effect can cause significant phenotypic shifts. Despite panmictic breeding and negligible demography *F. heteroclitus* displays surprising phenotypic divergence among microhabitats. This is unlikely due to environmentally induced plasticity but rather continuous selection on polygenic traits. Given sufficient standing genetic variation and large population sizes, polygenic selection may regenerate phenotypic divergence repeatedly every generation. While this does not lead to any long-term evolutionary change, such temporary phenotypic heterogeneity may be ecologically more relevant.

Virulence constrains transmission even in the absence of a genetic trade-off

[Godinho, DP \(1\)](#); [Rodrigues, LR \(1\)](#); [Lefevre, S \(2\)](#); [Delteil, L \(2\)](#); [Mira, AF \(1\)](#); [Fragata, IR \(1\)](#); [Magalhães, S \(1\)](#); [Duncan, AB \(2\)](#)

(1) CE3C - centre for ecology, evolution and environmental changes, FCUL University of Lisbon, Lisbon, Portugal; (2) ISEM - Institut des Sciences de l'Évolution, Université de Montpellier, Montpellier, France

The virulence-transmission trade-off predicts that parasite fitness peaks at intermediate virulence. Despite the centrality of this hypothesis, whether the correlation between virulence and parasite fitness has a genetic basis or is environmentally driven remains to be addressed. Disentangling among these alternatives is key to identifying conditions under which parasite traits can evolve independently, which could be applied to strategies for the management of parasite virulence. Most studies in support of the trade-off hypothesis used parasite isolates that differ genetically, but also in their recent ecological and evolutionary history, as they have different geographic origins. This may lead to spurious correlations among traits, masking which factors affect the trade-off. Here, we tackled this issue by infecting host plants with inbred lines created from the same population of the macro-parasitic spider-mite *Tetranychus urticae*. When transmission was not possible during the infection period, we observed a hump-shaped relationship between virulence and parasite fitness, as predicted by theory. This relationship was due to within-host density dependence rather than to a genetic correlation between traits. However, when transmission to uninfected hosts occurred during the infection period, virulence was positively, environmentally and genetically correlated with parasite fitness. In this case, more virulent genotypes suffer less from host exploitation by escaping to new hosts. Therefore, the virulence-transmission trade-off depends on within-host dynamics and on the timing of transmission, rather than on a genetic correlation. This fundamental correlation may thus be easier to manipulate than previously thought.

Mutation rate of SARS-CoV-2 and emergence of mutators during experimental evolution

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To understand how organisms evolve, it is fundamental to study how mutations emerge and establish. Here, we estimate the rate of mutation accumulation of SARS-CoV-2 and investigate the repeatability of its evolution when facing a new cell type but no immune or drug pressures. We perform experimental evolution with two strains of SARS-CoV-2, one carrying the originally described spike protein (CoV-2-D) and another carrying the D614G mutation that has spread worldwide (CoV-2-G). After 15 passages in Vero cells and whole genome sequencing, we characterized the spectrum and rate of the emerging mutations and looked for evidences of selection across the genomes of both strains. From the mutations accumulated, and excluding the genes with signals of selection, we estimated a spontaneous mutation rate of 1.25×10^{-6} per nucleotide, per infection cycle for both lineages of SARS-CoV-2. We further show that mutation accumulation is heterogeneous along the genome, with the spike gene accumulating mutations at rate five-fold higher than the genomic average. We also observe the emergence of mutators in the CoV-2-G background, likely linked to mutations in the RNA-dependent RNA polymerase and/or in the error-correcting exonuclease protein. These results provide valuable information on how spontaneous mutations emerge in SARS-CoV-2 and on how selection can shape its genome towards adaptation to new environments.

Wolbachia effects on Transposable Element mobilization

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Wolbachia is a bacterial endosymbiont that is maternally transmitted and widespread across insects and nematodes species. This endosymbiont affects many aspects of host biology and can also play a role in host defense. Wolbachia confers resistance against viral infection and affects abundance of piRNAs, an important mechanism of repressing transposable element (TE) mobilization in the germline of eukaryotes. To test this hypothesis that Wolbachia impacts TE mobilization in the host genome, we studied TE expression in flies from a panel of *Drosophila melanogaster* lines naturally infected with Wolbachia and for which we have information on TE insertions. We removed Wolbachia from 25 *D. melanogaster* genotypes from the *Drosophila* Genetic Reference Panel, to create a panel of 25 pairs of Wolbachia-positive and Wolbachia-negative lines. We characterized Wolbachia loads in adult females from the Wolbachia-positive genotypes and measured the transcription of 14 TEs of different families in adult females from each of the Wolbachia-positive and Wolbachia negative genotypes. We found variation in TE expression which depended on Wolbachia status, type of TE, and host genotype. Differences in TE expression with versus without Wolbachia mostly depended on host genotype, rather than on TE identity. These data suggest that Wolbachia may impact TE mobilization and the generation of novel genetic variants in host genomes.

Longevity-associated microbial and evolutionary signatures in the gut of old mice resemble youthful profiles

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Aging, one of the all-time challenges, is accompanied by several factors, including an increase in inflammation levels and alterations in the intestinal microbiota composition and evolution. Following a period of great fluctuations in the first years of life, the gut microbiota starts to stabilize around age three. This stability continues through adulthood but will inevitably be affected by aging, an important contributor to the loss of homeostasis. On the other hand, gut dysbiosis will also contribute to aging, e.g. by increasing gut permeability and giving rise to systemic inflammation. Nevertheless, how these events impact microbiota evolution and whether they could be involved in pathobiont selection is still unknown. Here we approach this question by comparing microbiota evolution in three sets of mice with different ages: young (6–9 weeks old), old (19 months old), and very old (25 months old). Specifically, previous studies have described the adaptation of a commensal strain of *E. coli* to the guts of young animals and have shown that it rapidly acquires metabolic-related mutations. In contrast, in the guts of old mice, *E. coli* adaptation shifts towards stress-related mutations, most likely due to an increase in inflammation and oxidative stress during aging, whereas the rise of metabolic adaptations becomes slower. Yet, to increase both the health and lifespan we need to understand how the (lucky) very old are different and how that impacts *E. coli* evolution. To tackle this question, we first compared the host environment that *E. coli* encounters upon colonization of the very old with the two previously studied age groups. For this, we measured the level of frailty, intestinal inflammation and characterized the microbiota composition. We found that the very old animals are the frailest, but do not show higher intestinal inflammation than the old mice. Interestingly, when compared to young and old animals, the very old show an increase in some health-associated bacteria, such as *Akkermansia muciniphila*, *Oscillospira*, and several Muribaculaceae members. Moreover, the adaptive pattern of *E. coli* colonizing the gut of the very old displays more metabolic than stress-related mutations, approaching the profile found in young animals. Together, these data raise the possibility that specific alterations to the microbiota and the gut environment during aging may not be exclusively dysbiotic and may even be associated with longevity. Future studies should try to understand whether only the healthier are able to reach very old age or whether this is a general possibility provided some reversion of dysbiosis occurs.

Can evolutionary change keep up with the fast-paced global warming? *Drosophila* says no.

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Adaptive evolution is key in mediating responses to global warming and may sometimes be the only solution for species to survive. Such evolution will expectedly lead to changes in the populations' thermal reaction norm and improve their ability to cope with stressful conditions. Conversely, evolutionary constraints might limit the adaptive response. Here, we test these expectations by performing a real-time evolution experiment in historically differentiated *Drosophila subobscura* populations. We address the phenotypic change after nine generations of evolution in a daily fluctuating environment with average constant temperature, or in a warming environment with increasing average and amplitude temperature across generations. Our results showed that (1) evolution under a global warming scenario does not lead to a noticeable change in the thermal response; (2) historical background appears to be affecting responses under the warming environment, particularly at higher temperatures; and (3) thermal reaction norms are trait dependent: although lifelong exposure to low temperature decreases fecundity and productivity but not viability, high temperature causes negative transgenerational effects on productivity and viability, even with high fecundity. These findings in such an emblematic organism for thermal adaptation studies raise concerns about the short-term efficiency of adaptive responses to the current rising temperatures.

Functional specialization of social and asocial learnings in *Drosophila melanogaster*

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Social and asocial learnings are required to cope with the complexity of the environment. They are behaviourally distinct. However, whether they use a single (general-purpose) or distinct (special-purpose) cognitive mechanisms remains elusive. A general-purpose mechanism comprises a single set of genes regulating the same biochemical pathways and neural circuits, while a special-purpose mechanism comprises two sets of genes, possibly affecting different biochemical pathways and/or neural circuits. To address this question, we firstly tested social and asocial learning abilities in 40 lines of the DGRP, a panel of several isogenic sequenced lines that together represent the genetic variation of a natural *Drosophila* population. For asocial learning, individual flies had to learn to avoid an oviposition-site where they associated an odour (conditioned stimulus, CS) with a bitter taste (unconditioned stimulus, US). For social learning, flies had to learn the oviposition-site choice of a group of conspecifics previously exposed to the CS and the US. Secondly, we performed a Genome-Wide Association Study – a statistical correlation between the genetic variants in the DGRP and each learning phenotype. We obtained two completely different sets of candidate genes for social and asocial learnings. Thirdly, to functionally validate the role of each gene on each learning phenotype, we used GAL4/RNAi-UAS lines to knockdown the genes. We found genes that affect both learnings and also cases of specialization. This is the first experimental evidence supporting the special-purpose cognitive mechanism hypothesis. Future work should focus on the extent of this specialization, concerning the biochemical pathways and the neural circuitry.

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Population structure of Brittany provides new insights on the introduction of steppe ancestry in Western Europe

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Present-day France lies at the confluence of the three migration waves that mostly contributed to the genetic ancestry of modern Europeans. However, little is known about the interaction between such population movements at their edge and how this process gave rise to modern population structure.

To fill in this gap, we generated ~850 high-coverage whole-genomes together with genome-wide data for >3,000 present-day individuals from the northern half of France and incorporated them into a panel containing 100s of publicly available modern and ancient Europe-wide samples. We also present, for the first time, ancient DNA from six Medieval individuals (300-1100 CE) from Western France to gain insights into the genetic impact of what is commonly known as the Migration Period in Europe. We document extensive fine-scale population structure in Northwestern France and an overall increased population differentiation between the northern and southern sides of the river Loire accompanied by different proportions of steppe and Neolithic-related ancestries. Samples from Western Brittany show the largest levels of steppe ancestry and high levels of allele sharing with Bell Beakers-associated individuals, which are only comparable with those found in other populations lying on the northwestern edges of Europe. Together, our analysis implies that modern-day samples from Western Brittany retain, to a larger extent, the legacy of the important genetic changes that followed the arrival of people associated with the Bell Beaker complex from north-central Europe ~2500 BCE, which reflect in their genetic proximity and the sharing of disease-related alleles with other present-day Western Britons and Irish.

Phylogenetic relationships and selective constraints in the visual pigments of the *Astyanax mexicanus* (Characiformes, Characidae) cavefish and surface populations

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Vision system in troglotic organisms is an outstanding topic in evolutionary biology. The cavefish characid *Astyanax mexicanus* has been a model to address evolutionary questions regarding the visual function and the selective pressures that have evolved the differentiated morphology of cave forms relative to their surface congeners. The dim-light visual pigment rhodopsin, located in the rod photoreceptors, has been subject to numerous studies concerning vision in dark environments, such as caves. However, it was not until recently that the cone opsins and other pigments related with the visual function have acquired relevance in the evolutionary studies of cavefish species. In this study we reconstruct the phylogeny and analyze the influence of selective pressures on the visual and non-visual opsins in cave and surface populations of *Astyanax mexicanus* through the analysis of Next Generation Sequencing data. Therefore, 36 visual and non-visual opsins were obtained from whole genome sequences (WGS) of 22 cave and surface populations. We found evidence of relaxed selective constraints in cave forms in comparison with surface populations for most of the opsins. Furthermore, we also identified several putative “Lost of Function” (Lof) mutations in the protein-codifying genomic regions for some of the cave populations that are not present in the opsins of surface individuals. Our study reveals the differentiated action of selection on the visual pigments of cave and surface populations of this species.

evALLution: translating evolution into touch, making evolution accessible for people with blindness

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39 million people have blindness worldwide and additional 246 million have impaired vision. Amounting to the difficulties deriving from sensory disability, people with blindness face socio-economic inequity and have limited access to education, a trend that is aggravated for scientific and natural history knowledge. The under-representation of people with visual impairment in the evolution research community is deeply connected with the vision-based communication of evolutionary biology and the accompanying lack of multisensory alternatives for learning. We developed an outreach project including, and dedicated to, people with blindness: evALLution. Based on an immersive and multisensory tree of life, we developed multiple haptic activities for the 20 taxa represented, including classical models for evolution research: bird beak morphology, butterfly camouflage, stickleback armor, cichlid adaptive radiations... Recurring mainly to touch and auditory narration, we were able to instruct and test participants from a wide range of ages on the basic evolution concepts of adaptation, natural selection, common ancestry and extinction. Our activities thus far have shown that regardless of age, education level and type of blindness, participants can successfully comprehend and predict evolutionary change. All it takes is creative investment in translating evolution knowledge into multisensory approaches. In a time when we strive for a more diverse and inclusive world and research community, it is imperative to gather our collective creativity to bring down any ableist barriers that obstruct anyone's access to biodiversity and evolutionary biology. We will share our process and what we have learned along the way.

Abstract of Poster presentations

Poster P1 Session 1, Room 1

The genomics of divergence and hybridization in South European hares

[Souto, J](#) (1,2,3); [Marques, JP](#) (1,2,3); [Farelo, L](#) (1,3); [Alves, PC](#) (1,2,3); [Boursot, P](#) (4); [Melo-Ferreira, J](#) (1,2,3)

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Hybridization leading to genetic exchanges between species is a ubiquitous evolutionary process that impacts the evolutionary trajectories of species since the split from a common ancestor. Characterizing patterns of genomic divergence and introgression between species, and the selective and demographic processes underlying the genetic exchanges, provide important insights on fundamental evolutionary mechanisms. It allows, for example, understanding how the genomes of the diverging entities become isolated (speciation), or the adaptive impact of interspecific genetic exchanges. Here, we will address these relevant evolutionary questions studying the process of divergence between two hare species from Europe: the broom hare (*Lepus castroviejoii*), distributed in the Cantabrian Mountains in Northern Spain, and the Italian hare (*L. corsicanus*), present in Central and Southern Italy, Sicily and introduced in Corsica. These species are the result of a recent split from a common ancestor and occupy geographic areas with environmental similarities in the Iberian and Italian Peninsulas. Both show evidence of ancient introgression from an arctic/boreal hare, the mountain hare (*L. timidus*) currently distributed in northern Eurasia and the Alps. Moreover, the broom hare possibly also hybridized with its current neighbouring species in the Iberian Peninsula. We will use this system and whole genome sequencing data to characterize and model the process of divergence between the sister broom and Italian hares, and infer the dynamics of ancient and possibly current hybridization affecting the species. These hybridization events resulted from complex dynamics of transient and novel contacts among south European hare species during the post-glacial environmental changes, which we will reconstruct. This work will allow understanding the relative importance of demographic and selective events shaping the divergence and genetic exchanges among species.

Poster P2 Session 1, Room 1

The impact of introgression during species replacements promoted by climate change

Juliana Alves (1,2,3), Liliana Farelo (1,2,3), Paulo C. Alves (1,2,3), Andrew Kitchener (4), Dolores Gavier-Widén (5), João Pimenta (1,2,3), José Melo-Ferreira (1,2,3)

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Anthropogenic changes in climate and habitats pose important challenges to biodiversity, forcing species to move or risk extinction unless they are able to adapt to the new environments. Among the most striking impacts of climate change are the important shifts of the distribution of species, such as retractions or fragmentations of vulnerable species or expansions of favoured ones. This is particularly relevant when species are invading the range of retracting close relatives and they hybridize. Introgressive hybridization may endanger the survival of species, introducing maladaptive variation, but may also create opportunities for adaptation, if the introgressed variation increase their adaptive potential in the new environmental settings. Quantifying the impact of introgressive hybridization in the interspecific dynamics of species facing climate change is therefore of utmost importance. Here, we investigate the genetic interaction between *Lepus timidus* (mountain hare), a retracting arctic/boreal species well adapted to cold environments, and *Lepus europaeus* (brown hare), an invading temperate species, in two contact areas, in Sweden and Scotland, where an invasion-retraction dynamics between the species is known. By using genome-wide single nucleotide polymorphism data from both species, we will characterize the patterns of genetic structure and genetic diversity on the two focal areas, inspect historical and contemporaneous patterns of hybridization during the range replacement, and model the demographic dynamics of the interacting species.

Poster P3 Session 1, Room 1

Finding lineage-specific regions: A comparison between the genomes of human and chimpanzee

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Repetitive sequences are frequent in vertebrate genomes. Both transposable elements and structural variation can leave a footprint of high repetitiveness in the genome. Their complement, high-complexity and transposon-free regions have long been associated with developmental genes, like the Hox cluster.

High-complexity regions can be identified by their dissimilarity to other genomic regions. We calculate the genome complexity of the human genome using the published program macle, and identify all unique regions, showing that these regions are strongly enriched for genes involved in neuron differentiation and morphogenesis processes. We further estimate that duplications older than 120 Million years have diverged to the point of being considered unique.

We expand this dissimilarity search to compare pairs of genomes and look for functionally significant lineage-specific regions (LSR) between the human and chimpanzee genomes.

Poster P4 Session 1, Room 1**Population genomics and inbreeding inference of Bermuda petrel****Afonso, RO (1); Madeiros, J (2); Campioni, L (3) Pina Martins, F (1), Silva, MC (1)**

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Pterodroma cahow, also known as Bermuda petrel, is an endangered seabird species, endemic to the Bermuda Islands. The settling of colonizers in the islands in the 17th century caused a drastic decline on this species to the point that was thought as extinct. Surprisingly, in 1951, a few pairs were found breeding in a few remote islets, which brought up an ambitious conservation programme, that has led to an incredible recovery until the present day. The approach embraced in cahow's recovery in the last years enabled the gathering of such ecology data considered very rare among wild populations and more commonly on captive ones. This project aims to bring a deeper knowledge on the Bermuda petrel through a genetic approach, comprising a high throughput sequencing technique (ddRAD-seq) and further bioinformatic tools. The main goals are to estimate cahow's genomic diversity and compare it to other sister taxa; estimate levels of inbreeding and relatedness and test its putative impact on the hatching success of the last few years; find genomic signatures of its demographic history, which is presumed to rely on a period of high diversity and abundance of individuals until an intense genetic bottleneck followed by an ongoing expansion. Also, this project intends to learn about the dynamic between drift and selection through sequencing and analysis of two immune system genes (TLRs), described as being under selection in many avian species.

Poster P5 Session 1, Room 2

Genomic dynamics of virulence and antibiotic resistance in bacterial genomes

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Antibiotics have become a serious threat to human, animal, and ecosystem health. Their overuse has had a serious impact on bacteria and has led to an alarming increase in antibiotic resistance which is particularly worrying in the case of pathogenic bacteria. The exposure to antibiotics is a driver of bacterial genome evolution, and as such, the genomic location of the resistome and the virulome may have a critical role on this dynamic. Recent works have demonstrated that there is a positive correlation between antibiotic resistance and virulence in microbial communities' metagenomes. In this work we aimed at evaluating the co-occurrence of antibiotic resistance, and virulence factor genes in the same genomic location in a dataset composed of 16632 bacterial complete reference genomes (from RefSeq). For that we have searched for all the gene orthologues to the Resfinder and MUSTARD antibiotic resistance (ARs), and the VFDB virulence factor (VFs) databases, and assigned them a genomic location: either on plasmids or on chromosomes. We concluded that an additional category of genomic element should be considered for those antibiotic resistance and virulence factor encoding genes that are present in both plasmids and chromosomes of the same bacterial genome, which may correspond to mobile genomic elements, such as Integrative and Conjugative Elements (ICE). Our results show that ICEs are enriched with ARs while VFs are preferentially located in chromosomes. We also show the distribution of the different categories of each ARs and VFs, and co-occurrences per genomic element.

Poster P6 Session 1, Room 2

Gut mélange à trois: fluctuating selection modulated by microbiota, host immune system, and antibiotics**Barreto, HC (1); Abreu, B (1); Gordo, I (1)**

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Iron is critical in host-microbe interactions, and its availability is under tight regulation in the mammalian gut. Antibiotics and inflammation are known to perturb iron availability in the gut, which could subsequently alter host-microbe interactions. Here, we show that an adaptive allele of *iscR*, encoding a major regulator of iron homeostasis of *Escherichia coli*, is under fluctuating selection in the mouse gut. In vivo competitions in immune-competent, immune-compromised, and germ-free mice reveal that the selective pressure on an *iscR* mutant *E. coli* is modulated by the presence of antibiotics, other members of the microbiota, and the immune system. Ex vivo assays show that iron availability is an important mediator of the *iscR* allele fitness benefits or costs. We identify Lipocalin-2, a host's innate immune system protein that prevents bacterial iron acquisition, as a major host mechanism underlying fluctuating selection of the *iscR* allele. Our results provide a remarkable example of strong fluctuating selection acting on bacterial iron regulation in the mammalian gut.

Poster P7 Session 1, Room 2**Addressing challenging evolutionary concepts through memes and integrative activities: An approach from interviews to secondary teachers in Granada (Spain)****Martín-Peciña, M (1,2); Rams, S (2)**

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Evolutionary Biology is a fundamental discipline that explains the evolution of all organisms in the planet. Despite this essential assignment, teaching Biological Evolution is not free of obstacles and several pedagogical difficulties of diverse origin has been reported in the literature regarding this discipline. In that respect, we have interviewed six pre-service and three in-service teachers of secondary education from Granada (Spain) to look into their perceptions about teaching difficulties when dealing with Evolutionary Biology. Interestingly, we found that pre-service teachers observe a higher number of difficulties than in-service teachers related to teaching-learning processes associated with Evolutionary Biology. However, both groups of teachers agree on the kind of difficulties detected: the teleological thinking, substitution of species, the concept of population, an anthropocentric view of Biological Evolution and the nature of science. These obstacles for the understanding of Evolutionary Biology were detected when teachers referred to the students more than to themselves. With this in mind, we designed a sequence of activities for the 4th year of the secondary education in order to address misconceptions about Biological Evolution. These activities start from a reflective discussion around memes as a playful thread and continue with cross-curricular activities to consider the integrative nature of Evolutionary Biology as a way to reinforce a meaningful knowledge of the discipline.

Poster P8 Session 1, Room 2

In-depth, whole-genome single cell evolution of relapsing colorectal cancer liver metastasis

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Despite significant improvements in metastatic colorectal cancer (mCRC) survival, tumor recurrence remains a critical clinical concern, as most patients will relapse within a short time period, primarily in the liver. While the high genetic heterogeneity, often observed in mCRC tumors, is expected to contribute to the observed variation in therapeutic response and patient survival, our current understanding of the mechanisms that metastatic cells use to resist treatment is so far limited. Importantly, unlike conventional sequencing strategies of bulk tumor samples - which collectively average the genomic information stemming from highly heterogeneous clonal populations -, single-cell DNA sequencing technologies currently enable the identification of specific malignant cell lineages that would be impossible to distinguish otherwise. As such, here we use heterochronous single-cell DNA sequencing data to identify specific malignant cell lineage/s responsible for the relapse in a mCRC patient with recurrent hepatic metastasis. By leveraging a robust Bayesian phylogenetic approach with sophisticated molecular profiling methods, we explored (i) *the evolutionary history of metastatic spread*, (ii) *the timing and clonality of cancer progression* and (iii) somatic variants and molecular patterns potentially contributing to the acquisition of therapeutic resistance.

Poster P9 Session 1, Room 3

Host-virus-viophage symbiotic interactions altered by antiviral exposure**del Arco, A (1); Fischer, M (2); Becks, L (1)**

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Species interactions shape population dynamics and community diversity. Such interactions are not fixed, but lay along a parasitic-mutualistic continuum where cost and benefits change by the interplay of ecological and evolutionary processes. In addition, species interactions might be disrupted by chemical exposures derived from anthropic activities, which in microbial communities can result in rapid evolutionary changes relevant at ecological time scales. Here, we use a marine heterotrophic flagellate to test host, virus and viroplage trait changes under antiviral exposures (oseltamivir of 0.1 mg/L of oseltamivir what is with Predicted No Effect Concentrations (PNEC)). Communities were established in chemostats for 50 days (~100 host generations) under three antiviral treatments: control, no exposure; pulse, one pulse of 0.1 mg/L; and, disturbed, one pulse of 0.1 mg/L every day. Host, virus and viroplage population dynamics and species ratio changed depending on antiviral exposure. Host population traits diversified from ancestor populations, It suggests they evolved during the experiment. Specifically, host survived virus infections, interestingly, especially host clones coming from the disturbed treatments where virus pressure was expected to be lower due to antiviral exposure. Virus and viroplage trait changes are still under study. To conclude, we show host diversification from ancestral populations influenced by antiviral pressures.

Poster P11 Session 1, Room 3

Geographic dispersion of Zika virus: a phylodynamic approach

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Zika virus (ZIKV), a mosquito-borne virus of the Flaviviridae family that induces microcephaly in newborns, caused a public health emergency of international concern in 2016 due to its rapid spread in the Americas. Although the overall number of ZIKV-related cases has declined sharply after 2016, the virus might still be circulating unnoticed. The virus was first isolated in 1947 in non-human primates in Africa and the first suggestion of inter-human transmission came from its detection in the antropophilic mosquito, *Aedes aegypti*, in 1966, in South-East Asia. The first reported outbreaks occurred in the Pacific islands of Micronesia in 2007. In 2013, in French Polynesia, an outbreak was associated with increased congenital and neurological syndromes, from where it radiated to the Americas. Following the American outbreaks, intensified surveillance efforts provided an opportunity to understand the patterns of genetic diversity, evolution and spread of ZIKV. We analyzed a curated dataset of 505 publicly available full-length coding region sequences with associated metadata that included geographical origin and collection date. Maximum likelihood tree reconstruction showed two main genetic clusters that separated the African from non-African sequences. We further examined the non-African (previously denominated “Asian”) cluster with a Bayesian model-based hierarchical clustering approach and identified substructures within it. We reported a genetic distance between Pre-American and American lineages of 5 %, while the distance between American subgroups was limited to ~0.5 %. This reduced genetic distance is expected from a very recent diversification. Ancestral character reconstruction indicated a spread from South-East Asia to Polynesia and from there reaching South America, particularly Brazil. Subsequently, multiple diversification events occurred in other South-Central American and Caribbean countries, giving rise to the North American cluster. The large number of low-frequency mutations that were detected in sequences originating from epidemic regions and that are distributed homogeneously across the genome, agrees with a demographic expansion scenario. We detected nine sites with evidence of positive selection that also harbored increased frequencies of alternative amino

acids in particular clades, for example, the non-African clade, the Central American clade and the Caribbean/North American clade. When restricting the detection of selection to the period of the earlier expansion of ZIKV in the Americas, we were able to identify another two sites with evidence of selection. We were unable to find evidence of recombination within ZIKV. The genetic subgroups that we identified in this study are the basis for a proposal of a new nomenclature that will constitute a helpful framework for future studies on ZIKV genomic variation.

Poster P12 Session 1, Room 4**Mapping the Stars – Geographic and Bathymetric Distribution of the Asteroidea****Carter, HF (1,2); Bribiesca-Contreras, G (1); Williams, S (1)**

(1) (NHM – Natural History Museum, London, UK; UCL – University College London, UK)

A latitudinal diversity gradient in species richness is one of the most consistently recognised patterns across a wide variety of terrestrial and aquatic habitats, but diversity patterns in the deep ocean (>200m) have rarely been investigated. Here, we have compiled and analysed a dataset of more than 250,000 coordinate records spanning the entirety of the world's oceans and covering the full taxonomic diversity of the Asteroidea, an entire class of charismatic marine invertebrates. We find evidence for a latitudinal gradient in diversity in shallow (0-200m) waters of both the Northern and Southern hemispheres, but diverging patterns of latitudinal species richness between the hemispheres with depth. The abyssal fauna (2000-6000m) is dominated by largely cosmopolitan species, with peaks in northern temperate and Antarctic/sub-Antarctic waters. We have used measurements of sea-floor environmental variables to investigate potential contributory factors shaping these observed patterns. We have also compiled a secondary database, containing geographic and bathymetric range and substrate preference for ~99% of currently described taxa and used this in combination with our coordinate dataset to analyse for the first time the interrelationships between global regional assemblages in this group. We identify the Philippines and the Caribbean as hotspots of global diversity, with high regional diversity around the Antarctic Peninsula and along the chain of the Aleutians. Finally, we produce the first global bathymetric overview of the Asteroidea and show that most families are shallow tropical specialists with deep sea diversity dominated by a highly restricted set of specialised families.

Poster P13 Session 1, Room 4**Large-scale evolution of body temperatures in land vertebrates****Moreira, MO (1,2); Qu, Y-F (2,3); Wiens, JJ (2,4)**

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Body temperature is a crucial variable in animals that affects nearly every aspect of their lives. Here we analyze for the first time largescale patterns in the evolution of body temperatures across terrestrial vertebrates (tetrapods: including amphibians, mammals, birds and other reptiles). Despite the traditional view that endotherms (birds and mammals) have higher body temperatures than ectotherms, we find they are not significantly different. However, rates of body-temperature evolution are significantly different, with lower rates in endotherms than ectotherms, and the highest rates in amphibians. We find that body temperatures show strong phylogenetic signal and conservatism over 350 million years of evolutionary history in tetrapods, and some lineages appear to have retained similar body temperatures over time for hundreds of millions of years. Although body temperatures are often unrelated to climate in tetrapods, we find that body temperatures are significantly related to day-night activity patterns. Specifically, body temperatures are generally higher in diurnal species than nocturnal species, both across ectotherms and, surprisingly, across endotherms also. Overall, our results suggest that body temperatures are significantly linked to phylogeny and diel-activity patterns within and among tetrapod groups, rather than just climate and the endotherm-ectotherm divide.

Poster P15 Session 1, Room 5

How deleterious mutations and migration can shape the genome of haplodiploids

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Genomic scans of differentiation are widely used to detect outliers potentially under divergent selection. However, the effect of removing deleterious mutations can confound these analyses. In addition, work done on migration and its effects on deleterious mutations are scarce while works measuring the effects of deleterious mutations on the genome focus on diploid autosomes, excluding for example haplodiploid populations. To quantify this effect, we model migration and deleterious mutations, using stochastic simulations of 100Kb chromosomes with SLiM. We compare genetic differentiation patterns in sex-limited hemizygous chromosomes (e.g. X/Z sex-chromosomes or haplodiploid autosomes) with diploid autosomes. Our results predict that background selection (BGS) increases differentiation, but this effect vanishes with increasing migration rates. For recessive and slightly deleterious mutations, we predict diploid chromosomes to be affected by associative overdominance (AOD) at low recombining regions, creating valleys of differentiation while maintaining diversity. Interestingly, such results were also found in hemizygous chromosomes but at a much narrower range of the parameter space. In addition, we report on the transition zone between AOD and BGS, which depends on the dominance of deleterious mutations and is influenced by the hemizygosity of the genome, with haplodiploids presenting the transition much sooner than diploids.

Our results indicate that AOD can exist in haplodiploids, contrary to our initial thoughts, and that migration has an impact on the differentiation between populations, eroding the peaks produced by BGS while also lowering the effects of AOD albeit at a much slower rate.

Poster P16 Session 1, Room 5

Introducing clumps: input tree-to-supertree distance-based partitioning of sets of partially overlapping phylogenetic trees

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Post-processing of trees often focuses on (multi)sets of phylogenetic trees on the same leaf set, which can be summarised or investigated using a variety of consensus and clustering methods. One post-processing method identifies islands of trees, the disconnected components of a graph where vertices are trees and edges connect sufficiently similar trees. This approach cannot be easily extended to (multi)sets of trees with partially overlapping leaf sets, such as those generated for phylogenomic studies, due to the confounding effects introduced by small trees (with small distances to potentially disparate larger trees) and by pairs of trees with insufficiently overlapping leaf sets. In an attempt to identify informative clusters of trees with partially overlapping leaf sets, we define a new subsetting approach that successively extracts subsets we term “clumps” from a set of trees. Clumping overcomes the problem of undefined distances between insufficiently overlapping input trees, by instead measuring the distances of the trees to a supertree computed for the as yet unclumped input trees. Clumps are those trees that are sufficiently similar to the supertree, with the supertree recalculated for the remaining trees after each round of clumping. Weighting is used to obviate problems otherwise caused by small input trees. While clumps were developed with the goal of minimising the negative effects introduced by small trees and avoiding comparisons of trees with non-overlapping leaf sets, they can be applied to (multi)sets of trees with identical taxonomic sampling. Time permitting we will introduce the concept of clumps, an analytical pipeline and an empirical example of clumping.

Poster P17 Session 1, Room 5

Inferring sex-biased admixture processes in human populations with Approximate Bayesian Computation: the case of Atlantic Slave Trade admixture in Cabo Verde and São Tomé e Príncipe.

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Recently admixed populations provide unique opportunities to understand how complex admixture processes influence genetic diversity. Since the 15th century, admixture triggered by European colonization and the Atlantic Slave Trade (AST) has been marked by sex-specific demographic processes leaving a peculiar signature along the genome. According to historical sources, much more males than females were forcibly displaced from Africa during the AST. However, population genetics studies revealed a strong sex-bias towards unions between African females and European males. In the patriarchal colonial context, enslaved and non-enslaved people formed two almost isolated communities, but unions between enslaved females and non-enslaved males were more likely tolerated. For this reason, the specific history of socio-cultural constraints on mating at play during admixture has strongly influenced genetic diversity of Afro-descendant populations.

We aim at reconstructing complex sex-specific admixture histories on the archipelagos of Cabo Verde and São Tomé e Príncipe, two of the earliest European peopling colonies in Sub-Saharan Africa and commercial platforms crucial to the history of AST. Both the archipelagos were not inhabited when the Portuguese first settled the islands in the 15th century. Portuguese settlers then intensified the peopling with enslaved Africans and tolerated the formation of a biologically and culturally admixed society. Although similar, the colonisation history of both archipelagos markedly differed, influencing processes of genetic admixture and the formation of creole cultures. We genotyped more than 2.5 million Single Nucleotide Polymorphisms (SNP) on autosomes, X-chromosome, NRY-chromosome and mitochondrial DNA from 350 individuals sampled on the main inhabited islands of both archipelagos.

We propose a novel method and accompanying computational and bioinformatics tools to infer, from autosomal and sex-specific genetic data, the complex sex-specific admixture history of admixed populations using Approximate Bayesian Computation (ABC). The recently developed software package MetHis, together with existing Machine Learning algorithms, allows for ABC inference of complex admixture histories based on explicit simulation of diploid (autosomal) genetic data under random mating. The aim of our project is to implement a sex-specific version of the MetHis software allowing for the joint simulation of diploid, haplo-diploid (X-chromosome), and haploid (NRY-chromosome, mtDNA) data under explicitly parameterized non-random mating. After in silico benchmarking of our method, will be able to disentangle female and male demographic processes during admixture in Cabo Verde and São Tomé e Príncipe to formally test which sex-specific admixture history best explains the observed genetic diversity in either archipelagos.

Poster P18 Session 1, Room 5

De novo assembly can help us deal with the lack of reference genomes to infer the demographic history of non-model species

Henrique, M (1); Tournebize, R (1); Lainé, H (1); Mourato, B (1, 2); Sgarlata, GM (1); Arredondo, A (2, 3); Rodríguez, W (2, 4); Sousa, AGG (1); Lilue, J (1); Boitard, S (5); Mazet, O (2,3); Chikhi, L (1, 6)

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Reconstructing the demographic history of species has an enormous importance for evolutionary and conservation biologists. The pairwise sequentially Markovian coalescent (PSMC) of Li and Durbin [1] uses the distribution of heterozygous sites along the genome of a single diploid individual to reconstruct the population demographic history. However, it also requires the use of a reference genome, which is mostly unavailable for non-model species. This causes people to use reference genomes from other species, which can introduce a bias when calling SNPs and lead to spurious results [2]. In this study, we assess the impact of the reference divergence by using high-quality reference genomes from increasingly divergent species. We first infer a human PSMC, using reference genomes from human, chimpanzee, a Western lowland gorilla, a Sumatran orangutan, a Northern white-cheeked gibbon, and a rhesus macaque. To further investigate the impact of the reference divergence, we compared the PSMCs inferred for each of these primates using as reference both its conspecific and the other primates' references assemblies. Results suggest that the divergence of the reference generate biases on the demographic inference. While we were able to recover a similar shape using the closer species as reference, the PSMC curves tended to be shifted towards the recent past and lower effective sizes, with increasingly divergent references showing a bigger shift or a drastic change of the curve shape. We also wanted to investigate whether using a de novo assembly from the target non-model species as reference would be a better approach compared to the use of a high-quality reference from a closely related species. To assess the impact of the quality of the reference on the PSMC, we generated de novo assemblies for the Chimpanzee and the Gray mouse lemur, we then compared the PSMC inferred using these as references versus using the high-quality reference genome for the same species. Results indicate that using a short read de novo assembly as reference, produces a very close demographic inference as the one obtained using a high-quality reference genome. Results also suggest that a de novo assembly might lead to a more accurate inference than the one obtained using a high-quality reference genome from a close species. This approach can be a valuable tool to infer the PSMC for species for which there are no high-quality reference genomes available.

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Poster P19 Session 2, Room 1

Real-time adaptation to evolutionary novel toxins in an insect herbivore

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Plants in the genus *Erysimum* (Brassicaceae) have gained the ability to produce cardenolides in addition to the conserved glucosinolate defences of all Brassicaceae. Cardenolides are a class of potent toxins that are functionally and biosynthetically unrelated to glucosinolates. Consistent with a co-evolutionary escape by the plant, several glucosinolate-adapted herbivore species no longer accept *Erysimum* as host plant. While some herbivores still feed on *Erysimum*, there appears to have been no evolution of specific resistance to cardenolides in any *Erysimum* herbivore. To study the consequences of phytochemical novelty and diversification for herbivore resistance, we expose a lepidopteran insect (*Plutella xylostella*) - with partial susceptibility to cardenolides - to strong selective pressures, and aim to observe the evolution of cardenolide resistance in action. Genomic responses to selection will be assessed using whole genome sequencing of pooled individuals. Candidate loci contributing to cardenolide resistance will be validated using CRISPR/Cas9 genome-edited *Plutella xylostella* reference lines on artificial 'cardenolide' diets.

Poster P20 Session 2, Room 1

The impact of gene flow in experimental evolving populations of *Tetranychus urticae* adapting to cadmium: a phenotypic and genomics approach

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From Fisher's characterization of adaptation in 1930, until now with the genomics era, understanding adaptation has been a topic under active research. In many taxa, there is evidence of local adaptation to different environments across the species range. Yet, little is known about how populations can adapt to new environments leading to local adaptation, especially when there is potential for gene flow. Theoretical studies predict that advantageous alleles in a given local environment can be lost due to gene flow, preventing adaptation. At the same time, other studies have shown that gene flow can bring new alleles that speed up local adaptation. To fulfil this knowledge gap, one can use experimental evolution, since it provides the possibility to control different selective pressures exerted in all replicated populations which in turn helps disentangle the impact of drift, migration and selection. More recently it was possible to combine Experimental Evolution with next-generation sequencing (NGS) and sequencing whole genomes of pools of individuals (PoolSeq), allowing to obtain estimates of allele frequencies at multiple SNPs for several replicated populations at different time points (Evolve and reseq). Therefore, I aim to tackle how populations can adapt to new environments by studying phenotypic and genomic changes through time in experimental evolution populations of *Tetranychus urticae* adapting to cadmium with and without gene flow. Namely, I aim to: (1) assess if populations can adapt to cadmium by analyzing changes in life-history traits through time; (2) identify genomic regions involved in adaptation to cadmium in the absence of gene flow; (3) compare genomic patterns of diversity and differentiation in regimes with and without migration; and (4) verify if the observed genomic patterns fit theoretical predictions, by simulating populations evolving according to the conditions used in experimental evolution. Here, we will present the plan for my Master thesis, describing the data and comparisons that we will do to achieve these goals.

Poster P21 Session 2, Room 1

Evolution in sympatry did not increase avoidance of reproductive interference between closely related spider mites**Cruz, MA (1); Sousa, VC (1,2); Magalhães, S (1,2); Zélé, F (3)**

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Costly reproductive interactions between species, termed reproductive interference, have recently regained attention as being a major driver of species exclusion. Thus, it is expected that, following secondary contact, sympatric populations engaging in these interactions will evolve strategies to mitigate or avoid reproductive interference in order to persist. Here, we tested this expectation using a system comprised of two closely related spider mites, *Tetranychus urticae* and *T. cinnabarinus*, which have been shown to engage in interspecific crosses that produce mostly sterile hybrids. We allowed these species to evolve in either allopatry or sympatry for 30 generations before testing the strength of reproductive interference in the system. By comparing offspring production by each species when alone versus in the presence of heterospecifics, we confirmed that both suffer from reproductive interference. However, the response of each species to reproductive interference did not change after evolution in sympatry, indicating that spider mites were unable to avoid costly interactions. This finding has important implications for spider mite population dynamics and distribution in nature, and raises the question of whether other strategies, such as niche partitioning, can serve as alternate means of avoiding reproductive interference.

Poster P22 Session 2, Room 2

How evolution is explored in portuguese basic education textbooks

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A recent analysis of Portuguese basic education biology curricula shows that some of the fundamental key ideas of evolution are not explicitly mentioned in the mandatory essential learnings to be achieved by the students. Although not specifically mentioned, these learning goals can still be taught in these grades by the teachers. To understand how evolution is explored in these educational levels, the textbooks from “Study of the environment” (from the 1st to the 4th grade) and “Natural Sciences” (from the 5th to the 9th grade) that are most used in Portugal were analysed. This educational resource was chosen for analysis because several studies show that textbooks are one of the resources that teachers use most in their classes. Using the Framework to Assess the Coverage of biological Evolution (FACE) we analysed the text, exercises, laboratorial activities and images appearing in these books. Each book was independently analysed by two researchers that identified and coded each unit of analysis that contained a FACE evolution key idea. When distinct results were obtained for a unit of analysis, they were discussed by the researchers until consensus was reached or otherwise removed from the analysis. According to our results, the FACE categories most often found in Portuguese basic education textbooks are “Evidence for evolution”, “History of life” and “Scientific Practices”. The categories “Evolutionary processes”, “Nature of Science” and “Studying evolution” are less frequent in these textbooks. Approximately 25% of the subcategories are not addressed in any of the textbooks, showing that several key evolution ideas are still missing in these basic educational resources. Our results suggest that, although textbooks explore more evolution key ideas than those explicitly mentioned in the official curricula for basic education in Portugal, several evolution key ideas are still missing or are scarcely mentioned, highlighting the importance of being explicitly addressed in the official curricula.

Poster P23 Session 1, Room 4**Evolution of high-resolution spatial vision in the conch snail group Stromboidea****Irwin, AR (1,2); Strong, EE (3); Harper, EM (4); Williams, ST (1)**

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Members of the gastropod superfamily Stromboidea are characterised by their elaborate shell morphologies and diverse eye structures. Estimates of visual acuity from histological data suggest surprisingly fine resolution vision in the large eyes of families Rostellariidae, Seraphsidae and Strombidae. In contrast, the small eyes of Aporrhaidae, Struthiolariidae and Xenophoridae provide much coarser resolution. Due to this variation in eye types and visual capabilities, the superfamily therefore provides an excellent opportunity for eye evolution studies. To this end, we use Sanger sequencing data for three mitochondrial genes (COI, 12S and 16S) and one nuclear gene (28S) to build a robust phylogenetic framework of the superfamily. Morphological traits (including eye size, aperture size, and lens diameter) are mapped onto the phylogeny to identify key transition points in the evolution of large, camera-type eyes and further explore how visual structures vary across the group. The stromboid fossil record is excellent, which allows for the use of fossil calibrations in phylogenetic analyses, to determine when these complex eyes originated.

Poster P24 Session 2, Room 2

The Azores archipelago harbours heterogeneous honey bee populations shaped by recent human-mediated processes**Henriques, D.; Lopes, AR; Pinto, MA**

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The Azores offers a unique stage for studying the impact of human-mediated processes on the genetic composition of honey bee populations. Through beekeeping activities, humans can shape gene pools directly, by selective breeding or by mediating gene flow between geographically isolated lineages, and indirectly, by introducing novel parasites and pathogens. These processes can change dramatically and rapidly in insular populations, due to their geographical isolation and their typically small effective population sizes. Recently, we performed a genetic survey of the Azorean honey bee populations (N=474) using a combination of mtDNA and SNP markers. This survey revealed a very heterogeneous composition across the archipelago, which has been shaped by historical and contemporary human-mediated processes. The most ubiquitous haplotypes (62%) were of African ancestry (sub-lineage AIII), supporting an introduction of the Iberian honey bee *Apis mellifera iberiensis* from the north of mainland Portugal during historical times. However, a tentative breeding program in the 1980s, involving the importation of honey bee queens from a highly divergent eastern European lineage (aka lineage C), associated with the accidental arrival of the dangerous ectoparasitic mite *Varroa destructor* in 2000, led to a dramatic change in the composition of populations from Pico, Faial and Graciosa and, to a lesser extent, from Terceira, São Miguel, Flores, and especially Santa Maria. The SNP and mitochondrial data were not concordant ($r^2=0.082$). In São Miguel, most of the individuals did not show any signal of C-lineage introgression in the nuclear genome although 27% of the colonies harbored a C-lineage mitotype. Contrarily, in Terceira and São Jorge, C-lineage mitotypes were undetected, yet many individuals (84%) showed some level of nuclear introgression ($0.050=Q\text{-values}=0.181$). Graciosa, Pico, and Faial harbour the most introgressed population, as revealed by both markers, and the latter two islands are also colonized by *V. destructor*. Santa Maria harbours the best preserved population, with virtually no C-lineage introgression at both nuclear and mitochondrial compartments, and it is free of *V. destructor*. This is the first genetic study performed in the Azores, offering unique baseline data that can be used for better managing and preserving Azorean populations.

Poster P26 Session 2, Room 3

Transcriptional changes between sexes, tissues and ontogenetic stages associated with the presence of a B chromosome in the grasshopper *Eyprepocnemis plorans*

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B chromosomes are supernumerary and dispensable elements that are found in the genome of many eukaryotes in addition to the standard set of chromosomes, also known as A chromosomes. They often behave like genomic parasites for the host genome, but the true nature of this intragenomic conflict is still poorly understood. Here, we address this issue by means of a comprehensive RNA-seq experiment, comparing transcriptomes of B-carrying and B-lacking male and female embryos and adults, including legs and gonads, of the grasshopper *Eyprepocnemis plorans*. The results showed that B chromosome presence is associated with gene expression changes for a high number of A chromosome genes, in addition to those inherent to the protein-coding genes located in the B chromosome. The highest number of differentially expressed genes (DEGs) due to B presence was found in gonads (ovary= 643 DEGs, testis= 306 DEGs), followed by embryos (female= 95 DEGs, male= 130 DEGs) and finally in hind legs (female= 81 DEGs, male= 36 DEGs). Furthermore, while B-carrying embryos showed a pronounced up-regulation of transposable elements (~38% of all DEGs), gene expression changes in B-carrying adults mainly involved protein-coding genes (~50%, considering both up- and down-regulations). In particular, these changes were more apparent in the ovary with ~36% of protein-coding DEGs showing down-regulation, a figure being only ~15% in testis. Moreover, we found a slight increase of DEGs in embryos that received a maternal B in respect to embryos which inherited a paternal B chromosome. These findings outline a scene in which the B chromosome in testis, where they are eliminated postmeiotically from spermatids, triggers fewer changes in gene expression than in ovaries. Finally, the meaning of the higher transcriptional effects of B chromosome presence on the ovary could entail a response to manage the B-drive that takes place in this organ for *E. plorans*, as these chromosomes show a transmission advantage during female meiotic drive during oogenesis.

Poster P27 Session 2, Room 3

Evolutionary constrains in the tetrapod neck bauplan**Martins, R (1); Castanhinha, R (1,2)**

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The vertebral column consists of repetitive skeletal elements, organized in homologous series, the vertebrae, and is of paramount importance for evolutionary analyses. Its standardization is regulated by an extremely conserved group of Hox genes that regulate embryonic development. From over 30,000 amniote species there are almost 10,000 reptiles that present a large variation of pre-sacral vertebral count. Mammals (Synapsida) and reptiles (Sauropsida) show great divergences in the plasticity of their axial development since the beginning of tetrapod evolution. Curiously, there is still no consensus on how to define cervical vertebrae. The more common definition is topological: all vertebrae anterior to the first vertebra connected to the sternum by a complete rib. Synapsids are an extremely typical example of conservation, with 7 cervical vertebrae. Exceptions include the genera *Bradypus*, *Choloepus*, and *Trichechus*. In the case of sauropsids, they have greater plasticity, reaching up to 72 cervical vertebrae in *Elasmosaurus platyurus*. However, they also demonstrate segmental conservation in the Crocodylia and Testudinata clades, with 9 and 8 cervical vertebrae, respectively. On the other hand, in birds they range from 10 in *Nymphicus hollandicus* to 25 cervical vertebrae in *Cygnus*. There are multiple studies centered on the variation of the vertebral count as a whole or on the conserved cervical regionalization of mammals. To clarify how cervical regionalization evolved over millions of years, we conducted a comprehensive survey of pre-sacral vertebral counts focusing on intraspecific and interspecific variations in more than 400 tetrapod taxa (extinct and extant). We mapped vertebral counts into amniotic phylogeny as well as into more detailed trees within the group. This allowed to test several hypotheses regarding the relationship between the number of presacral vertebrae vs: total size, total weight, and length of the neck. We also calculated intraspecific variation in order to find patterns of variation. Finally, we used embryos from 3 model species *Gallus gallus*, *Anas platyrhincus*, and *Coturnix coturnix* to analyze the frequency with which these meristic changes occurred. Our study demonstrates a substantial variation in the number of cervical vertebrae in some species of the most diverse groups of tetrapods, suggesting the absence of strong selection against intraspecific and interspecific changes in the number of cervical vertebrae. Contrary to the initial hypothesis, the inverse relationship between intraspecific variation and increase in cervical vertebrae numbers may be explained by developmental constrains that limit the intraspecific variation in long neck species.

Poster P28 Session 2, Room 3

The Impact of Sub-Lethal Temperatures on Spider Mite Reproduction

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Due to climate change, organisms are being increasingly exposed to longer and more intense periods of heat stress, which critically affect their life-history traits. Reproduction is generally more sensitive to high temperatures than survival, although most studies focus on the latter trait. This suggests that populations will be affected by climate change earlier than predicted by current knowledge. To test the influence of temperature on reproduction, we addressed how sub-lethal high temperatures affect this trait in *Tetranychus urticae*, a haplodiploid agricultural pest of great economic importance. Although several studies have tackled the effect of temperature on this species, as well as their reproductive behaviour, few have addressed the interaction temperature – reproductive behaviour. First, we measured fertility and survival of both sexes at high temperatures, to identify the temperature that critically impairs fertility but not survival. This is seen in females by decreased fecundity and in males by reduced ratio of female offspring. Results showed that 36 °C best fits this condition, with males being more sensitive than females. Then, we measured how this temperature affected offspring paternity share, as the pattern of first male sperm precedence seen in this species may change when the first male is sterile due to temperature. Results suggest that this is the case. Moreover, females mated with sterilized males had higher remating eagerness, which led to restored offspring sex-ratio levels after they remated with fertile males. We also tested if, and how fast, sterilized males regain fertility once placed at an optimal temperature. Results indicate that there is no recovery at least after two days at an optimal temperature. This project thus provides new insights regarding the effects of climate change on reproductive traits in an important crop pest, paving the way to future studies in both sexual selection and adaptation to abiotic stresses.

Poster P30 Session 2, Room 4

Coping with anthropogenic stress: the role of gut-associated bacteria in a freshwater isopod

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Human activity is a major driver of environmental change and can act as a significant evolutionary force. Although responses of organisms to anthropogenic changes are extensively studied, most work to date does not integrate responses of host-associated microbiomes, even though they can be a key determinant of host fitness. Chemical pollutants - often introduced to streams via wastewater treatment plant effluents - are pervasive anthropogenic stressors that can affect the fate of individuals, populations, and ecosystems. We use *Asellus aquaticus*, a freshwater isopod with high environmental tolerance, to study the impact of pollution on organismal fitness and to explore the hypothesis that gut-microbiome may mediate adaptation to environmental stress. We specifically aim to understand how wastewater contaminants, including chemical compounds and microbes, affect *A. aquaticus*' performance and microbiome. Laboratory and semi-natural flume experiments revealed that chemical pollution can lead to mortality of the host at high concentrations, while more realistic concentrations affect growth and feeding rates (i.e. host performance). 16S amplicon sequencing of digestive tissues further revealed that exposure to wastewater can also alter composition of the gut microbiota. Our results provide insight into host-microbiome responses to anthropogenic change.

Poster P31 Session 2, Room 4

Mate-choice copying in fruit flies is regulated by appetitive dopaminergic neurons

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Dopamine is a neuromodulator that controls the formation of appetitive and aversive memories during the associative learning process. Mate-choice copying (MCC) is a type of associative learning during which females observe the mating interactions of other females and copy their choices. MCC is known to be regulated by dopamine but is unclear whether it depends on appetitive or aversive memories, as females can learn to copy preferences (appetitive memory) or rejections (aversive memory). As motivation is necessary for reproduction and appetitive learning increases motivation, MCC probably involves the formation of appetitive memories. To find out, we studied the role of appetitive (PAM) and aversive (PPL1) dopaminergic neurons in modulating MCC, in *Drosophila melanogaster*. We used transgenic lines to silence dopaminergic signaling in the PAM and PPL1 clusters. We compared the behaviour of transgenic with control flies. We found that PAM flies were incapable of MCC, unlike control flies. PPL1 flies also failed to learn but learned better than PAMs (although the sample size is small). This confirms that the formation of appetitive memories during MCC is certainly an adaptive mechanism. For this reason, there may be a smaller contribution from aversive memories, however, our study leaves this hypothesis still open.

Poster P32 Session 1, Room 3

The heat is on! Female mating behaviour under stress

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The changing climate, in particular the rising temperature, is one of the most alarming problems of the XXI century. This temperature rise will have a huge impact on biodiversity across the globe. Ectotherms, in particular insects, could be amongst the most affected organisms by the rising temperature, namely, due to negative repercussions on reproduction and, consequently, on population persistence. This phenomenon could be linked to sterility induced by heat stress, with strong evidence suggesting that males are more affected than females. Male sterility has a higher prevalence at high temperatures and is a major issue for the species' subsistence, especially in monandrous species, where typically only one male sire all the offspring of the female. Here we aim to understand the impact of history - different genetic backgrounds associated to the distinct bio-geographical origin of the populations - and thermal selection - different thermal selective regimes that populations are subjected to - on male sterility induced by a heat have, and consequently on the evolution of the mating system of *D. subobscura*, a monandrous species that is a model organism in evolutionary biology. To tackle these questions, we will use an experimental setup addressing the real-time evolution of two bio-geographical distinct populations subjected to a global warming scenario. We will evaluate if populations evolving in warming environment can cope better with heat stress and subsequently male sterility, by altering their mating behaviour. Specifically, we aim to test if male sterility is transient or not and posteriorly, evaluate if evolved females remate with multiple males to ensure reproductive success, and or if evolved females choose between different males according to their fertility condition. Understanding if and how monandrous species change their mating behaviour under heat stress will be key to assess how likely is population persistence.

Poster P33 Session 2, Room 4

Rapid spread of adaptive evolutionary events in social microbiomes**Frazão, N (1); Gordo, I (1)**

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Background and objectives: Social networks can influence the ecology of gut bacteria shaping the species composition of the gut microbiome in humans and other animals. Gut commensals can also evolve and adapt at a reasonable pace when colonizing healthy hosts. Here, we aimed at assessing the impact of the host's social regime on bacterial molecular evolution in the mammalian gut. Methodology: Using an in vivo experimental evolution approach, we investigated how the pattern of molecular adaptation of *Escherichia coli* colonizing the mouse gut is influenced by the host's social environment. Results: We found high transmission rates of newly colonizing *E. coli* strains in mice inhabiting the same environment, with horizontal gene transfer (HGT) events between phylogenetic distinct *E. coli* strains being pervasive under these conditions. A simple population genetics model of mutation-selection-migration predicts that, after hundreds to thousands of generations of gut adaptation, the level of parallelism of evolutionary events is greatly enhanced in co-housed mice when compared to animals living asocially. Moreover, under a social regime, evolutionary events reach global higher frequencies and can lead to swamping of locally selected evolutionary events. Conclusions and implications: The observed pattern of mutation and HGT sharing under sociality is consistent with a massive role of migration shaping the adaptive evolution of new strains that invade the gut microbiomes of healthy hosts. Strong directional selection is observed, where fixation of alleles and swamping of locally selected evolutionary events are to be expected, which may have important implications for the spread of antibiotic resistant strains across mammalian microbiomes.

Statistics

The XVII ENBE gathered 112 participants from 40 different host institutions, and from 11 different countries.

Table 1. The top 10 institutions in terms of number of participants.

<i>Institution</i>	<i>Country</i>	<i>Number of Participants</i>
<i>cE3c, University of Lisbon</i>	Portugal	23
<i>Intituto Gulbenkian de Ciência</i>	Portugal	14
<i>FCUL, University of Lisbon</i>	Portugal	10
<i>Biopolis/CIBIO, University of Porto</i>	Portugal	9
<i>Universidade de Aveiro</i>	Portugal	9
<i>Natural History Museum, London</i>	UK	4
<i>iBiMED, University of Aveiro</i>	Portugal	3
<i>Universidad de Vigo</i>	Spain	3
<i>INIAV</i>	Portugal	2
<i>FCUP, University of Porto</i>	Portugal	2



Figure 1. Distribution of the affiliation country of the participants. World map with the absolute number of participants per country.

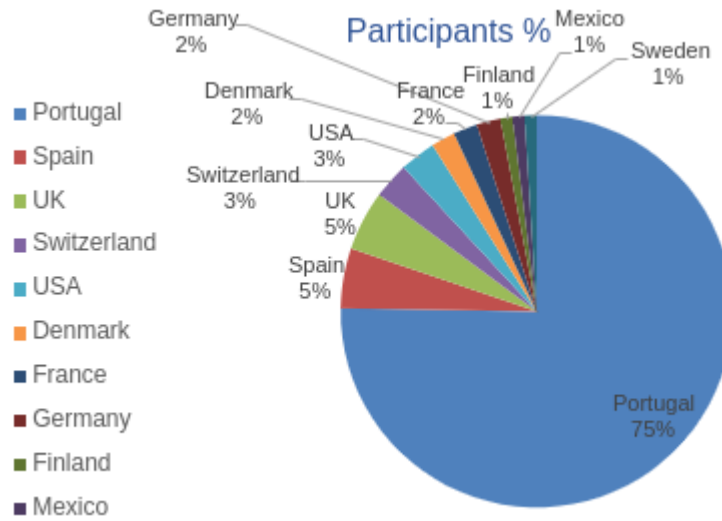


Figure 2. Distribution of the affiliation country of the participants. Percentage of participants per country.

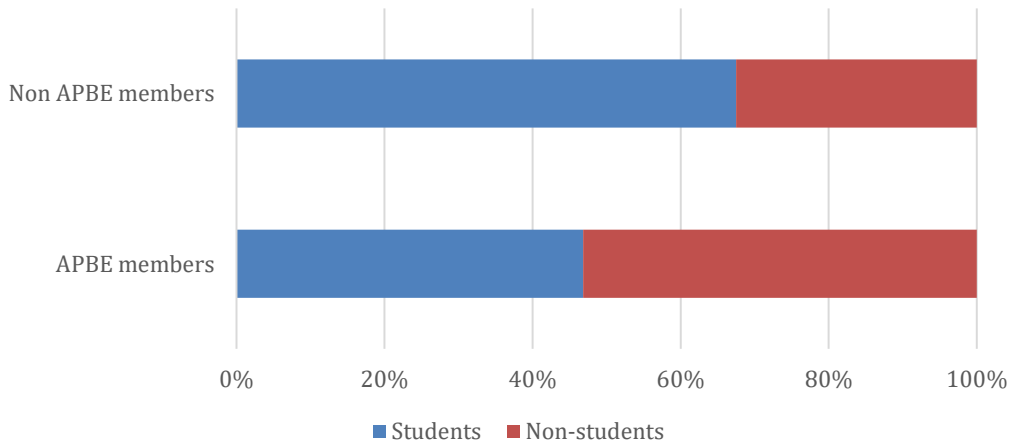


Figure 3. Percentage of participants that are students and non-students among participants which are APBE members (bottom figure) and those who are not members of the APBE (top figure).