ENBE 2025

XXI International Meeting of the Portuguese Association for Evolutionary Biology

BOOK OF ABSTRACTS

18th-19th December 2025

Bragança

ENBE 2025

XXI International Meeting of the Portuguese Association for Evolutionary Biology

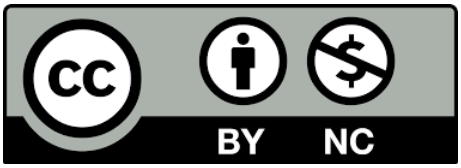
Title: Book of abstracts of the XXI International Meeting of the Portuguese Association for Evolutionary Biology

Editors: M. Alice Pinto, Ana Rita Lopes & Dora Henriques, CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal.

Published by: Instituto Politécnico de Bragança – 2025

ISBN: 978-972-745-368-9

Design: Ana Rita Lopes



ENBE 2025

XXI International Meeting of the Portuguese Association for Evolutionary Biology

18th-19th December 2025

Bragança, Portugal

Edited by

M. Alice Pinto

Dora Henriques

Ana Rita Lopes

Instituto Politécnico de Bragança, Portugal

December, 2025

Committees

Organising committee

M. Alice Pinto (CIMO, IPB, Bragança) – Chair
Ana Rita Lopes (CIMO, IPB, Bragança)
Dora Henriques (CIMO, IPB, Bragança)
Carolina Peralta (MPI-EvolBio, Germany)
Manuel Curto (CIBIO, Vairão)
Rita Ponce (ESE-IPS Setúbal, ICNOVA, Lisboa)
Susana Almeida (CCMAR, CIMAR LA, Faro)
Vitor Sousa (CE3C, FCUL, Lisboa)
Xana Sá Pinto (CIDTFF, UA, Aveiro)

Scientific committee

M. Alice Pinto (CIMO, IPB, Bragança) - chair
Ana Rita Lopes (CIMO, IPB, Bragança)
Carolina Peralta (MPI-EvolBio, Germany)
Dora Henriques (CIMO, IPB, Bragança)
Élio Sucena (ce3c, FCUL, Lisboa)
Filipe Castro (CIIMAR, UP; Porto)
Mónica Marques (CIIMAR, UP; Porto)
Patrícia Beldade (CE3C, FCUL, Lisboa)
Rita Ponce (ESE-IPS Setúbal, ICNOVA, Lisboa)
Rui Faria (CIBIO, Vairão)
Sara Magalhães (CE3C, FCUL, Lisboa)
Susana Almeida (CCMAR, CIMAR LA, Faro)
Vitor Sousa (CE3C, FCUL, Lisboa)
Xana Sá Pinto (CIDTFF, UA, Aveiro)

Student volunteers

Aicha Meliani (CIMO, IPB, Bragança)
António Pérez-Pérez (CIMO, IPB, CIAPA, Bragança)
Carlos Yadró (CIMO, IPB, Bragança)
Daniela Barbosa (CIMO, IPB, Bragança)
Fernanda Li (CIMO, IPB, Bragança)
Larissa Cunha (CIMO, IPB, Bragança)
Maíra Costa (CIMO, IPB, Bragança)

Index

Committees **5**

Welcome message **11**

Organisation **12**

Sponsors **12**

Venue **13**

Internet access **14**

Discover the Bragança region **14**

Detailed program **15**

Oral Communications **19**

TOPIC 1| GENOME ARCHITECTURE, STRUCTURAL EVOLUTION AND BIOGEOGRAPHY **20**

PLENARY TALK| THE EVOLUTION OF SEX AND RECOMBINATION – LESSONS FROM THE BEE HIVE 20

TALK 1| STRUCTURAL ORGANIZATION AND EVOLUTIONARY DYNAMICS OF HUMAN SATELLITE 1B (HSAT1B) ACROSS PRIMATE GENOMES 21

TALK 2| BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS 22

TALK 3| GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES 23

TALK 4| FCRL6 THROUGHOUT THE LINEAGES: WHAT'S THE HISTORY BEHIND THE FIRST FCRL THAT WAS DESCRIBED? 24

TALK 5| GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB 25

TALK 6| EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG 26

TOPIC 2| DOMESTICATION, POPULATION GENOMICS AND CONSERVATION **27**

TALK 7| EVIDENCE FOR TWO MAJOR DOMESTICATION EVENTS DURING THE EVOLUTIONARY HISTORY OF *SACCHAROMYCES CEREVISIAE* 27

TALK 8| UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS 28

TALK 9| INCOMPLETE LINEAGE SORTING AND THE RECURRENT EVOLUTION OF PARTHENOGENESIS IN TIMEMA STICK INSECTS 29

TALK 10| MACRO- AND MICROEVOLUTIONARY GENOMICS OF THE BLUE SHARK (*PRIONACE GLAUCA*) 30

TALK 11| SEEDLING EVOLUTION UNDERSTANDING TO PROMOTE POSITIVE ATTITUDES TOWARDS BIODIVERSITY CONSERVATION: A STUDY WITH ELEMENTARY SCHOOL STUDENTS 31

TALK 12| HARNESS THE POWER OF NGS: LATEST APPLICATIONS IN DNA AND RNA RESEARCH (NOVOGENE-GOLD SPONSOR) 32

TOPIC 3| EXPERIMENTAL EVOLUTION AND ADAPTATION 33

PLENARY TALK| THE ROLE OF HISTORY, CHANCE, AND SELECTION DURING ADAPTATION – FROM NATURE TO THE LAB 33

TALK 13| DETRIMENTAL IMPACT OF A HEATWAVE ON MALE REPRODUCTIVE BEHAVIOUR AND FERTILITY 35

TALK 14| MATERNAL EFFECTS MEDIATE THE INTERACTIVE EFFECT OF TEMPERATURE AND POPULATION STRUCTURE ON SPIDER MITE SEX RATIO AND BODY SIZE 36

TALK 15| FROM GENOMES TO "HEAT": THE MOLECULAR ORIGIN OF ADAPTATION IN DESERT MAMMALS 37

TALK 16| THE IMPORTANCE OF ENVIRONMENTAL HETEROGENEITY FOR THE GENOMIC SIGNATURE OF ADAPTATION TO CADMIUM 38

TALK 17| TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) 39

TALK 18| EXPERIMENTAL EVOLUTION IN SYMPATRY LEADS TO HIGHER GROWTH RATES, BUT DOES NOT ALLEVIATE THE COSTS OF COMPETITION AND REPRODUCTIVE INTERFERENCE 40

TALK 19| DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS 41

TOPIC 4| CO-EVOLUTION, HOST–PATHOGEN AND PARASITE EVOLUTION 42

TALK 20| VIRAL EVOLUTION IN ISOLATION: HOW VARROA INVASION SHAPED DEFORMED WING VIRUS AND LAKE SINAI VIRUS IN AZOREAN HONEYBEES 42

TALK 21| RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING? 43

TALK 22| ECO-EVOLUTIONARY DYNAMICS OF *ESCHERICHIA COLI* INVASION ACROSS HUMAN GUT MICROBIOTAS 44

TALK 23| ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS 45

TALK 24| PHYLOGENETIC INFERENCE WITH NOT-SO-RARE MUTATIONS AND WEE TINY ORGANISMS 46

TOPIC 5| HYBRIDISATION, INTROGRESSION, AND PHENOTYPIC DIVERSITY 47

PLENARY TALK| MUSEUM COLLECTIONS AS WINDOWS INTO SPECIES FORMATION AND INTROGRESSION IN A MOVING HYBRID ZONE OF BIRDS 47

TALK 25| HYBRIDIZATION AS A SOURCE OF PHENOTYPIC DIVERSITY: THE GENOMIC BASIS OF YELLOW COAT COLOUR IN IBERIAN WOLVES 48

TALK 26| HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES 49

TALK 27| THE GENOMIC AFTERMATH OF THE ICE AGES IN EUROPEAN HARES 50

TALK 28| IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS 51

TALK 29| AVIAN STRCTURAL COLORATION DIVERSITY EXPLAINED BY CHANGES IN FEATHER KERATINIZATION 52

TALK 30| MORPHOLOGICAL RESPONSES OF *MUS MUSCULUS* TO THE ENVIRONMENTAL CONDITIONS OF CABO VERDE 53

TALK 31| GENOME STORIES: HOW LOSING GENES BUILDS NEW PHENOTYPES 54

Poster Communications 55

TOPIC 1| GENOME ARCHITECTURE, STRUCTURAL EVOLUTION AND BIOGEOGRAPHY 56

POSTER 1| OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH 56

POSTER 2| PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER 57

POSTER 3| FIRST PHYLOGEOGRAPHIC ASSESSMENT OF THE DIADEMED SAND SNAKE (COLUBRIDAE: *LYTORHYNCHUS*) ACROSS THE SAHARO-ARABIAN DESERT BELT 58

POSTER 4| GENOMIC ARCHITECTURE OF SHELL COLOUR POLYMORPHISM IN *LITTORINA* MARINE SNAILS: THE ROLE OF CHROMOSOMAL INVERSIONS AND GENE FLUX 59

POSTER 5| A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME 60

TOPIC 2| DOMESTICATION, POPULATION GENOMICS AND CONSERVATION 61

POSTER 6| ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS 61

POSTER 7| HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC 63

POSTER 8| VARIATION IN GARUM RECIPES ACROSS THE ROMAN EMPIRE AND THE MICROBIAL COMMUNITIES DRIVING THEIR FERMENTATION 64

POSTER 9| METABARCODING OF MEDITERRANEAN MONK SEAL (*MONACHUS MONACHUS)* SCATS REVEALS A DIVERSE PISCIVOROUS DIET 65

POSTER 10| RECONSTRUCTING POPULATION DYNAMICS OF THE EUROPEAN SARDINE (*SARDINA PILCHARDUS*) USING PALAEOGENOMICS 66

POSTER 11| ADAPTATION AND (EPI)GENOMIC EROSION IN SMALL, ISOLATED POPULATIONS: INSIGHTS FROM THE CRITICALLY ENDANGERED APENNINE BROWN BEAR 67

POSTER 12| UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING 68

POSTER 13| EVALUATING DNA COLLECTION METHODS FOR NON-INVASIVE GENETIC MONITORING IN DESERT CONDITIONS 69

POSTER 14| THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE 70

POSTER 15| BLUEFINDB: A MULTI-MARKER, "HUMAN-IN-THE-LOOP" ARCHITECTURE FOR PRECISION eDNA REFERENCE DATABASE CURATION 71

POSTER 16| POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, *PARAMURICEA CLAVATA* IN THE PARC NATIONAL DES CALANQUES (FRANCE) 72

POSTER 17| WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 73

POSTER 18| UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S 75

TOPIC 3| EXPERIMENTAL EVOLUTION AND ADAPTATION 76

POSTER 19| PAST SELECTIVE HISTORY INFLUENCES ADAPTATION TO ORAL INFECTION IN DROSOPHILA MELANOGASTER 76

POSTER 20| THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX* 77

POSTER 21| LONG-TERM EVOLUTION EXPERIMENTS FULLY REVEAL THE POTENTIAL FOR THERMAL ADAPTATION 78

POSTER 22| ADAPT, ADJUST OR MOVE: CAN THE SPIDER MITES *TETRANYCHUS CINNABARINUS* DO IT ALL IN RESPONSE TO HEAT? 79

POSTER 23| DO MATING SYSTEMS SHAPE THERMAL FERTILITY? 80

POSTER 24| THE EGG OR THE CHICKEN? REVISITING AGLOMERULISM AND THE EMERGENCE OF ANTI-FREEZE GLYCOPROTEINS, RENAL FUNCTION, AND WATER BALANCE IN NOTOTHENIOIDS 81

POSTER 25| LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE 82

TOPIC 4| CO-EVOLUTION, HOST–PATHOGEN AND PARASITE EVOLUTION 84

POSTER 26| EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS 84

POSTER 27| PATHOGENS AGAINST THE MACHINE: EVOLUTIONARY SHIFTS OF *PHYTOPHTHORA INFESTANS* ACROSS EUROPEAN BIOREGIONS AND THEIR IMPLICATIONS FOR PREDICTIVE MODELLING 85

POSTER 28| HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL 86

POSTER 29| HOW DOES THE EVOLUTION OF DIRECT AND INDIRECT INTERACTIONS AFFECT ECOSYSTEM RESILIENCE? 87

POSTER 30| INTRA-POPULATION VARIABILITY IN A DARWINIAN SELECTION PROGRAM FOR *VARROA* RESISTANCE IN *APIS MELLIFERA IBERIENSIS* 88

POSTER 31| BENCHMARKING LAMP PRIMER DESIGN PLATFORMS FOR PYRETHROID RESISTANCE SNP DETECTION IN *VARROA DESTRUCTOR* 89

POSTER 32| NO EVIDENCE FOR A TRADE-OFF BETWEEN HOST AVOIDANCE BEHAVIOUR AND PATHOGENICITY TOWARDS ECOLOGICALLY ASSOCIATED BACTERIA IN CAENORHABDITIS ELEGANS 90

TOPIC 5| HYBRIDIZATION, INTROGRESSION, AND PHENOTYPIC DIVERSITY 91

POSTER 33| DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? 91

POSTER 34| NEW ASSESSMENTS ON GEOGRAPHIC AND SEXUAL SKULL VARIATION IN THE SUBGENUS *CHARRONIA* (*MARTES FLAVIGULA* AND *MARTES GWATKINSII*) (CARNIVORA; MUSTELIDAE) 93

POSTER 35| PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS 94

POSTER 36| EXPLORING THE CELLULAR BASIS OF VARIATION IN CRANIOFACIAL FEATURES OF CICHLID FISHES 95

POSTER 37| WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS 96

POSTER 38| HARNESSING MITOCHONDRIAL DIVERGENCE IN *APIS MELLIFERA* TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY 97

List of Authors 98

List of Participants 121

Welcome message

It is our great pleasure to welcome you to **ENBE 2025 – XXI International Meeting of the Portuguese Association for Evolutionary Biology,** held in Bragança from **18 to 19 December 2025**. This XXI edition is jointly organised by *Associação Portuguesa de Biologia Evolutiva* (APBE), *Centro de Investigação de Montanha* (CIMO), and *Instituto Politécnico de Bragança* (IPB). ENBE is a unique event where young and senior scientists share and celebrate their research achievements in Evolutionary Biology, strengthening collaborations and fostering new connections.

ENBE 2025 will bring together more than 100 participants who will contribute to a diverse scientific programme featuring 31 oral communications and 38 posters across five thematic areas: (i) genome architecture, structural evolution and biogeography; (ii) domestication, population genomics and conservation; (iii) experimental evolution and adaptation; (iv) co-evolution, host–pathogen and parasite evolution; and (v) hybridisation, introgression and phenotypic diversity. The programme will also include exciting keynote lectures from three renowned scientists: Margarida Matos (University of Lisbon, Portugal), Matthew Webster (Uppsala University, Sweden), and Ricardo Pereira (Stuttgart State Museum of Natural History, Germany).

In addition, this XXI edition will, for the first time, host a roundtable focusing on improving engagement between evolutionary biologists, science communicators, educators, and journalists. This topic will be debated by a panel of eminent contributors from the science communication, media, and education sectors.

I am confident that this will be a successful event, and this success is the result of the commitment of our keynote speakers and roundtable participants, who readily accepted our invitation, as well as our session chairs and all participants, whose dedication and enthusiasm make this meeting possible. Last but not least, I would like to express my deepest gratitude to all supporting institutions and sponsors, and especially to the organising committee, the scientific committee, and student volunteers, whose hard work and dedication were essential in bringing this event to life.

Bragança welcomes you with its beautiful historic centre, including a remarkably well-preserved castle, and a rich cultural heritage. The region is also renowned for its exceptional gastronomy. We invite you to take the opportunity to discover the flavours and traditions of the *Nordeste Transmontano*.

I wish you all an inspiring and productive conference and a Merry Christmas.

M. Alice Pinto, Chair of ENBE 2025, CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300- 253 Bragança, Portugal.

Organisation

Instituto Politécnico de Bragança (IPB)

Centro de Investigação de Montanha (CIMO)

Laboratório Associado para a Sustentabilidade e Tecnologia nas Regiões de Montanha (SUSTEC)

Associação Portuguesa de Biologia Evolutiva (APBE)

Sponsors

Gold

Novogene

STAB vida
Your easy genetics laboratory

Silver

Grupo I.L.C.

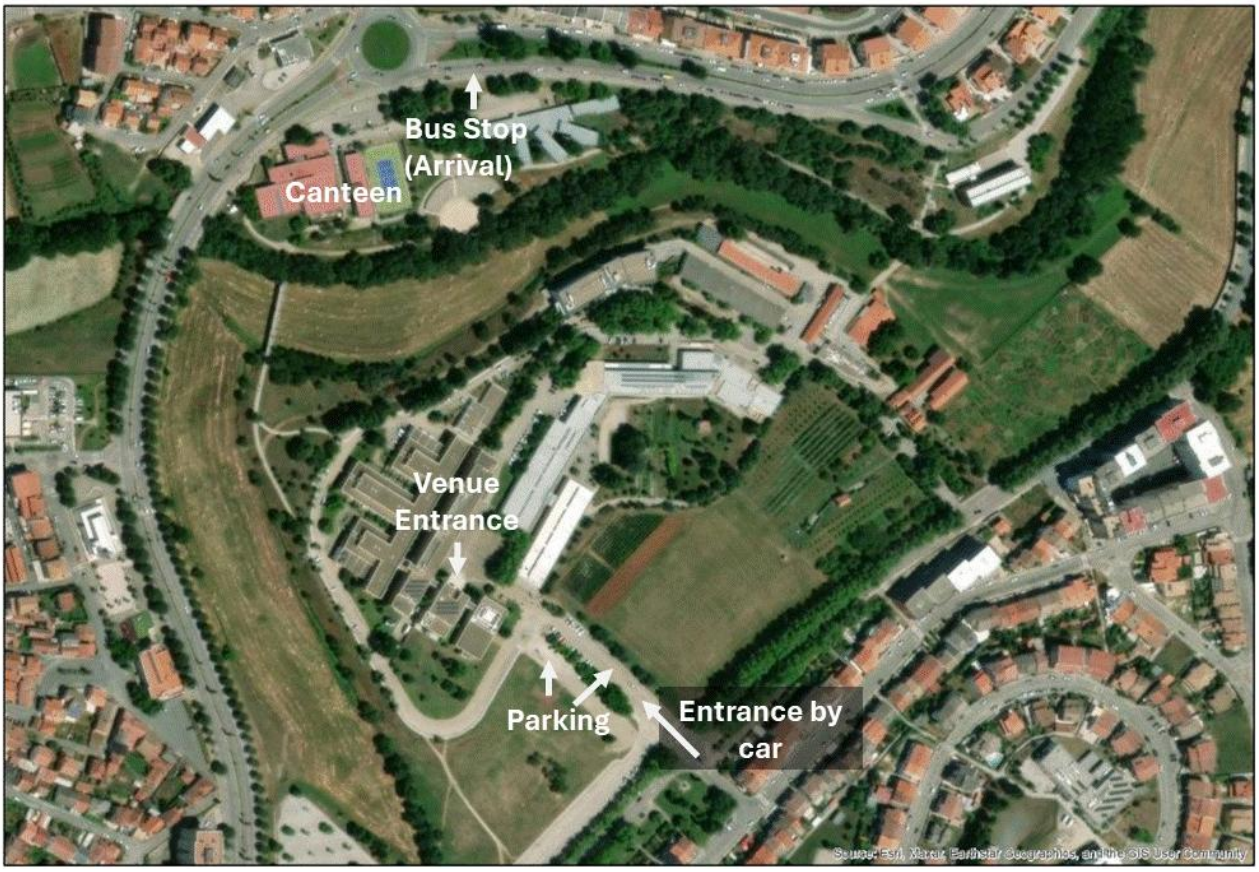
frilabo

Quilaban
uma fórmula de vida

avantor™

Venue

The ENBE 2025 takes place at the Auditorium of the Escola Superior de Tecnologia e Gestão (ESTIG), Instituto Politécnico de Bragança (IPB), Campus de Santa Apolónia, Bragança.



GPS Coordinates: 41°47'47.1"N 6°46'06.8"W

Maps Link: https://maps.app.goo.gl/sKsFrxB7XrbtprXp8

Internet access

Wireless internet is available campus-wide to participants of the conference via Eduroam.

Discover the Bragança region

The district of Bragança lies in Trás-os-Montes, in the northeast of Portugal, a region celebrated for its rich traditions, handicrafts, gastronomy, and breathtaking landscapes. It is home to the Montesinho Natural Park, the International Douro Park, and the Protected Landscape of Azibo, where visitors can enjoy stunning scenery filled with diverse flora and fauna.

Visitors can explore an ancient culture with roots that reach back to pagan times. Traditional festivities, such as the Boys' Festivity (Festa dos Rapazes), the Caretos, and the Pauliteiros War Dances, bring the region's vibrant heritage to life, accompanied by the rhythmic sounds of bagpipes. Local craftsmanship is equally remarkable, from copper, leather, and woodwork to weaving, basketry, and the famous "Caretos" masks.

Bragança is also renowned for its gastronomic delights, including the succulent "Posta à Mirandesa" (a traditional beef steak), Montesinho lamb, trout, game meats (partridge, wild boar, hare), and the delicious "Folar de Bragança", a savoury bread filled with assorted meats.

In the city of Bragança, history and culture await at every corner. Do not miss a walk around the castle, with its Watchtower, the Domus Municipalis, a unique Romanesque building found only on the Iberian Peninsula, and a visit to the Graça Morais Contemporary Art Museum.

For more information, visit: turismo.cm-braganca.pt/

Link to a video about Bragança: turismo.cm-braganca.pt/videos/video-in-english

Detailed program

DAY 1: 18th December 2025

11:00: Registration and Poster placement

13:30: Opening Ceremony

Session 1	**Chairs: Rui Faria and Susana Almeida**		
	TIME	**SPEAKER**	**TOPIC 1| Genome Architecture, Structural Evolution and Biogeography**
	14:00	Matthew Webster	**Plenary Talk|** The evolution of sex and recombination – lessons from the bee hive
	14:40	Carlos Vila-Verde	**Talk 1|** Structural organisation and evolutionary dynamics of human satellite 1b (HSAZ1b) across the primate genome
	14:52	Jorge Pereira	**Talk 2|** Bat genome evolution: karyotypic conservation and repetitive sequence dynamics
	15:04	Matthew Moreira	**Talk 3|** Global diversity patterns are explained by diversification rates and dispersal at ancient, not shallow, timescales
	15:16	Maria Carolina Matos	**Talk 4|** FCRL6 throughout the lineages: what's the history behind the first FCRL that was described?
	15:28	Mónica Lopes-Marques	**Talk 5|** Gene loss and evolutionary adaptations in cetaceans: insights from the gene loss db
	15:40	João Moutinho	**Talk 6|** Exon duplication and loss in cldn18 punctuates the evolution of the gnathostome stomach and lung

---

16:00: Coffee Break

Session 2	Chairs: Vítor Sousa e Dora Henriques		
	TIME	**SPEAKER**	**TOPIC 2| Domestication, Population Genomics and Conservation**
	16:35	Isabel Alves	**Talk 7|** Evidence for two major domestication events during the evolutionary history of *Saccharomyces cerevisiae*
	16:47	Catarina Ginja	**Talk 8|** Unveiling genome-wide diversity and selection signatures in Portuguese sheep breeds
	16:59	João Souto	**Talk 9|** Incomplete lineage sorting and the recurrent evolution of parthenogenesis in Timema stick insects
	17:11	Sofia Alves	**Talk 10**| Macro- and microevolutionary genomics of the blue shark (*Prionace glauca*)
	17:23	Xana Sá-Pinto	**Talk 11|** Seedling evolution understanding to promote positive attitudes towards biodiversity conservation
	17:35	Alejandro Garcia	**Talk 12|** Harness the power of NGS: latest applications in DNA and RNA research (Novogene-gold sponsor talk)

Session 3	Chairs: Rita Ponce e Xana Sá-Pinto	
	TIME	**Mesa Redonda| Evolução com todos: pontes entre ciência, educação e comunicação**
	18:00	**Bruno Sousa**, *Agrupamento de Escolas de Albufeira Poente (online)* **Ivone Fachada**, *Ciência Viva - Agência Nacional* para a Cultura Científica e Tecnológica **João Faiões**, *Jornalista da SIC* **Maria Vicente**, *Ciência Viva - Agência Nacional* para a Cultura Científica e Tecnológica **Ricardo Pereira,** *Stuttgart State Museum of Natural History* **Tiago Ramalho**, *Jornalista do Público*

19:30: Live musical moment and Porto wine

DAY 2: 19 December 2025

	Chairs: Margarida Matos and M. Alice Pinto		
Session 4	**TIME**	**SPEAKER**	**TOPIC 3| Experimental Evolution and Adaptation**
	9:00	Margarida Matos	**Plenary Talk |** The role of history, chance, and selection during adaptation – from nature to the lab
	9:40	Afonso Grandela	**Talk 13|** Detrimental impact of a heatwave on male reproductive behaviour and fertility
	9:52	Sofia G. Costa	**Talk 14|** Maternal effects mediate the interactive effect of temperature and population structure on spider mite sex ratio and body size
	10:04	André Silva	**Talk 15|** From genomes to "heat": the molecular origin of adaptation in desert mammals
	10:16	Marta Ferreira	**Talk 16|** The importance of environmental heterogeneity for the genomic signature of adaptation to cadmium
	10:28	R. Alexandre Barroso	**Talk 17|** Toxicity in the reef: evolutionary insights and proteomic
	10:40	Miguel Cruz	**Talk 18|** Experimental evolution in sympatry leads to higher growth rates, but does not alleviate the costs of competition and reproductive interference
	10:52	Pedro Humberto Castro	**Talk 19|** Discovery of an evolutionarily conserved molecular mechanism for iodine detoxification in plants

11:05: Coffee Break

	Chairs: Sara Magalhães and Ana Rita Lopes		
Session 5	**TIME**	**SPEAKER**	**TOPIC 4| Co-evolution, Host–Pathogen and Parasite Evolution**
	11:35	Ana Rita Lopes	**Talk 20|** Viral evolution in isolation: how *Varroa* invasion shaped deformed wing virus and Lake Sinai virus in Azorean honeybees
	11:47	António Pérez	**Talk 21|** Rethinking the evolution of *Varroa destructor* resistance to amitraz: what is happening?
	11:59	Hugo Barreto	**Talk 22|** Eco-evolutionary dynamics of *Escherichia coli* invasion across human gut microbiotas
	12:11	Raquel Tomé	**Talk 23|** Estimating trait heritability and variation in predator-prey dynamics
	12:23	Rui Borges	**Talk 24|** Phylogenetic inference with not-so-rare mutations and wee tiny organisms

12:35 Group Photo

12:45 Lunch Break (IPB Cantina)

Session 6	Chairs: Élio Sucena and Mónica Marques		
	TIME	**SPEAKER**	**TOPIC 5| Hybridisation, Introgression, and Phenotypic Diversity**
	14:15	Ricardo Pereira	**Plenary Talk|** Museum collections as windows into species formation and introgression in a moving hybrid zone of birds
	14:55	Catarina Garcês	**Talk 25|** Hybridisation as a source of phenotypic diversity: the genomic basis of yellow coat colour in Iberian wolves
	15:07	Fernanda Li	**Talk 26|** Human-mediated rapid evolutionary change in European honey bees
	15:19	José Costa	**Talk 27|** The genomic aftermath of the ice ages in European hares
	15:31	João Moreno	**Talk 28|** Impact of introgression on thermal stress responses in Iberian chubs: a proteomic-level approach uncovers widespread transgressive protein expression in hybrids
	15:43	Rita Afonso	**Talk 29|** Avian structural colouration diversity explained by changes in feather keratinisation
	15:55	Lara Almeida	**Talk 30|** Morphological responses of *Mus musculus* to the environmental conditions of Cabo Verde
	16:07	Raquel Ruivo	**Talk 31|** Genome stories: how losing genes builds new phenotypes

16:20 Coffee Break

16:45 Poster Session

18:00 Closing Ceremony

18:15 APBE General Assembly

Oral Communications

TOPIC 1 | GENOME ARCHITECTURE, STRUCTURAL EVOLUTION AND BIOGEOGRAPHY

MATTHEW WEBSTER (Uppsala University, Uppsala, Sweden)

Matthew Webster gained his D.Phil. from the University of Oxford in 2001 and then moved to Uppsala University, Sweden, where he is now professor of genomics, specialising in evolutionary genomics and population genetics. He is interested in topics including the genetic basis of local adaptation, the evolution of recombination rate, the speciation process, and conservation genomics, working mainly with bees and other social insects.

See more at https://www.uu.se/en/contact-and-organisation/staff?query=N1-581

PLENARY TALK| THE EVOLUTION OF SEX AND RECOMBINATION – LESSONS FROM THE BEE HIVE

The evolutionary advantages of sex and recombination are still not fully understood. Meiotic recombination rates vary greatly among animal and plant taxa, and some species have evolved extremely high rates of crossing over, but the causes of this are unclear. Similarly, the genetic signals that give rise to males and females are highly diverse and rapidly evolving, but few examples of evolutionary shifts in sex-determination have been studied. The honeybee *Apis mellifera* is an ideal organism to study both of these processes, as a) it has one of the highest rates of meiotic recombination of all animals, and b) it has a recently-evolved sex determination gene. Here, I will present our recent research addressing these two topics.

Knowledge of the genetic architecture of variation in recombination rate is important for understanding its evolution. In *A. mellifera*, the haploid nature of males enables direct inference of recombination landscapes by comparing drone genomes to those of their diploid mothers. We use whole-genome sequences of 1,508 drones derived from 184 queens to identify individual crossover events and quantify extensive inter-individual variation in recombination rate. A genome-wide association analysis revealed a strong association between this variation and mlh1, a key recombination gene. This is the first major locus found to be associated with recombination rate variation in insects and provides a potential mechanism underlying the evolution of elevated crossover rates in honeybees.

In *A. mellifera*, sex is determined by the complementary sex determiner (csd) gene. However, this gene is not present in other closely-related bee species, and the sex-determination gene used by other bees is not known. We used genome sequencing of diploid males and females to map the sex-determining locus in the red mason bee, *Osmia bicornis*. We identified a 2-kb region overlapping the long noncoding RNA ANTSR, previously identified as the sex-determining gene in an ant species. The locus shows extreme haplotype diversity and signatures of balancing selection, and its orthologs exhibit elevated diversity across multiple bee and ant genera, suggesting a conserved, ancestral role in sex determination.

Together, these results illuminate the genetic architecture of two fundamental processes—recombination and sex determination—enabling future research into how they evolve.

TALK 1| STRUCTURAL ORGANIZATION AND EVOLUTIONARY DYNAMICS OF HUMAN SATELLITE 1B (HSAT1B) ACROSS PRIMATE GENOMES

Vila-Verde, C (1,2); Eleutério, D (1,2); Chaves, R (1,2,3,4); Louzada, S (1,2)

(1) CytoGenomics Lab, Department of Genetics and Biotechnology (DGB), University of Trás-OsMontes and Alto Douro (UTAD), 5000-801 Vila Real, Portugal; (2) BioISI – Biosystems & Integrative Sciences Institute, Faculty of Sciences, University of Lisboa, 1749-016 Lisbon, Portugal; (3) RISE-Health - Health Research Network, Faculty of Medicine, University of Porto, Porto, Portugal; (4) CACTMAD-Centro Académico Clínico de Trás-os-Montes e Alto Douro, University of Trás-osMontes and Alto Douro (UTAD), Vila Real, Portugal

Keywords: primate evolution; satellite DNA; T2T assemblies; bioinformatics; HSat1B

Abstract

Human satellite 1B is among the human classical satellite DNA (satDNA) families. HSat1B arrays have been described in the human genome, located in (peri)centromeric region of acrocentric autosomes as well as in the Y chromosome. The availability of the T2T genome assemblies from humans and other primates allows access to more detailed sequence information at the chromosome level. This work aimed to analyse the structural organisation and evolutionary dynamics of HSat1B to understand its potential roles in chromosome architecture and its evolutionary trail. Available genome assembly data were analysed by determining the genomic distributions of HSat1B across ten different primate species in which genomes have been sequenced telomere-to-telomere. We employed bioinformatics methodologies to accurately annotate this satellite in the various genomes, from the human assembly up to the lemur assembly. HSat1B arrays were identified in all analysed species. Each HSat1B monomer exhibits a conserved tripartite structure: an AluY fragment (approximately 290 bps), an AT-rich region (approximately 1600 bps, showing some divergence across primates), and a GC-rich region, here named H1B (approximately 560 bp). Interestingly, this structure is present only in some of the primates analysed, while the others had only H1B and H1B sequence variants. A syntenic analysis was also performed addressing the different species and their homologous regions, suggesting that this satellite DNA accompanied the evolution of primates' genomes. Future research will focus on further exploring comparative genomic analyses in other primate families and on investigating the potential role of satDNA in primate speciation and chromosomal organisation.

Acknowledgements/Funding
This work was supported by the Scientific Employment Stimulus (CEECIND/01825/2017), attributed to S.L., by FCT (Portugal). D.E. is recipient of a fellowship (2024.04110.BD) from FCT (Portugal).

TALK 2| BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS

Pereira, JC (1,4); Costa, S (1); Torres, V (1); Escudeiro, A (1); Barros, P (3,5); Chaves, R (1,4); Cabral, J (5); Adega, F (1,2)

(1) CytoGenomics Lab – Department of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal; (2) BioISI – Biosystems & Integrative Sciences Institute, Polo UTAD, Vila Real, Portugal; (3) Laboratory of Applied Ecology, University of Trás-os-Montes e Alto Douro, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal; (4) RISE-Health, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal; (5) CITAB - Centre for the Research and Technology of Agro-Environmental and Biological Sciences, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal

Keywords: bats; karyotype evolution; repetitive sequences; transposable elements; phylogenetics

Abstract

Bats (order *Chiroptera*) are among the most diverse mammalian groups, exhibiting unique evolutionary adaptations. Within Vespertilionidae, a highly conserved chromosome number (2n = 44) conceals subtle rearrangements that may influence evolutionary trajectories. We investigated the karyotypic architecture and repetitive sequence dynamics of three Iberian *Myotis* species—*M. daubentonii*, *M. blythii*, and *M. escalerai*—using Zoo-FISH with human whole-chromosome painting probes. Comparative maps revealed extensive synteny among species and with the human genome, consistent with the putative ancestral karyotype of Vespertilionidae. However, minor intrachromosomal rearrangements were detected, likely driven by repetitive elements such as transposable elements (TEs) and ribosomal DNA clusters. These sequences act as genomic "architects," promoting structural variation and potentially influencing adaptive traits. Understanding the interplay between conserved karyotypes and repetitive sequence dynamics provides insights into phylogenetic relationships within *Myotis* and highlights the role of repetitive elements in shaping genome architecture. Integrating cytogenomic and sequencing approaches will further clarify the evolutionary impact of these sequences on bat genome organisation.

TALK 3| GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES

Stephens, P (1); Farrell, M (2); Davies, J (3); Gittleman, J (4); Meiri, S (5); **Moreira, M** (6); Roll, U (7); Wiens, J (8)

(1) Oklahoma State University, United States; (2) University of Glasgow, United Kingdom; (3) University of British Columbia, Canada; (4) University of Georgia, United States; (5) Tel-Aviv University, Israel; (6) BIOPOLIS, Portugal; (7) Ben-Gurion University of the Negev, Israel; (8) University of Arizona, United States

Keywords: climate; colonization time; diversification rate; latitudinal diversity gradient; species richness

Abstract

Explaining global species richness patterns is a major goal of evolution, ecology, and biogeography. These richness patterns are often attributed to spatial variation in diversification rates (speciation minus extinction). Surprisingly, prominent studies of birds, fish, and plants have reported higher speciation and/or diversification rates at higher latitudes, where species richness is lower. We hypothesize that these surprising findings are explained by the focus of those studies on relatively recent macroevolutionary rates, within the last ~20 million years. Here, we analyse global richness patterns among 10,213 squamates (lizards and snakes) and explore their underlying causes. We find that when diversification rates were quantified at more recent timescales, we observed mismatched patterns of rates and richness, similar to previous studies in other taxa. Importantly, diversification rates estimated over longer timescales were instead positively related to geographic richness patterns. These observations may help resolve the paradoxical results of previous studies in other taxa. We found that diversification rates were largely unrelated to climate, even though climate and richness were related. Instead, higher tropical richness was related to the ancient occupation of tropical regions, with colonization time the variable that explained the most variation in richness overall. We suggest that large-scale diversity patterns might be best understood by considering climate, deep-time diversification rates, and the time spent in different regions, rather than recent diversification rates alone.

TALK 4| FCRL6 THROUGHOUT THE LINEAGES: WHAT'S THE HISTORY BEHIND THE FIRST FCRL THAT WAS DESCRIBED?

Matos, MC (1,2,3); Davis, RS (4) and Esteves, PJ (1,2,3)

(1) CIBIO-UP, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus Agrário de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal; (2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, 4485-661 Vairão, Portugal; (3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4169-007 Porto, Portugal; (4) Departments of Medicine, Microbiology, and Biochemistry & Molecular Genetics, Comprehensive Cancer Center, University of Alabama at Birmingham, Birmingham, AL 35294, USA

Keywords: FCRL; FCGR; immunoreceptors; birth-and-death evolution

Abstract

The Fc receptor-like (FCRL) multigene family exhibits marked genetic similarity to the classical Fc receptors (FCR) for IgG and IgE and are predicted to derive from a common ancestor. FCRL4 is expressed in B cells in humans, displays dual regulatory properties, and is a receptor for systemic IgA. FCRL6 is one of the most diverse members of the FCRLs and, in humans, functions as an inhibitory receptor of cytotoxic T and NK lymphocytes via binding to MHCII. To investigate the evolutionary history of FCRL6, we gathered all available sequences for Monotremata and Marsupialia to assess their relationship with those of placental mammals. We also analysed this genomic location, uncovering an *FCRL6-like* gene in some placental mammal species and another potential *FCRL* in Monotremata. Phylogenetic analyses show FCRL6 is conserved throughout evolution, except for the monotremes, where the gene present in the typical *FCRL6* locus is classified as *FCRL4,* and very close to it, in the *FCRL6-like* locus, is a gene classified as *FCRL6*. These sequences were the most divergent and prompted additional analysis, where we included FCRL4 and FCGR representatives. This wider phylogenetic analysis confirmed the described sister relationship between FCRL's and FCGR's, while also revealing lineage-specific adaptations. Monotremes have FCGR and FCRL members that are exclusive to their lineage, whereas marsupials lost all FCGR1 representatives, retained one copy of FCGR3, and have an expansion of FCGR2 genes. When we focus on FCRLs, there are clear orthologs for FCRL4 and FCRL6 in placental mammals and marsupials. Contrastingly, the monotreme's receptors occupy a basal position within the FCRL branch, displaying a distinct relationship with them while maintaining a separate identity. Together, these findings highlight both the conservation and diversification of FCRL6 across mammals. They underscore the unique evolutionary trajectories of monotremes and marsupials, suggesting lineage-specific pressures that shaped the FCRL family.

TALK 5| GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB

Themudo, G (1); Ruivo, R (1); Valente, R (1); Artilheiro, N (1,2); Oliveira, D (1,2); Amorim, I (1); Castro, L (1,2); **Lopes-Marques, M** (1, 2)

(1) CIIMAR/CIMAR LA, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Matosinhos, Portugal; (2) Department of Biology, Faculty of Science, University of Porto, Rua Campo Alegre s/n, 4169-007 Porto, Portugal

Keywords: gene inactivation, evolution, marine mammals, adaptation, biocuration

Abstract

The transition of cetaceans from terrestrial to fully aquatic life involved several anatomical, physiological, and genomic changes. Understanding the genomic modifications underlying these evolutionary adaptations is essential for establishing genotype–phenotype correlations and linking evolutionary traits to genomic changes. Within this context, gene loss or pseudogenization, resulting from the accumulation of ORF-disrupting mutations or gene/exon deletions, has gained attention as a mechanism underlying lineage-specific adaptations, particularly in cetaceans. Using the recently released Gene Loss DB (http://geneloss.org), which compiles 1872 gene loss events across 57 cetacean species and an additional 1321 events in other mammalian taxa, we conducted a comparative analysis of cetacean gene loss patterns, mechanisms, and functional implications. In cetaceans, gene losses are enriched in categories related to skin structure and keratinisation, immune and inflammatory responses, and lipid metabolism, consistent with their aquatic adaptations. Furthermore, losses shared between mysticetes and odontocetes highlight early evolutionary events in the cetacean ancestor linked to the transition to an aquatic lifestyle, including complete skin remodelling and the loss of fur, hair, and sebaceous glands. In contrast, lineage-specific losses reflect later, unique adaptations such as the retention of teeth in odontocetes and the loss of tooth-development genes in mysticetes, which present keratinised baleen plates instead. Our findings highlight the value of manually curated, searchable resources such as Gene Loss DB for the meta-analysis of gene loss in a specific species or order. This resource enables researchers to obtain a comprehensive overview of the major metabolic pathways affected by gene loss, an insight that would otherwise demand extensive effort and considerable time to assemble from numerous manuscripts. This overview also provides critical perspectives on gene essentiality and illustrates how gene loss can be linked to phenotypic innovation, metabolic rewiring, and environmental adaptation.

Acknowledgements/Funding

FCT - Fundação para a Ciência e Tecnologia I.P. (2022.00397.CEECIND/CP1728/CT0006 to M.L.-M., 2023.07615.CEECIND/CP2848/CT0007 to R.R., and CEECINST/00133/2018/CP1510/CT0004 to L.F.C.C). This research was funded by national funds through FCT and by the European Commission's Recovery and Resilience Facility, within the scope of UID/04423/2025, UID/PRR/04423/2025, LA/P/0101/2020, and project ATLANTIDA II (ref. NORTE2030-FEDER-01799200), co-financed by the European Union through the NORTE 2030 Regional Program and the European Regional Development Fund (ERDF) and funded by the Research Council of Norway Marma-Detox (project no. 334739).

TALK 6| EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG

Moutinho, J (1); Machado, A (1); Ferreira, P (2); Ruivo, R (1); Lopes-Marques, M (1); Wilson, J (2); Froufe, E (1); Castro, L (1)

(1) CIIMAR/CIMAR LA, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Matosinhos, Portugal; (2) Department of Biology, Faculty of Science, University of Porto, Porto, Portugal; (2) Wildfrid Laurier University, Canada

Keywords: gene duplication; alternative splicing; gastric evolution; exon loss; pleiotropy

Abstract

Understanding the evolutionary origin of anatomical novelties is fundamental to revealing the history of life forms. Innovative morphological archetypes, behaviours, and organs are central to adaptation and the colonisation of new ecological niches. The stomach associated gastric glands, and digestive function first evolved alongside the appearance of jaws in gnathostomes, with multiple secondary losses occurring across diverse lineages. This simplification of the gut was accompanied by the loss of several genes involved in acid secretion and protein digestion. Here, we investigate the evolutionary history of claudin 18 (Cldn18), a transmembrane protein essential for tight-junction formation, across jawed vertebrates. In mammals, Cldn18 displays a dual expression profile in gastric and lung alveolar epithelium, regulated by alternative splicing isoforms. Recent studies have reported the loss of a Cldn18 gene (a 3R duplicate) in agastric teleost species, but not in the stomachless platypus, suggesting that pleiotropy may act as a selective force maintaining Cldn18 in monotremes. We show that Cldn18 originated in the ancestor of gnathostomes but was independently and convergently lost in chimaeras and lungfishes. We further demonstrate that the emergence of alternative splicing generating gastric- and lung-specific isoforms predates the invasion of terrestrial habitats. In monotremes (platypus and echidna), we identify the targeted loss of the gastric-specific exon, coinciding with the absence of gastric glands in this lineage. Our findings illuminate a complex evolutionary scenario combining gene duplication, alternative splicing innovation, and secondary exon loss, underpinning the evolution of stomach and lung phenotypes in jawed vertebrates.

TALK 7| EVIDENCE FOR TWO MAJOR DOMESTICATION EVENTS DURING THE EVOLUTIONARY HISTORY OF *SACCHAROMYCES CEREVISIAE*

Alves, I (1); Loegler, V (1); Friedrich, A (1); Schacherer, J (1)

(1) UMR 7156 – Molecular Gene5cs, Genomics and Microbiology (GMGM); CNRS – University of Strasbourg, France

Keywords: yeast; population genomics; demographic inference

Abstract

The budding yeast *Saccharomyces cerevisiae* has been used worldwide for a wide range of human activities such as winemaking, brewing, baking, and distilling for tens of centuries. It is a widely studied model organism from which wild and domesticated populations have been previously described. Despite its tight link to our species, very little is known about the evolutionary trajectories of domestication processes. Here, we compiled complete genome sequences of more than 3,000 *S. cerevisiae* isolates from around the world, and we characterised patterns of population diversity and genetic clustering within domesticated and wild strains. We developed a series of complex demographic models taking into account the complexities of the species' life-cycle and used a composite-likelihood approach to infer the best-fitting model and the underlying demographic parameters. Patterns of differentiation show genetic proximity between clades associated with wine-fermentation as well as between clades related to fermentation processes in Asia. We also found that wine strains are associated with the largest decrease in nucleotide diversity, with 1.1 to 4.46-fold relative to the average *S. cerevisiae* diversity. We also found a significant increase in allele sharing between wild populations from East Asia and European domesticated strains. Our demographic modelling approach revealed that patterns of genetic variation in yeast are not consistent with a single episode of domestication, in which a common ancestral population gives rise to all domesticated strains. Instead, it is compatible with an earlier split of European domesticated strains, followed by a more recent split between Asian domesticated strains and most wild East Asian conspecifics.

TALK 8| UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS

Gaspar, D (1); Usié, A (2); Bruno de Sousa, C (1); Matos, J (3); Matos, C (4); Pires, AE (1, 5); **Ginja, C** (1)

(1) BIOPOLIS/CIBIO - Program in Genomics, Biodiversity and Land Planning, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO - Laboratório Associado, Universidade do Porto, Vairão, Portugal; (2) CEBAL, Centro de Biotecnologia Agrícola e Agro-Alimentar do Alentejo, Instituto Politécnico de Beja, Portugal e MED - Mediterranean Institute for Agriculture, Environment and Development and CHANGE - Global Change and Sustainability Institute, Beja, Portugal; (3) INIAV, I.P. – Instituto Nacional de Investigação Agrária e Veterinária, Unidade de Biotecnologia e recursos Genéticos, Oeiras, Portugal; (4) ACOS - Agricultores do Sul, Beja, Portugal; (5) Faculdade de Medicina Veterinária, Universidade Lusófona-Centro Universitário de Lisboa and I-MVET Investigação Medicina Veterinária, Lisboa, Portugal.

Keywords: *Ovis aries*; Portuguese native sheep; high-throughput sequencing; population genomics; selection signatures

Abstract

In the Iberian Peninsula, extensive sheep husbandry and transhumance fostered a great diversity of native breeds. Sheep are raised in agrosilvopastoral systems that promote environmental sustainability and preserve rural landscapes. Native breeds are classified into Merino (fine wool), Bordaleiro (intermediate wool), and Churro (coarse wool) based on fleece characteristics. This study characterises the genomic diversity and population structure of native Portuguese sheep breeds, aiming to investigate their evolutionary history and assess the impact of demographic events such as bottlenecks and admixture. Whole-genome resequencing data were generated for 101 individuals comprising 10 breeds: Campaniça, Serra da Estrela, Merino Branco, Merino Preto, Churra Algarvia, Churra da Terra Quente, Churra Badana, Churra Galega Mirandesa, Churra Galega Bragançana Branca, Churra Galega Bragançana Preta. High-quality SNPs were used to estimate genetic diversity and infer population structure using Principal Components Analysis and Bayesian clustering. Wright's fixation index (F_{ST}) was used to measure genetic differentiation and infer selection signatures. Portuguese sheep exhibited moderate nucleotide diversity ($1.35x10\text{-}3 < \pi < 2.03x10\text{-}3$) and heterozygosity ($0.28 \leq HO \leq 0.34$; $0.30 \leq HE \leq 0.35$). Evidence of moderate inbreeding ($F_{IS} \sim 0.11$) was found in Churra Algarvia and Churra Badana, which were well-differentiated from all other breeds, consistent with geographic isolation and demographic bottlenecks. We also observed a separation between fine and coarse wool breeds. F_{ST} analyses identified four regions of strong genetic differentiation between these breed groups ($F_{ST} \geq 0.3$), including a region on chromosome 6 containing QTLs associated with milk, meat, and growth traits. Genes linked to tail length (HOXB13, chromosome 11) and fleece characteristics (EIF2S2, chromosome 13) were also located in regions of high genetic differentiation. Mitochondrial phylogenies showed that all individuals belonged to haplogroup B, the predominant maternal lineage in European sheep. This study provides an assessment of genomic diversity, breed relationships and admixture in Portuguese sheep, offering valuable resources for their conservation, breeding and management. https://doi.org/10.54499/2022.04843.PTDC

Acknowledgements/Funding: ARIES project - https://doi.org/10.54499/2022.04843.PTDC

TALK 9| INCOMPLETE LINEAGE SORTING AND THE RECURRENT EVOLUTION OF PARTHENOGENESIS IN TIMEMA STICK INSECTS

Souto, J (1,2), Mérel, V (1), Goudet, J (1,2*), Schwander, T (1*)

(1) Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland; (2) Swiss Institute of Bioinformatics, University of Lausanne, Lausanne, Switzerland

*Co-senior authors

Keywords: incomplete lineage sorting (ILS); phylogenomic conflict; introgression; liftover; parthenogenesis

Abstract

The repeated evolution of similar traits in related species can result from the independent selection of shared ancestral variants, producing gene and species tree discordances known as incomplete lineage sorting (ILS). In *Timema* stick insects, parthenogenesis has evolved multiple times independently via the same cellular mechanism, offering an exceptional system to test whether ILS promoted recurrent transitions to parthenogenesis. Using whole-genome data from ten *Timema* species (five sexual and five parthenogenetic), we benchmarked two variant detection strategies, “single reference” and “liftover”, to identify the most suitable approach for interspecific comparisons across highly divergent lineages (~30 MYA). The lift over approach, which maps reads to species-specific genomes and converts coordinates through whole-genome alignments, improved the reliability of genotype calls and recovered up to 19% more callable sites. Genome-wide D-statistics revealed limited introgression (0.2–0.7% of the genome) but substantial phylogenetic conflict, implying that ILS is the main source of discordance among *Timema* species. Comparative genomic analyses did not identify any genomic regions shared across all parthenogenetic–sexual pairs, suggesting a polygenic or dispersed genetic basis for parthenogenesis. Ongoing analyses are focusing on loci with excess shared variation between parthenogenetic lineages to clarify the role of ancestral polymorphisms in the recurrent evolution of parthenogenesis.

TALK 10| MACRO- AND MICROEVOLUTIONARY GENOMICS OF THE BLUE SHARK (*PRIONACE GLAUCA*)

Alves, JS (1,2,3,4); Marques, JP (1, 3); Farelo, L (1, 3); Arnaud-Haond, S (4); Queiroz, N (1, 3); Melo-Ferreira, J (1,2,3)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal; (2) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal; (3) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal; (4) UMR248 MARBEC, Univ. Montpellier, Ifremer, IRD, CNRS, Sète, France

Keywords: comparative genomics; population genomics; whole-genome sequencing; climate change; panmixia

Abstract

Rapid ocean change and overfishing threaten the persistence of many marine predators. The blue shark (*Prionace glauca*), the most widely distributed and heavily fished shark, is particularly vulnerable to ocean warming and deoxygenation due to its ectothermic physiology and high-energy predatory behaviour. However, it remains unclear how these pressures affect the species and whether it has the capacity to adapt and persist, partly because its genomic diversity is still poorly characterised. Previous studies relied on a limited number of markers, capturing weak but geographically coherent population structure. Whole-genome data can provide a finer characterisation of population history and structure, while also enabling the detection of selection and offering hints about potential adaptation. Here, we apply whole-genome sequencing at two evolutionary scales. At the macroevolutionary level, we use high-quality genomes of 23 shark species to investigate the evolution of three traits linked to environmental adaptation - diving behaviour, thermal niche, and metabolic rate. These traits have evolved repeatedly across shark lineages, providing an opportunity to detect possible genomic signatures of convergent evolution. These analyses are ongoing, and the framework will be presented. At the microevolutionary level, we examine the genetic diversity and structure of the blue shark across the Atlantic and Mediterranean. Linkage disequilibrium decay analyses revealed low LD across the genome, consistent with weak structure and no signs of recent bottlenecks. Similarly, population structure analyses showed no detectable genetic structure, supporting a largely panmictic population with unrestricted gene flow in the Atlantic and Mediterranean. Follow-up analyses will reconstruct the species' demographic parameters and scan the genome for putative signals of selection, which will then be compared with macroevolutionary patterns. This study provides the most comprehensive genomic assessment to date of the species' current genetic status and offers an interdisciplinary foundation for predicting how it may respond to future ocean conditions.

TALK 11| SEEDLING EVOLUTION UNDERSTANDING TO PROMOTE POSITIVE ATTITUDES TOWARDS BIODIVERSITY CONSERVATION: A STUDY WITH ELEMENTARY SCHOOL STUDENTS

Pessoa, P (1,2,3); Lopes, JB (2); Pinto, A (3); **Sá-Pinto, X** (1)

(1) CIDTFF.UA: Centro de Investigação em Didática e Tecnologia na Formação de Formadores, Departamento de Educação e Psicologia, Universidade de Aveiro, Aveiro, Portugal; (2) UTAD: Universidade de Trás-os-Montes e Alto Douro, Vila Real, Portugal; (3) ESE.IPP: Escola Superior de Educação do Instituto Politécnico do Porto, Porto, Portugal

Keywords: biodiversity conservation; evolutionary literacy; education for sustainability; elementary school students; evolution education.

Abstract

The biodiversity crisis demands urgent and informed conservation efforts. Despite the crucial role of intraspecific biodiversity in allowing species to adapt to environmental change, its importance remains largely unknown to the public and overlooked in educational programmes. Promoting scientific knowledge about intraspecific diversity, as well as positive attitudes toward its conservation, is therefore essential. Understanding natural selection is expected to support such attitudes; however, to our knowledge, no studies have yet examined this relationship in young learners. This study addresses this gap by investigating the impact of a socioscientific issues (SSI)-based educational intervention, grounded in evolutionary principles, on elementary students' attitudes toward intraspecific biodiversity and their understanding of evolution. The intervention involved 80 Portuguese third-grade students (8–9 years old) who participated in hands-on activities linking evolutionary mechanisms to a real-world challenge related to agriculture and food security. Data were collected through pre- and post-intervention semi-structured interviews assessing attitudes and reasoning about intraspecific diversity, along with a questionnaire measuring students' Level of Understanding of Evolution by Natural Selection (LUENS). Results showed a significant increase in both pro-biodiversity attitudes and LUENS scores after the intervention. While none of the students used evolutionary arguments beforehand, 48% did so afterwards, and evolutionary reasoning was significantly associated with pro-biodiversity choices. Students with higher LUENS scores were more likely to use evolutionary justifications and to choose to plant seeds containing intraspecific diversity, although this latter trend was not statistically significant. These findings highlight the value of integrating evolutionary literacy into primary education to strengthen students' capacity to apply evolutionary reasoning in sustainability-related decision-making. Future research should examine the replicability of these results in diverse contexts and investigate the impact of teacher-led implementation. It is also important to design and evaluate professional development strategies that empower elementary teachers to address SSI through an evolutionary lens.

TALK 12| HARNESS THE POWER OF NGS: LATEST APPLICATIONS IN DNA AND RNA RESEARCH (NOVOGENE-GOLD SPONSOR)

Alejandro Garcia (1)

(1) Novogene Europe

Keywords: Next-generation sequencing**,**

Abstract

Next-generation sequencing (NGS) has fundamentally transformed life sciences research, enabling comprehensive genome- and transcriptome-wide analyses to address complex biological questions. Genomics and transcriptomics now play a central role in uncovering the molecular mechanisms underlying adaptation, stress responses, development, and disease. In this presentation, we will explore how these technologies are driving new discoveries and demonstrate how Novogene's customised sequencing and bioinformatics solutions can help researchers efficiently translate biological questions into high-quality, actionable data.

TOPIC 3 | EXPERIMENTAL EVOLUTION AND ADAPTATION

MARGARIDA MATOS (Centre for Ecology, Evolution and Environmental Changes, University of Lisbon, Lisbon, Portugal)

Margarida Matos is a Full Professor at the Department of Biology of the Faculty of Sciences of the University of Lisbon (Ciências). With a PhD in Genetics in 1997, she is a Researcher at the Centre for Ecology, Evolution and Environmental Changes (CE3C), leading the Local Adaptation in *Drosophila* Research Group. Between 2009 and 2025, she was a member of the Executive Committee of CE3C. She is the Coordinator of the PhD programme Biodiversity, Genetics and Evolution (BIODIV/Ciências). At Ciências, she has taught many disciplines in Bachelor and Master Courses, namely in Evolutionary Ecology, Evolutionary Biology, and Experimental Evolution. She supervised (or co-supervises) 9 PhD theses (one ongoing) and 4 Post-Docs. Her research field is Evolutionary Ecology, using mainly Experimental Evolution as a tool.

The main line of her research for several decades now has been the study of the evolutionary patterns and processes during adaptation to novel environments, with a focus on the transition between Nature and the Laboratory. This has been done by analysing the real-time evolution of repeated colonisations of *Drosophila subobscura* populations to a laboratory environment, at several biological levels, as a way to understand the role of History and Selection during Adaptation. Her research has highlighted that populations have abundant standing genetic variation to adapt, with selection quickly erasing the signs of history in fitness-related traits, while genetic differentiation between populations is maintained at the inversion frequency and genome-wide level. Her most recent project (ADAPTCLIMWARM PI Pedro Simões, former PhD student), analyses how historically differentiated populations adapt to climate change at the phenotypic, genomic, and transcriptomic levels. Findings until now illustrate the relevance of different genetic backgrounds on the rate of evolution and specific genetic paths, as well as the contrasting conclusions across biological levels.

She has authored more than 70 scientific publications, including 2 books and more than 50 articles in journals of recognised merit in Evolutionary Biology. As she approaches retirement, what makes her most proud is seeing how her former students have flourished in their own careers, whether following in her footsteps in Evolutionary Biology or pursuing other paths.

See more at https://www.ce3c.pt/research/research-groups/evolutionary-perspectives-in-a-changing-world/local-adaptation-in-drosophila and https://orcid.org/0000-0001-6998-5133

PLENARY TALK| THE ROLE OF HISTORY, CHANCE, AND SELECTION DURING ADAPTATION – FROM NATURE TO THE LAB

In this lecture, Margarida Matos will highlight some of the main results of the several decades of her research. The main line of her research has been the study of the evolutionary patterns and processes during adaptation to novel environments, with a focus on the transition between Nature and the Laboratory. This has been done by analysing the real-time evolution of repeated colonisations of

Drosophila subobscura populations to a laboratory environment, at several biological levels, as a way to understand the role of History, Chance, and Selection during Adaptation. Her research has highlighted that populations have abundant standing genetic variation to adapt to the laboratory, tending to converge at the life-history trait level, both among recently founded populations and between them and long-term established populations. In fact, selection quickly erased the signs of history in fitness-related traits between populations derived from contrasting European latitudes. On the other hand, genetic differentiation was maintained both at the inversion frequency and the genome-wide level. Thus, different biological levels lead to different outcomes. After decades of characterising adaptation to the laboratory, her team (led by Pedro Simões, her former PhD student) turned from convergent to divergent evolution, tackling how historically differentiated populations adapt to a rising temperature at the phenotypic, genomic, and transcriptomic levels. They found that thermal adaptation was rather slow and contingent on the genetic background of populations. Interestingly, many candidate genes evolved relatively fast in their expression, in contrast with a much slower detection of thermal adaptation at the life-history traits level. They also found indications of an interplay between adaptive plasticity and thermal evolution, partially explaining differences between populations. As she approaches retirement, what makes her most proud is seeing how her former students have flourished in their own careers, either following her footsteps in Evolutionary Biology or pursuing other paths.

TALK 13| DETRIMENTAL IMPACT OF A HEATWAVE ON MALE REPRODUCTIVE BEHAVIOUR AND FERTILITY

Grandela, A (1,2); Antunes, MA (1,2); Santos, MA (1,2); Matos, M (1,2); Rodrigues, LR (1,2); Simões, P (1,2)

(1) Centre for Ecology, Evolution and Environmental Changes (cE3c) & CHANGE–Global Change and Sustainability Institute, Lisbon, Portugal; (2) Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal

Keywords: climate change; heat stress; mating behaviour; fertility; *Drosophila*

Abstract

Understanding how heatwaves impact different aspects of mating behaviour and fertility is getting increasingly important. In this context, laboratory fertility and mating experiments involving the manipulation and exposure of insects to different thermal conditions are common procedures. To conduct such experiments, practical methods such as dyes are needed for an easy, non-invasive discrimination of individuals. We report here a study measuring the effect of an extended heat stress applied to males on several parameters of mating behaviour and fertility of laboratory populations of *Drosophila subobscura* derived from two distinct European locations. We found highly detrimental effects of heatwave on mating behaviour—with longer (courtship and copulation) latencies and lower mating occurrence, but no changes in mating duration—and fertility, with reduced fecundity and reproductive success. Furthermore, we also tested the efficacy of food dye as a marker for individual discrimination and mating occurrence. While food dye did not allow for to infer the occurrence of a mating based on a transfer of coloration from male to female, it did not affect mating and fertility, attesting its utility has a method for discriminating individuals within mating experiments in the context of thermal studies. Importantly, despite the fact that the heatwave was only applied in males, we observed an impact on behaviour of females that mated with stressed males, by often refusing their nuptial feeding. This opens possibilities for further integrated research on the changes of female and male mating behaviour and fertility under different thermal scenarios.

TALK 14| MATERNAL EFFECTS MEDIATE THE INTERACTIVE EFFECT OF TEMPERATURE AND POPULATION STRUCTURE ON SPIDER MITE SEX RATIO AND BODY SIZE

Costa, S (1); Chokechaipaisarn, C (2); Gardner, A (2); Magalhães, S (1,3,*); Rodrigues, L (1,*)

(1) Centre for Ecology, Evolution and Environmental Changes & CHANGE – Global Change and Sustainability Institute (cE3c), Faculty of Sciences, University of Lisbon, Lisbon, 1749-016 Portugal; (2) School of Biology, University of St Andrews, St Andrews, Fife, United Kingdom; (3) Wissenschaftskolleg zu Berlin, Institute for Advanced Study, Berlin, Germany.

*Co-last authors

Keywords: global warming; local mate competition; maternal effect; sex allocation; spider mites

Abstract

Population structure and temperature are two important environmental stresses, often affecting organismal traits. Although their effect has been studied independently, their potential interactive effects remain poorly understood, particularly in haplodiploids. Indeed, population structure is predicted to affect sex allocation, as a female-biased sex ratio is favoured in small populations, whereas high temperatures often lead to male-biased sex ratios due to fertilisation failures. Moreover, both population structure and temperature have been documented to affect body size, which in turn also affects sex ratio. Here, we addressed this knowledge gap by exposing the spider mite *Tetranychus cinnabarinus* to a sublethal or control temperature under high or low population structure (*i.e.*, patches founded by 2 or 10 females, respectively) over two generations. We found that males were consistently smaller under heat in a high population structure across generations. In contrast, heat increased female body size in both generations, but its interaction with population structure emerged in the second generation only. Sex ratio was also affected by heat exposure, being more male-biased only in the second generation, pointing to the importance of maternal effects on both sex ratio and female size outcomes. Unlike classical predictions and earlier findings, population structure did not affect sex ratio. To interpret these findings, we developed a theoretical model to predict the optimal sex ratio assuming different numbers of founding females and proportions of constrained females (*i.e.*, females with no fertilised offspring), whose frequency increases with temperature due to heat-induced male sterility. We found that a relatively high incidence of constrained females erases the difference in sex ratio under high and low population structure, traditionally predicted by theory. Our findings highlight how the interaction between population structure and thermal stress can shape key biological traits that may influence how species persist in changing environments.

TALK 15| FROM GENOMES TO "HEAT": THE MOLECULAR ORIGIN OF ADAPTATION IN DESERT MAMMALS

Silva, AFF (1,2); Oliveira, D (1,2); Machado, A (1); Ruivo, R (1); Cordeiro, JM (1); Castro, LFC (1,2)

(1) CIIMAR–Interdisciplinary Centre of Marine and Environmental Research, Matosinhos, Portugal; (2) FCUP- Faculty of Sciences, University of Porto, Portugal

Keywords: gene duplication; cholesterol, Heteromyidae, heterothermy

Abstract

Deserts are harsh environments with high temperatures and low precipitation, posing challenges for life. However, specific species have adapted to these conditions by regulating body temperature and minimizing water loss. To understand the genetic and molecular foundations of their phenotypes, we aim to analyse how small mammals have converged on arid environment adaptations at the molecular level, investigate the role of gene duplication in adaptation to extreme environments, and identify the molecular changes that underlie adaptations to different desert settings. An in-house bioinformatic pipeline was used to identify events of gene expansion and gene loss in a set of selected species (e.g., Heteromyidae), followed by manual annotation in Geneious R11.1.5 and phylogenetic analysis in PhyML. Gene expression was evaluated using publicly available RNA-Seq datasets. These analyses revealed multiple clade specific gene expansions of cholesterol related genes in several Heteromyidae species (*Perognathus longimembris*; *Dipodomys* spp.). Gene sequence analysis and tissue expression patterns also indicate phenotypic changes underpinning higher cholesterol levels. Our results suggest a radical shift in the regulation of cholesterol uptake and metabolism in Heteromyidae, in agreement with the high serum cholesterol levels reported for *Dipodomys merriami*. We propose that gene expansions are expected to promote gene functional plasticity. Given the role of cholesterol in membrane fluidity upon temperature shifts, such molecular events could promote ecotype-specific adaptations to arid environments.

TALK 16| THE IMPORTANCE OF ENVIRONMENTAL HETEROGENEITY FOR THE GENOMIC SIGNATURE OF ADAPTATION TO CADMIUM

Ferreira, MC (1); Godinho, DP (2); Magalhães, S (1,3); Sousa, VC (1,3); Fragata, I (1,3)

(1) Centre for Ecology, Evolution and Environmental Changes and CHANGE; (2) Gulbenkian Institute for Molecular Medicine; (3) Department of Biology, Faculdade de Ciencias da Universidade de Lisboa

Keywords: *Tetranychus urticae*; pool-seq; experimental evolution, environmental heterogeneity

Abstract

Heavy metals can propagate across all levels of ecosystems. Their short-term effects are well known across taxa, leading to oxidative stress and cell death. However, we know little about the long-term impact of heavy metals on organisms. Moreover, metal accumulation in plants is spatially heterogeneous, allowing for herbivores to either adapt to polluted environments or shift their range to non-contaminated plants. Thus, understanding how spatial heterogeneity in heavy metal pollution impacts herbivores is key to understanding the role of these pollutants in shaping ecological communities. To address this knowledge gap, we performed 55 generations of experimental evolution of the two-spotted spider mite, *Tetranychus urticae,* on tomato plants (a) without cadmium (control), (b) with high cadmium concentrations (homogeneous environment), and (c) with and without cadmium (heterogeneous environment). For the homogeneous and heterogeneous selection regimes, we quantified changes in performance under cadmium and shifts in allele frequencies (using Pool-seq) relative to the control selection regime. We detected significant changes in allele frequencies in SNPs, in both cadmium-exposed regimes, consistent with the action of positive selection. Interestingly, we detected more SNPs under selection in the heterogeneous environment compared to the homogeneous environment. Although the SNPs under selection were distributed along the genome in both regimes, they were more concentrated in a small region on the first chromosome in the heterogeneous regime. Interestingly, for both cadmium regimes we found changes in genes associated with neurotransmission, response to oxidative stress, transport channels and gustatory sensors. We also identified regime specific genomic changes: genes associated with lysosomal pathways were only observed in the heterogeneous regime, whereas changes in genes associated with the Golgi complex were found exclusively in the homogeneous regime. Overall, our results suggest that, despite a common response to cadmium, spider mites evolved different strategies to deal with it in their cells. Thus, our results highlight that environmental heterogeneity can modulate adaptation to environmental stressors.

TALK 17| TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA)

Barroso, RA (1,2); Ramos, L (1,2); Moreno, H (1,2); Rodrigues, T (1,2); Ledoux, JB (1); Campos, A (1); Turkina, MV (3); Antunes, A (1,2)

(1) CIIMAR/CIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Porto, Portugal; (2) Department of Biology, FCUP University of Porto, Porto, Portugal; (3) Department of Biomedical and Clinical Sciences, MEDFAK Linköping University, Linköping, Sweden

Keywords: cnidaria, stony corals, venom evolution, gene duplication, omics data

Abstract

Stony corals (Scleractinia, Cnidaria) are colonial heterotrophic animals that form the structural foundation of coral reefs. Resembling other cnidarians, including sea anemones and jellyfish, they discharge nematocysts for prey capture and defence, yet the molecular diversity and evolution of their toxins remain poorly understood. Here, we performed a comprehensive evolutionary analysis on stony coral neurotoxins, known as *Cnidaria Small Cysteine-Rich Proteins* (SCRiPs), and examined the transcriptomes and proteomes of five newly sequenced species (*Acropora muricata*, *Blastomussa wellsi*, *Catalaphyllia jardinei*, *Micromussa lordhowensis,* and *Montipora foliosa*) to identify additional toxins. Across 117 cnidarian genomes and 103 transcriptomes, we identified 168 new putative SCRiPs in 36 stony coral and 12 sea anemone species, classifying them into four subfamilies (α, β, γ, δ). Most SCRiPs appear to be under purifying selection, although signatures of adaptive evolution in specific scleractinian lineages suggest neofunctionalization and fine-tuning of toxin potency. In the five newly sequenced species, transcriptomic analysis showed that approximately 5% of the secretome encodes putative toxins (50 to 286 per species), and proteomic data validated several candidates, including SCRiPs and pore-forming actinoporins. Phylogenetic analyses showed that most stony coral actinoporins are closely related to those of Corallimorpharia and black corals (Antipatharia), separated from sea anemones (Actiniaria), with evidence of multiple lineage-specific duplication and diversification events. Structural modelling further revealed that most SCRiPs adopt a βdefensin-like fold, whereas actinoporins exhibit architectures consistent with those of sea anemones. Together, our findings reveal novel insights into stony coral venoms, highlighting their evolutionary significance and potential as sources of novel bioactive compounds.

Acknowledgements/Funding
R.A.B. was supported by the Ph.D. grant 2022.09707.BD provided by FCT—*Fundação para a Ciência e a Tecnologia*. A.A. was partially supported by the Strategic Funding U-IDB/04423/2020 and UIDP/04423/2020 through national funds provided by the FCT and the European Regional Development Fund (ERDF) in the framework of the program PT2020 and by the European Structural and Investment Funds (ESIF) through the Competitiveness and Internationalization Operational Program—COMPETE 2020. This project was also supported by the European Union (H2020 program/Horizon Europe Blueshellfish Project Grant agreement ID: 101086234).

TALK 18| EXPERIMENTAL EVOLUTION IN SYMPATRY LEADS TO HIGHER GROWTH RATES, BUT DOES NOT ALLEVIATE THE COSTS OF COMPETITION AND REPRODUCTIVE INTERFERENCE

Cruz, MA (1); Sousa, VC (1,2); Zélé, F (3); Magalhães, S (1,2)

(1) CE3C - Centre for Ecology, Evolution and Environmental Changes & CHANGE - Global Change and Sustainability Institute, Faculdade de Ciências da Universidade de Lisboa, Lisboa, Portugal; (2) Departamento de Biologia Animal, Faculdade de Ciências da Universidade de Lisboa, Lisboa, Portugal; (3) ISEM, Université de Montpellier, CNRS, IRD, Montpellier, France

Keywords: coexistence theory; adaptation; trophic interactions; sexual interactions; partial reproductive isolation

Abstract

Evolution in sympatry is known to drive character displacement, which should facilitate coexistence between species by alleviating competition for food and reproductive interference. However, only a few studies have investigated how evolving with heterospecifics shapes the evolutionary trajectories of these two interactions and how this ultimately changes the likelihood of coexistence. To fill this gap, we measured these features in two competing spider mite species, *Tetranychus urticae* and *T. cinnabarinus*, subjected to experimental evolution either in allopatry or in sympatry for more than 20 generations in a homogeneous environment. We found that most responses after evolution in sympatry were only transiently detected (i.e., at different time points), suggesting an important role of fluctuating selection. Indeed, depending on the experiment, we found higher intrinsic growth rates of both species in sympatry, which came at an apparent cost of increased sensitivity to interspecific competition and a lower induction of reproductive interference in *T. urticae*. This hints at the existence of a growth-competition trade-off in this system, along with other correlations among traits underlying trophic and sexual interactions, which may be hampering species divergence in this system. Finally, predictions for coexistence between the two species support this hypothesis as they did not change significantly after evolution in the presence of heterospecifics. Possibly, a more complex environment, for example, with more varied food sources, may be necessary to enable trait changes facilitating coexistence.

TALK 19| DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS

Lourenço, T (1,2,3,4); Esperança, A (1,2,3); Freitas, S (1,2,3); Vignols, F (4), Azevedo, H (1,2,3); Dubos, C (4); **Castro, PH** (1,2)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal; (2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal; (3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal; (4) IPSIM, Université de Montpellier, CNRS, INRAE, Institut Agro, Montpellier, France;

Keywords: biofortification; crops; functional genomics; halides; halide methyltransferase

Abstract

Iodine is well known for its essential role in human nutrition. In plants, however, its function remains less explored. Even so, iodine is regarded as a beneficial element that, at appropriate concentrations, can enhance growth and improve tolerance to environmental stresses. When present in excessive amounts, whether through human activities or naturally occurring in certain ecosystems, iodine can become toxic to plants, a condition referred to as Reclamation Akagare disease. Maintaining a balanced internal iodine level is therefore crucial. To prevent toxicity, plants have evolved efficient mechanisms to regulate iodine content. One such mechanism is iodine volatilisation, carried out by halide methyltransferase (HMT) enzymes. These enzymes methylate iodide, enabling its release into the atmosphere. Consequently, HMTs play a key role in iodine homeostasis and are considered an important detoxification pathway in plants. In this study, we investigated the evolutionary conservation of the HMT gene family in plants. Phylogenetic analyses revealed that the family is highly conserved across plant lineages. To explore their functional roles, we generated Arabidopsis T-DNA insertion mutants, overexpression lines, and complementation lines, and exposed them to different concentrations of iodide salts. We assessed the resulting morphological and physiological changes and quantified iodine accumulation in each line, demonstrating a direct correlation between the presence of HMT and reduced iodine tolerance. Finally, our cross-species analysis showed that the absence of HMT is associated with increased iodine accumulation. Together, these findings provide a foundation for a deeper understanding of iodine regulation in plants and offer valuable perspectives for improving iodine tolerance and advancing biofortification strategies in crops.

Acknowledgements/Funding
Work co-financed by the European Union through the NORTE 2030 Regional Programme under the NORTE2030-FEDER-02130700 project. T.L. was supported by FCT/MCTES, NORTE2020, and UE/FSE (SFRH/BD/05206/2021).

TALK 20| VIRAL EVOLUTION IN ISOLATION: HOW VARROA INVASION SHAPED DEFORMED WING VIRUS AND LAKE SINAI VIRUS IN AZOREAN HONEYBEES

Lopes, Ana R (1); Low, M (2); Martín-Hernández, R (3); de Miranda, J (2); Pinto, M. Alice (1)

(1) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Bragança, Portugal; (2) Department of Ecology, Swedish University of Agricultural Sciences, 750-07 Uppsala, Sweden; (3) Centro de Investigación Apícola y Agroambiental (CIAPA). IRIAF. Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal, 19180 Marchamalo, Spain

Keywords: *Apis mellifera*; evolution; viruses; qPCR; high-throughput sequencing

Abstract

Geographically isolated ecosystems provide exceptional opportunities to study evolutionary processes. The Azores archipelago, with its heterogeneous distribution of the mite *Varroa destructor*, the major threat to honeybees, and a well-documented invasion history, serves as a natural laboratory to investigate how varroa pressure shapes honey bee viruses' evolution. Varroa has been well-established on Pico since 2000, on Flores since 2001, and on Faial since 2008, with the remaining islands being naive to this parasite. In 2014–2015 and 2020, 494 colonies were sampled from across the archipelago and were then analysed using high-throughput amplicon sequencing to assess the diversity and phylogenetic structure of two major RNA viruses: Deformed wing virus (DWV) and Lake Sinai virus (LSV). All three DWV variants (A, B, and C) were detected, but their distribution varied geographically. Phylogenetic analyses showed that DWV sequences from São Miguel and Santa Maria clustered mainly with DWV-C (rare variant), whereas those from Pico, Faial, Flores, and Graciosa grouped with DWV-A and -B (variants linked to mite transmission). The co-occurrence of DWV variants within 73.5% of the colonies suggests a long-standing viral presence, with DWV-C likely representing the ancestral variant before varroa invasion. Restricted honey bee movement is maintaining this rare variant, while varroa-mediated transmission has favoured the spread of A and B variants in infested islands. Although LSV has not been proven to be associated with varroa, it exhibited a pronounced geographic structure. LSV-2 (32.8%) dominated all varroa-infested islands, whereas LSV-3 (39.4%) and LSV-9 (25.8%) were prevalent in the varroa-free islands Graciosa and Terceira, and São Miguel and Santa Maria, respectively. The consistent genetic clustering of Santa Maria and São Miguel populations across both viruses suggests island-specific evolutionary trajectories. These findings demonstrate how pathogen invasions and geographic isolation interact to structure viral communities and influence honeybee virome evolution.

TALK 21| RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING?

Pérez-Pérez, A (1); Bartolomé, C (2); Sagastume, S (1); Meana, A (3); Martín-Hernández, R (1); Maside, X (4), Higes, M (1)

(1) Laboratorio de Patología Apícola, Centro de Investigación Apícola y Agroambiental de Marchamalo, (CIAPA), Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal de Castilla-La Mancha (IRIAF), Marchamalo, Spain; (2) Fundación Pública Galega de Medicina Xenómica (FPGMX); Hospital Clínico Universitario de Santiago; Edificio de Consultas, planta (-2)R/ Choupana s/n 15706 - Santiago de Compostela, Galiza, Spain; (3) Department of Animal Health, Faculty of Veterinary Medicine, Complutense University of Madrid, 28040 Madrid, Spain; (4) Dpto. de Zoologia, Genética e Antropologia Física Faculdade de Biologia Universidade de Santiago de Compostela; Rua Lope Gómez de Marzoa s/n Bloque A – 4º Andar (ascensor 2) 15782 - Santiago de Compostela, Galiza, Spain.

Keywords: *Apis mellifera*, *Varroa destructor*, amitraz, acaricide resistance, *Octβ2R* gene.

Abstract

The ectoparasitic mite *Varroa destructor* represents one of the most significant threats acting on *Apis mellifera* populations worldwide, and its control is essential for colony survival. Chemical acaricides, particularly amitraz, are widely used; however, resistance has been increasingly reported. Different studies suggest that mutations in the octopamine receptor gene *Octβ2R* are directly associated with this resistance. From an evolutionary perspective, the presence of the mutation should increase or remain stable as long as the selective factor, the acaricide, is present. On the other hand, if this selective factor is absent, the allele frequency should decrease. In this study, we analysed the genetic variation of *Octβ2R* in *Varroa destructor* populations exposed to different management systems: organic (oxalic acid) and conventional (amitraz). To explore whether the use of acaricides is shaping allele frequencies, a total of 83 mites from 14 apiaries (three of them have not been treated with amitraz for at least five years) were individually genotyped by amplifying and sequencing a 1064 bp fragment of *Octβ2R*. The analysis of the sequences showed that a mutation in the DNA fragment related to F290L was detected at a high frequency (89%), with no significant difference between organic or conventionally treated apiaries. No additional mutations reported in the literature were identified in this study. The high and widespread frequency of the F290L allele, combined with its predominance in homozygous individuals, suggests that this mutation is not directly associated with the use of amitraz in honey bee hives. These results highlight the importance of considering both historical and contemporary evolutionary processes when interpreting resistance patterns. Further research integrating temporal sampling and population genetic modelling will be critical to determine whether F290L confers a true adaptive advantage and how selection, drift, and gene flow interact to shape the evolutionary dynamics of resistance in *Varroa* populations.

Acknowledgements/Funding
Study funded by a national project with funds from the Predoctoral Contract Aid for the Training of Doctors PRE2022-103811 and Project PID2021-128882ORI00.

TALK 22| ECO-EVOLUTIONARY DYNAMICS OF *ESCHERICHIA COLI* INVASION ACROSS HUMAN GUT MICROBIOTAS

Barreto, HC (1); Steiner, C (1); Magnan, M (1); Tenaillon, O (1)

(1) Université Paris Cité, CNRS, Inserm, Institut Cochin, F-75014 Paris, France

Keywords: colonization resistance; microbiota; eco-evolutionary dynamics

Abstract

The human gut microbiota provides protection against pathogen colonisation, a phenomenon known as colonisation resistance. However, the mechanisms enabling commensal bacteria to bypass colonisation resistance remain poorly understood. Using MiniBioReactor Arrays, *in vitro* systems that simulate the human gut environment, we investigated the colonisation ability of 26 barcoded commensal *Escherichia coli* natural isolates across 16 distinct gut microbiotas from healthy donors. *E. coli* invaded and colonised all donor microbiotas, with colonisation levels varying by up to three orders of magnitude between donors, indicating donor-specific differences in susceptibility to invasion. The diversity of the invading *E. coli* population decreased in most donors over time. Barcode-level tracking of individual *E. coli* strains revealed that initial diversity loss was driven by strain-level differences in competitive success rather than within-strain evolution, as barcode dynamics showed little evidence of adaptive selection within winning strains. Furthermore, invasion success was decoupled from the initial abundance of *Enterobacteriaceae*, the phylogenetically closest competitors of *E. coli* within the gut microbiota. In contrast, we observed an inverse relationship between microbiota α-diversity and invasion susceptibility, with low-diversity communities being more permissive to *E. coli* establishment. Our results indicate that invasion success depends on both microbiota diversity and *E. coli* genomic background, highlighting the importance of these factors in determining colonisation outcomes.

Acknowledgements/Funding

Hugo Barreto was supported by the DREAM ANR-20-AMR-0002 grant from ANR, and by the HORIZONMSCA-2023-PF-01 project number 101148351 - MICROINVADER, funded by the European Union (https://european-union.europa.eu/). Views and opinions expressed are, however, those of the authors only and do not necessarily reflect those of the European Union or the European Research Executive Agency. Neither the European Union nor the granting authority can be held responsible for them. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

TALK 23| ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS

Tomé, R (1); Wonner, T (1); Adánez, J (1); Gueye, J-B (1); Lima, A (1); Henriques, S (1); King, J (1); Fragata, I (1)

(1) CE3C - Centre for Ecology, Evolution, and Environmental Changes & CHANGE – Global Change and Sustainability Institute, Faculty of Sciences, University of Lisbon, Portugal.

Keywords: predator-prey interactions; broad-sense heritability; prey preference; functional response

Abstract

Prey-predator interactions are prevalent in ecosystems, as most organisms are either consuming prey, being predated, or both. Prey population age structure dictates the availability of each prey stage and has been shown to impact the persistence of predator-prey systems. In addition, different levels of genetic variation in the predator and/or prey population can also determine the persistence of the system. However, most studies do not link the genetic variation observed in the system to traits involved in the predator-prey interactions and predator preference. Such knowledge is key to predicting how predator-prey systems and their evolutionary dynamics can unfold over time. Here, we aim to tackle this gap by performing functional response experiments and direct behavioural observations in a system composed of an outbred population or several isogenic lines of the predatory mite *Amblyseius swirskii,* and its prey, the spider-mite, *Tetranychus urticae*. We observed a clear prey preference for juveniles and eggs in the outbred predator population through functional response assays, although this preference changed depending on prey population structure. In contrast, when we performed direct observations in the predator isogenic lines, we found a preference for adult females compared to juveniles. The discrepancy between the functional response assays and direct observation can be explained by the low success in predation of adult females. Beyond this, we also saw that the duration of attack and handling time were both lower for eggs compared to adult females and juveniles. Finally, we found genetic variation for the success rate of the predators and duration of attack, but not for prey preference and handling time. Overall, these results suggest that prey population age structure and predator preference may interact, shaping predator-prey population dynamics. Eventually, these may alter the eco-evolutionary dynamics of this system through the evolution of predator success rate and attack time, traits that are not typically considered in predator-prey literature.

TALK 24| PHYLOGENETIC INFERENCE WITH NOT-SO-RARE MUTATIONS AND WEE TINY ORGANISMS

Rui Borges (1)

(1) University of St Andrews, United Kingdom

Keywords: recurrent mutations; boundary mutations; phylogenetic inference; viral evolution

Abstract

A common assumption in mathematical models of molecular evolution is that mutations are rare. One example is the boundary mutation assumption, which posits that mutations occur so infrequently that, by the time a new mutation arises, the previous one has already been fixed or lost in the population. However, this assumption ignores recurrent mutations and can be problematic for highly diverse organisms, such as bacteria and viruses. Here, we challenge the assumption of infrequent mutation in phylogenetic inference. To do so, we compare two mutation models: one that incorporates recurrent mutations and another that allows only boundary mutations. We evaluate these models across simulated datasets and three empirical case studies of medical and epidemiological relevance, demonstrating that failing to account for recurrent mutations leads to systematic biases in phylogenetic inference. We conclude by highlighting the importance of incorporating recurrent mutations in phylogenetic analyses of highly diverse organisms.

TOPIC 5 | HYBRIDISATION, INTROGRESSION, AND PHENOTYPIC DIVERSITY

RICARDO PEREIRA (Stuttgart State Museum of Natural History, Baden-Württemberg, Germany)

How are species formed, and how do they persist in a changing environment? These questions first sparked my curiosity in childhood—from watching my grandfather breed canaries with a mix of fascination and horror to reading about human evolution. They crystallised during my academic career, where I studied a variety of biological systems (lizards, salamanders, copepods, grasshoppers) in which hybridisation reveals the genes underlying species formation or provides pathways for rapid adaptation. After earning my PhD on salamander hybrid zones at UC Berkeley and the University of Porto, I investigated hybrid fitness using experimental copepod populations at the Scripps Institution of Oceanography. My Marie-Curie research at the National History Museum in Denmark and later group leader roles at LMU Munich allowed me to combine lab and field studies on grasshopper hybrids to identify genes involved in reproductive isolation and explore how incompatibilities are resolved in hybrids. Now, as head of Biodiversity Monitoring at the State Museum of Natural History Stuttgart, I use museum time series and monitoring collections to understand the drivers of intraspecific variation and identify genes enabling species to adapt to changing environments. As a longtime beneficiary of ENBE, I'm excited to share ongoing research on a bird hybrid zone that sheds light on the genetic basis of species formation and persistence in a warming world.

See more at https://www.naturkundemuseum-bw.de/en/research/biodiversity-monitoring/team-biodiversity-monitoring/ricardo-pereira

PLENARY TALK| MUSEUM COLLECTIONS AS WINDOWS INTO SPECIES FORMATION AND INTROGRESSION IN A MOVING HYBRID ZONE OF BIRDS

Divergence in sexual traits often evolves earliest during species formation, leading evolutionary biologists to rank their importance "far ahead of all other" species barriers. However, it remains unclear whether sexual selection alone can maintain species boundaries over time—especially amid extensive hybridisation driven by ongoing environmental change. In this study, we demonstrate the value of natural history museum collections by integrating collectomics, museomics, and the extended specimen concept to investigate speciation in a moving hybrid zone between black-headed and red-headed buntings. Using collectomics, we analyzed distributional and environmental data from specimen records and ecological niche models, revealing previously unrecognized ecological differences between species and evidence of asymmetric range expansions during the current interglacial period. Genomic analyses of both historical and contemporary specimens through museomics supported these findings and showed that up to 1.5% of the genome exhibits elevated differentiation consistent with selection against gene flow. Morphological measurements from fresh and museum specimens, following the extended specimen approach, indicated that sexual selection on male plumage traits imposes stronger reproductive barriers than natural selection on morphometric traits associated with ecological adaptation. Ongoing research using morphological and genomic data from admixed individuals at the center of the hybrid zone aims to map phenotypes under natural and sexual selection to their causal genes. Analyses of specimens spanning 25 generations in this moving hybrid zone will further elucidate the interplay between traits under natural and sexual selection in maintaining species boundaries despite notable distributional changes. This integrated approach highlights how natural history collections provide essential data for a comprehensive understanding of the processes driving early speciation and enabling species persistence in changing environments.

TALK 25| HYBRIDIZATION AS A SOURCE OF PHENOTYPIC DIVERSITY: THE GENOMIC BASIS OF YELLOW COAT COLOUR IN IBERIAN WOLVES

Garcês, C (1,2,3); Lobo, D (1,3,4); López-Bao, J.V. (5); Godinho, R (1,2,3)

(1) CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos, InBio Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal; (2) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal; (3) BIOPOLIS - Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, Vairão, Portugal; (4) Dept. of Biotechnology and Life Sciences, University of Insubria, Busto Arsizio, Italy; (5) Biodiversity Research Institute (CSIC-Oviedo University-Principality of Asturias), Mieres, Spain

Keywords: hybridization; introgression; structural variants; haplotype

Abstract

In Northwest Galicia (Spain), an atypical uniform yellow coat colour has been observed in Iberian wolves (*Canis lupus signatus*) living alongside wildtype conspecifics. Although yellow pigmentation is widespread in domestic dogs, where it results from structural variation at the ventral and hair-cycle promoters (VP1–HCP1) of the Agouti Signalling Protein (*ASIP*) gene, the genetic basis of this phenotype in wolves had not been determined. Given that wolf–dog hybridisation has been documented in this region, we hypothesised that the yellow phenotype in Iberian wolves could result from the introgression of dog *ASIP* promoter haplotypes. To investigate this, we used a targeted enrichment strategy to capture a 64-kb genomic region containing *ASIP* and its two 5' regulatory promoters. This panel was applied to both high- and low-quality DNA samples previously identified as carrying the “dog-yellow” genotype. After variant calling, we phased the data using multiple phasing methods to ensure robustness across algorithms. We then reconstructed haplotype relationships using maximum-likelihood phylogenetic inference and generated haplotype networks for the full *ASIP* region as well as for the VP and HCP promoters separately. Across analyses, Iberian wolves with the yellow phenotype carried the same VP1–HCP1 structural variant combination characteristic of yellow domestic dogs. Both the phylogeny and the haplotype networks showed that the yellow wolf haplotype group together with those of domestic dogs, rather than with the haplotypes of wild-type wolves. The absence of divergent wolf-specific yellow haplotypes suggests that this variant likely entered the wolf population through a single dog-to-wolf introgression event, followed by subsequent spread within the Galician wolf population. Our results demonstrate that the unusual yellow coat colour in Galician wolves is not a retained ancestral polymorphism but reflects recent introgression at the *ASIP* locus from domestic dogs, showcasing how hybridisation can introduce visible phenotypic variation into wild populations.

Acknowledgements/Funding
This work is under development with partial funding from FEDER through the COMPETE 2030 Programme, under the project WOLF-IB_2023.17017.ICDT. CG worked under a research fellowship funded by ECOGEN-CIBIO-BIOPOLIS own funds. DL is supported by a postdoctoral fellowship under the project PRIN 2022 “Epigenetics and conservation of small populations: microevolution and adaptive divergence in relict bear populations”, funded by the EU – Next Generation EU (CUP J53D2300669006). RG works under a PI research contract from FCT (2022.07926.CEECIND).

TALK 26| HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES

Li, F (1); Lopes, AR (1); Taliadoros, D (2); Costa, M (1); Yadró, CA (1); Cunha, L (1); Henriques, D (1); Martin-Hernandez, G (2); de Graaf, DC (3); Webster, M (2); Pinto, MA (1)

(1) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Bragança, Portugal; (2) APINOV – Centre de Recherche & Formations Apicoles, France; (2) Department of Medical Biochemistry and Microbiology, Science for Life Laboratory, Uppsala University, Uppsala, Sweden; (3) LMEB - Laboratory of Molecular Entomology and Bee Pathology, Faculty of Sciences, Ghent University, Ghent, Belgium;

Keywords: evolutionary lineages, *Apis mellifera*, introgression, diversity, haplotypes

Abstract

In its vast distributional range, spanning Africa, Europe, the Middle East, and western Asia, the honey bee *Apis mellifera* diversified into 30 subspecies grouped into four major evolutionary lineages. Two of these lineages, M (western/northern European) and C (southeastern European), are parapatric in Europe. However, increasingly intensified queen trading is likely eroding the natural genetic boundaries and altering the continent's diversity patterns. To evaluate the impact of this recent human-mediated gene flow, we conducted an unprecedented survey spanning 33 countries and sampling more than 1,300 colonies, including 139 from conservation apiaries of the M-lineage subspecies *A. m. mellifera*. We used a dual-marker approach combining the hypervariable mitochondrial $tRNA^{Leu}$–cox2 intergenic region with nuclear genome-wide single-nucleotide polymorphisms (SNPs). Both markers were highly concordant at the lineage level and European scale, showing that in the native area of M-lineage, which covers western and northern Europe, C-lineage ancestry is now predominant. This pattern is congruent with widespread commercial dissemination of C-lineage subspecies (*A. m. carnica*, *A. m. ligustica*), which is leading to introgressive hybridisation and, in many regions, to almost complete replacement of native subspecies. The exceptions to this trend are the Iberian Peninsula, Ireland, and conservation apiaries, which retain almost exclusively native M-lineage ancestry. Remarkably, even within the native C-lineage range in the Mediterranean and southeastern Europe, the Italian subspecies *A. m. ligustica*, the most widely favoured subspecies worldwide, shows worrying levels of introgression from its C-lineage neighbour *A. m. carnica*. Equally striking is the widespread presence of African-lineage mitotypes, whose routes of introduction remain unclear. Altogether, these findings raise serious concerns about the genetic integrity of native subspecies and the consequences of admixture for adaptation in a rapidly changing environment shaped by climate change and emerging parasites and pathogens. Further, these changes may affect the gene pools of wild *A. mellifera* populations, recently classified as Endangered by the IUCN.

Acknowledgements/Funding
This work was conducted in the framework of the project Better-B, funded by the European Union, the Swiss State Secretariat for Education, Research, and Innovation, and UK Research and Innovation under the UK government's Horizon Europe funding guarantee (grant number 10068544). It was further supported by national funding by FCT, Foundation for Science and Technology, through the individual research grant 2024.05645.BD of Fernanda Li, as well as by national funds through FCT/MCTES (PIDDAC): CIMO, UIDB/00690/2020 (DOI: 10.54499/UIDB/00690/2020) and UIDP/00690/2020 (DOI: 10.54499/UIDP/00690/2020); and SusTEC, LA/P/0007/2020 (DOI:10.54499/LA/P/0007/2020).

TALK 27| THE GENOMIC AFTERMATH OF THE ICE AGES IN EUROPEAN HARES

Costa, J (1,2,3,4); Marques, JP (1,2,3); Farelo, F (1,2,3); Boursot, P (4); Melo-Ferreira, J (1,2,3)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, 4485-661 Vairão, Portugal; (2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, 4485-661 Vairão, Portugal; (3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, 4099-002 Porto, Portugal; (4) Institut des Sciences de l'Évolution Montpellier (ISEM), Université de Montpellier, CNRS, IRD, Montpellier, France.

Keywords: introgression; genomics; evolution; hybridization; hares

Abstract

Hares provide a powerful system for studying how climatic fluctuations and range dynamics shape genomic variation. During the Pleistocene glacial cycles, the repeated advances and retreats of ice sheets across Europe drove range contractions and expansions among European hare species, creating opportunities for contact and hybridisation. These dynamics left clear genomic footprints, particularly in mitochondrial DNA (mtDNA): all European hare species exhibit mtDNA introgression from the mountain hare (*Lepus timidus*), a cold-adapted species that colonised much of central Europe during the Last Glacial Maximum and is now restricted to northern regions and the Alps. This signal is most striking in the broom hare (*L. castroviejoi*) and the Italian hare (*L. corsicanus*), two sister species isolated in the Iberian and Italian Peninsulas, respectively, whose native mitochondrial lineages were completely replaced by those of the mountain hare. Using Bayesian demographic modelling and neural-network-based machine learning applied to high-coverage genomes, we identified a major genome-wide introgression event from the mountain hare into the ancestor of the broom and Italian hares approximately 900,000 years ago, which likely explains the complete mtDNA replacement. Additionally, smaller introgression events occurred as recently as 20,000 years ago. The introgressed regions that are fixed or nearly fixed in both species represent roughly 0.5% of their current genomes and are gene-poor, which is consistent with purifying selection acting to eliminate introgressed variants. However, these regions also include loci associated with mitochondrial function, which could indicate co-introgression of mitonuclear interacting genes. These results show that genomic analyses are powerful in detecting and characterising very ancient introgression events. They also suggest that the persistence of the anciently introgressed variants could have been promoted by the maintenance of mitonuclear compatibility following complete mitochondrial genome replacement.

TALK 28| IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS

Moreno, JM (1,2); Mendes, SL (1); Moço, M (1); Bernardo, C (1); Faustino, E (1); Santos, R (2); Sousa, VC (1)

(1) cE3c –Centre for Ecology, Evolution and Environmental Changes & CHANGE - Global Change and Sustainability Institute, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal; (2) MARE – Marine and Environmental Sciences Centre & ARNET—Aquatic Research Network, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal

Keywords: hybridization; freshwater fish; climate change; proteomics

Abstract

Hybridisation and introgression can generate novel regulatory variation, yet their effects on proteome-level responses to environmental stress remain poorly understood. We investigated thermal stress responses (20ºC vs. 26ºC) in two Iberian chub species, *Squalius caetobrigus* (Sado basin; Grândola population) and *S. pyrenaicus* (Tagus basin; Canha population), and a population from São Martinho (Sado basin) with introgression from both species (hybrid population) using a simulated heatwave experiment and label-free mass spectrometry. Across populations, more than 3,300 proteins were quantified. São Martinho exhibited the strongest response to warming, with 54 differentially expressed proteins compared to 11 in Grândola and 23 in Canha. Although all populations showed a conserved heat-shock response, the hybrid proteomic profile was distinct and unexpectedly more similar to Canha than to Grândola, as São Martinho and Grândola inhabit the same river basin. Midparent scaling revealed that ~60% of quantified proteins in the hybrid population displayed transgressive expression, exceeding the parental range in either direction, while additive and dominance-like patterns were less common. This highlights a strong contribution of novel regulatory effects in hybrids. Difference-in-Differences analysis further showed nearly balanced proportions of convergent and divergent responses across comparisons, indicating that hybrids combine parental-like and unique regulatory strategies. Functional enrichment analyses identified shared mitochondrial metabolic pathways across all populations under warming. However, hybrids showed distinctive enrichment in glutathione metabolism and fatty-acid biosynthesis, suggesting enhanced oxidative stress regulation and metabolic adjustment compared to parental species. Together, these results demonstrate that hybridization and introgression can reshape proteomic plasticity, producing both parental-like and novel molecular responses. This hybrid-specific flexibility may enhance resilience to warming and contribute to the persistence of introgressed populations under climate change.

Acknowledgements/Funding
This project is funded by FCT Strategic project UIDB/00329/2020 granted to cE3c and UIDB/04292/2020 awarded to MARE, the project LA/P/0069/2020 granted to the Associate Laboratory ARNET. The project is further financed by the Human Frontier Science Program Young Research Grant (RGY0081/2020) and the FCT SR&TD Project grant (PTDC/BIA-EVL/43457/2021, https://doi.org/10.54499/PTDC/BIA-EVL/4345/2021). JMM is funded by FCT PhD fellowship (SFRH/BD/143199/2019) and SLM is funded by an FCT fellowship (SFRH/BD/145153/2019). VCS and RS are further supported by Scientific Employment Stimulus – Institutional Call (https://doi.org/10.54499/CEECINST/00032/2018/CP1523/CT0008 and https://doi.org/10.54499/CEECINST/00032/2018/CP1523/CT0006, respectively).

TALK 29| AVIAN STRCTURAL COLORATION DIVERSITY EXPLAINED BY CHANGES IN FEATHER KERATINIZATION

Rita Afonso (1)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal

Keywords: structural coloration; bird feathers; colour genetics

Abstract

Animals produce colour through light-absorbing pigments or light-scattering structural mechanisms. While pigment-based coloration has a well-characterized molecular basis, far less is known about the genomic determinants of structural colours. Thanks to the availability of many colour mutations with simple inheritance patterns and large phenotypic effects that arose during avian domestication, bird feathers represent a powerful system to tackle these questions. Here, we integrate genetic mapping, high-resolution single-cell transcriptomics, gene expression and function analyses, microscopy, and photonics to characterize the molecular basis of artificially selected structural blue colour variation in lovebirds. We found that transglutaminase-mediated keratin cross-linking during feather morphogenesis is essential for assembling photonic nanostructures in the medullary region of feather barbs. Modulation of transglutaminase expression and activity also influences the quasi-ordered arrangement of keratin fibres and air cavities, thereby fine-tuning the resulting structural colour hues. The generalization of our findings to non-parrot species revealed a novel genetic mechanism generating colour diversity via nanostructural reorganization of bird feathers, contributing to our understanding of vertebrate colour evolution beyond classical pigmentary pathways.

TALK 30| MORPHOLOGICAL RESPONSES OF *MUS MUSCULUS* TO THE ENVIRONMENTAL CONDITIONS OF CABO VERDE

Almeida, L (1,2,3); Macedo, T (1,2,3); Lopes, E (1,4); Boratyński, Z (1,2); Vasconcelos, R (1,2,5)

(1) CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Universidade do Porto, Portugal; (2) BIOPOLIS - Program in Genomics, Biodiversity and Land Planning, Universidade do Porto, Portugal; (3) Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Portugal; (4) ISECMAR - Instituto de Engenharia e Ciências do Mar, UTA, Universidade Técnica do Atlântico, Cabo Verde; (5) Departamento de Ciências da Vida, Faculdade de Ciências e Tecnologias da Universidade de Coimbra, Portugal.

Keywords: evolution, invasive species, Island biogeography, photo analysis, rodents

Abstract

The evolution of species on islands reveals much about how evolutionary and geographical processes shape biodiversity. Studying the colonisation of islands by exotic species provides an opportunity to better understand evolutionary processes, how species cope with different ecological conditions and resource limitations, and the influence of these factors on morphological changes. Studies have shown that *Mus musculus* accidentally introduced to islands exhibit morphological variations compared to their continental populations of origin. These variations include changes in tooth size and coat pattern, which are associated with local adaptations. This study aimed to understand how environmental differences influenced the morphological changes of *Mus musculus* on the different islands of Cabo Verde. More than 300 individuals from most of the islands in the archipelago were studied. Analyses included measurements of weight, head width, ear height, foot length, body length, and tail length in order to identify significant differences between island populations. Photographs of over 200 individuals were also used to assess coat variation between islands. The study revealed significant size differences and notable variations in coat colour across the islands. Lighter or yellowish substrates, such as those found on Sal Island in its more arid habitats, predict lighter and more chromatic coats, whereas darker substrates, such as those found on Fogo Island due to its lava cover, predict darker and less chromatic coats. Five hundred years is sufficient time for differences in size and coat colour to emerge in mice on the Cabo Verde islands.

TALK 31| GENOME STORIES: HOW LOSING GENES BUILDS NEW PHENOTYPES

Ruivo, R (1)

(1) CIIMAR/CIMAR LA, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, Avenida General Norton de Matos, S/N 4450-208 Matosinhos, Portugal

Keywords: Cetacea, seahorses, genomes, gene Loss, adaptation

Abstract

How are Phenotypes "built"? A question that has fascinated biologists from Aristotle's Historia animalium to Darwin's On the Origin of Species. And yet, we marvel at the "adaptive unknowns" of the aerodynamic swimming of a penguin, the deep diving hunt of a sperm whale, or the energy-saving movements of a seahorse: examples that crystallize key concepts in Biology, such as that of Adaptation and the Phenotype. A central challenge of contemporary evolutionary biology is thus to understand how novelty emerges and evolves at the molecular level; how an inherent gene set gives rise to the phenotype (the genotype–phenotype link), and how these processes interact with adaptive landscapes. This challenge has greatly benefited from the revolution in omics technologies, which now offer an unforeseen capacity to decipher the molecular origin of complex traits. In this talk, I will explore several examples that highlight the power of comparative genomics in uncovering the dynamics of extant genomes. Specifically, I will focus on episodes of secondary gene loss, paralleling abrupt habitat transitions (e.g., land-to-water) and life history trait adaptations in specific Metazoan lineages (e.g., metabolic rewiring).

Acknowledgements/Funding
FCT- Fundação para a Ciência e Tecnologia I.P. (2023.07615.CEECIND/CP2848/CT0007). This research was funded by national funds through FCT and by the European Commission's Recovery and Resilience Facility, within the scope of UID/04423/2025, UID/PRR/04423/2025, LA/P/0101/2020, and project ATLANTIDA II (ref. NORTE2030-FEDER-01799200), co-financed by the European Union through the NORTE 2030 Regional Program and the European Regional Development Fund (ERDF) and funded by the Research Council of Norway Marma-Detox (project no. 334739).

Poster Communications

TOPIC 1 | GENOME ARCHITECTURE, STRUCTURAL EVOLUTION AND BIOGEOGRAPHY

POSTER 1| OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH

Teixeira, J (1); Ferreira, P (2); Machado, A (3); Santos, A (3); Ruivo, R (3); Wilson, J (4); Castro, F (1)

(1) University of Porto, CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, Matosinhos, Portugal; (2) University of Otttawa; (3) CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, Matosinhos, Portugal; (4) Wilfrid Laurier University, Canada

Keywords: stomach; *Chondrichthyes*; gene loss; agastric; comparative genomics

Abstract

The origin of evolutionary novelty and the mechanisms by which new traits and structures arise remain central, unresolved questions in evolutionary biology. The stomach, an organ with gastric function and widely retained in jawed vertebrates, provides a compelling example, as its loss has occurred independently in several lineages, for instance, monotremes and a few teleost groups (e.g, *Cyprinidae, Syngnathidae*). In *Chondrichthyes*, a similar loss of a stomach phenotype was found, yet it was observed only in *Holocephali* (chimaeras), whereas *Elasmobranchs* (sharks, rays, and skates) retain the stomach and its associated gastric functions. This loss is often attributed to the disappearance, alteration, or inactivation of key genes involved in acid secretion, such as Atp4A and Atp4B, which encode core subunits of the gastric proton pump. To investigate the genomic basis of stomach loss in chondrichthyans, we will employ a comparative genomic and transcriptomic framework. First, by performing phylogenetic and synteny analyses of gastric-related genes to determine whether gene loss events occurred independently in Holocephali and to assess the conservation of the surrounding genomic regions. Second, transcriptomic data from multiple tissues and species will be examined to determine whether candidate gastric genes remain active in the agastric Holocephali lineage. This study aims to understand the molecular network responsible for the gastric physiology in cartilaginous fish; establish when and how these adaptations emerged and whether gene loss is a key adaptive process; compare the patterns that influence these two major cartilaginous groups with the known events in teleost fish; lastly, assess how and when are genes expressed in gastric species of sharks and rays. Regarding previous findings in other organisms and ongoing analysis, we expect the Holocephali lineage to exhibit similar absence or pseudogenization of key gastric genes, while being retained and functional in gastric Elasmobranchs.

POSTER 2| PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER

Morel, M (1); Rambaud, L (2); Rudall, P (3); Bateman, R (3); Boussau, B (1*); Scutt, C (2*); Tavares, R (4*)

(1) Laboratoire de Biométrie et Biologie Evolutive, Université de Lyon; Université Lyon 1; CNRS; UMR 5558, Villeurbanne, France; (2) Laboratoire de Reproduction et Développement des Plantes, Ecole Normale Supérieure de Lyon; UMR 5667, Lyon, France; (3) Royal Botanic Gardens, Kew, United Kingdom; (4)CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Associação Biopolis, Campus de Vairão, Universidade do Porto, Vairão, Portugal

*co-last authors

Keywords: gene family evolution; origin of flower; phylogeny; synteny; plant evo-devo

Abstract

The YABBY multigene family encodes transcription factors found across angiosperms and gymnosperms, as well as in some lycophytes, bryophytes, and green algae. In seed plants, YABBY genes are typically expressed in the abaxial domain of lateral shoot organs—including leaves and reproductive structures—where they are required for organ expansion. Outside their two conserved domains, YABBY coding sequences have diverged extensively, complicating the reconstruction of their evolutionary history. The branching order of YABBY lineages in seed plants remains unresolved. Here, we combine specific phylogenetic reconstruction approaches with analyses of gene structure and conservation of genomic context (synteny) to refine the evolutionary trajectory of the YABBY family. Integrating these results with fossil evidence and functional data from angiosperms, we propose an evo-devo scenario for ovule development, a crucial trait in the angiosperm flower. Our findings underscore both the challenges and the biological significance of tracing the evolution of gene families over hundreds of millions of years, and highlight the methodological precautions required for such analyses.

POSTER 3| FIRST PHYLOGEOGRAPHIC ASSESSMENT OF THE DIADEMED SAND SNAKE (COLUBRIDAE: *LYTORHYNCHUS*) ACROSS THE SAHARO-ARABIAN DESERT BELT

Mota, R (1,2,3); Gonçalves, D (4); Brito, JC (1,2,3); Licata, F (1,2); Crochet, P (5); Liz, AV (1,6)

(1) CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal; (2) BIOPOLIS - Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, Vairão, Portugal; (3) Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Portugal; (4) CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, Matosinhos, Portugal; (5) CEFE, CNRS, Univ Montpellier, EPHE, IRD, Montpellier, France; (6) GEMAP, Departamento de Xeografía, Universidade de Santiago de Compostela, Spain

Keywords: *Lytorhynchus*; saharo-Arabian desert; phylogeography; systematics; desert biogeography

Abstract

The Saharo-Arabian desert belt has experienced considerable palaeoclimatic and landcover changes since the Miocene, which have influenced the evolution and distribution of its biota. The diademed sand snake, *Lytorhynchus diadema*, is a non-venomous, nocturnal colubrid that inhabits xeric environments in the region, being typically found in vegetated dunes, gravel plains, and salt flats. Despite its extensive range, the genetic diversity and population structure of this species remain largely unstudied. We gathered over 30 tissue samples across the species' range, including Egypt, Mauritania, Morocco, Sudan, Tunisia, Israel, Kuwait, Oman, Saudi Arabia, and the United Arab Emirates, which are now curated at CIBIO and partner collections. Our genetic analyses focused on three mitochondrial markers (16S, cyt-b, COI) and one nuclear locus (C-mos) to establish preliminary phylogenetic insights. Morphological data extracted from photographic analyses, along with genetic results, were used to assess potential diversity and identify a new candidate species from the Atlantic Sahara coastal desert. These findings advance our understanding of diversification processes in the world's largest continuous arid region, which remains mostly unexplored.

POSTER 4| GENOMIC ARCHITECTURE OF SHELL COLOUR POLYMORPHISM IN *LITTORINA* MARINE SNAILS: THE ROLE OF CHROMOSOMAL INVERSIONS AND GENE FLUX

Bezerra, L (1,2,3); Sousa, VC (3); Pereira, P (1,2); Faria, R (1,2,4)

(1) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal; (2) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Campus de Vairão, Vairão, Portugal; (3) CE3C - Centre for Ecology, Evolution and Environmental Changes & CHANGE Global Change and Sustainability Institute, Department of Biology, Ciências, University of Lisbon, Lisbon, Portugal, Portugal; (4) Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal

Keywords: *Littorina*; colour polymorphism; genetic basis; gene flux; chromosomal inversions

Abstract

Colour polymorphism is one of the most remarkable forms of phenotypic variation found in nature, and it is an informative phenotype for studying the relationships between genetics, development, and natural selection. In the marine snail *Littorina saxatilis*, a model system to study adaptation in the intertidal, shell colour variation was partially associated with one chromosomal inversion. However, it is not clear whether this happens across other *Littorina* species. Here, we will present a recently initiated project using whole-genome sequencing data to investigate the genetic basis of colour polymorphism in *L. obtusata*, *L. fabalis*, and *L. saxatilis*, with three main goals: i) identify regions associated with colour polymorphism, ii) determine whether chromosomal inversions are involved, and iii) infer whether gene flux occurred between arrangements associated with colour polymorphism. Preliminary results of pooled sequencing in *L. fabalis* show a large region of high differentiation between two colour morphs (yellow and brown), corresponding to a region where an inversion has been described in *L. saxatilis*. In *L. obtusata*, results show three smaller differentiation peaks within and near the same region, but without signatures of an inversion. These results suggest that shell colour polymorphism can have different genetic architectures across these species that are not always associated with a chromosomal inversion. Future steps include Pool-seq analysis of *L. saxatilis* and individual sequencing analysis of *L. fabalis* individuals, including modeling to detect gene flux between inversion arrangements. Ultimately, we hope to clarify the evolutionary dynamics of chromosomal inversions and their role in maintaining phenotypic diversity, as well as to clarify the importance of gene flux within inversions in maintaining balanced polymorphisms.

POSTER 5| A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME

Campos, R (1); Louzada, S (1,2); Barros, P (3); Cabral, J (4); Chaves, R (1,5); Pereira JC (1,5); Adega, F (1,2)

(1) CytoGenomics Lab, Department of Genetics and Biotechnology (DGB), University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal; (2) BioISI – Biosystems & Integrative Sciences Institute, Polo UTAD, Vila Real, Portugal; (3) Laboratory of Applied Ecology, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal; (4) RISE-Health, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal; (5) CITAB - Centre for the Research and Technology of Agro-Environmental and Biological Sciences, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal

Keywords: bats; transposable elements; iInflammation-related genes; innate immunity; comparative genomics

Abstract

Bats (Order Chiroptera) possess long and healthy life spans and exhibit a remarkable ability to tolerate viral infections without developing excessive inflammation, a trait that contrasts sharply with the (often) severe inflammatory responses in humans. Inflammatory responses in mammals are orchestrated by pathways such as NF-κB, cGAS–STING, and the NLRP3 inflammasome, which, when dysregulated, contribute to chronic inflammation and autoimmune diseases in humans. Understanding how bats modulate these pathways at the genomic level can provide valuable insights into inflammation control mechanisms. Recently, studies suggest that immune-related gene profiles in some bat species differ from other mammals (loss/gain; nucleotide sequence; gene expression), potentially explaining their viral tolerance. Focusing on key inflammation-related genes, including *NLRP3 and OAS1,* we explored gene regulation patterns across two bat species: *Myotis daubentonii* and *Rhinolophus ferrumequinum,* which were selected based on their availability and representation of distinct phylogenetic lineages and immune strategies. Transposable elements (TEs) are DNA sequences capable of mobilizing within the genome, affecting genome structure and gene expression, and contributing to evolution and adaptation. Although most TEs in mammals are inactive, some bats retain active DNA transposons and endogenous retrovirus-derived elements (ERVs) that integrate into the genome and are vertically inherited. Given that TE insertions can alter gene or protein function, we hypothesize that they may influence bats' ability to control virus induced pathogenesis. Here we present a preliminary comparative *in silico* analysis of human and bat genomes to identify differences in inflammation-related genes and their regulatory regions, with a focus on TE insertion patterns. Our findings may enhance our understanding of immune modulation and inspire novel anti-inflammatory therapies in humans.

POSTER 6| ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS

Yadró Garcia, CA (1,2,3); Henriques, D (1); Haddad, N (4); Obeidat, WM (5); AlShagour, B (4); Necati Muz, M (6); Arab, A (7); Eissa, AA (8); Hosri, C (9); Lamghari, F (10); Arruda, J (10); Rufino, J (11); Martin-Hernandez, R (12); Nanetti, A (13); Pinto, MA (1)

(1) CIMO/LA SusTEC - Centro de Investigação de Montanha, Instituto Politécnico de Bragança, Bragança, Portugal; (2) Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal; (3) CIBIO- Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Vila do Conde, Portugal; (4) NARC-National Agriculture Research Center, Amman, Jordan; (5) The University of Jordan, School of Agriculture, Department of Plant Protection, Amman 11942, Jordan; (6) Department of Parasitology, Faculty of Veterinary Medicine, University of Namik Kemal, Tekirdag, Turkey; (7) Department of Animal Science, College of Agriculture and Natural Resources, University of Tehran, Islamic Republic of Iran; (8) Plant Protection Research Institute, Agricultural Research Center, Dokki, Giza, Egypt; (9) UL- Lebanese University, Faculty of Agriculture, Beirut, Lebanon; (10) Fujairah Research Centre, Fujairah, UAE; (11) CeDRI SusTEC - Research Centre in Digitalization and Intelligent Robotics, Instituto Politécnico de Bragança, Bragança, Portugal; (12) CIAPA - Centro de Investigación Apícola y Agroambiental. IRIAF. Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal, Marchamalo, Spain; (13) CREA-AA - Research Centre for Agriculture and Environment, Bologna, Italy

Keyword: *Apis mellifera*, environmental adaptation, genome scans

Abstract

The Middle East is home to a large number of *Apis mellifera* subspecies that have evolved under extreme aridity and desertic conditions. Therefore, they represent a unique opportunity to disentangle the genetic basis of adaptation to such challenging environmental conditions. We arranged a collection of 514 drone samples (haploid males) split into two latitudinal transects. Transect 1 comprised 342 samples: 66 *A. m. lamarckii* (Egypt), 197 *A. m. syriaca* (Jordan), 30 *A. m. syriaca* (Lebanon), 21 *A. m. meda* (southeastern Turkey), and 27 *A. m. anatoliaca* (Anatolia, Turkey). Transect 2 comprised 173 samples: 14 *A. m. jemenitica* (Oman), 9 *A. m. jemenitica* (UAE), 75 *A. m. meda* (Iran), and 75 *A. m. caucasia* (northeastern Turkey). For all samples, whole genomes were resequenced, and environmental and bioclimatic variables were retrieved from WorldClim. For each transect, we applied three genotype–environment association methods (Samβada, pRDA, and LFMM) and one outlier-detection approach (PCAdapt) to identify SNPs associated with environmental adaptation. SNPs were annotated, and the intersection of genes between the four methods in each transect was analysed for gene enrichment. In both transects, enriched terms included genes related to biological regulation through endocrine, neuroendocrine, and neurotransmitter pathways. The regulation of gene expression was also enriched, including several transcription factors, especially HOX genes. Transmembrane and ionic transporters also seem to play a central role in environmental adaptation in these subspecies. Finally, neurogenesis, synapse establishment, and neural system development were also enriched. When gene enrichment analysis was set to exclude electronic annotations (automatically assigned, non-curated GO terms), enriched terms included processes such as behaviour, learning or memory, cognition, and associative and olfactory learning and behaviour. Our findings point to a complex suite of regulatory and sensory

pathways that collectively shape the environmental adaptation of honey bee subspecies that have evolved in arid environments.

Acknowledgements/Funding
C.A.Y.G. was funded by Fundação para a Ciência e a Tecnologia (FCT) through the individual research grant 2021.06948.BD (DOI: 10.54499/2021.06948.BD). This research was funded by the project MEDIBEES - Monitoring the Mediterranean Honey Bee Subspecies and their Resilience to Climate Change for the Improvement of Sustainable Agro-Ecosystems. MEDIBEES is part of the PRIMA programme supported by the European Union. This research was also supported by national funds through FCT/MCTES (PIDDAC): CIMO UID/00690/2025 (10.54499/UID/00690/2025) and UID/PRR/00690/2025 (10.54499/UID/PRR/00690/2025); SusTEC, LA/P/0007/2020 (DOI: 10.54499/LA/P/0007/2020).

POSTER 7| HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC

Themudo, G (1); Rey-Iglesia, A (2); dos Santos, MI (1,3); Netels, R (1); López, A (4); Martínez-Cedeira, J (4), da Fonseca, R (2); Campos, PF (1)

(1) CIIMAR, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões Avenida General Norton de Matos, S/N; (2) The Globe Institute, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark; (3) University of Minho; (4) CEMMA, Coordinadora para o Estudio dos Mamiferos Mariños, Apdo 165, 36380 Gondomar, Spain

Keywords: population genomics, ancient DNA, whaling, population dynamics, Cetacea

Abstract

The North Atlantic right whale (NARW, *Eubalaena glacialis*) was the primary target for early industrial whalers, particularly the Basques. Once abundant on both sides of the North Atlantic, inhabiting its temperate and subpolar waters, these whales are now functionally extinct in the Northeast Atlantic and critically endangered according to the IUCN Red List. Despite their fragmentary remains, bones are abundant in the archaeological and historical records and reveal a long history and extensive tradition connected to the exploitation of these marine resources. Using state of the art ancient DNA techniques, we aim to genetically characterize the functionally extinct population of NARW from the Northeast Atlantic. We sequenced 17 full genomes from historical specimens collected in the Cantabrian Sea, dating from the 13-18th century. These data were compared with genomes of modern individuals from the extant population in the Northwest Atlantic. Our results highlight differences in genetic diversity over time, shedding light on the impact of whaling on this species. Our results suggest that the NARW population was panmictic, and that there was a significant decrease in diversity since the Middle Ages to the present, with the extinction of most of the lineages present at the time. This work clearly points to the devastating effects commercial whaling had on the population of North Atlantic Right Whales in the Cantabrian Sea and the NARW population.

Acknowledgements/Funding
This research was partially supported by the Strategic Funding UIDB/04423/2020 and UIDP/04423/2020, through national funds provided by FCT and European Regional Development Fund (ERDF), in the framework of the programme PT2020. PFC was partially supported by national funds through FCT, I.P., under the Scientific Employment Stimulus Initiative, reference CEECIND/01799/2017, 2023.05877.CEECIND and SARDINOMICS 2022.03142.PTDC. Sequencing data was obtained thanks to an EASI Genomics grant PID 14751, conceded to PFC.

POSTER 8| VARIATION IN GARUM RECIPES ACROSS THE ROMAN EMPIRE AND THE MICROBIAL COMMUNITIES DRIVING THEIR FERMENTATION

Netels, R (1); dos Santos, I (1,2); Themudo, G (1); Campos, P (1)

(1) CIIMAR/UP - Centro Interdisciplinar de Investigação Marinha e Ambiental, University of Porto, Porto, Portugal; (2) – UM – University of Minho, School of Biological Sciences, Braga, Portugal

Keywords: fish; fermentation; microbiome; ancient DNA

Abstract

Romans were among the earliest societies to fully exploit marine resources. Small pelagic fish, such as sardines, mackerels, sprats, anchovies and whiting, species typically regarded as low-value, were commonly processed into fermented fish sauces, including *garum, liquamen*, *allec* and *muria*. Among these products, *garum* was the most highly valued and widely distributed across the Roman Empire. It was primarily used as a seasoning and condiment in a wide range of dishes, conferring a distinctive umami flavour derived from protein breakdown during fermentation. Roman producers were also able to modulate the sensory properties of *garum* by incorporating additional ingredients. These could be added either during the fermentation, like various shellfish (e.g., crustaceans and molluscs), or post-fermentation, when *garum* was blended with several other products like wine, vinegar, honey, spices, or Mediterranean herbs. The elevated salt concentrations (around 20%) required for fermentation ensured microbial safety and created an environment favouring halophilic bacteria and other salt-tolerant organisms responsible for the biochemical transformation of the fish substrate. Moreover, factors such as habitat, raw material composition, and fermentation time (at least 9 months) likely contributed to selecting the final fermentation microbiome. In this study, remains from different production sites across regions of France, Spain, and Portugal are analysed using state-of-the-art ancient DNA techniques to investigate variability in recipes and microbial community structure of *garum* produced throughout the Roman Empire.

POSTER 9| METABARCODING OF MEDITERRANEAN MONK SEAL (*MONACHUS MONACHUS*) SCATS REVEALS A DIVERSE PISCIVOROUS DIET

Vijayakumar, S (1); Themudo, GE (1); Carneiro, J (1); Campos, PF (1)

(1) CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Porto, Portugal;

Keywords: metabarcoding; *Monachus monachus*; trophic ecology; fisheries conflict; Madeira

Abstract

The Mediterranean monk seal (*Monachus monachus*), Europe's most endangered marine mammal, faces critical conservation challenges, with a remnant population of ~25 individuals near Madeira. This study employs high-throughput DNA metabarcoding of fecal samples to elucidate the trophic ecology of this isolated population. Fourteen samples from Madeira and Desertas were amplified using dual universal MiFish primers targeting the mitochondrial 12S rRNA gene region (~170– 180 bp), enabling simultaneous detection of bony and cartilaginous fishes. Sequencing was performed on the Illumina NovaSeq 6000 platform, generating 150PE reads. Data were processed using Cutadapt and VSEARCH for demultiplexing, primer trimming, quality filtering, merging, dereplication, chimera removal, and OTU clustering, ensuring robust handling of pooled datasets. The analysis revealed 60 unique fish species (39 native, 21 non-native/migratory) as part of the seals' diet. This confirms an opportunistic generalist feeding strategy. Frequency of Occurrence (FO%) analysis confirmed the dominance of the Sparidae family in the diet (avg. FO ~79%), with seven core species present in all samples (100% FO). The dual MiFish primer approach provided superior taxonomic resolution, documenting elasmobranchs in the diet for the first time and molecularly detecting the presence of previously unrecorded species like *Fistularia petimba* and *Diplodus puntazzo* in Madeira waters. The diet also demonstrated notable overlap with commercial fisheries, suggesting resource competition. The high occurrence of *Sparus aurata* (78.5% FO) indicates potential interaction with local aquaculture, but the overall dietary diversity suggests reliance on wild stocks. Non-target DNA was also detected, including host DNA and frequent *Teira dugesii* signals. Overall, the results provide high-resolution dietary insights essential for conservation management and assessing human–seal conflict.

POSTER 10| RECONSTRUCTING POPULATION DYNAMICS OF THE EUROPEAN SARDINE (*SARDINA PILCHARDUS*) USING PALAEOGENOMICS

dos Santos, I (1,2); Netels, R (2); Themudo, G (2); da Fonseca, R (3); Campos, P (2)

(1) UM – University of Minho, Braga, Portugal; (2) CIIMAR - Centro Interdisciplinar de Investigação Marinha e Ambiental, University of Porto, Porto, Portugal; (3) Centre for Global Mountain Biodiversity, GLOBE Institute, University of Copenhagen, Universitetsparken 15, 2100 Copenhagen, Denmark

Keywords: garum; marine resource exploitation; overfishing; roman empire

Abstract

Overfishing has severely affected numerous marine species, reducing their effective population sizes to a fraction of their historical levels. Yet, because reliable catch records are often lacking, our understanding of how these pressures have shaped species' evolutionary trajectories remains limited. One of the most impacted species is the European sardine (*Sardina pilchardus*), a key pelagic resource in Atlantic waters and of major economic importance, particularly in Southern Europe and Morocco, where it is the primary target of purse-seine fisheries and a critical source of income for coastal communities. The species ranges from the southern Celtic Sea and North Sea to Mauritania and Senegal, including the Azores, Madeira, and the Canary Islands, and is also abundant throughout the Mediterranean. Current populations form three genetic clusters: one comprising individuals from the Azores and Madeira; a second encompassing Iberian populations, which occupy the centre of the sampling range; and a third containing Mediterranean and Canary Islands individuals, with Iberian sardines showing signs of admixture. In this study, we apply state-of-the-art ancient DNA approaches to specimens predating periods of intensive fishing and compare their genetic profiles with those of modern, post-exploitation populations. This enables us to examine genetic continuity over time and compare levels of genetic diversity before and after exploitation—providing essential baselines for stock delineation, fisheries management, and determining appropriate fishing effort across the various FAO areas.

POSTER 11| ADAPTATION AND (EPI)GENOMIC EROSION IN SMALL, ISOLATED POPULATIONS: INSIGHTS FROM THE CRITICALLY ENDANGERED APENNINE BROWN BEAR

Lobo, D (1,2,3); Colangelo, P (4,5); Gramolini, L (4); Ciucci, P (6); Bonapace, IM (1)

(1) Department of Biotechnology and Life Sciences, University of Insubria, Busto Arsizio, Italy; (2) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Vairão, Portugal; (3) BIOPOLIS, Program in Genomics, Biodiversity and Land Planning, Vairão, Portugal; (4) Research Institute on Terrestrial Ecosystems, National Research Council, Rome, Italy; (5) National Biodiversity Future Center (NBFC) - National Biodiversity Future Center, Palermo, Italy; (6) Department of Biology and Biotechnologies "Charles Darwin", University of Rome La Sapienza, Rome, Italy.

Keywords: Apennine brown bear; epigenomics; genomic erosion

Abstract

Adaptation in small and isolated populations is constrained by strong genetic drift and reduced efficacy of selection. Epigenetic mechanisms may partly compensate by enabling rapid, plastic responses to environmental change. The Apennine brown bear (*Ursus arctos marsicanus*), a critically endangered population, represents an extreme case of long-term isolation and low effective population size in Europe. We investigated how genomic erosion has shaped both genetic and epigenetic potential in this relict lineage using 44 medium-high coverage genomes spanning all European brown bear populations. Apennine bears exhibited the lowest heterozygosity and the highest number of fixed variants, including 21,748 SNPs unique to this population and associated with 3,420 genes, 123 of which carried high or moderate impact variants enriched in neurodevelopmental, cognitive, and morphological functions. These may underlie distinctive phenotypes such as smaller body size and reduced aggressiveness. To assess potential effects on epigenetic potential, we identified SNPs that create or disrupt CpG dinucleotides. Apennine bears showed the lowest proportion of CpG disruptive variants (17.5%) and the highest of CpG-creative ones (16.4%), yet fixed variants were disproportionately CpG-disruptive (23.9%). Our results suggest that genomic erosion may progressively constrain epigenetic potential, although the elevated CpG content in the Apennine bear genome may still support phenotypic plasticity under continued isolation.

Acknowledgements/Funding
This work was funded by the project PRIN 2022 "Epigenetics and conservation of small populations: microevolution and adaptive divergence in relict bear populations", funded by the EU – Next Generation EU (CUP J53D2300669006).

POSTER 12| UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING

Viana, A (1,2,3); Carvalho, J (2,3); Farelo, L (2,3); Rodrigues, M (4); Santos-Reis, M (4); Fernandes, CR (4); Zub, K (5); Miranda, I (2,3); Melo-Ferreira, J (1,2,3)

(1) Departamento de Biologia, Faculdade de Ciências da Universidade do Porto, Porto, Portugal; (2) CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Universidade do Porto, Vairão, Portugal; (3) BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal; (4) CE3C – Centre for Ecology, Evolution and Environmental Changes & CHANGE – Global Change and Sustainability Institute, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal; (5) Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland

Keywords: population genetics; phylogenetics; demography; whole-genome resequencing

Abstract

Understanding the evolutionary history of a species is fundamental to elucidate the processes generating and maintaining diversity and to better inform targeted conservation strategies. The least weasel (*Mustela nivalis*) is one of the most widely distributed carnivorans in the Northern Hemisphere, displaying substantial morphological diversity, which has been used as evidence for its subdivision into more than 20 recognised subspecies. Previous studies have characterised population structure based on mitochondrial (mtDNA) markers, showing that genetic structure does not coincide with morphology-based subdivisions. Here, we use whole-genome sequencing (WGS) data to more effectively probe the evolutionary history and extant population structure of the least weasel. Sampling combines publicly available (N = 6) with newly generated sequencing (N = 8) data, representing most of Eurasia and spanning all the most relevant subgroups identified by previous mtDNA analyses. More specifically, we will characterise genome-wide population structure and genetic diversity, infer phylogenetic relationships among individuals using both WGS and complete mtDNA sequences, and estimate changes in effective population sizes over time. The results of this study will help shed new light on the evolutionary history of the least weasel, providing the first genome-wide characterisation of this species' population structure and phylogenetic relationships.

POSTER 13| EVALUATING DNA COLLECTION METHODS FOR NON-INVASIVE GENETIC MONITORING IN DESERT CONDITIONS

Mostajeran, M (1,2,3); Khalatbari, L (1,2); Lobo, D (1,2,4); Godinho, R (1,2,3,5)

(1) CIBIO – Research Centre in Biodiversity and Genetic Resources - InBIO Associate Laboratory, University of Porto, Vairão, Portugal; (2) BIOPOLIS, Vairão, Portugal; (3) University of Porto, Porto, Portugal; (4) University of Insubria, Varese, Italy; (5) University of Johannesburg, Johannesburg, South Africa

Keywords: non-invasive samples; genetic monitoring; arid environments; scat swabbing

Abstract

Non-invasive genetic sampling is an essential tool for studying elusive carnivores, particularly in remote and arid environments where direct observation or capture is difficult. However, the success rate of genetic analyses depends strongly on how samples are collected and preserved. This study compares two non-invasive sampling methods for the Arabian wolf (*Canis lupus arabs)*: direct DNA extraction from dry-collected scats and DNA obtained by swabbing the mucous layer of the same scats in the field. 232 samples were collected at the AlUla region, Saudi Arabia, between the years 2024 and 2025. The success rate for species identification was evaluated based on sequencing results for a mitochondrial D-loop fragment, confirming 176 samples as canids. A total of 91 scats (51.7%) and 85 swabs (48.3%) were successfully identified to species. A chi-square test comparing results for the two sample types showed no significant association between sample type and species identification success (χ^2 (1) = 0.825, p = 0.364), indicating similar performance between methods for this parameter. The next phase of the study involves nuclear genotyping of confirmed canine samples using 17 microsatellite markers optimized for the Arabian wolf, followed by an evaluation of genotyping success, allelic dropout, and false allele rates for each sample type. This assessment will help determine whether swabbing samples, which requires simpler storage and transport, can match or exceed the effectiveness of direct dry-scat extraction. The results will contribute to establishing best practices for non-invasive genetic monitoring of carnivores in arid landscapes.

Acknowledgements/Funding
This study was conducted within the scope of the Predator Prey Model project (CW11830), funded by the Royal Commission for AlUla (RCU), which supported data collection and analysis. MM and LK were supported by the same project. RG is supported by an FCT Principal Researcher contract (2022.07926.CEECIND), and DL by is supported by a postdoctoral fellowship under the project PRIN 2022 “Epigenetics and conservation of small populations: microevolution and adaptive divergence in relict bear populations”, funded by the EU – Next Generation EU (CUP J53D2300669006).

POSTER 14| THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE

Meliani-Rodríguez, A (1); McCormack, G (2); de Miranda, JR (3); Oleksa, A (4); Requier, F (5); Rogenstein, S (6); Pinto, MA (1)

(1) CIMO– Centro de Investigação de Montanha , LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal; (2) Zoology, School of Natural Sciences and Ryan Institute, National University of Ireland, Galway, Galway, Ireland; (3) Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden; Department of Genetics; (4) Faculty of Biological Sciences, Kazimierz Wielki University, Powstańców Wielkopolskich 10, Bydgoszcz 85-090, Poland; (5) Université Paris- Saclay, CNRS, IRD, UMR Évolution, Génomes, Comportement et Écologie, Gif-sur-Yvette, France; (6) The Ambeessadors, Berlin, Germany Honey Bee Watch, Galway, Ireland

Keywords*: Apis mellifera*; wild honey bees; genomics; conservation; natural selection

Abstract

While the risks faced by managed honey bee (*Apis mellifera*) colonies have been extensively documented in scientific literature, knowledge of the status of wild bee colonies, also known as free-living colonies (FLCs), remains limited. This lack of knowledge has long led to the assumption that FLCs were extinct in Europe. However, recent studies indicate that forests containing cavity-bearing trees across Europe could potentially support more than 80,000 bee colonies (although this figure is likely conservative), indicating the potential presence of stable, self-sustaining populations of wild native honey bees. Recently, wild 'black' honey bees (e.g., *A. m. mellifera* and *A.m. iberiensis*) have been listed as threatened within the European Union, according to the IUCN Red List of Threatened Species, due to the combined threats of the invasive ectoparasite *Varroa destructor* and interbreeding with commercial bee races used in beekeeping. Such FLCs represent an important component of Europe's native biodiversity, as well as providing *in-situ* conservation of locally adapted genetic diversity that is potentially valuable for developing resistance or tolerance mechanisms to varroa and other exotic diseases, and which is promoted by adaptation and recovery in small isolated populations. Studying FLCs may therefore provide crucial insights into their role as a genetic reservoir and their role as part of the ecological heritage of this key organism. In this context, the FREE-B project aims to investigate FLCs across a latitudinal gradient in Europe. The project will address several key questions, including whether long-surviving FLCs retain specific genomic components of native *A. mellifera* subspecies (e.g., *A. m. iberiensis* in Portugal), whether they show signs of genetic introgression from managed colonies, and whether they possess genomic adaptations that enable survival in the wild. These and related questions will be explored through six dedicated work packages, each targeting specific objectives, which will be briefly described.

Acknowledgements/Funding
This research is funded by Biodiversa+, the European Biodiversity Partnership, in the context of the FREE-B project under the 2023–2024 BiodivNBS joint call. It is co-funded by the European Commission (GA No. 101052342) and the national funding through *Fundação para a Ciência e a Tecnologia* (Ref. FCT: BiodivNBS/0004/2023).

POSTER 15| BLUEFINDB: A MULTI-MARKER, "HUMAN-IN-THE-LOOP" ARCHITECTURE FOR PRECISION eDNA REFERENCE DATABASE CURATION

Vijayakumar, S (1); Kuruppuarachchi, K (1); Themudo, G (1); Campos, P (1); João Carneiro (1)

(1) CIIMAR, - Centro Interdisciplinar de Investigação Marinha e Ambiental, University of Porto, Porto, Portugal

Keywords: eDNA metabarcoding; reference database curation; human-in-the-loop; tiered rescue architecture; primer validation

Abstract

The reproducibility of environmental DNA (eDNA) metabarcoding depends on transparent and replicable workflows for creating a complete and curated reference database. Conventional curation tools (RESCRIPT, CRUX, and OBI tools) tend to operate as non-flexible workflows, discarding valid taxa due to minor primer mismatches or failing when specific marker sequences are absent. BlueFinDB addresses this issue through an open-source, multi-marker pipeline (12S, COI, 16S, 18S) that builds highly accurate project-specific reference libraries using standard primer sets (e.g., MiFish, Leray-XT, Vences V4, and Stoeck V9) according to the preferences of the researcher and the data being analysed. BlueFinDB differentiates itself through a novel Tiered intelligent rescue architecture. The core engine first initiates Tier 1, which fetches marker-specific sequences and validates them via *in-silico* PCR (using *Cutadapt*) to ensure primer accuracy. If this fails, then it automatically triggers a Tier 2 protocol where it mines for complete mitochondrial genomes or whole-genome assemblies and performs virtual PCR to cut and retrieve the target amplicons. This mechanism ensures high-quality data recovery that most standard scrapers miss, significantly reducing false negatives caused by database fragmentations. Beyond automation, BlueFinDB addresses the “reproducibility vs. flexibility" conflict through a user-centric, human-in-the-loop design. Instead of silently failing, the pipeline generates an interactive "Patch Script” for problematic cases, such as missing taxonomy or private sequence injection, allowing researchers to manually fill the gaps without interrupting the automated audit trail. It is integrated with Smart caching to stop duplicate API calls and ensure consistent outputs. BlueFinDB provides a dynamic, transparent, and gap-free alternative to static databases, automating tedious curation while preserving human oversight so researchers can build robust, traceable reference libraries tailored to their needs.

https://github.com/SUBRAMANIAM96/BlueFinDB

POSTER 16| POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, *PARAMURICEA CLAVATA* IN THE PARC NATIONAL DES CALANQUES (FRANCE)

Ramos, I (1); Aurelle, D (3); Cornette, F (4); Estaque, T (5); Garrabou, J (6); Mérigot, B (4); Schull, Q (4); Ledoux, J-B (2)

(1) UAlg-Universidade do Algarve, Faro, Portugal; CIIMAR; (2) CIIMAR -Centro Interdisciplinar de Investigação Marinha e Ambiental, Universidade do Porto, Matosinhos, Portugal; (3) Institut Systématique Evolution Biodiversité,MNHN,CNRS,Sorbonne Université,EPHE,Université des Antilles,Paris,FR; (4) MARBEC, Univ Montpellier, Ifremer, IRD, CNRS, Sète, France; (5) Septentrion Environnement, Marseille, France; (6) ICM-CSIC - Institute of Marine Sciences, Barcelona, Spain;

Keywords: population genomics; marine protected area; *Paramuricea clavata*; connectivity; deep refugia hypothesis

Abstract

Population genetics studies are still poorly considered by biodiversity managers when creating effective conservation measures; however, recent improvements in sequencing technologies and bioinformatics are expanding the potential contribution of this field to biodiversity management and conservation. This case study aims to demonstrate how population genetics can support management efforts in a marine protected area, the Parc National des Calanques (PNC, France), focusing on the Mediterranean red gorgonian, *Paramuricea clavata*. *P. clavata* is a habitat-forming octocoral (Cnidaria, Anthozoa) with a key structural role in biodiversity-rich benthic communities; however, its shallow populations (until 40m depth) are of particular conservation concern due to mass mortality events induced by recurrent marine heatwaves. The intensity of this stressor dramatically contrasts with the low resilience of *P. clavata* and raises questions about its evolutionary trajectory. Moreover, the impact of these events on the species' genetic make-up remains unclear. Crucial questions regarding, for instance, the ability of deep populations to recolonize shallow and impacted areas ("deep refugia hypothesis"), are still open. Using state-of-the-art bioinformatics and population genomics to analyse whole-genome sequencing data from 20 shallow to mesophotic populations from the PNC and its neighbouring, we aim to i) map the pattern of genetic diversity, ii) characterize the connectivity among populations within the PNC, and between the PNC and nearby populations looking for potential spillover effect of the MPA, and iii) test the deep refugia hypothesis. Here, we will present an overview of an ongoing work, which will improve our understanding of *P. clavata* ecology and evolution in the context of climate change and provide a genomic baseline to guide conservation and restoration efforts for this habitat-forming species, in an emblematic protected area.

Acknowledgements/Funding
This research was funded by PureOceanFoundation and the national funds through FCT-Fundação para a Ciência e a Tecnologia, I.P., and by the European Commission's Recovery and Resilience Facility, within the scope of UID/04423/2025, UID/PRR/04423/2025, and LA/P/0101/2020.

POSTER 17| WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1

Li, F (1); Lima, D (1,2); Bashir, S (1); Yadró, CA (1); De Graaf, DC (3); De Smet, L (3); Verbinnen, G (3); Rosa-Fontana, A (1); Rufino, J (4,5); Martín-Hernandez, R (6); Medibees Consortium; Pinto, M. Alice (1); Henriques, D (1)

(1) CIMO – Centro de investigação de Montanha, LA SusTEC, Instituto Politécnico de Bragança, Bragança, Portugal; (2) Pontificia Universiade de Minas Gerais, Belo Horizonte MG, Brasil; (3) LMEB - Laboratory of Molecular Entomology and Bee Pathology, Department of Biochemistry and Microbiology, Faculty of Sciences, Ghent University, Ghent, Belgium; (4) SusTEC – Laboratório Associado para a Sustentabilidade e Tecnologia em Regiões de Montanha, Instituto Politécnico de Bragança, Bragança, Portugal; (5) CeDRI – Research Centre in Digitalization and Intelligent Robotics, Instituto Politécnico de Bragança, Bragança, Portugal; (6) CIAPA – Laboratorio de Patología Apícola, Centro de Investigación Apícola y Agroambiental de Marchamalo , IRIAF – Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal de Castilla-La Mancha, Marchamalo, Spain

Keywords: protein evolution; cytochrome p450; protein modelling

Abstract

Cytochrome P450 enzymes are central to pesticide metabolism and resistance, yet how these proteins diversify substrate specificity while maintaining catalytic function remains poorly understood. A genome-wide analysis of CYP336A1 (a nicotine-metabolizing P450) across 1467 *Apis mellifera* males from 25 countries spanning the Mediterranean, Middle East, Europe, and Cuba revealed an intricate haplotype architecture. Despite the detection of only 28 single-nucleotide variants (SNPs), 45 distinct haplotypes were detected for CYP336A1. Among these, 23 haplotypes carried at least four SNPs, and four harboured more than 10. A five-SNP haplotype (D202G; M207I; I222V; V226I; Q238K) dominated at 36% frequency, far exceeding the next most common single-SNP haplotype (D262N, 9%). Interestingly, this dominant haplotype was completely absent from the Iberian Peninsula, North Africa, and Oman and, consequently, from five *A. mellifera* subspecies: *iberiensis, intermissa, jemenitica, mellifera and sahariensis*. To investigate the functional impact of the identified variants, individually and in combination, we used *in sillico* protein structural approaches. Protein models were generated with trRosetta, validated with MolProbity, and evaluated using TM-score and RMSD via TM-Align. Structural modelling revealed remarkable fold congruency: the enzyme encoded by the five-SNP haplotype retained a near-identical fold as compared to the wild-type enzyme (TM-score = 0.998, RMSD = 0.34 Å), as did a rarer 13-SNP haplotype (2%) (TM-score = 0.998, RMSD = 0.38 Å). Individual SNPs also produced minimal backbone displacement (0.32–0.54 Å), suggesting that P450 diversification proceeds through subtle structural adjustments rather than major disruption. Moreover, most SNPs clustered within substrate-recognition regions, whereas catalytic residues remained invariant across haplotypes, demonstrating a partitioning between substrate-recognition/binding evolution and preservation of catalytic machinery. Importantly, single-variant effects cannot predict multi-variant haplotype outcomes. As such, heavy reliance on individual SNPs for pesticide risk assessment may misestimate real metabolic capacity.

Acknowledgements/Funding

This work was conducted in the framework of the projects MEDIBEES - Monitoring the Mediterranean Honey Bee Subspecies and their Resilience to Climate Change for the Improvement of Sustainable Agro-Ecosystems funded by PRIMA, and Bee3Pomics: Omics insights into molecular effects of plant protection products in honey bees (*Apis* mellifera) funded by the RESTART-FCT. It was further supported by national funding by FCT, Foundation for Science and Technology, through the individual research grant 2024.05645.BD of Fernanda Li,

as well as by national funds through FCT/MCTES (PIDDAC): CIMO, UIDB/00690/2020 (DOI: 10.54499/UIDB/00690/2020) and UIDP/00690/2020 (DOI: 10.54499/UIDP/00690/2020); and SusTEC, LA/P/0007/2020 (DOI:10.54499/LA/P/0007/2020).

POSTER 18| UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S

Ribeiro, M (1,2); Gawran, J (3); Barros, S (1); Neves, D (1,4); Navarro-Martín, L (3); Santos, MM (1,2); Neuparth, T (1)

(1) CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, Endocrine Disruptors and Emerging Contaminants Group, University of Porto, Porto, Portugal; (2) FCUP - Department of Biology, Faculty of Sciences, University of Porto, Porto, Portugal; (3) IDAEA-CSIC - Institute of Environmental Assessment and Water Research, Barcelona, Spain; (4) ICBAS - Institute of Biomedical Sciences Abel Salazar, University of Porto, Porto, Portugal

Keywords: transcriptomics; DNA methylation; epigenetics; zebrafish and Bisphenol S; environmental risk assessment

Abstract

Bisphenol S(BPS), one of the primary alternatives for Bisphenol A(BPA), has been detected in surface waters at rising concentrations (ng/L to low µg/L), mostly due to its extensive industrial use, particularly in the manufacture of polycarbonate plastics and epoxy resins. Given the current scarcity of knowledge concerning BPS toxicity after long-term exposure and its impact on subsequent generations indirectly exposed, this study aims to evaluate the ecological risks of BPS in aquatic ecosystems through an intergenerational bioassay with Danio rerio (zebrafish). The first generation(F0) was exposed to environmentally relevant concentrations of BPS (0.4, to 10µg/L) for 4 months, and the subsequent generation(F1) was grown in clean water. We collected apical, biochemical, and molecular data to disclose cause-effect relationships and contribute to a deeper understanding of the mechanisms underlying BPS toxicity. In F0, females exposed to 0.4µg/L of BPS showed significant histological changes in gonads (atretic oocytes and inflammatory responses) alongside with an increased gonadosomatic index. Regarding F1, changes in length, heart rate, and behaviour were observed mainly in embryos/larvae descended from the F0 0.4µg/L BPS treatment. To further elucidate the observed effects, we performed transcriptomic analyses on F0 female gonads and on F1 embryos from the 0.4µg/L BPS lineage. In parallel, enzymatic methyl-sequencing was carried out on the same biological samples to assess DNA methylation patterns and evaluate their potential role in epigenetic inheritance. With this conceptual approach, we aim to contribute to a more comprehensive evaluation of the environmental risks associated with BPS exposure. By addressing intergenerational effects and their potential underlying epigenetic mechanisms, we seek to elucidate how BPS may influence the evolutionary trajectories of exposed populations. These insights are essential for understanding the long-term consequences of BPS contamination in aquatic species and highlight the urgent need to integrate evolutionary and intergenerational perspectives into environmental risk assessment frameworks.

Acknowledgements/Funding
This work was supported by projects TRANSEPIC10.54499/2022.02922.PTDC, financed by the Portuguese Foundation for Science and Technology (FCT). Marta Ribeiro acknowledges FCT for her PhD grant 2022.12763.BD.

POSTER 19| PAST SELECTIVE HISTORY INFLUENCES ADAPTATION TO ORAL INFECTION IN DROSOPHILA MELANOGASTER

Lafuente, E (1); Akyaw, PA (2); Madaan, T (3); Roque, D (1); Sucena, E (1)

(1) Centre for Ecology, Evolution, and Environmental changes (CE3C); (2) University of Edinburgh, United Kingdom; (3) Institute of Science & Technology Austria, Austria

Keywords: historical contingency; experimental evolution; immunity

Abstract

Historical contingency - the influence of past selective processes on subsequent evolution - can determine whether adaptation is facilitated or constrained in new contexts. We explored this by taking advantage of two *Drosophila melanogaster* populations maintained in the lab with distinct histories: one previously adapted to systemic infection with *Pseudomonas entomophila* (BactSys) and its control population (ContSys). We confirmed that, after several generations of relaxed selection, BactSys flies still showed improved survival upon systemic infection. We subjected both populations to a new selection regime consisting of infecting flies to the same pathogen through a different (oral) route. Over 24 generations, both populations evolved increased survival, but BactSys flies showed a faster rate of adaptation, particularly females. The adaptive response appears to have occurred in two phases: a steep improvement within the initial 8 generations, followed by a slower rate of change. We also investigated the patterns for bacterial clearance and fecundity. Interestingly, both traits mirror the dynamics observed for survival. In early generations, BactSysOral flies cleared infections faster and became more fecund than controls, but these advantages diminished or reversed in later generations. Together, our results suggest that prior adaptation to systemic infection initially conferred a generalist advantage, which later may have given way to trade-offs or specialization. Our findings show how infection through two different infection routes can cross-talk both physiologically and evolutionarily. In addition, this work further sustains that past selective history can shape adaptive trajectories differently and affect the balance between traits in a historically contingent manner.

POSTER 20| THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX*

Diéguez-Antón, A (1,2); Rodríguez-Flores, MS (3); Castaño-Serna, JS (3); Meno, L (3); Escuredo, O (3); Saker, Y (3); Harbane, S (3); Seijo, MC (3)

(1) BV1-Pranta, Solo e Aproveitamento de Subproductos, Departamento de Bioloxía Vexgetal e Ciencias so Solo, Facultade de Ciencias, Universidade de Vigo, Ourense, Spain; (2) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, Bragança, Portugal; (3) GISA—Grupo de Investigación en Sistemas Agroambientales, Departamento de Bioloxía Vexgetal e Ciencias so Solo, Facultade de Ciencias, Universidade de Vigo, Ourense, Spain

Keywords: invasive species; adaptation; yellow-legged hornet; *Vespa velutina nigrithorax*

Abstract

Vespa velutina nigrithorax, commonly known as the yellow-legged hornet, has emerged as one of the most rapidly expanding invasive species in Europe over the past two decades. The successful establishment of this species is attributed to a combination of its intrinsic biological traits, the absence of natural enemies, predators, or direct competitors, and the habitats it invades, which offer abundant food resources and adequate shelter. Moreover, the favourable climatic conditions for the species that provide optimal temperature and humidity are the key factors examined in this study. We monitored the hornets' pressure in 14 apiaries in Galicia (NW Spain) for two years. Temperature (ºC) and relative humidity (%) of each apiary were recorded, and a hunting camera was used to show the presence of the hornet. The camera was placed in front of the studied colonies at a distance that allowed distinguishing between hornets and honey bees. The camera was programmed to take photographs every hour from 6 am to 11 pm. The results of our study showed that the air temperature and relative humidity in the apiary affected the number of hornets that appeared in front of the hive throughout the day. Temperature was the factor with the highest correlation with the number of hornets in front of the hives. It was seen that with atypical temperature values of 5 °C and 38 °C, hornets were seen in front of the hives with hunting activity, contrary to what is described in South Korea, where it was observed that at temperatures higher than 35 ºC there was no hunting activity by hornets. The species demonstrates a wider thermal tolerance than previously reported, suggesting high ecological plasticity. The ecological plasticity of *Vespa velutina* enhances its invasive success by enabling rapid phenotypic adjustments to new environments, an early stage of local adaptation.

Acknowledgements/Funding

A special acknowledgement is due to the Agrupación Apícola de Galicia for their support in this research. Ana Diéguez-Antón expresses her gratitude for the support of Postdoctoral Financial Aid of Xunta de Galicia and the University of Vigo, grant number ED481B-2025/080, founded by Consellería de Educación, Ciencia, Universidades e Formación Profesional.

POSTER 21| LONG-TERM EVOLUTION EXPERIMENTS FULLY REVEAL THE POTENTIAL FOR THERMAL ADAPTATION

Antunes, MA (1,2); Grandela, A (1,2); Matos, A (1,2); Simões, P (1,2)

(1) CE3C - Center for Ecology, Evolution and Environmental Changes (CE3C) & CHANGE – Global Change and Sustainability Institute, Lisboa, Portugal; (2) Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal

Keywords: thermal adaptation; experimental evolution; long-term evolution; climate change; fertility; *Drosophila*

Abstract

Evolutionary responses may be crucial in allowing organisms to cope with the prolonged effects of climate change. However, a clear understanding of the dynamics of adaptation to warming environments is still lacking. Addressing how reproductive success evolves in such deteriorating environments is extremely relevant, as this trait is constrained at temperatures below critical thermal limits. Experimental evolution under a warming environment can elucidate the potential of populations to respond to rapid environmental changes. The few studies following such a framework lack analysis of long-term response. We here focus on the long-term thermal evolution of two *Drosophila subobscura* populations, from different European latitudes, under warming temperatures. We tested the reproductive success of these populations in the ancestral (control) and warming environment after ~50 generations of thermal evolution. We found a general adaptive response to warming temperatures in the long term, since populations evolving in the warming environment showed increased performance in that environment relative to the respective control populations. On the other hand, no clear response was observed in the ancestral environment. Coupled with data from previous generations, we highlight a slow pace of adaptive response and differences in that response between populations of distinct histories. These findings demonstrate the need for long-term evolution experiments to fully reveal the potential for thermal adaptation. It also highlights that the scrutiny of different populations is needed as a measure of variation in evolutionary responses within a species. Accounting for these sources of variation - both temporal and spatial - will allow for more robust assessments of climate change evolutionary responses.

POSTER 22| ADAPT, ADJUST OR MOVE: CAN THE SPIDER MITES *TETRANYCHUS CINNABARINUS* DO IT ALL IN RESPONSE TO HEAT?

Gaspar, R (1); Costa, S (1); Nunes, S (1); Magalhães, S (1); Rodrigues, LR (1)

(1) CE3C -Centre for Ecology, Evolution and Environmental Changes & CHANGE-Global Change and Sustainability Institute, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal

Keywords: global warming; crop pests; dispersal; plasticity; adaptive potential

Abstract

Organisms have been exposed to increasingly frequent heat waves and higher long-lasting local temperatures, conditions that can ultimately lead to their extinction. However, individuals may be capable of coping with heat if they adjust their response plastically, adapt to these new conditions or move to places with better resources. Because these strategies are non-exclusive and are not necessarily independent, it is important to assess them all together in the same organism. We have done just that using the spider mite, *Tetranychus cinnabarinus*, an important economic pest, exposed to a control (25°C) or one of two high temperatures (33°C and 36°C). We found that body size and fecundity were lower at high temperatures than at 25°C, suggesting there is no clear advantageous adjustment in trait values at high temperatures. To determine if temperature promotes movement, we installed females onto a patch connected to two others by bridges and assessed the number of eggs. Females maintained at 36°C seemed to move more and lay more eggs away from their initial location than those maintained at 25°C, suggesting there is increased dispersal at high temperature. Finally, resorting to a set of isogenic lines of the same species, we found significant genetic variance at 36°C in all traits measured, suggesting there is potential for adaptation at high temperatures. A positive genetic correlation observed between daily fecundity and body size, and a lack of correlation between these traits and dispersal, suggest that selection for more fecund, necessarily bigger, females at 36°C is genetically independent from selection for females that disperse more. All in all, our results suggest that *T. cinnabarinus* has the tools to cope with high temperature stress, either by evolving to disperse to cooler locations or to become more fecund at high temperature.

POSTER 23| DO MATING SYSTEMS SHAPE THERMAL FERTILITY?

Santos, R (1,2); Grandela, A (1,2); Rodrigues, LR (1,2); Simões, P (1,2)

(1) cE3c – Centre for Ecology, Evolution and Environmental Changes & CHANGE – Global Change and Sustainability Institute, FCUL University of Lisbon, Lisbon, Portugal; (2) FCUL - Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Lisbon, Portugal

Keywords: fertility; mating system; *Drosophila*; thermal evolution; climate change

Abstract

Rising temperatures have a detrimental effect on many organisms, particularly ectotherms, with reproductive functions often impaired at lower thermal thresholds than survival. In many taxa, male fertility is sensitive to heat-induced sterility, whereas females are affected at warmer temperatures than males. This means that females can buffer the effect of heat on male fertility. However, this rescue depends on species-specific mating systems (e.g., monandry vs polyandry), with monandrous females having fewer opportunities to compensate for male sterility compared to polyandrous ones. We will present a study devised to address how different mating systems affect the evolution of reproductive traits, including fertility, in both sexes, under thermal stress. This will be done by performing a comparative analysis among *Drosophila* species with different mating systems. This work will shed light on the relevance of mating systems in shaping populations' adaptation to rising temperatures, clarifying implications for population persistence in the face of climate change.

POSTER 24| THE EGG OR THE CHICKEN? REVISITING AGLOMERULISM AND THE EMERGENCE OF ANTI-FREEZE GLYCOPROTEINS, RENAL FUNCTION, AND WATER BALANCE IN NOTOTHENIOIDS

Teixeira, J (1); Pinto, B (2); Wilson, J (3); Guerreiro, P (4); Castro, F (2)

(1) CIIMAR/CIMAR LA, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Matosinhos, Portugal; Universidade do Algarve; (2) CIIMAR/CIMAR LA, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Matosinhos, Portugal; (3) Wilfrid Laurier University, Canada; (4) Centro de Ciências do Mar do Algarve (CCMAR)

Keywords: ecodevo; fish renal function; notothenioid; glomerulus; antifreeze glycoprotein

Abstract

The dominance of notothenioid fishes in the Southern Ocean is supported by extreme physiological adaptations, most notably the evolution of antifreeze glycoproteins (AFGPs). It is thought that to prevent the urinary loss of these metabolically expensive molecules, these fish evolved aglomerular kidneys. Yet, the genetic mechanisms underscoring this phenotypic loss remain unclear. Strikingly, glomeruli-associated genes, such as podocin and nephrin, appear to be retained rather than lost, as previously shown in other teleost lineages (e.g. syngnathids). This project explores the hypothesis that aglomerulism in notothenioids might not be a static condition, but a regulatory state that may vary during development. To investigate this, we will analyse transcriptomic profiles of larval stages and expose juveniles to environmental challenges designed to favour glomerular filtration. By combining genomics and physiological data, we aim to clarify the mechanisms driving this puzzling morphological transition. Understanding these regulatory backgrounds is crucial not only for understanding the evolutionary drivers of this specific trait but also for understanding how these fish might cope with rapid environmental shifts in Antarctic waters.

Acknowledgements/Funding
This project is funded by PROPOLAR – Portuguese Polar Program.

POSTER 25| LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE

Lima, D (1,2), Li, F (1), Bashir, S (1); Yadró, CA (1); Taliadoros, D (3); Webster, M (3); Rufino, J (4,5); Roessink, I (6); Buddendorf, B (6); van der Steen, J (7); Murcia, M (8); Fernández-Alba, AR (8); De Graf, D (9); Lopes, AR (1); Pinto, MA (1); Henriques, D (1)

(1) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300- 253 Bragança, Portugal; (2) Pontificia Universiade de Minas Gerais , 30140-108, Belo Horizonte MG, Brasil; (3) Department of Medical Biochemistry and Microbiology, Science for Life Laboratory, Uppsala University, 75237 Uppsala, Sweden; (4) Laboratório Associado para a Sustentabilidade e Tecnologia em Regiões de Montanha (SusTEC), Instituto Politécnico de Bragança, Bragança, Portugal; (5) Research Centre in Digitalization and Intelligent Robotics (CeDRI), Instituto Politécnico de Bragança,Campus de Santa Apolónia, Portugal; (6) Wageningen Environmental Research (WENR), Droevendaalsesteeg 3, NL-6708 PB Wageningen, The Netherlands; (7) Alveus AB Consultancy, Kerkstraat 96, NL-5061 EL Oisterwijk, The Netherlands; (8) Chemistry and Physics Department, University of Almeria, Agrifood Campus of International Excellence (ceiA3), 04120 Almería, Spain; (9) Laboratory of Molecular Entomology and Bee Pathology (LMEB), Department of Biochemistry and Microbiology, Faculty of Sciences, Ghent University, Ghent, Belgium

Keywords: *Apis mellifera*; pesticide exposure; genomic–environment association (GEA); environmental adaptation

Abstract

Widespread pesticide use associated with intensive agriculture has been proven to impact the Western honey bee (*Apis mellifera*). However, despite evidence of declines in survival, development, foraging efficiency, and overall colony health, the genomic underpinning of this abiotic stressor is largely unknown. This study involved 102 whole-genome sequences from honey bee colonies from across Europe, sampled under the Better-B project, to search for genetic correlations to pesticide exposure using Genomic-Environment Association (GEA) analyses. The environmental exposure data were collected within the framework of the INSIGNIA-EU project, which used APIStrips (in-hive pesticide-adsorbing strips) to quantify pesticide residues brought into the hive by foraging in many of the sampled colonies. The APISTRIP data were complemented by modelled exposure grids from PEST-CHEMGRIDS and agriculture zones from the CORINE Land Cover. Employing three complementary GEA approaches—SAMBADA (spatial analysis tool), LFMM (latent factor mixed models), and RDA (Redundancy Analysis)—we identified SNPs in the bee's genome significantly correlated with agricultural pressure and pesticide use. Notably, several genes with known roles in detoxification and stress response, including venom carboxylesterase6 and CYP336A1, were highlighted. These variants point to molecular pathways targeted by agrochemical toxicity, offering insights into the consequences of pesticide use. Such findings may, in the future and upon further validation, help refine risk assessment frameworks, support the development of resilience-oriented breeding programs, and promote sustainable apicultural practices.

Acknowledgements/Funding

This work was conducted in the framework of the projects Better-B, funded by the European Union, the Swiss State Secretariat for Education, Research and Innovation, and UK Research and Innovation, under the UK government's Horizon Europe funding guarantee (grant number 10068544), Bee3Pomics: Omics insights into molecular effects of plant protection products in honey bees (Apis mellifera) funded by the

RESTART-FCT and INSIGNIA-EU: Preparatory action for monitoring of environmental pollution using honeybees (Procurement procedure ENV/2021/OP/0014 of 28-09-2021)

POSTER 26| EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS

Costa, M (1); Pérez-Pérez, A (2); Santos, AC (1); Prado, R (1); Lopes, D (1); Lopes, AR (1); Yadró, CA (1); Martín-Hernández, R (2); Higes, M (2); Pinto, MA (1); Henriques, D (1)

(1) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal; (2) IRIAF—Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal, Centro de Investigación Apícola y Agroambiental (CIAPA), Marchamalo, Spain.

Keywords: *Varroa destructor*; historical; amitraz; resistance; mutation

Abstract

Varroa destructor is one of the main parasites of the honey bee (*Apis mellifera*), causing significant colony losses worldwide. The control of this mite often relies on acaricides, with amitraz being among the most widely used products in Portugal and Spain over the last decade. However, the continuous and persistent use of the same active substance exerts strong selective pressure on parasite populations, potentially favouring alleles associated with treatment resistance. Recently, a point mutation resulting in a phenylalanine-to-leucine substitution at position 290 (F290L) was identified in *V. destructor* populations from Spain, putatively associated with amitraz resistance. This mutation has been detected at high frequency in recent samples, suggesting resistance may have evolved due to sustained amitraz use. To assess whether the F290L mutation was already present before the widespread amitraz adoption, DNA extraction and sequencing analysis will be performed on mites collected since 2006, prior to the massive use of this treatment in Iberian beekeeping. This approach will clarify whether the allele frequency of F290L increased because of the selective pressure exerted by amitraz or if it already existed in high frequencies in earlier populations. This study will contribute to a better understanding of the evolution of resistance and to the development of more effective monitoring and management strategies to combat *V. destructor*.

Acknowledgements/Funding
This work was supported by the project "MITE- Varroa e vírus transmitidos: MonItorização de muTações e dEsenvolvimento de ferramentas moleculares inovadoras" funded by National Beekeeping Programme 2023-2027; FCT/MCTES (PIDDAC): CIMO UID/00690/2025 (10.54499/UID/00690/2025) and UID/PRR/00690/2025 (10.54499/UID/PRR/00690/2025); SusTEC, LA/P/0007/2020 (DOI: 10.54499/LA/P/0007/2020);and Project PID2021-128882OR-I00.

POSTER 27| PATHOGENS AGAINST THE MACHINE: EVOLUTIONARY SHIFTS OF *PHYTOPHTHORA INFESTANS* ACROSS EUROPEAN BIOREGIONS AND THEIR IMPLICATIONS FOR PREDICTIVE MODELLING

Castaño Serna, JS (1,2); Meno Fariñas, L (1); Diéguez Antón, A (2,3,4); Escuredo Pérez, O (1,2); Seijo Coello, MC (1,2)

(1) GISA – Grupo de Investigación en Sistemas Agroambientales, Bioloxía Vexetal e Ciencias do Solo, Universidade de Vigo, Ourense, España; (2) IAA – Instituto de Agroecoloxía e Alimentación, Universidade de Vigo, Campus Auga, Ourense, España; (3) BV1-Pranta, Solo e Aproveitamento de Subproductos, Departamento de Bioloxía Vexgetal e Ciencias so Solo, Facultade de Ciencias, Universidade de Vigo, Ourense, Spain; (4) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, Bragança, Portugal.

Keywords: population genetics; pathogen evolution; late blight; bioregions; predictive modelling

Abstract

Understanding how rapidly evolving pathogen populations interact with climate variability is essential for improving disease forecasting and for designing sustainable crop protection strategies. *Phytophthora infestans*, the causal agent of potato late blight, has experienced substantial genetic and phenotypic turnover across Europe during the past two decades, driven by the emergence of aggressive, thermotolerant, and fungicide-resistant clonal lineages. In this work, we integrated EuroBlight genotype records with European bioregions to examine spatial and temporal patterns of lineage dispersal in Spain, Portugal, France, and neighbouring regions. By aggregating clonal types within Köppen–Geiger climate zones, we characterised how environmental and agronomic contexts structure pathogen populations and modulate the geographic expansion of emergent clones. Our analyses reveal distinctive bioregional signatures of lineage composition, including a marked increase in metalaxyl-resistant and warm-adapted clones within southern Atlantic and Mediterranean regions since 2018. These shifts coincide with increased climatic variability, shifts in cultivar use, and modified agronomic practices, suggesting active evolutionary responses to novel agro-ecological pressures. When compared with commonly used decision support systems (DSS), several of these emergent lineages show climatic niches and epidemic dynamics that partly exceed the thresholds assumed by classical rule-based models, especially under warmer and more variable conditions. These findings highlight the importance of integrating pathogen population genetics, bioregional climate stratification, and updated biological parameters into future DSS frameworks. By adopting an evolutionary, spatially explicit perspective, this work aims to improve model calibration, anticipate pathogen adaptation, and strengthen the resilience of European potato production systems under ongoing climate change.

Acknowledgements/Funding
Funded by: "Sustainable strategy for integrated disease management in potato crops" with reference FEADER 2023/013B.

POSTER 28| HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL

Costa, M (1); Sánchez, S (1); Lopes, AR (1); Yadró, CA (1); Pérez-Pérez, A (2); Martín-Hernández, R (2); Higes, M (2); Pinto, MA (1); Henriques, D (1)

(1) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal; (2) IRIAF—Instituto Regional de Investigación y Desarrollo Agroalimentario y Forestal, Centro de Investigación Apícola y Agroambiental (CIAPA), Marchamalo, Spain

Keywords: *Varroa destructor*; Resistance; Mutation; Octβ2R; F290L.

Abstract

The Western honey bee (*Apis mellifera*) has a crucial role in pollination and apicultural production but faces a major threat from the ectoparasitic mite *Varroa destructor*. This parasite causes varroosis and acts as a vector for multiple viruses, undermining colony health and survival. Chemical control relies mainly on two classes of synthetic acaricides: pyrethroids (fluvalinate and flumethrin) and formamidines (amitraz). However, the repeated and prolonged use of these compounds has promoted the development of resistance in *V. destructor* populations. Amitraz resistance has been associated with mutations in the Octopamine-like β-adrenergic receptor (Octβ2R), including N87S (France), Y215H (USA), F290L (Spain), and Y337F (Turkey). Until now, the distribution of these resistance alleles had not been investigated in Portugal. To address this gap, mites collected from different regions of the country were analysed through DNA extraction, PCR with specific primers, and Sanger sequencing. The results revealed an unexpectedly high frequency (98.3%) of the F290L allele, which has also been reported in Spanish populations, suggesting a strong potential selective pressure resulting from the prolonged use of amitraz. This atypically high frequency raises important questions regarding the origin and evolutionary trajectory of this resistance allele in Portugal. Therefore, a retrospective analysis of mite samples collected before the widespread adoption of amitraz is proposed. This approach will clarify whether the F290L allele was already present in ancestral *V. destructor* populations or whether its current prevalence arose from recent selective pressure. Integrating this data will be essential for understanding the evolutionary dynamics of resistance and for supporting the development of more effective monitoring and management strategies against this parasite.

Acknowledgements/Funding
This work was supported by the project "MITE- Varroa e vírus transmitidos: MonItorização de muTações e dEsenvolvimento de ferramentas moleculares inovadoras" funded by National Beekeeping Programme 2023-2027; FCT/MCTES (PIDDAC): CIMO UID/00690/2025 (10.54499/UID/00690/2025) and UID/PRR/00690/2025 (10.54499/UID/PRR/00690/2025); SusTEC, LA/P/0007/2020 (DOI: 10.54499/LA/P/0007/2020).

POSTER 29| HOW DOES THE EVOLUTION OF DIRECT AND INDIRECT INTERACTIONS AFFECT ECOSYSTEM RESILIENCE?

Adánez, J (1,2); Rodrigues, LR (1,2); Fragata, I (1,2)

(1) Centre for Ecology, Evolution and Environmental Changes (CE3C), Faculdade de Ciências, Universidade de Lisboa; (2) CHANGE, Global Change and Sustainability Institute, Lisboa, Portugal.

Keywords: ecosystem resilience; experimental evolution; tri-trophic system; interactions; population dynamics

Abstract

Ecosystems are exposed to a wide range of disturbances, and their stability and resilience to these perturbations are key to determining their long-term persistence. However, the factors that determine such persistence are still largely unexplored, namely due to the complexity of natural ecosystems. As the complexity of ecological networks increases, both direct (e.g., herbivory or predation) and indirect (via trophic cascades or apparent competition) interactions between species rise in number; however, the number of indirect interactions increases faster, which has been shown to lead to more stable ecosystems. How such stability influences system evolution remains unclear. Furthermore, theoretical work predicts that the evolution of species and their interactions may increase system stability and ecosystem resilience, but empirical evidence for this remains limited. I set out to fill these knowledge gaps with my PhD. One way to incorporate complexity in the laboratory is to use tri-trophic systems, which are ubiquitous and relatively simple to handle. The system I will be working with, composed of a plant (*Brassica rapa*), a herbivore (the spider mite *Tetranychus urticae*), and its predator (the predatory mite *Amblyseius swirskii*), includes direct interactions such as predation and herbivory, and indirect interactions, with predators benefiting the plants by predating on the herbivore. Specifically, the aims of my work are to study 1) how does ecosystem stability affect evolutionary dynamics and shape ecosystem resilience, and 2) how does the evolution of both direct and indirect interactions affect species evolution and ecosystem resilience. With this work, I hope to significantly contribute to a better understanding of the role of eco-evolutionary dynamics on ecosystem resilience, a timely issue when considering the current unpredictability of environmental change.

POSTER 30| INTRA-POPULATION VARIABILITY IN A DARWINIAN SELECTION PROGRAM FOR *VARROA* RESISTANCE IN *APIS MELLIFERA IBERIENSIS*

Cunha, L (1,2); Lopes, AR (1); Kotrschal, S (3); Panziera, D (3); de Graaf, DC (4); Pinto, MA (1)

(1) CIMO, LA SusTEC, IPB - Polytechnic Institute of Bragança, Bragança, Portugal; (2) Federal University of Technology of Paraná, Dois Vizinhos, Brazil; (3) Biointeractions and Plant Health, Wageningen University & Research, Wageningen, Netherlands; (4) University of Ghent, Belgium.

Keywords: natural selection; co-evolution; *Varroa* destructor; variability

Abstract

Varroa destructor, originally parasitising *Apis cerana*, has co-evolved with this host and developed adaptations that limit its pathogenicity. After shifting to *A. mellifera* in the mid–twentieth century, infestations in managed colonies began to be controlled mainly with acaricides, suppressing natural selective pressure and preventing the emergence of resistance. Understanding resistance and tolerance mechanisms to varroa is essential for elucidating the host-parasite relationship. Darwinian Selection (DS) offers a practical approach, whereby the colonies that survive selective pressure transmit advantageous resistance alleles to subsequent generations DS requires continuous monitoring of colonies and environment to detect measurable effects and the co-evolutionary trends. This study evaluates the performance of *A. m. iberiensis* colonies exposed to DS by monitoring varroa infestation using the mite fall method. Forty-three colonies from twenty families were monitored during the second year of selection over a six-month period (May-October 2025). Mites were collected on chromatographic plates placed on the hive's sanitary tray for 72 hours and counted manually. Infestation was standardised as mite fall per day. A clear temporal pattern was observed, with mean infestation increasing from 6,4 mites/day in May to a significant peak in September (16.2 mites/day, $p<0.01$), followed by a slight decline in October (13.5 mites/day). This trend likely reflects seasonal brood dynamics and mite reproduction. Although no significant differences were found between families, substantial variation occurred between colonies. Two colonies showed extreme values (1,12 and 39,95 mites/day; $p<0,01$). Four infestation groups were identified: <5 (25.6%); 5 to 10 (27.9%); 10 to 30 (39.5%), and >30 mites/day (7.0%). The intra-population variability is fundamental to host-parasite coevolution and for the success of DS programmes, highlighting the need for individual-level monitoring to identify resistant phenotypes. Consequently, continuous natural selection favours the evolution of *A. m. iberiensis* towards resistance to *V. destructor*, reducing the dependence on chemical treatments in beekeeping.

Acknowledgements/Funding
This work was conducted in the framework of the project BETTER-B - Improving bees' resilience to stressors by restoring harmony and balance, funded by the European Union, the Swiss State Secretariat for Education, Research and Innovation, and UK Research and Innovation, under the UK government's Horizon Europe funding guarantee (grant number 10068544).

POSTER 31| BENCHMARKING LAMP PRIMER DESIGN PLATFORMS FOR PYRETHROID RESISTANCE SNP DETECTION IN *VARROA DESTRUCTOR*

Bejaoui, M (1); Costa, M (1); Pinto, MA (1); Henriques, D (1)

(1) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal

Keywords: *Varroa destructor;* pyrethroid resistance; voltage-gated sodium channel; LAMP diagnostics; evolutionary acaricide resistance monitoring

Abstract

Varroa destructor, an ectoparasitic mite of *Apis mellifera*, is a driver of colony and pollination service declines. Widely used pyrethroid acaricides targeting the mite voltage-gated sodium channel (VGSC) have selected for resistance mutations at codons 918 and 925 in Domain II. Genotyping 100 mites from 35 apiaries at the locus revealed ~40% pyrethroid-resistant haplotypes, with the double-resistant M918L/L925V variant at 43%, establishing the Portuguese baseline. PCR-based assays at this locus are robust but laboratory-bound, whereas loop-mediated amplification (LAMP) offers an isothermal, rapid, low-cost alternative for field resistance surveillance. Using this baseline, we benchmarked mutation-focused LAMP primer sets with PrimerExplorer V5, NEB LAMP Designer, and LAMP Designer v1.16 under shared, explicitly defined thermodynamic constraints. We constrained outer primers and inner-primer Tm to 55–70 °C, loops to ≈62–65 °C, GC to 40–70%, F2–B2 span to 120–180 bp, and filtered candidates using ΔG thresholds for hairpins and dimers. PrimerExplorer V5 provided flexible control over primer geometry around codons and loop placement, but required a loop-primer step and external specificity checks. NEB LAMP Designer rapidly generated optimised sets with conservative end-stability and self-dimer filtering, although limited parameter tuning and absence of BLAST restricted mutation-centred optimization. LAMP Designer v1.16 delivered an exhaustive thermodynamic assessment of hairpins, self-dimers, and cross-dimers together with BLAST-supported specificity and evaluation, at the cost of a steeper learning curve and reliance on proprietary software. In NEB LAMP Designer and LAMP Designer v1.16, targeted codons were embedded in distinct inner-primer segments (918 in F2, F1c; 925 in F1c, B1c, respectively), whereas PrimerExplorer V5 was used to design assays on codon 925 alone, given that M918L never occurred without L925V. Collectively, these comparisons show how software architecture and Tm/ΔG criteria shape LAMP primer solutions for resistance SNPs and inform the design of field-deployable diagnostics for evolutionary surveillance.

Acknowledgements/Funding
This work was supported by the project "MITE – Varroa e vírus transmitidos: MonItorização de muTações e dEsenvolvimento de ferramentas moleculares inovadoras" funded by National Beekeeping Programme 2023–2027; FCT/MCTES (PIDDAC): CIMO UID/00690/2025 (10.54499/UID/00690/2025) and UID/PRR/00690/2025 (10.54499/UID/PRR/00690/2025); SusTEC, LA/P/0007/2020 (10.54499/LA/P/0007/2020); and Project PID2021-128882OR-I00.

POSTER 32| NO EVIDENCE FOR A TRADE-OFF BETWEEN HOST AVOIDANCE BEHAVIOUR AND PATHOGENICITY TOWARDS ECOLOGICALLY ASSOCIATED BACTERIA IN CAENORHABDITIS ELEGANS

Vilas Boas, J (1); Ferreira, G (1); Osório, J (1)

(1) Centre for Ecology, Evolution and Environmental Changes (cE3c) & CHANGE–Global Change and Sustainability Institute, Lisbon, Portugal.

Keywords: host-pathogen evolution; avoidance behaviour; *Caenorhabditis elegans*

Abstract

Host fitness costs imposed by pathogens can be mitigated through behavioural avoidance and/or immune responses. Host-pathogen theory predicts that these two defence strategies should covary negatively if they carry fitness costs and are functionally redundant. Alternatively, these two strategies could covary positively if they are complementary or share an underlying genetic basis. Here, we test these hypotheses in the nematode *Caenorhabditis elegans* by quantifying pathogen avoidance behaviour and pathogenicity in response to ecologically associated bacteria. For this, we employed a panel of twelve divergent wild isolates of *C. elegans* and a diverse collection of naturally associated bacterial strains to the nematodes. First, we assessed the pathogenicity of twenty-nine bacterial strains to be able to choose bacteria that represent a gradient of bacterial pathogenicity for the behavioural assays. For this, we conducted replicated fitness assays in the reference strain of *C. elegans* by measuring nematode population growth in the different bacteria. From these assays, we selected nine focal bacteria - three highly pathogenic, three of intermediate pathogenicity, three non-pathogenic - and one beneficial reference strain. Second, we then quantified two avoidance behaviours and population growth across the twelve host genotypes in response to these ten bacterial strains. Our results reveal broad, specific, and significant interactions between host genotype and bacterial strain for both avoidance behaviour and pathogenicity. However, we found no significant covariation between these two defensive traits in either a given host across bacteria, or in a bacteria across hosts. These findings challenge prevailing theoretical expectations regarding trade-offs in host–pathogen evolution and highlight the need for further investigation into the coevolutionary processes shaping avoidance behaviour.

POSTER 33| DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS?

Pinilla, L (1,2*); Garcês, C (1,2*); Ravagni, S (3); Caniglia, R (4); Fabbri, E (4); Leonard, J (5); Skrbinsek, T (6); Vernesi, C (7); Stronen, A (6); Vilà, C (5); Ciucci, P (3); Lobo, D (1,2,8+); Godinho, R (1,2,9+)

(1) CIBIO/InBIO, University of Porto, Vairão, Portugal; (2) BIOPOLIS, Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal; (3) Dept. of Biology and Biotechnologies "Charles Darwin", Sapienza University of Rome, Rome, Italy; (4) BIO-CGE, Unit for Conservation Genetics, Istituto Superiore per la Protezione e la Ricerca Ambientale, Bologna, Italy; (5) CSIC-Doñana Biological Station, Seville, Spain; (6) Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia; (7) Research and Innovation Centre, Fondazione Edmund Mach, S. Michele all'Adige, Italy; (8) Dept. of Biotechnology and Life Sciences, University of Insubria, Busto Arsizio, Italy; (9) Dept. de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal

*Shared first authorship

+Shared senior authorship

Keywords: wolf-dog hybridization; genomics; dog introgression; anthropogenic hybridization; human-dominated landscapes

Abstract

Hybridisation disrupts species barriers and enables gene flow, generating hybrid genomes. However, gene exchange is not uniform across the genome, resulting in regions with different levels of permeability to introgression. In canids, a compelling example is the hybridisation between grey wolves (*Canis lupus*) and domestic dogs (*C. l. familiaris*), a process largely facilitated by human influence (i.e., anthropogenic hybridisation). As European wolf populations recover and recolonise increasingly human-dominated landscapes, encounters with dogs are expected to rise, potentially increasing hybridisation events. In this study, we investigate wolf-dog hybridisation at both the European and regional scale to identify genomic regions that are either resistant or permeable to the introgression of dog-derived variants into wolf genomes. We analysed whole genomes from 39 individuals with recent wolf-dog ancestry across three European populations: the Iberian Peninsula (N=7), Italy (N=15), and the Dinaric region (N=17). First, we assessed global ancestry and pedigree information to classify individuals into recent backcrosses with wolves (BC1-BC2) or later-generation backcrosses (BC3-BC5). We then applied local ancestry inference to estimate dog ancestry at each genomic locus. Across all populations combined, we identified 56 highly permeable regions (≥99th percentile) and 26 strongly resistant regions (≤1st percentile) to dog introgression, distributed across nine and six chromosomes, respectively, with no overlap between them. At the population level, we detected 153 permeable and 115 resistant regions in the Italian population, and 40 permeable and 58 resistant regions in the Dinaric population. Due to the limited sample size, results from the Iberian population were not sufficiently robust for population-specific inference. Identifying genomic regions that resist or facilitate introgression will help determine whether they harbour genes associated with physiological, morphological, and behavioural traits characteristic of wolves or dogs. These insights will be essential for understanding the evolutionary dynamics of anthropogenic hybridisation and for informing conservation strategies for European wolf populations.

Acknowledgements/Funding
This work was funded by the BioDiversa+ WOLFNESS project (DivProtect/0012/2021). LP and CG worked under a research fellowship funded by ECOGEN's group private funds. DL is supported by a postdoctoral fellowship under the project PRIN 2022 "Epigenetics and conservation of small populations: microevolution and adaptive divergence in relict bear populations", funded by the EU – Next Generation EU (CUP J53D2300669006). RG has a Principal Investigator research contract funded by FCT (2022.07926.CEECIND).

POSTER 34| NEW ASSESSMENTS ON GEOGRAPHIC AND SEXUAL SKULL VARIATION IN THE SUBGENUS *CHARRONIA* (*MARTES FLAVIGULA* AND *MARTES GWATKINSII*) (CARNIVORA; MUSTELIDAE)

Sicuro, FL (1,2,3); Abramov, AV (4); Perini, FA (5)

(1) IBRAG – Institute of Biology Roberto Alcantara Gomes, Department of Physiological Sciences, University of the State of Rio de Janeiro, Rio de Janeiro, Brazil; (2) CESAM – Centre for Environmental and Marine Studies, Department of Biology, University of Aveiro, Aveiro, Portugal; (3) PICTIS – International Program for Science, Technology and Innovation in Health, Ílhavo, Portugal; (4) ZIN RAS – Zoological Museum, Zoological Institute of the Russian Academy of Sciences, Saint Petersburg, Russia; (5) ICB – Institute of Biological Sciences, Department of Zoology, Federal University of Minas Gerais, Belo Horizonte, Brazil.

Keywords: morphometrics; Mustelidae; sexual dimorphism; geographic variation; cranial morphology

Abstract

The subgenus *Charronia* (Mustelidae; *Martes*) comprises two species with disjunct distribution patterns: the widely distributed *M. flavigula*, ranging from southern Siberia to the Sunda region, and *M. gwatkinsii*, restricted to the Western Ghats in India. Although *Charronia* is typically associated with forested habitats and exhibits flexible feeding and hunting behaviours, the extent of cranial morphological diversification linked to geography or sex remains insufficiently characterised, and several taxonomic issues persist. Here, we provide an expanded assessment of morphometric and functional skull variation in *M. flavigula* and *M. gwatkinsii*, integrating 141 individuals of both sexes from 13 countries across Eastern and Southeastern Asia, representing the largest sample of *Charronia* analysed to date. Seventeen linear cranial measurements were collected and analysed using univariate and multivariate statistical approaches to examine sexual dimorphism and geographic structuring. Overall patterns reveal marked sexual differences across measurements. *M. flavigula* from continental Asia exhibits substantial overlap, while still suggesting broad geographic structuring, including gradients between Indochinese and southern Chinese populations. Specimens from southern Siberia display consistently larger dimensions, whereas individuals from the Sunda Islands remain clearly differentiated from continental regions. Measurements of *M. gwatkinsii* fall within the lower range of *M. flavigula*, with proportional similarities between the single male and two female individuals examined. This expanded framework offers improved resolution for evaluating morphological diversification in *Charronia* and provides a foundation for refining its taxonomic boundaries.

Acknowledgements/Funding
FLS is funded by national funds through FCT – Fundação para a Ciência e a Tecnologia I.P., under the project CESAM-Centro de Estudos do Ambiente e do Mar, reference UID/50017/2025 (doi.org/10.54499/UID/50017/2025) and LA/P/0094/2020 (doi.org/10.54499/LA/P/0094/2020); FAP is supported by a Research Productivity Grant (CNPq) #311224/2025-3.

POSTER 35| PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS

Sousa, P (1,2,3); Costa, J (1,2,3,4); Farelo, L (1,3); Letty, J (5); Kaerle, C (6); Queney, G (6); Alves, PC (1,2,3,7); Bedson, CPE (8,9), Pimenta, J (1,3); Melo-Ferreira, J (1,2,3); Marques, JP (1,3)

(1) CIBIO, Research Centre in Biodiversity and Genetic Resources, Universidade do Porto, Vairão, Portugal; (2) DBIO-FCUP - Departamento de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal; (3) BIOPOLIS - Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal; (4) ISEM - Institut des Sciences de l'Évolution Montpellier, Université Montpellier, Montpellier, France; (5) ONCFS - Research Department, National Hunting and Wildlife Agency, Juvignac, France; (6) ANTAGENE - Animal Genomics Laboratory, Lyon, France; (7) EBM - Estação Biológica de Mértola, CIBIO, Mértola, Portugal; (8) Natural England, Eastbrook, Cambridge, UK; (9) Department of Natural Sciences, Manchester Metropolitan University, Manchester, UK.

Keywords: genomics; hares; introgression; biodiversity conservation

Abstract

Human activities have profound impacts on ecosystems, with land-use changes, the introduction of non-native species, and accelerated climate change reshaping the distributions of many organisms. Such human-induced range shifts can lead to changes in hybridisation dynamics in contact zones between closely related species. Understanding how hybridisation affects genetic variation is essential for conservation. Gene flow can compromise genetic integrity by introducing deleterious or maladaptive traits, but can also facilitate the transfer of adaptive genetic variants, potentially enhancing species resilience. In this work, we investigate admixture patterns between Mountain hares (*Lepus timidus*) and European hares (*L. europaeus*) in two contrasting scenarios: the French Alps, where both species naturally overlap, and the Peak District, where Mountain hares were reintroduced into an area occupied by European hares. Both species are largely allopatric across most of Eurasia, with few contact zones occurring where competition and interbreeding can threaten Mountain hares' persistence. In these areas, the European hare, better adapted to current environmental conditions, can competitively displace Mountain hares, increasing the likelihood of hybridisation and potentially eroding their genetic integrity. Using ddRADseq data, we examined hybridisation patterns across these regions. Our analyses revealed contrasting dynamics: ancient and localised gene flow in the French Alps, versus more widespread and recent admixture in the Peak District. Admixture in the French Alps occurs mainly in peripheral areas, highlighting regions where human-driven environmental change is likely to shape contact dynamics between species. Both species show latitudinal structure across alpine populations, with central populations acting as a genetic bridge between northern and southern groups. In contrast, the higher levels of admixture in the Peak District reflect the recent human-mediated contact. Genetic signals also indicate past translocations from Ireland to Scotland. This work leverages cutting-edge genomic analyses to reveal how interspecific gene flow occurs across different ecological and anthropogenic contexts.

POSTER 36| EXPLORING THE CELLULAR BASIS OF VARIATION IN CRANIOFACIAL FEATURES OF CICHLID FISHES

Duarte, Pr (1); Marconi, A (1); Soto-Bajo, I (1); Elkin, J (1); Santos, M (1)

(1) Zoology Department, University of Cambridge, Cambridge, United Kingdom

Keywords: cichlid fishes; evo-devo; craniofacial diversification; single nucleus transcriptomics; neural crest

Abstract

Vertebrates are known to display incredibly complex and diverse phenotypes, ranging from pigmentation patterns to specialized craniofacial structures and sensory features. Several of these traits derive from a transient embryonic cell population - the (cranial) neural crest - and are known to have emerged as evolutionary adaptations to novel environments. East African cichlids have undergone successive waves of adaptive radiations, resulting in low levels of interspecific genetic divergence, but remarkable variation in their morphology and trophic ecology. As such, cichlid fishes arise as a powerful model for the study of the developmental and molecular basis of species divergence. Here, we explore the cellular basis of cichlid phenotypic diversity by harnessing single nucleus transcriptomics. We take a special focus on tissues contributing towards craniofacial features diversification, hypothesising that the neural crest could be a major driver of interspecific diversity in cichlids. We identified a total of 93 cell type subpopulations across relevant embryonic stages (segmentation, early pharyngula, and mid pharyngula), all of them conserved between three morphologically and ecologically divergent eastern African cichlid species: *Tropheops* sp. 'mauve', *Astatotilapia calliptera,* and *Aulonocara stuartgranti*. We show that species-specific cell type enrichment and interspecific transcriptome divergence are more relevant for the diversification of cichlid craniofacial traits than the emergence of novel cell types. We observe eye and (cranial neural crest and mesoderm-derived) head mesenchyme related subclusters to be particularly variable across our three target species. Using a combination of differential gene expression analyses and genomic approaches, we identify candidate genes potentially driving craniofacial and eye divergence between species. Taken together, our results suggest that both the "novel" neural crest and the most "ancient" mesoderm derived mesenchyme might have played an important role in the establishment of highly variable craniofacial variation along cichlid evolution.

POSTER 37| WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS

Faustino, E (1); Mendes, SL (1); Carvalho, J (1); Perea, S (2); Doadrio, I (2); Pheulner, P (3); Sousa-Santos, C (4); Sousa, V (1)

(1) Centre for Ecology, Evolution and Environmental Changes (CE3C), Portugal; (2) MNCN - Museo Nacional de Ciencias Naturales, José Gutiérrez Abascal 2, 28006 Madrid, Spain; (3) Department of Fish Ecology and Evolution, Eawag—Swiss Federal Institute of Aquatic Science and Technology, Switzerland; (4) MARE/ARNET ISPA – Instituto Universitário de Ciências Psicológicas, Sociais e da Vida, Portugal.

Keywords: demographic modelling; reference genome bias; freshwater fish; gene flow

Abstract

Hybridization, the mating between genetically distinct lineages, is widespread throughout the evolutionary tree. Our understanding of hybridization and its prevalence has been made possible due to the generation of population genomics data for an increasing number of species, coupled with the development of different methods, such as demographic modelling. Freshwater fish stand out with some of the highest rates of hybridization in animals. Yet, if and how hybridization can lead to speciation remains debatable. Here, we investigate two potential cases of hybridization in Iberian chubs, previously described using low-coverage data. By using whole-genome population genomic data, we aim to uncover the demographic history and relationship of the Iberian chubs. These species have been shown to have experienced gene flow throughout their evolutionary history. We generated high-coverage(>17x) whole-genome re-sequencing data for 35 individuals comprising *S. pyrenaicus*, *S. carolitertii*, *S. tartessicus*, *S. caetobrigus,* and two outgroup species, *S. torgalensis* and *S. aradensis*. We used D-statistics to distinguish incomplete lineage sorting from gene flow and found that the relationship between *S. pyrenaicus*, *S. carolitertii*, *S. tartessicus,* and *S. caetobrigus* cannot be explained by simple bifurcating trees, with evidence of gene flow, in agreement with previous results using genotyping-by-sequencing and low-coverage data. Demographic modelling showed evidence of an admixed population of *S. caetobrigus*, after extensive gene flow (50%) from *S. pyrenaicus* recently in time (~10kya). These results highlight the complexity of the relationship between *Squalius* species, with several instances of gene flow between different species. Furthermore, this ongoing project aims to determine the extent to which reference genome choice can impact demographic inference, comparing choosing the reference genome of one of the species in the dataset or choosing an equidistant reference to all species in the dataset. We expect to find reference genome bias towards one species in the former rather than the latter, which should generate the same bias for all species.

POSTER 38| HARNESSING MITOCHONDRIAL DIVERGENCE IN *APIS MELLIFERA* TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY

Honrado, M (1,2); Henriques, D (1); Santos, J (1); Yadró García, CA (1); MEDIBEES Consortium; Pinto, MA (1) Amaral, JS (1)

(1) CIMO, LA SusTEC, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal; (*2*) LAQV-REQUIMTE & Department of Chemistry, University of Aveiro, Campus Universitário de Santiago, Aveiro, 3810-193, Portugal

Keywords: *Apis mellifera*, honey, mitochondrial DNA, entomological origin

Abstract

The Mediterranean region holds one of the highest levels of *Apis mellifera* subspecific diversity, exhibiting a rich evolutionary history shaped by long-term geographic isolation, climatic variation, and, more recently, by human-driven processes. As part of the international project MEDIBEES, we developed a DNA-metabarcoding approach to characterise the entomological origin of honey, focusing on mitochondrial lineages A (African), M (Western European), C (Eastern European), and O (Middle Eastern). To build a robust reference database, DNA was extracted from 1280 honeybees representing 16 *A. mellifera* subspecies (*A.m. sahariensis, A.m. intermisa, A.m. siciliana, A.m. ruttneri, A.m. iberiensis, A.m. ligustica, A.m. macedonica, A.m. adami, A.m. cecropia, A.m. cypria, A.m. caucasica, A.m. meda, A.m. anatoliaca, A.m. syriaca, A.m. jemenitica, A.m. lamarcki*) and whole genomes were sequenced. Mitochondrial genomes were assembled using MitoZ, resulting in 769 assemblies, which were individually aligned against the reference mitochondrial genome using MEGA. Only mitogenomes corresponding to native *subspecific* ancestry were retained, producing a final curated database of 355 sequences. This database was then used to calculate the fixation index (F_{ST}) pairwise values, and a 400 bp sliding window was used to identify single-nucleotide polymorphisms (SNPs) that effectively differentiate (F_{ST}>0.98) the four lineages. Three promising regions emerged for primer design: one in the COI gene, one in the ND1 gene, and one in the CYTB gene. The resulting primers were first validated using 36 honeybee samples of known lineage representing all 16 subspecies and subsequently applied to 83 honey samples from Lebanon, Jordan, Türkiye, Italy, Algeria, Malta, UAE, and Oman. Among the three markers, ND1 showed the highest discriminatory power, correctly assigning all reference honeybee samples to their respective lineage. The COI and CYTB primers also showed strong potential, and the observed error rates (5.8% in COI and 1.7% for CYTB) provide useful thresholds for interpreting the DNA-metabarcoding results in honey samples. Overall, this study demonstrates how patterns of mitochondrial divergence shaped by long-term evolutionary processes can be harnessed for applied DNA-metabarcoding on food authenticity.

Acknowledgements/Funding

M. Honrado and C. Yadró acknowledge the PhD scholarship from FCT (2021.08119.BD, 2021.06948.BD). This research was funded by the project MEDIBEES - Monitoring the Mediterranean Honey Bee Subspecies and their Resilience to Climate Change for the Improvement of Sustainable Agro-Ecosystems. MEDIBEES is part of the PRIMA programme supported by the European Union. This research was also supported by national funds through FCT/MCTES (PIDDAC): CIMO UID/00690/2025 (10.54499/UID/00690/2025) and UID/PRR/00690/2025 (10.54499/UID/PRR/00690/2025); SusTEC, LA/P/0007/2020 (DOI: 10.54499/LA/P/0007/2020).

List of Authors

AUTHOR	NUMBER OF ABSTRACTS	TITLE [COMMUNICATION TYPE]
A Marconi	1	• EXPLORING THE CELLULAR BASIS OF VARIATION IN CRANIOFACIAL FEATURES OF CICHLID FISHES **[Poster]**
Afonso Grandela	3	• LONG-TERM EVOLUTION EXPERIMENTS FULLY REVEAL THE POTENTIAL FOR THERMAL ADAPTATION **[Poster]** • DO MATING SYSTEMS SHAPE THERMAL FERTILITY? **[Poster]** • DETRIMENTAL IMPACT OF A HEATWAVE ON MALE REPRODUCTIVE BEHAVOUR AND FERTILITY **[Oral]**
Agostinho Antunes	1	• TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) **[Oral]**
Aicha Meliani Rodríguez	1	• THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE **[Poster]**
Alba Rey-Iglésia	1	• HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC **[Poster]**
Alexandre Campos	1	• TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) **[Oral]**
Alexandre Esperança	1	• DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS **[Oral]**
Alexandre Pinto	1	• SEEDLING EVOLUTION UNDERSTANDING TO PROMOTE POSITIVE ATTITUDES TOWARDS BIODIVERSITY CONSERVATION: A STUDY WITH ELEMENTARY SCHOOL STUDENTS **[Oral]**
Alexei Abramov	1	• NEW ASSESSMENTS ON GEOGRAPHIC AND SEXUAL SKULL VARIATION IN THE SUBGENUS CHARRONIA (*MARTES FLAVIGULA* AND *MARTES GWATKINSII*) (CARNIVORA; MUSTELIDAE) **[Poster]**
Alfredo López	1	• HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC **[Poster]**
Alireza Arab	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Amadeo Rodríguez Fernández-Alba	1	• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]**
Ana Clara Santos	1	• EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]**

Ana Diéguez Antón	2	• PATHOGENS AGAINST THE MACHINE: EVOLUTIONARY SHIFTS OF PHYTOPHTHORA INFESTANS ACROSS EUROPEAN BIOREGIONS AND THEIR IMPLICATIONS FOR PREDICTIVE MODELLING **[Poster]** • THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX* **[Poster]**
Ana Elisabete Pires	1	• UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS **[Oral]**
Ana Escudeiro	1	• BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS **[Oral]**
Ana Lima	1	• ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS **[Oral]**
Ana R. Lopes	6	• VIRAL EVOLUTION IN ISOLATION: HOW *VARROA* INVASION SHAPED DEFORMED WING VIRUS AND LAKE SINAI VIRUS IN AZOREAN HONEYBEES **[Oral]** • LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (APIS MELLIFERA) TO PESTICIDE PRESSURE **[Poster]** • EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]** • HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL [Poster] • INTRA-POPULATION VARIABILITY IN A DARWINIAN SELECTION PROGRAM FOR VARROA RESISTANCE IN APIS MELLIFERA IBERIENSIS **[Poster]** • HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]**
Ana Usié	1	• UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS **[Oral]**
André Liz	1	• FIRST PHYLOGEOGRAPHIC ASSESSMENT OF THE DIADEMED SAND SNAKE (COLUBRIDAE: LYTORHYNCHUS) ACROSS THE SAHARO-ARABIAN DESERT BELT **[Poster]**
André Machado	3	• OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH **[Poster]** • EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG **[Oral]** • FROM GENOMES TO “HEAT”: THE MOLECULAR ORIGIN OF ADAPTATION IN DESERT MAMMALS **[ORAL]**
André Santos	1	• OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH **[Poster]**
André Silva	1	• FROM GENOMES TO “HEAT”: THE MOLECULAR ORIGIN OF ADAPTATION IN DESERT MAMMALS **[ORAL]**
André Viana	1	• UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]**
Andrejz Oleksa	1	• THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE **[Poster]**

Andy Gardner	1	• MATERNAL EFFECTS MEDIATE THE INTERACTIVE EFFECT OF TEMPERATURE AND POPULATION STRUCTURE ON SPIDER MITE SEX RATIO AND BODY SIZE **[Oral]**
Anne Friedrich	1	• EVIDENCE FOR TWO MAJOR DOMESTICATION EVENTS DURING THE EVOLUTIONARY HISTORY OF SACCHAROMYCES CEREVISIAE **[ORAL]**
Annelise Rosa-Fontana	1	• WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]**
Antonio Nanetti	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Antonio Pérez-Pérez	3	• RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING? **[Oral]** • EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]** • HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL **[Poster]**
Aránzazu Meana	1	• RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING? **[Oral]**
Astrid Stronen	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Banan Al-Shagour	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Bas Buddendorf	1	• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]**
Bastien Boussau	1	• PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER **[Poster]**
Bastien Mérigot	1	• POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, *PARAMURICEA CLAVATA* IN THE PARC NATIONAL DES CALANQUES (FRANCE) **[Poster]**
Bernardo Pinto	1	• THE EGG OR THE CHICKEN? REVISITING AGLOMERULISM AND THE EMERGENCE OF ANTI-FREEZE GLYCOPROTEINS, RENAL FUNCTION AND WATER BALANCE IN NOTOTHENIODS **[Poster]**
Carla Sousa-Santos	1	• WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS **[Poster]**
Carles Vilà	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Carlos Yadró	6	• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]** • ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]** • WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]** • HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]**

		• EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]** • HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL **[Poster]** • HARNESSING MITOCHONDRIAL DIVERGENCE IN APIS MELLIFERA TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY **[Poster]**
Carlos P.E. Bedson	1	• PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
Carlos Rodríguez Fernandes	1	• UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]**
Carlos Vila-Verde	1	• STRUCTURAL ORGANIZATION AND EVOLUTIONARY DYNAMICS OF HUMAN SATELLITE 1B (HSAT1B) ACROSS PRIMATE GENOMES **[Oral]**
Carmen Seijo Coello	1	• PATHOGENS AGAINST THE MACHINE: EVOLUTIONARY SHIFTS OF PHYTOPHTHORA INFESTANS ACROSS EUROPEAN BIOREGIONS AND THEIR IMPLICATIONS FOR PREDICTIVE MODELLING **[Poster]**
Carolina Bartolomé	1	• RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING? **[Oral]**
Carolina Bruno-de-Sousa	1	• UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS **[Oral]**
Caroline Steiner	1	• ECO-EVOLUTIONARY DYNAMICS OF *ESCHERICHIA COLI* INVASION ACROSS HUMAN GUT MICROBIOTAS **[Oral]**
Catarina Bernardo	1	• IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS **[Oral]**
Catarina Garcês	2	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]** • HYBRIDIZATION AS A SOURCE OF PHENOTYPIC DIVERSITY: THE GENOMIC BASIS OF YELLOW COAT COLOUR IN IBERIAN WOLVES **[Oral]**
Catarina Ginja	1	• UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS **[Oral]**
Cécile Kaerle	1	• PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
Chadi Hosri	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Charlie Scutt	1	• PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER **[Poster]**
Chedhawat Chokechaipaisarn	1	• MATERNAL EFFECTS MEDIATE THE INTERACTIVE EFFECT OF TEMPERATURE AND POPULATION STRUCTURE ON SPIDER MITE SEX RATIO AND BODY SIZE **[Oral]**
Christian Dubos	1	• DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS **[Oral]**

Claudino Matos	1	• UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS **[Oral]**
Cristiano Vernesi	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Daniel Eleutério	1	• STRUCTURAL ORGANIZATION AND EVOLUTIONARY DYNAMICS OF HUMAN SATELLITE 1B (HSAT1B) ACROSS PRIMATE GENOMES **[Oral]**
Daniel Gaspar	1	• UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS **[Oral]**
Daniela Barbosa	1	• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]** • WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]**
David Neves	1	• UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S **[Poster]**
Delphine Panziera	1	• INTRA-POPULATION VARIABILITY IN A DARWINIAN SELECTION PROGRAM FOR *VARROA* RESISTANCE IN *APIS MELLIFERA IBERIENSIS* **[Poster]**
Demetris Taliadoros	2	• HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]** • LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]**
Diana Lobo	4	• ADAPTATION AND (EPI)GENOMIC EROSION IN SMALL, ISOLATED POPULATIONS: INSIGHTS FROM THE CRITICALLY ENDANGERED APENNINE BROWN BEAR **[Poster]** • DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]** • HYBRIDIZATION AS A SOURCE OF PHENOTYPIC DIVERSITY: THE GENOMIC BASIS OF YELLOW COAT COLOUR IN IBERIAN WOLVES **[Oral]** • EVALUATING DNA COLLECTION METHODS FOR NON-INVASIVE GENETIC MONITORING IN DESERT CONDITIONS **[Poster]**
Didier Aurelle	1	• POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, PARAMURICEA CLAVATA IN THE PARC NATIONAL DES CALANQUES (FRANCE) **[Poster]**
Diogo Oliveira	2	• GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB **[Oral]** • FROM GENOMES TO “HEAT”: THE MOLECULAR ORIGIN OF ADAPTATION IN DESERT MAMMALS **[Oral]**
Diogo Prino Godinho	1	• THE IMPORTANCE OF ENVIRONMENTAL HETEROGENEITY FOR THE GENOMIC SIGNATURE OF ADAPTATION TO CADMIUM *[Oral]*
Diogo Roque	1	• PAST SELECTIVE HISTORY INFLUENCES ADAPTATION TO ORAL INFECTION IN *DROSOPHILA MELANOGASTER* **[Poster]**
Dirk C. de Graaf	2	• WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]** • HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]**

		• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]** • INTRA-POPULATION VARIABILITY IN A DARWINIAN SELECTION PROGRAM FOR VARROA RESISTANCE IN APIS MELLIFERA IBERIENSIS **[Poster]**
Dora Henriques	8	• EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]** • ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]** • HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL [Poster] • WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]** • HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]** • LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]** • BENCHMARKING LAMP PRIMER DESIGN PLATFORMS FOR PYRETHROID-RESISTANCE SNP DETECTION IN *VARROA DESTRUCTOR* **[Poster]** • HARNESSING MITOCHONDRIAL DIVERGENCE IN APIS MELLIFERA TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY **[Poster]**
Doralinda Lopes	1	• EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]**
Duarte Gonçalves	1	• FIRST PHYLOGEOGRAPHIC ASSESSMENT OF THE DIADEMED SAND SNAKE (COLUBRIDAE: LYTORHYNCHUS) ACROSS THE SAHARO-ARABIAN DESERT BELT **[Poster]**
Eissa Asma A.	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Elena Fabbri	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Élio Sucena	1	• PAST SELECTIVE HISTORY INFLUENCES ADAPTATION TO ORAL INFECTION IN *DROSOPHILA MELANOGASTER* **[Poster]**
Elsa Froufe	1	• EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG **[Oral]**
Elvira Lafuente	1	• PAST SELECTIVE HISTORY INFLUENCES ADAPTATION TO ORAL INFECTION IN *DROSOPHILA MELANOGASTER* **[Poster]**
Estevão Faustino	1	• IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS **[Oral]** • WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS **[Poster]**

Evandro Lopes	1	• MORPHOLOGICAL RESPONSES OF *MUS MUSCULUS* TO THE ENVIRONMENTAL CONDITIONS OF CABO VERDE **[Oral]**
Fabrice Requier	1	• THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE **[Poster]**
Fernanda Li	3	• WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]** • HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]** • LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]**
Fernando Perini	1	• NEW ASSESSMENTS ON GEOGRAPHIC AND SEXUAL SKULL VARIATION IN THE SUBGENUS CHARRONIA (*MARTES FLAVIGULA* AND *MARTES GWATKINSII*) (CARNIVORA; MUSTELIDAE) *[Poster]*
Fernando Sicuro	1	• NEW ASSESSMENTS ON GEOGRAPHIC AND SEXUAL SKULL VARIATION IN THE SUBGENUS CHARRONIA (*MARTES FLAVIGULA* AND *MARTES GWATKINSII*) (CARNIVORA; MUSTELIDAE) **[Poster]**
Filipe Castro	2	• THE EGG OR THE CHICKEN? REVISITING AGLOMERULISM AND THE EMERGENCE OF ANTI-FREEZE GLYCOPROTEINS, RENAL FUNCTION AND WATER BALANCE IN NOTOTHENIODS. **[Poster]** • OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH **[Poster]**
Filomena Adega	2	• A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME **[Poster]** • BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS **[Oral]**
Flore Zélé	1	• EXPERIMENTAL EVOLUTION IN SYMPATRY LEADS TO HIGHER GROWTH RATES, BUT DOES NOT ALLEVIATE THE COSTS OF COMPETITION AND REPRODUCTIVE INTERFERENCE **[Oral]**
Florence Cornette	1	• POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, *PARAMURICEA CLAVATA* IN THE PARC NATIONAL DES CALANQUES (FRANCE) *[Poster]*
Florence Vignols	1	• DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS **[Oral]**
Fouad Lamghari	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Fulvio Licata	1	• FIRST PHYLOGEOGRAPHIC ASSESSMENT OF THE DIADEMED SAND SNAKE (COLUBRIDAE: LYTORHYNCHUS) ACROSS THE SAHARO-ARABIAN DESERT BELT **[Poster]**
Giles Verbinnen	1	• WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]**
Giselle Martin Hernandez	1	• HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]**
Goncalo Themudo	6	• VARIATION IN GARUM RECIPES ACROSS THE ROMAN EMPIRE AND THE MICROBIAL COMMUNITIES DRIVING THEIR FERMENTATION **[Poster]**

		• METABARCODING OF MEDITERRANEAN MONK SEAL (MONACHUS MONACHUS) SCATS REVEALS A DIVERSE PISCIVOROUS DIET **[Poster]** • RECONSTRUCTING POPULATION DYNAMICS OF THE EUROPEAN SARDINE (*SARDINA PILCHARDUS*) USING PALAEOGENOMICS **[Poster]** • BLUEFINDB: A MULTI-MARKER, "HUMAN-IN-THE-LOOP" ARCHITECTURE FOR PRECISION eDNA REFERENCE DATABASE CURATION **[Poster]** • GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB **[Oral]** • HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC **[Poster]**
Grace McCormack	1	• THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE **[Poster]**
Guilherme Ferreira	1	• NO EVIDENCE FOR A TRADE-OFF BETWEEN HOST AVOIDANCE BEHAVIOUR AND PATHOGENICITY TOWARDS ECOLOGICALLY ASSOCIATED BACTERIA IN CAENORHABDITIS ELEGANS **[Poster]**
Guillaume Queney	1	• PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
Herlander Azevedo	1	• DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS [Oral]
Hugo Barreto	1	• ECO-EVOLUTIONARY DYNAMICS OF ESCHERICHIA COLI INVASION ACROSS HUMAN GUT MICROBIOTAS **[Oral]**
Hugo Moreno	1	• TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) **[Oral]**
I Soto-Bajo	1	• EXPLORING THE CELLULAR BASIS OF VARIATION IN CRANIOFACIAL FEATURES OF CICHLID FISHES **[Poster]**
Ian Marc Bonapace	1	• ADAPTATION AND (EPI)GENOMIC EROSION IN SMALL, ISOLATED POPULATIONS: INSIGHTS FROM THE CRITICALLY ENDANGERED APENNINE BROWN BEAR **[Poster]**
Ignacio Doadrio	1	• WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS **[Poster]**
Inês Amorim	1	• GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB **[Oral]**
Inês Fragata	3	• THE IMPORTANCE OF ENVIRONMENTAL HETEROGENEITY FOR THE GENOMIC SIGNATURE OF ADAPTATION TO CADMIUM **[Oral]** • HOW DOES THE EVOLUTION OF DIRECT AND INDIRECT INTERACTIONS AFFECT ECOSYSTEM RESILIENCE? **[Poster]** • ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS **[Oral]**
Inês M. dos Santos	2	• HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST

		ATLANTIC **[Poster]** • RECONSTRUCTING POPULATION DYNAMICS OF THE EUROPEAN SARDINE (*SARDINA PILCHARDUS*) USING PALAEOGENOMICS **[Poster]**
Inês Miranda	1	• UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]**
Inês Ramos	1	• POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, *PARAMURICEA CLAVATA* IN THE PARC NATIONAL DES CALANQUES (FRANCE) **[Poster]**
Inês Santos	1	• VARIATION IN GARUM RECIPES ACROSS THE ROMAN EMPIRE AND THE MICROBIAL COMMUNITIES DRIVING THEIR FERMENTATION **[Poster]**
Isabel Alves	1	• EVIDENCE FOR TWO MAJOR DOMESTICATION EVENTS DURING THE EVOLUTIONARY HISTORY OF *SACCHAROMYCES CEREVISIAE* **[Oral]**
Ivo Roessink	1	• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]**
J. Elkin	1	• EXPLORING THE CELLULAR BASIS OF VARIATION IN CRANIOFACIAL FEATURES OF CICHLID FISHES **[Poster]**
J. Bernardino Lopes	1	• SEEDLING EVOLUTION UNDERSTANDING TO PROMOTE POSITIVE ATTITUDES TOWARDS BIODIVERSITY CONSERVATION: A STUDY WITH ELEMENTARY SCHOOL STUDENTS **[Oral]**
J.V. López-Bao	1	• HYBRIDIZATION AS A SOURCE OF PHENOTYPIC DIVERSITY: THE GENOMIC BASIS OF YELLOW COAT COLOUR IN IBERIAN WOLVES **[Oral]**
James Arruda	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Janan Gawran	1	• UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S **[Poster]**
Jean-Baptiste Gueye	1	• ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS **[Oral]**
Jean-Baptiste Ledoux	2	• TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) **[Oral]** • POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, PARAMURICEA CLAVATA IN THE PARC NATIONAL DES CALANQUES (FRANCE) **[Poster]**
Jennifer Leonard	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Jérôme Goudet	1	• INCOMPLETE LINEAGE SORTING AND THE RECURRENT EVOLUTION OF PARTHENOGENESIS IN TIMEMA STICK INSECTS **[Oral]**
Jérôme Letty	1	• PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
Jessica King	1	• ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS **[Oral]**

Joana Amaral	1	• HARNESSING MITOCHONDRIAL DIVERGENCE IN APIS MELLIFERA TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY **[Poster]**
Joachim de Miranda	1	• VIRAL EVOLUTION IN ISOLATION: HOW *VARROA* INVASION SHAPED DEFORMED WING VIRUS AND LAKE SINAI VIRUS IN AZOREAN HONEYBEES **[Oral]** • THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE **[Poster]**
Joana Vilas Boas	1	• NO EVIDENCE FOR A TRADE-OFF BETWEEN HOST AVOIDANCE BEHAVIOUR AND PATHOGENICITY TOWARDS ECOLOGICALLY ASSOCIATED BACTERIA IN *CAENORHABDITIS ELEGANS* **[Poster]**
Joana Santos	1	• HARNESSING MITOCHONDRIAL DIVERGENCE IN APIS MELLIFERA TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY **[Poster]**
João Cabral	2	• A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME **[Poster]** • BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS **[Oral]**
João Carneiro	2	• METABARCODING OF MEDITERRANEAN MONK SEAL (*MONACHUS MONACHUS*) SCATS REVEALS A DIVERSE PISCIVOROUS DIET **[Poster]** • BLUEFINDB: A MULTI-MARKER, "HUMAN-IN-THE-LOOP" ARCHITECTURE FOR PRECISION eDNA REFERENCE DATABASE CURATION **[Poster]**
João Carvalho	2	• UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]** • WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS **[Poster]**
João Cordeiro	1	• FROM GENOMES TO “HEAT”: THE MOLECULAR ORIGIN OF ADAPTATION IN DESERT MAMMALS **[Oral]**
João M Moreno	1	• IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS **[Oral]**
João Moutinho	1	• EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG **[Oral]**
João Pedro Marques	3	• THE GENOMIC AFTERMATH OF THE ICE AGES IN EUROPEAN HARES **[Oral]** • MACRO- AND MICROEVOLUTIONARY GENOMICS OF THE BLUE SHARK (*PRIONACE GLAUCA*) **[Oral]** • PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
João Picão Osório	1	• NO EVIDENCE FOR A TRADE-OFF BETWEEN HOST AVOIDANCE BEHAVIOUR AND PATHOGENICITY TOWARDS ECOLOGICALLY ASSOCIATED BACTERIA IN CAENORHABDITIS ELEGANS **[Poster]**

João Pimenta	1	• PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
João Souto	1	• INCOMPLETE LINEAGE SORTING AND THE RECURRENT EVOLUTION OF PARTHENOGENESIS IN TIMEMA STICK INSECTS **[Oral]**
João Teixeira	1	• OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH **[Poster]**
Joaquim Garrabou	1	• POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, PARAMURICEA CLAVATA IN THE PARC NATIONAL DES CALANQUES (FRANCE) **[Poster]**
John Gittleman	1	• GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES **[Oral]**
John Wiens	1	• GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES **[Oral]**
Jonathan Davies	1	• GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES **[Oral]**
Jonathan S Castaño-Serna	1	• THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX* **[Poster]** • PATHOGENS AGAINST THE MACHINE: EVOLUTIONARY SHIFTS OF PHYTOPHTHORA INFESTANS ACROSS EUROPEAN BIOREGIONS AND THEIR IMPLICATIONS FOR PREDICTIVE MODELLING **[Poster]**
Jonathan Wilson	3	• THE EGG OR THE CHICKEN? REVISITING AGLOMERULISM AND THE EMERGENCE OF ANTI-FREEZE GLYCOPROTEINS, RENAL FUNCTION AND WATER BALANCE IN NOTOTHENIODS. **[Poster]** • OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH **[Poster]** • EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG **[Oral]**
Jorge C Pereira	1	• BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS **[Oral]**
Jorge Pereira	1	• A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME **[Poster]**
José Brito	1	• FIRST PHYLOGEOGRAPHIC ASSESSMENT OF THE DIADEMED SAND SNAKE (COLUBRIDAE: LYTORHYNCHUS) ACROSS THE SAHARO-ARABIAN DESERT BELT **[Poster]**
José Costa	2	• THE GENOMIC AFTERMATH OF THE ICE AGES IN EUROPEAN HARES **[Oral]** • PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
José Martínez-Cedeira	1	• HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC **[Poster]**
José Matos	1	• UNVEILING GENOME-WIDE DIVERSITY AND SELECTION SIGNATURES IN PORTUGUESE SHEEP BREEDS **[Oral]**

José Melo-Ferreira	4	• THE GENOMIC AFTERMATH OF THE ICE AGES IN EUROPEAN HARES **[Oral]** • MACRO- AND MICROEVOLUTIONARY GENOMICS OF THE BLUE SHARK (*PRIONACE GLAUCA*) **[Oral]** • UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]** • PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
José Rufino	2	• WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]** • LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]** • ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS n
José Teixeira	1	• THE EGG OR THE CHICKEN? REVISITING AGLOMERULISM AND THE EMERGENCE OF ANTI-FREEZE GLYCOPROTEINS, RENAL FUNCTION AND WATER BALANCE IN NOTOTHENIODS **[Poster]**
Joseph Schacherer	1	• EVIDENCE FOR TWO MAJOR DOMESTICATION EVENTS DURING THE EVOLUTIONARY HISTORY OF *SACCHAROMYCES CEREVISIAE* **[Oral]**
Jozef van der Steen	1	• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE [Poster]
Juan Adánez	2	• HOW DOES THE EVOLUTION OF DIRECT AND INDIRECT INTERACTIONS AFFECT ECOSYSTEM RESILIENCE? **[Poster]** • ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS **[Oral]**
Juliana Sofia Alves	1	• MACRO- AND MICROEVOLUTIONARY GENOMICS OF THE BLUE SHARK (*PRIONACE GLAUCA*) **[Oral]**
K.A.S.U. Kuruppuarachchi	1	• BLUEFINDB: A MULTI-MARKER, "HUMAN-IN-THE-LOOP" ARCHITECTURE FOR PRECISION eDNA REFERENCE DATABASE CURATION **[Poster]**
Karol Zub	1	• UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]**
L. Filipe C. Castro	1	• GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB **[Oral]**
Laia Navarro-Martin	1	• UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S **[Poster]**
Lara Almeida	1	• MORPHOLOGICAL RESPONSES OF *MUS MUSCULUS* TO THE ENVIRONMENTAL CONDITIONS OF CABO VERDE [Oral]
Larissa Cunha	2	• INTRA-POPULATION VARIABILITY IN A DARWINIAN SELECTION PROGRAM FOR *VARROA* RESISTANCE IN *APIS MELLIFERA IBERIENSIS* **[Poster]** • HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]**

Laura Gramolini	1	• ADAPTATION AND (EPI)GENOMIC EROSION IN SMALL, ISOLATED POPULATIONS: INSIGHTS FROM THE CRITICALLY ENDANGERED APENNINE BROWN BEAR **[Poster]**
Laura Meno	1	• THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX* **[Poster]**
Laura Meno Fariñas	1	• PATHOGENS AGAINST THE MACHINE: EVOLUTIONARY SHIFTS OF PHYTOPHTHORA INFESTANS ACROSS EUROPEAN BIOREGIONS AND THEIR IMPLICATIONS FOR PREDICTIVE MODELLING **[Poster]**
Léa Rambaud	1	• PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER **[Poster]**
Leili Khalatbari	1	• EVALUATING DNA COLLECTION METHODS FOR NON-INVASIVE GENETIC MONITORING IN DESERT CONDITIONS **[Poster]**
Leonor Bezerra	1	• GENOMIC ARCHITECTURE OF SHELL COLOUR POLYMORPHISM IN LITTORINA MARINE SNAILS: THE ROLE OF CHROMOSOMAL INVERSIONS AND GENE FLUX **[Poster]**
Leonor R. Rodrigues	3	• MATERNAL EFFECTS MEDIATE THE INTERACTIVE EFFECT OF TEMPERATURE AND POPULATION STRUCTURE ON SPIDER MITE SEX RATIO AND BODY SIZE **[Oral]** • DETRIMENTAL IMPACT OF A HEATWAVE ON MALE REPRODUCTIVE BEHAVOUR AND FERTILITY **[Oral]** • HOW DOES THE EVOLUTION OF DIRECT AND INDIRECT INTERACTIONS AFFECT ECOSYSTEM RESILIENCE? **[Poster]**
Leonor Rodrigues	2	• ADAPT, ADJUST OR MOVE: CAN THE SPIDER MITES *TETRANYCHUS CINNABARINUS* DO IT ALL IN RESPONSE TO HEAT? **[Poster]** • DO MATING SYSTEMS SHAPE THERMAL FERTILITY? **[Poster]**
Liliana Farelo	4	• THE GENOMIC AFTERMATH OF THE ICE AGES IN EUROPEAN HARES **[Oral]** • MACRO- AND MICROEVOLUTIONARY GENOMICS OF THE BLUE SHARK (*PRIONACE GLAUCA*) **[Oral]** • UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]** • PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
Lina De Smet	1	• WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]**
Lorena Pinilla	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Luana Ramos	1	• TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) **[Oral]**
Luís Castro	2	• EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG **[Oral]** • FROM GENOMES TO “HEAT”: THE MOLECULAR ORIGIN OF ADAPTATION IN DESERT MAMMALS **[Oral]**

M. Alice Pinto	11	• EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]** • VIRAL EVOLUTION IN ISOLATION: HOW VARROA INVASION SHAPED DEFORMED WING VIRUS AND LAKE SINAI VIRUS IN AZOREAN HONEYBEES **[Oral]** • HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL **[Poster]** • ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]** • LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]** • INTRA-POPULATION VARIABILITY IN A DARWINIAN SELECTION PROGRAM FOR *VARROA* RESISTANCE IN *APIS MELLIFERA IBERIENSIS* **[Poster]** • THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE **[Poster]** • WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]** • HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]** • BENCHMARKING LAMP PRIMER DESIGN PLATFORMS FOR PYRETHROID-RESISTANCE SNP DETECTION IN *VARROA DESTRUCTOR* **[Poster]** • HARNESSING MITOCHONDRIAL DIVERGENCE IN APIS MELLIFERA TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY **[Poster]**
Maíra Costa	4	• EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]** • HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL **[Poster]** • HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]** • BENCHMARKING LAMP PRIMER DESIGN PLATFORMS FOR PYRETHROID-RESISTANCE SNP DETECTION IN *VARROA DESTRUCTOR* **[Poster]**
Margarida Matos	2	• LONG-TERM EVOLUTION EXPERIMENTS FULLY REVEAL THE POTENTIAL FOR THERMAL ADAPTATION **[Poster]** • DETRIMENTAL IMPACT OF A HEATWAVE ON MALE REPRODUCTIVE BEHAVOUR AND FERTILITY **[Oral]**
Margarida Santos-Reis	1	• UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]**
María Carmen Seijo	1	• THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX* **[Poster]**

Maria Carolina Matos	1	• FCRL6 THROUGHOUT THE LINEAGES: WHAT'S THE HISTORY BEHIND THE FIRST FCRL THAT WAS DESCRIBED? **[Oral]**
Maria Murcia	1	• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE [Poster]
María Shantal Rodríguez-Flores	1	• THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX* **[Poster]**
María Soledad Sagastume	1	• RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING? **[Oral]**
Maria V. Turkina	1	• TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) **[Oral]**
Mariana Moço	1	• IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS **[Oral]**
Mariano Higes	3	• RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING? **[Oral]** • EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]** • HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN *VARROA DESTRUCTOR* POPULATIONS FROM PORTUGAL **[Poster]**
Marie Morel	1	• PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER **[Poster]**
Marta A. Antunes	1	• DETRIMENTAL IMPACT OF A HEATWAVE ON MALE REPRODUCTIVE BEHAVOUR AND FERTILITY **[Oral]** • LONG-TERM EVOLUTION EXPERIMENTS FULLY REVEAL THE POTENTIAL FOR THERMAL ADAPTATION **[Poster]**
Marta A. Santos	1	• DETRIMENTAL IMPACT OF A HEATWAVE ON MALE REPRODUCTIVE BEHAVOUR AND FERTILITY **[Oral]**
Marta Cardoso Ferreira	1	• THE IMPORTANCE OF ENVIRONMENTAL HETEROGENEITY FOR THE GENOMIC SIGNATURE OF ADAPTATION TO CADMIUM **[Oral]**
Marta Ribeiro	1	• UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S **[Poster]**
Maryam Mostajeran	1	• EVALUATING DNA COLLECTION METHODS FOR NON-INVASIVE GENETIC MONITORING IN DESERT CONDITIONS **[Poster]**
Mathew Low	1	• VIRAL EVOLUTION IN ISOLATION: HOW *VARROA* INVASION SHAPED DEFORMED WING VIRUS AND LAKE SINAI VIRUS IN AZOREAN HONEYBEES **[Oral]**
Mathew Webster	1	• HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES **[Oral]**
Matthew Moreira	1	• GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES **[Oral]**

Matthew Webster	1	• LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]**
Maxwell Farrell	1	• GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES **[Oral]**
Me Santos	1	• EXPLORING THE CELLULAR BASIS OF VARIATION IN CRANIOFACIAL FEATURES OF CICHLID FISHES **[Poster]**
Medibees Consortium	1	• WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]** • HARNESSING MITOCHONDRIAL DIVERGENCE IN APIS MELLIFERA TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY **[Poster]**
Mélanie Magnan	1	• ECO-EVOLUTIONARY DYNAMICS OF *ESCHERICHIA COLI* INVASION ACROSS HUMAN GUT MICROBIOTAS **[Oral]**
Miguel A Cruz	1	• EXPERIMENTAL EVOLUTION IN SYMPATRY LEADS TO HIGHER GROWTH RATES, BUT DOES NOT ALLEVIATE THE COSTS OF COMPETITION AND REPRODUCTIVE INTERFERENCE **[Oral]**
Miguel Machado Santos	1	• UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S **[Poster]**
Mohamed Khalil Bejaoui	1	• BENCHMARKING LAMP PRIMER DESIGN PLATFORMS FOR PYRETHROID-RESISTANCE SNP DETECTION IN *VARROA DESTRUCTOR* **[Poster]**
Mónica Honrado	1	• HARNESSING MITOCHONDRIAL DIVERGENCE IN APIS MELLIFERA TO DETERMINE THE ORIGIN OF MEDITERRANEAN HONEY **[Poster]**
Mónica Lopes-Marques	2	• GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB **[Oral]** • EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG **[Oral]**
Mónica Rodrigues	1	• UNDERSTANDING THE EVOLUTIONARY HISTORY OF LEAST WEASELS (*MUSTELA NIVALIS*) USING WHOLE GENOME SEQUENCING **[Poster]**
Mustafa Necati Muz	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Nádia Artilheiro	1	• GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB **[Oral]**
Nizar Haddad	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Nuno Queiroz	1	• MACRO- AND MICROEVOLUTIONARY GENOMICS OF THE BLUE SHARK (PRIONACE GLAUCA) **[Oral]**
Olga Escuredo	1	• THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX* **[Poster]**
Olga Escuredo Pérez	1	• PATHOGENS AGAINST THE MACHINE: EVOLUTIONARY SHIFTS OF PHYTOPHTHORA INFESTANS ACROSS EUROPEAN BIOREGIONS AND THEIR IMPLICATIONS FOR PREDICTIVE MODELLING **[Poster]**
Olivier Tenaillon	1	• ECO-EVOLUTIONARY DYNAMICS OF *ESCHERICHIA COLI* INVASION ACROSS HUMAN GUT MICROBIOTAS **[Oral]**

Paolo Ciucci	2	• ADAPTATION AND (EPI)GENOMIC EROSION IN SMALL, ISOLATED POPULATIONS: INSIGHTS FROM THE CRITICALLY ENDANGERED APENNINE BROWN BEAR **[Poster]** • DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Paolo Colangelo	1	• ADAPTATION AND (EPI)GENOMIC EROSION IN SMALL, ISOLATED POPULATIONS: INSIGHTS FROM THE CRITICALLY ENDANGERED APENNINE BROWN BEAR **[Poster]**
Patrícia Ferreira	2	• OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH **[Poster]** • EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG **[Oral]**
Patrícia Pessoa	1	• SEEDLING EVOLUTION UNDERSTANDING TO PROMOTE POSITIVE ATTITUDES TOWARDS BIODIVERSITY CONSERVATION: A STUDY WITH ELEMENTARY SCHOOL STUDENTS **[Oral]**
Patrick Stephens	1	• GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES **[Oral]**
Paula Campos	1	• BLUEFINDB: A MULTI-MARKER, "HUMAN-IN-THE-LOOP" ARCHITECTURE FOR PRECISION eDNA REFERENCE DATABASE CURATION **[Poster]**
Paula F. Campos	4	• HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC **[Poster]** • VARIATION IN GARUM RECIPES ACROSS THE ROMAN EMPIRE AND THE MICROBIAL COMMUNITIES DRIVING THEIR FERMENTATION **[Poster]** • METABARCODING OF MEDITERRANEAN MONK SEAL (*MONACHUS MONACHUS*) SCATS REVEALS A DIVERSE PISCIVOROUS DIET **[Poster]** • RECONSTRUCTING POPULATION DYNAMICS OF THE EUROPEAN SARDINE (*SARDINA PILCHARDUS*) USING PALAEOGENOMICS **[Poster]**
Paula Rudall	1	• PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER **[Poster]**
Paulo Barros	2	• A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME **[Poster]** • BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS **[Oral]**
Paulo Célio Alves	1	• PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
Paulo Pereira	1	• GENOMIC ARCHITECTURE OF SHELL COLOUR POLYMORPHISM IN LITTORINA MARINE SNAILS: THE ROLE OF CHROMOSOMAL INVERSIONS AND GENE FLUX **[Poster]**
Pedro Guerreiro	1	• THE EGG OR THE CHICKEN? REVISITING AGLOMERULISM AND THE EMERGENCE OF ANTI-FREEZE GLYCOPROTEINS,

		RENAL FUNCTION AND WATER BALANCE IN NOTOTHENIODS **[Poster]**
Pedro Humberto Castro	1	• DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS **[Oral]**
Pedro J. Esteves	1	• FCRL6 THROUGHOUT THE LINEAGES: WHAT'S THE HISTORY BEHIND THE FIRST FCRL THAT WAS DESCRIBED? **[Oral]**
Pedro Simões	3	• LONG-TERM EVOLUTION EXPERIMENTS FULLY REVEAL THE POTENTIAL FOR THERMAL ADAPTATION **[Poster]** • DO MATING SYSTEMS SHAPE THERMAL FERTILITY? **[Poster]** • DETRIMENTAL IMPACT OF A HEATWAVE ON MALE REPRODUCTIVE BEHAVOUR AND FERTILITY **[Oral]**
Pedro Sousa	1	• PATTERNS OF GENETIC ADMIXTURE IN NATURAL AND INTRODUCED HARE POPULATIONS **[Poster]**
Philine G. D. Pheulner	1	• WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS **[Poster]**
Pierre Boursot	1	• THE GENOMIC AFTERMATH OF THE ICE AGES IN EUROPEAN HARES **[Oral]**
Pierre-André Crochet	1	• FIRST PHYLOGEOGRAPHIC ASSESSMENT OF THE DIADEMED SAND SNAKE (COLUBRIDAE: LYTORHYNCHUS) ACROSS THE SAHARO-ARABIAN DESERT BELT **[Poster]**
Pr Duarte	1	• EXPLORING THE CELLULAR BASIS OF VARIATION IN CRANIOFACIAL FEATURES OF CICHLID FISHES **[Poster]**
Priscilla A. Akyaw	1	• PAST SELECTIVE HISTORY INFLUENCES ADAPTATION TO ORAL INFECTION IN *DROSOPHILA MELANOGASTER* **[Poster]**
Quentin Schull	1	• POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, PARAMURICEA CLAVATA IN THE PARC NATIONAL DES CALANQUES (FRANCE) **[Poster]**
R. Alexandre Barroso	1	• TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) **[Oral]**
Rafaela Prado	1	• EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]**
Randall S. Davis	1	• FCRL6 THROUGHOUT THE LINEAGES: WHAT'S THE HISTORY BEHIND THE FIRST FCRL THAT WAS DESCRIBED? **[Oral]**
Raquel Chaves	3	• STRUCTURAL ORGANIZATION AND EVOLUTIONARY DYNAMICS OF HUMAN SATELLITE 1B (HSAT1B) ACROSS PRIMATE GENOMES **[Oral]** • A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME **[Poster]** • BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS **[Oral]**
Raquel Gaspar	1	• ADAPT, ADJUST OR MOVE: CAN THE SPIDER MITES TETRANYCHUS CINNABARINUS DO IT ALL IN RESPONSE TO HEAT? **[Poster]**
Raquel Godinho	3	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]** • HYBRIDIZATION AS A SOURCE OF PHENOTYPIC DIVERSITY: THE GENOMIC BASIS OF YELLOW COAT COLOUR IN IBERIAN WOLVES **[Oral]**

		• EVALUATING DNA COLLECTION METHODS FOR NON-INVASIVE GENETIC MONITORING IN DESERT CONDITIONS **[Poster]**
Raquel Martín-Hernández	6	• RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING? **[Oral]** • EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS **[Poster]** • VIRAL EVOLUTION IN ISOLATION: HOW *VARROA* INVASION SHAPED DEFORMED WING VIRUS AND LAKE SINAI VIRUS IN AZOREAN HONEYBEES **[Oral]** • HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN VARROA DESTRUCTOR POPULATIONS FROM PORTUGAL [Poster] • ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]** • WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]**
Raquel Ruivo	5	• GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB **[Oral]** • OF LOSS AND DUPLICATION: THE GENETIC EVOLUTION OF GASTRIC FUNCTION IN CARTILAGINOUS FISH **[Poster]** • EXON DUPLICATION AND LOSS IN CLDN18 PUNCTUATES THE EVOLUTION OF THE GNATHOSTOME STOMACH AND LUNG [Oral] • FROM GENOMES TO “HEAT”: THE MOLECULAR ORIGIN OF ADAPTATION IN DESERT MAMMALS **[Oral]** • GENOME STORIES: HOW LOSING GENES BUILDS NEW PHENOTYPES **[Oral]**
Raquel Tavares	1	• PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER **[Poster]**
Raquel Tomé	1	• ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS **[Oral]**
Raquel Vasconcelos	1	• MORPHOLOGICAL RESPONSES OF *MUS MUSCULUS* TO THE ENVIRONMENTAL CONDITIONS OF CABO VERDE **[Oral]**
Raul Valente	1	• GENE LOSS AND EVOLUTIONARY ADAPTATIONS IN CETACEANS: INSIGHTS FROM THE GENE LOSS DB **[Oral]**
Rebecca Netels	2	• HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC **[Poster]** • VARIATION IN GARUM RECIPES ACROSS THE ROMAN EMPIRE AND THE MICROBIAL COMMUNITIES DRIVING THEIR FERMENTATION **[Poster]** • RECONSTRUCTING POPULATION DYNAMICS OF THE EUROPEAN SARDINE (*SARDINA PILCHARDUS*) USING PALAEOGENOMICS **[Poster]**
Ricardo Campos	1	• A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME **[Poster]**

Ricardo Mota	1	• FIRST PHYLOGEOGRAPHIC ASSESSMENT OF THE DIADEMED SAND SNAKE (COLUBRIDAE: LYTORHYNCHUS) ACROSS THE SAHARO-ARABIAN DESERT BELT **[Poster]**
Ricardo Santos	1	• DO MATING SYSTEMS SHAPE THERMAL FERTILITY**? [Poster]**
Richard Bateman	1	• PHYLOGENY AND SYNTENY OF YABBY TRANSCRIPTION FACTORS PROVIDE INSIGHTS INTO THE EARLY EVOLUTION OF THE ANGIOSPERM FLOWER **[Poster]**
Rita Afonso	1	• AVIAN STRUCTURAL COLORATION DIVERSITY EXPLAINED BY CHANGES IN FEATHER KERATINIZATION **[Oral]**
Romana Santos	1	• IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS **[Oral]**
Romolo Caniglia	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Rui Borges	1	• PHYLOGENETIC INFERENCE WITH NOT-SO-RARE MUTATIONS AND WEE TINY ORGANISMS **[Oral]**
Rui Faria	1	• GENOMIC ARCHITECTURE OF SHELL COLOUR POLYMORPHISM IN LITTORINA MARINE SNAILS: THE ROLE OF CHROMOSOMAL INVERSIONS AND GENE FLUX **[Poster]**
Rute da Fonseca	1	• HISTORIC OVEREXPLOITATION, GENETIC EROSION AND LOCAL EXTINCTION: PALAEOGENOMIC INSIGHTS INTO THE DECLINE OF EUBALAENA GLACIALIS IN THE NORTHEAST ATLANTIC **[Poster]**
Rute R. da Fonseca	1	• RECONSTRUCTING POPULATION DYNAMICS OF THE EUROPEAN SARDINE (SARDINA PILCHARDUS) USING PALAEOGENOMICS **[Poster]**
Sana Bashir	2	• WHY SINGLE SNP ANALYSES FAIL: EPISTATIC STRUCTURAL EFFECTS IN HONEY BEE CYP336A1 **[Poster]** • LANDSCAPE-SCALE GENOMIC RESPONSES OF THE WESTERN HONEY BEE (*APIS MELLIFERA*) TO PESTICIDE PRESSURE **[Poster]**
Sandra Louzada	2	• STRUCTURAL ORGANIZATION AND EVOLUTIONARY DYNAMICS OF HUMAN SATELLITE 1B (HSAT1B) ACROSS PRIMATE GENOMES **[Oral]** • A POSSIBLE ROLE OF TRANSPOSABLE ELEMENTS IN IMMUNE REGULATION: THE FASCINATING BAT GENOME **[Poster]**
Sara Costa	1	• BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS **[Oral]**
Sara Freitas	1	• DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS **[Oral]**
Sara Magalhães	4	• MATERNAL EFFECTS MEDIATE THE INTERACTIVE EFFECT OF TEMPERATURE AND POPULATION STRUCTURE ON SPIDER MITE SEX RATIO AND BODY SIZE **[Oral]** • EXPERIMENTAL EVOLUTION IN SYMPATRY LEADS TO HIGHER GROWTH RATES, BUT DOES NOT ALLEVIATE THE COSTS OF COMPETITION AND REPRODUCTIVE INTERFERENCE **[Oral]** • ADAPT, ADJUST OR MOVE: CAN THE SPIDER MITES TETRANYCHUS CINNABARINUS DO IT ALL IN RESPONSE TO HEAT? **[Poster]**

		• THE IMPORTANCE OF ENVIRONMENTAL HETEROGENEITY FOR THE GENOMIC SIGNATURE OF ADAPTATION TO CADMIUM **[Oral]**
Sara Ravagni	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Sara Sánchez	1	• HIGH PREVALENCE OF THE F290L AMITRAZ-RESISTANCE ALLELE IN VARROA DESTRUCTOR POPULATIONS FROM PORTUGAL **[Poster]**
Severine Kotrschal	1	• INTRA-POPULATION VARIABILITY IN A DARWINIAN SELECTION PROGRAM FOR VARROA RESISTANCE IN APIS MELLIFERA IBERIENSIS **[Poster]**
Shai Meiri	1	• GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES **[Oral]**
Silvia Perea	1	• WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS **[Poster]**
Sofia G. Costa	1	• MATERNAL EFFECTS MEDIATE THE INTERACTIVE EFFECT OF TEMPERATURE AND POPULATION STRUCTURE ON SPIDER MITE SEX RATIO AND BODY SIZE **[Oral]**
Sofia Henriques	1	• ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS **[Oral]**
Sofia L Mendes	1	• IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS **[Oral]** • WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS **[Poster]**
Sofia Nunes	1	• ADAPT, ADJUST OR MOVE: CAN THE SPIDER MITES TETRANYCHUS CINNABARINUS DO IT ALL IN RESPONSE TO HEAT? **[Poster]**
Sonia Harbane	1	• THERMAL TOLERANCE AND INVASION SUCCESS OF *VESPA VELUTINA NIGRITHORAX* **[Poster]**
Sophie Arnaud-Haond	1	• MACRO- AND MICROEVOLUTIONARY GENOMICS OF THE BLUE SHARK (PRIONACE GLAUCA) **[Oral]**
Steve Rogenstein	1	• THE FREE-B PROJECT: STUDYING EVOLUTIONARY AND ECOLOGICAL PATTERNS OF WILD HONEY BEE COLONIES IN EUROPE **[Poster]**
Subramanian Vijayakumar	2	• METABARCODING OF MEDITERRANEAN MONK SEAL (*MONACHUS MONACHUS*) SCATS REVEALS A DIVERSE PISCIVOROUS DIET **[Poster]** • BLUEFINDB: A MULTI-MARKER, "HUMAN-IN-THE-LOOP" ARCHITECTURE FOR PRECISION eDNA REFERENCE DATABASE CURATION **[Poster]**
Susana Barros	1	• UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S **[Poster]**
Tamara Wonner	1	• ESTIMATING TRAIT HERITABILITY AND VARIATION IN PREDATOR-PREY DYNAMICS **[Oral]**
Tanja Schwander	1	• INCOMPLETE LINEAGE SORTING AND THE RECURRENT EVOLUTION OF PARTHENOGENESIS IN TIMEMA STICK INSECTS **[Oral]**

Tanvi Madaan Madaan	1	• PAST SELECTIVE HISTORY INFLUENCES ADAPTATION TO ORAL INFECTION IN *DROSOPHILA MELANOGASTER* **[Poster]**
Teresa Neuparth	1	• UNRAVELLING THE IMPACT ON ZEBRAFISH OFFSPRING AFTER PARENTAL EXPOSURE TO BISPHENOL S **[Poster]**
Tiago Lourenço	1	• DISCOVERY OF AN EVOLUTIONARILY CONSERVED MOLECULAR MECHANISM FOR IODINE DETOXIFICATION IN PLANTS **[Oral]**
Tiago Macedo	1	• MORPHOLOGICAL RESPONSES OF *MUS MUSCULUS* TO THE ENVIRONMENTAL CONDITIONS OF CABO VERDE **[Oral]**
Tomás Rodrigues	1	• TOXICITY IN THE REEF: EVOLUTIONARY INSIGHTS AND PROTEOMIC ANALYSIS OF TOXIN FAMILIES FROM STONY CORALS (SCLERACTINIA, CNIDARIA) **[Oral]**
Tomaz Skrbinsek	1	• DOG INTROGRESSION IN THE WOLF GENOME: RANDOM PROCESS OR KEY GENOMIC REGIONS? **[Poster]**
Tristan Estaque	1	• POPULATION GENOMICS FOR THE CONSERVATION OF THE MEDITERRANEAN RED GORGONIAN, PARAMURICEA CLAVATA IN THE PARC NATIONAL DES CALANQUES (FRANCE) **[Poster]**
Uri Roll	1	• GLOBAL DIVERSITY PATTERNS ARE EXPLAINED BY DIVERSIFICATION RATES AND DISPERSAL AT ANCIENT, NOT SHALLOW, TIMESCALES **[Oral]**
Vera Torres	1	• BAT GENOME EVOLUTION: KARYOTYPIC CONSERVATION AND REPETITIVE SEQUENCE DYNAMICS **[Oral]**
Victor Loegler	1	• EVIDENCE FOR TWO MAJOR DOMESTICATION EVENTS DURING THE EVOLUTIONARY HISTORY OF *SACCHAROMYCES CEREVISIAE* **[Oral]**
Vincent Mérel	1	• INCOMPLETE LINEAGE SORTING AND THE RECURRENT EVOLUTION OF PARTHENOGENESIS IN TIMEMA STICK INSECTS **[Oral]**
Vítor C. Sousa	5	• EXPERIMENTAL EVOLUTION IN SYMPATRY LEADS TO HIGHER GROWTH RATES, BUT DOES NOT ALLEVIATE THE COSTS OF COMPETITION AND REPRODUCTIVE INTERFERENCE **[Oral]** • GENOMIC ARCHITECTURE OF SHELL COLOUR POLYMORPHISM IN LITTORINA MARINE SNAILS: THE ROLE OF CHROMOSOMAL INVERSIONS AND GENE FLUX **[Poster]** • IMPACT OF INTROGRESSION ON THERMAL STRESS RESPONSES IN IBERIAN CHUBS: A PROTEOMIC-LEVEL APPROACH UNCOVERS WIDESPREAD TRANSGRESSIVE PROTEIN EXPRESSION IN HYBRIDS **[Oral]** • WIDESPREAD GENE FLOW AND REFERENCE BIAS SHAPE DEMOGRAPHIC INFERENCE IN IBERIAN CHUBS **[Poster]** • THE IMPORTANCE OF ENVIRONMENTAL HETEROGENEITY FOR THE GENOMIC SIGNATURE OF ADAPTATION TO CADMIUM **[Oral]**
Wisam M Obeidat	1	• ADAPTIVE GENOMIC VARIATION IN HONEY BEES FROM ARID REGIONS **[Poster]**
Xana Sá-Pinto	1	• SEEDLING EVOLUTION UNDERSTANDING TO PROMOTE POSITIVE ATTITUDES TOWARDS BIODIVERSITY CONSERVATION: A STUDY WITH ELEMENTARY SCHOOL STUDENTS **[Oral]**
Xulio Maside	1	• RETHINKING THE EVOLUTION *VARROA DESTRUCTOR* RESISTANCE TO AMITRAZ: WHAT IS HAPPENING? **[Oral]**

Yasmine Saker	1	• THERMAL TOLERANCE AND INVASION SUCCESS *OF VESPA VELUTINA NIGRITHORAX* **[Poster]**
Zbyszek Boratyński	1	• MORPHOLOGICAL RESPONSES OF *MUS MUSCULUS* TO THE ENVIRONMENTAL CONDITIONS OF CABO VERDE **[Oral]**

List of Participants

NAME	AFFILIATION	COUNTRY
AFONSO GRANDELA	CE3C/FCUL	PORTUGAL
AICHA MELIANI RODRÍGUEZ	CIMO/SUSTEC - IPB	PORTUGAL
ALEJANDRO GARCIA	NOVOGENE CORPORATION, INC.	SPAIN
ALEXANDRE BARROSO	CIIMAR/UP	PORTUGAL
ANA CLARA SANTOS	CIMO/SUSTEC - IPB	PORTUGAL
ANA DIÉGUEZ ANTÓN	UNIVERSITY OF VIGO	SPAIN
ANA ELISABETE PIRES	FMV/ULUSÓFONA	PORTUGAL
ANA RITA LOPES	CIMO/SUSTEC - IPB	PORTUGAL
ANDRÉ SILVA	CIIMAR/UP	PORTUGAL
ANDRÉ VIANA	FCUP/UP	PORTUGAL
ANTONIO PÉREZ PÉREZ	CIAPA MARCHAMALO	SPAIN
CARLOS VILA-VERDE	UTAD	PORTUGAL
CARLOS YADRO	CIMO/SUSTEC - IPB	PORTUGAL
CATARINA GARCÊS	CIBIO-BIOPOLIS/UP	PORTUGAL
CATARINA GINJA	CIBIO-BIOPOLIS/UP	PORTUGAL
CELESTE FALCÃO	QUILABAN	PORTUGAL
CRISTIANA REIS	IPB	PORTUGAL
DANIELA BARBOSA	CIMO/SUSTEC - IPB	PORTUGAL
DIANA LOBO	CIBIO-BIOPOLIS/ UP/UNIVERSITY OF INSUBRIA	ITALY
DIOGO ROQUE	CE3C/FCUL	PORTUGAL
DORA HENRIQUES	CIMO/SUSTEC - IPB	PORTUGAL
DRAGAN STAJIC	CE3C/FCUL	PORTUGAL
ESTÊVÃO FAUSTINO	CE3C/FCUL	AUSTRIA
FERNANDA LI	CIMO/SUSTEC - IPB	PORTUGAL
FERNANDO SICURO	IBRAG-UERJ / CESAM-UA / PICTIS	PORTUGAL
FILOMENA ADEGA	UTAD	PORTUGAL
FRANCISCO BASTOS	CE3C/FCUL	PORTUGAL
GONÇALO THEMUDO	CIIMAR/UP	PORTUGAL
HUGO BARRETO	INSTITUT COCHIN	FRANCE
INÊS FRAGATA	CE3C/FCUL	PORTUGAL
INÊS MIRANDA	CIBIO-BIOPOLIS/UP	PORTUGAL
INÊS NOGUEIRO	ESS/IPB	PORTUGAL
INÊS RAMOS	CIIMAR/UALG	PORTUGAL
INÊS SANTOS	CIIMAR/UP/UM	PORTUGAL
ISABEL ALVES	UNIVERSITY OF STRASBOURG	FRANCE
IVONE FACHADA	CIÊNCIA VIVA - AGÊNCIA NACIONAL PARA A CULTURA	PORTUGAL
JOÃO CARVALHO	CIBIO-BIOPOLIS/UP	PORTUGAL
JOÃO FAIÕES	SIC	PORTUGAL
JOÃO MORENO	CE3C/MARE/FCUL	PORTUGAL
JOÃO MOUTINHO	CIIMAR/UP	PORTUGAL

JOÃO PICÃO OSÓRIO	CE3C/FCUL	PORTUGAL
JOÃO SOUTO	UNIVERSITY OF LAUSANNE	SWITZERLAND
JOÃO CARLOS TEIXEIRA	CIBIO-BIOPOLIS/UP	PORTUGAL
JOÃO TEIXEIRA	UNIVERSITY OF PORTO	PORTUGAL
JONATHAN CASTAÑO-SERNA	UNIVERSITY OF VIGO	SPAIN
JORGE PEREIRA	RISE/UTAD	PORTUGAL
JOSÉ TEIXEIRA	CIIMAR/UP	PORTUGAL
JOSÉ COSTA	CIBIO-BIOPOLIS/ISEM/UP	PORTUGAL
JUAN ADÁNEZ	CE3C/FCUL	PORTUGAL
JULIANA SOFIA ALVES	CIBIO-BIOPOLIS/ UNIVERSITY OF MONTPELLIER	PORTUGAL
KETRIN KUBIAK	CIMO/SUSTEC - IPB	PORTUGAL
LARA ALMEIDA	CIBIO-BIOPOLIS/UP	SPAIN
LARISSA CUNHA	CIMO/SUSTEC - IPB	PORTUGAL
LEONOR BEZERRA	CIBIO-BIOPOLIS/UP/CE3C/FCUL	PORTUGAL
LEONOR RODRIGUES	CE3C/FCUL	PORTUGAL
LORENA PINILLA	CIBIO-BIOPOLIS/UP	PORTUGAL
M. ALICE PINTO	CIMO/SUSTEC - IPB	PORTUGAL
MAÍRA COSTA	CIMO/SUSTEC - IPB	PORTUGAL
MANUEL CURTO	BOKU UNIVERISTY	AUSTRIA
MARGARIDA MATOS	CE3C/FCUL	PORTUGAL
MARIA CAROLINA MATOS	CIBIO-BIOPOLIS/UP	PORTUGAL
MARIA VICENTE	CIÊNCIA VIVA - AGÊNCIA NACIONAL PARA A CULTURA	PORTUGAL
MARTA FERREIRA	CE3C/FCUL	PORTUGAL
MARYAM MOSTAJERAN	CIBIO-BIOPOLIS/UP	PORTUGAL
MATTHEW MOREIRA	CIBIO-BIOPOLIS/UP	PORTUGAL
MATTHEW WEBSTER	UNIVERSITY OF UPPSALA	SWEDEN
MIGUEL CRUZ	CE3C/FCUL	PORTUGAL
MOHAMED KHALIL BEJAOUI	CIMO/SUSTEC - IPB	PORTUGAL
MÓNICA HONRADO	CIMO/SUSTEC - IPB	PORTUGAL
MÓNICA LOPES MARQUES	CIIMAR/UP	PORTUGAL
NUNO MOREDO	CIMO/SUSTEC - IPB	PORTUGAL
PATRÍCIA DUARTE	UNIVERSITY OF CAMBRIDGE	UK
PAULA CAMPOS	CIIMAR/UP	PORTUGAL
PEDRO HUMBERTO CASTRO	CIBIO-BIOPOLIS/UP	PORTUGAL
PEDRO SIMÕES	CE3C/FCUL	PORTUGAL
PEDRO SOUSA	CIBIO-BIOPOLIS/UP	PORTUGAL
RAFAELA PRADO	IPB	PORTUGAL
RAFFAELA H. C. BENETTI	CIMO/SUSTEC - IPB	PORTUGAL
RAQUEL GODINHO	CIBIO-BIOPOLIS/UP	PORTUGAL
RAQUEL RUIVO	CIIMAR/UP	PORTUGAL
RAQUEL TOMÉ	CE3C/FCUL	PORTUGAL
REBECCA NETELS	CIIMAR/UP	PORTUGAL
RICARDO MOTA	CIBIO-BIOPOLIS/UP	PORTUGAL
RICARDO CAMPOS	UTAD	PORTUGAL

RICARDO JORGE LOPES	CE3C/FCUL	PORTUGAL
RICARDO PEREIRA	STUTTGART STATE MUSEUM OF NATURAL HISTORY	GERMANY
RICARDO SANTOS	CE3C/FCUL	PORTUGAL
RITA AFONSO	CIBIO-BIOPOLIS/UP	PORTUGAL
RITA PONCE	ESE-IPS/ICNOVA	PORTUGAL
RUI BORGES	UNIVERSITY OF ST ANDREWS	UK
RUI FARIA	CIBIO-BIOPOLIS/UP	PORTUGAL
RUTE FONSECA	UNIVERSITY OF COPENHAGEN	DENMARK
SARA MAGALHÃES	CE3C/FCUL	PORTUGAL
SARA SÁNCHEZ	CIMO/SUSTEC - IPB	PORTUGAL
SARRA BEN YOUNES	IPB	PORTUGAL
SOFIA COSTA	CE3C/FCUL	PORTUGAL
SUSANA ALMEIDA	CIIMAR/UP	PORTUGAL
TERESA NEUPARTH	CIIMAR/UP	PORTUGAL
TIAGO RAMALHO	JORNAL PÚBLICO	PORTUGAL
VÍTOR SOUSA	CE3C/FCUL	PORTUGAL
XANA SÁ-PINTO	CIDTFF-UA	PORTUGAL