

VI IBERIAN CONGRESS OF BIOLOGICAL SYSTEMATICS



LA LAGUNA, TENERIFE
October 27 - 30, 2025

Museum of Science and the Cosmos (MCC)

BOOK OF ABSTRACTS

Table of Contents

INDEX.....	2
Welcome to CISA 2025!.....	13
Scientific and Local Committees	14
PLENARY TALKS.....	16
Prof. Miquel Arnedo	17
Dr. Patricia Álvarez-Campos	18
Dr. Amrita Srivathsan	19
Dr. Lisa Pokorny	20
TALKS & SPEED TALKS	21
TAXONOMY, PHYLOGENY & SYSTEMATICS	22
Unravelling a pseudo-cryptic species complex in <i>Lewinskya</i> (Orthotrichaceae, Bryophyta) across the Mediterranean–Macaronesian islands	23
Aguado-Ramsay, Pablo, Draper, Isabel, Patiño, Jairo, Calleja, Juan Antonio, Garilleti, Ricardo & Lara, Francisco	
<i>Syllis prolifera</i> species complex: new data from the Eastern Mediterranean Sea.....	24
Belvis, Fernando, Martín-Hervás, M. Rosario, Ruiz, Víctor, del Olmo, Irene & Álvarez-Campos, Patricia	
Vanishing of giant ecomorphs of chaffinches in the Azores revealed by ancient DNA ..	25
Illera, Juan Carlos; Rando, Juan Carlos; Alcover, Josep Antoni; Montero, Karina; Lalueza-Fox, Carles; Stervander, Martin; Irestedt, Martin; Ravinet Mark & Bover, Pere	
Stitch or cluster? A comparison of alternative phylogenomic dataset assembly strategies for blenny fish.....	26
Muñoz-Sánchez, Álvaro, Kulikov, Nikita & Irisarri, Iker	
Testing the adequacy of amino acid substitution models across different timescales ..	27
Giacomelli, Mattia, Domènech, Marc, Galán-Luque, Inés, Suresh, Megha, Arañó-Ansola, Javier, Pisani, Davide & Lozano-Fernández, Jesús	
The imaginable, the possible and the recognisable: modelling morphospace under biological and taxonomic constraints in Kinorhyncha.....	28
González-Casarrubios, Alberto	
Patterns of evolution within Tardigrada unveiled by time-calibrated multilocus phylogeny	29
López-López, Alejandro, Gąsiorek, Piotr, Morek, Witold & Michalczyk, Łukasz	

Non-biting midge that lived alongside Australian dinosaurs held for dear life in the Jurassic Lake.....	30
Viktor Baranov, Matthew R. McCurry, André P. Amaral, Robert Beattie, Steven A. Trewick	
<i>Divide et vinctes</i>. Taxonomical advances and challenges of the <i>Andricus</i> oak gall wasp genus (Hymenoptera: Cynipidae: Cynipini).....	31
Cuesta-Porta, Víctor, Nicholls, James A., Stone, Graham N., Tang, Chang-Ti, Melika, George & Pujade-Villar, Juli	
Phylogenetic relationships and species synonymization of cetacean parasites of the genus <i>Bolbosoma</i> Porta, 1908 (Acanthocephala: Polymorphidae).....	32
García-Gallego, Alicia, Aznar, Francisco J., Hernández-Orts, Jesús S., Davison, Nicholas J., Briscoe, Andrew G., Loizaga, Rocío, Littlewood, D. Timothy J., Fraija-Fernández, Natalia	
Multiple matrices to disentangle signals at the root of Metazoa	33
Galán-Luque, Inés, Giacomelli, Mattia, Domènech, Marc, Arañó-Ansola, Javier & Lozano-Fernández, Jesús	
Hidden Diversity in Island Pollinators: Insights from <i>Osmia submicans</i> in the Canary Islands	34
Patiño-Sauma, Diego, Lugo, David & Ruiz, Carlo	
Taxonomic challenges of Rajidae for conservation and management	35
Pérez, Trinidad, Piedrafita Clara, Gómez-Lobo Daniel, Borrell, Yaisel J., Miralles Laura	
Biogeodynamics of orogenic arcs and their biodiversity hotspots in the Western Mediterranean.....	36
Mas-Peinado, Paloma, Jiménez-Robles, Octavio, Galve,- J.P., & Booth-Rea, Guillermo	
Updating of the taxonomy and systematics of the Iberian freshwater fish based on genomic and morphological data	37
Perea, Silvia, Sousa-Santos, Carla, Robalo, Joana, López-Solano, Alfonso, Casal-López, Miriam, Mendes, Sofia, Sousa, Vitor & Doadrio, Ignacio	
Application of MALDI-TOF to Kinorhyncha identification: a combined morphological, genetic and proteomic approach.....	38
Sánchez, Nuria, González-Casarrubios, Alberto, Rossel, Sven, Khodami, Sahar & Martínez Arbizu, Pedro	
A new system classification of the current <i>Gibbula</i> concept (Vetigastropoda, Trochidae, Cantharidininae) based on integrative taxonomy	39
Templado, José; Uribe, Juan E.; Herbert, David G. & Zardoya, Rafael	
Genomic analysis of <i>Plebejus</i> Kluk (Lycaenidae: Polyommatainae) clarifies taxonomy within Europe.....	40
Toro-Delgado, Eric, Gauthier, Jérémy, Hinojosa, Joan C., Dincă, Vlad, Dapporto, Leonardo, Talavera, Gerard, Álvarez, Nadir & Vila, Roger	
Widespread but not uniform: cryptic diversity in the cave-adapted pseudoscorpion <i>Troglobisium racovitzae</i> (Ellingsen, 1912).....	41
Domènech, Marc, Hlebec, Dora, Giacomelli, Mattia, Ribera, Carles & Lozano-Fernandez, Jesus	

Species boundaries and phylogenetic relationships within Iberian *Alzoniella* Giusti & Bodon, 1984 (Gastropoda: Hydrobiidae): An integrative taxonomic approach 42

García Guerrero, Fernando, Miller, Jonathan P., Novo, Marta & Delicado, Diana

Unravelling hidden lineages and ecological preferences of the *Allolobophora chlorotica* species complex in the western Mediterranean 43

Piris, Alberto, Martínez Navarro, Alejandro, Tilikj, Natasha, Dupont, Lise, Marchán, Daniel F. & Novo, Marta

Studying host diversification and habitat specialization in squat lobsters from vulnerable mesophotic and deep-sea ecosystems through ultra-conserved elements . 44

Paula C. Rodríguez-Flores

BIODIVERSITY MONITORING & COMMUNITY ECOLOGY 45

Improving the reliability of metabarcode inventory and monitoring of arthropod communities 46

Eisele, Marius, Emerson, Brent C. & Andújar, Carmelo

Island-like environments through the lens of meiofaunal diversity: a metabarcoding approach 47

García-Cobo, Marta, Cattano, Petra, Fontaneto, Diego, Di Nezio, Francesco, Pardos, Fernando, Sánchez, Nuria & Martínez, Alejandro

Is it me or my circumstances? A study of oligochaete microbiome 48

de Sosa, Iren, Taboada, Sergi & Riesgo, Ana

Biodiversity drivers and community assembly on islands and continents 49

Macías-Hernández, N.; Domènech, M. Ramos C.; Arnedo M. Emerson B., Borges, P.A.V.; Cardoso, P.

Discovering animal diversity through phylogenetic placement of 18S metabarcoding data 50

Arañó-Ansola, Javier, Lozano-Fernandez, Jesus, Giacomelli, Mattia

Challenges and Opportunities in the Generation of Reference Genomes: Experiences from the Centre Balear de Biodiversitat..... 51

Arboleda, Enrique, de Oliveira Magalhães, Carolina, Moragues-Solanas, Lluís, Oliver-Riera, Bartomeu, Perez, Rafaela, Schöninger-Almaraz, Karen D., Triginer-Llabrés, Laura, & Capa, Maria

Integrating megabarcoding and metabarcoding to unlock hidden biodiversity and overcome data shortfalls 52

Santos-Perdomo, Irene, Salces-Castellano, A., Moraza, M. L., Mateos, E., Muñoz-Barrera, A., González-Montelongo, R., Suárez, D., Vega-Pita, N., Falcón-López, L., Lorenzo-Salazar, J. M., Flores, C., Arribas, P., Andújar, C.

Testing island biogeography theory belowground: soil mesofauna on islands of contrasting age..... 53

Salces-Castellano, Antonia; Vega-Pita, Nira; Santos-Perdomo, Irene; López, Heriberto; González-Montelongo, Rafaela; Rubio-Rodríguez, Luís A.; Emerson, Brent C.; Andújar, Carmelo; Arribas, Paula

Tiny consumers, big insights: uncovering kinorhynch diets with metabarcoding	54
Khodami, Sahar, Sánchez, Nuria, González-Casarrubios, Alberto & Martínez Arbizu, Pedro	
One Phylum, Two Worlds: Microbiome Contrasts in Freshwater and Marine Sponges .	55
Álvarez-Fernández, Almudena, Corral, Andrea, Gracia Sancha, Carlota, Lorente-Sorolla, Jose, Conejero, María, Turon, Marta, Taboada, Sergio, Díez-Vives, Cristina & Riesgo Gil, Ana	
eDNA reveals multifaceted impacts of invasive <i>Gambusia holbrooki</i> on endangered killifish populations of the Iberian Peninsula	56
Nester, Tessa Lynn, López-Solano, Alfonso, Perea, Silvia & Doadrio, Ignacio	
Spatio-temporal metabarcoding surveys in ports reveal homogenised communities with high genetic diversity of non-indigenous species.....	57
Zarcelo, Jesús, Antich, Adrià, Fernández-Tejedor, Margarita, Palacin, Cruz, Wangenstein, Owen S., Rius, Marc & Turon, Xavier	
Genomic monitoring of biodiversity in the Canary Islands	58
López Delgado, Julia, Zurita Pérez, Nieves, Arechavaleta Hernández, Manuel & Delgado Luzardo, Asunción	
How many samples do I need to take for community studies?.....	59
Martinez Arbizu, Pedro	
Tracking marine invasive species with marine sponges, possibilities and future directions	60
Gallego, Ramón, Corral-Lou, Andrea, Ramón-Laca, Ana, Alcaraz, Lourdes, Taboada, Sergi, Lanna, Emilio, Cavalcanti, Fernanda & Riesgo Gil, Ana	
Bridging Scales in Plant-Animal Interactions: Integrating Citizen Science with Field Data in the Pyrenees	61
Platania, Leonardo, Pérez-Lorenzo, Iván, Palazzesi, Luis, & Hidalgo Oriane	
Increased fish detection sensitivity with environmental RNA.....	62
Ramón-Laca, Ana, Gallego, Ramón, Duque, Carmen, Doadrio, Ignacio Parsons, Kim M., Nichols, Krista M., Engster, Samantha, Wells, Abigail, & Riesgo, Ana	

EVOLUTIONARY BIOLOGY..... 63

Independent genomic trajectories shape adaptation to life on land across animal lineages	64
Martínez-Redondo, Gemma I. Eleftheriadi, Klara, Salces-Ortiz, Judit, Escudero, Nuria, Fernández-Álvarez, Fernando Ángel, Carbonetto, Belén, Vargas-Chávez, Carlos, García-Vernet, Raquel, Palma-Guerrero, Javier, Rentería, Libe, Rojo, Iñaki, Chiva, Cristina, Sabidó, Eduard, Bombarely, Aureliano & Fernández, Rosa	
Evolution and diversity of venom-producing cells in ribbon worms	65
Verdes, Aida, Álvarez-Campos, Patricia, del Olmo, Irene, Emili, Elena, Koutsouveli, Vassiliki, Cuesta-Martín, David, Solana, Jordi & Bermúdez-Díaz, Isabel	

The first chromosome-scale assemblies of <i>Dugesia</i> shed light on the genome size evolution in flatworms	66
Daniel Dols-Serrate, Ignacio Tenaguillo-Arriola, Vadim A. Pisarenco, Marta Olivé-Muñiz, Julio Rozas & Marta Riutort	
Comparative genomics of conotoxin gene organization in cone snails.....	67
Herráez-Pérez, Ana, Pardos-Blas, José Ramón, Jiménez Tenorio, Manuel & Zardoya, Rafa	
Conserved and lineage-specific mechanisms underlying regeneration in the annelid <i>Ophryotrocha labronica</i>.....	68
Del Olmo, Irene, Herranz, María, Worsaae, Katrine, Verdes, Aida, & Álvarez-Campos, Patricia	
Evolutionary consequences of hybridisation: genomic evidence of hybrid speciation in insular beetles	69
Noguerales, Víctor, Eisele, Marius, Andújar, Carmelo & Emerson, Brent	
Functional specialization and lineage-specificity shape the evolution of ribbon worm venoms	70
Andrés, Elena, Muñoz-Santiago, José, Koutsouveli, Vassiliki, Verdes, Aida	
FANTASIA: user-friendly pipeline based on Natural Language Processing models illuminates the dark proteome across the Eukaryote Tree of Life.....	71
Belén Carbonetto, Gemma I. Martínez-Redondo, Francisco M. Perez-Canales, Ildefonso Cases, Iñigo de Martín-Agirre, Aureliano Bombarely, Ana M. Rojas & Rosa Fernández	
Evolution for Everyone: Integrating Palaeontology, DNA, and Ecosystems in the Casa de la Ciencia Sevilla (CSIC) Science Outreach Centre.....	72
Inshyna, Valentyna, Pérez Gutiérrez, Clara Elena, Ferreira Palomo, Ismael	
Transcriptomic insights into early developmental stages of a marine gastropod	73
Paula Moreno-Martín, Ana Herráez-Pérez, Patricia Álvarez-Campos, Cristina Grande & Rafael Zardoya	
Chemosensory gene family diversity and evolution in red devil <i>Dysdera</i> spiders	74
Pisarenco, Vadim A., Olivé-Muñiz, Marta, Sánchez-Gracia, Alejandro, Guirao-Rico, Sara and Rozas, Julio	
Adaptive Radiation and Trophic Specialization in <i>Dysdera</i> Spiders: A Genomic Perspective	75
Olivé-Muñiz, Marta, Garcia-Juan, Silvia, Escuer, Paula, Pisarenco, Vadim A., Macías-Hernández, Nuria, Arnedo, Miquel A., Sánchez-Gracia, Alejandro, Guirao-Rico, Sara and Rozas, Julio	
Sex Chromosomes and Polygenic Sex Determination Systems in Sponges.....	76
Lorente-Sorolla, Jose, Verdes, Aida, de Sosa, Irene, Galiá-Camps, Carles, Tonzo, Vanina, Turon, Marta, Rossi, Eleonora, Conejero, María, Koutsouveli, Vasiliki, Leiva, Carlos, Díez-Vives, Cristina, Álvarez-Presas, Marta, Grau-Bové, Xavier, Hermoso, Juan Antonio, El Hilali, Sami, Taboada, Sergi, Álvarez-Campos, Patricia, Alison Wright, & Riesgo, Ana	
Decoding Earthworms' Slumber: An Interdisciplinary Perspective at the Tissue Level .	77
Tilikj, Natasha, Conejero, María, Riesgo, Ana, Fernandez Marchán, Daniel, Świątek, Piotr, Díaz Cosín, Darío J & Novo, Marta	

Transcriptomic responses to dietary plasticity in the migratory painted lady butterfly (*Vanessa cardui*).....78

Mara Vicelja, Gemma Díaz, Aurora García-Berro, Javier Temes, Gerard Talavera

Water vs. Land: Gene Battles in the Evolution of Arthropod Respiration via a scRNA Perspective79

Tatsis, Polychronis, Salces, Judit, Solana, Jordi, Salamanca-Díaz, David, Fernández, Rosa

An asexual scandal! Genomic consequences of long-term asexuality in freshwater planarians80

Tenaguillo-Arriola, Ignacio, Riutort, M.

PHYLOGEOGRAPHY AND POPULATION GENETICS81

Population connectivity and adaptation patterns of the deep-sea sponge ground forming *Geodia hentscheli* across its geographic range82

Taboada, Sergi, Turon, Marta, Díez-Vives, Cristina, Arias, María Belén, Galià-Camps, Carles, Martín Huete, Marta, Riesgo, Ana

Effect of land-use heterogeneity on fairy-shrimps (*Anostraca*) dispersal across human-modified landscapes83

Sainz-Escudero, Lucía, Rosas-Ramos, Natalia, Gutiérrez-Rodríguez, Jorge, Perea, Silvia & García-París, Mario

Genomic insights into the montane lizards of the genus *Iberolacerta* (Lacertidae, Squamata)84

Talavera, A., Burriel-Carranza, Bernat, Mochales-Riaño, Gabriel, Estarellas, Maria, Arribas, Oscar, Tejero-Cicuéndez, Héctor, Salces-Ortiz, Judit, Fernández-Guiberteau, Daniel, Amat, Fèlix, Niell, Manel, Fernández, Rosa, S. Mikheyev, Alexander, Carranza Salvador

Deciphering genomic signatures of climatic adaptation and phenotypic diversity in a polyploid earthworm species complex85

Martínez Navarro, Alejandro, Caproni, Leonardo, Dell'Acqua, Matteo, Mager, Svenja, Gracia, Carlota, Taboada, Sergi, Trigo, Dolores, Marchán, Daniel F., Novo, Marta

Dissecting the genomics of migration in the Painted Lady butterfly86

García-Berro, Aurora, Shipilina, Daria, Backström, Niclas, Suchan, Tomasz, Palahí, Aleix, Collins C., Steve, Martins J., Dino, Pierce E., Naomi, Vila, Roger & Talavera, Gerard

Spatial patterns of phylogenetic diversity in the Asteraceae across the Canary Islands87

Jairo Patiño, Louis S. Jay-García, Oscar Castillo, J. Alfredo Reyes-Betancort, Javier Morente-López, Marcos Salas-Pascual, Agustín Naranjo-Cigala, Guillermo Sicilia-Pasos, Miguel A. Padrón-Mederos, Raúl Orihuela-Rivero, Rafaela González-Montelongo and Yurena Arjona

Second chance speciation in the clouded Apollo butterfly (*Parnassius mnemosyne*)...88

J. Lancho-Silva, L. Spilani, V. Marques, C. Bruschini, V. Dinca, M. Mutanen, M. Franzén, D. Adams, L. Dapporto, R. Vila

Genome architecture and photo-symbiont flexibility underpin colonization success of the small giant clam <i>Tridacna maxima</i> across the Indo-Pacific	89
Leiva, Carlos, Fauvelot, Cecile, Neo, Mei Lin, Lee, Li Keat, Reimer, James, Conaco, Cecilia, Torrado, Héctor, Combosch, David, Lemer, Sarah	
Phylogeography and colonization history of cryptic <i>Poecilia</i> species in the Nicaraguan lakes	90
Barluenga, Marta, Perea, Silvia, Garita-Alvarado, Carlos & Ornelas-García, Claudia Patricia	
Evolutionary history of a rapid post glacial radiation in the songbird genus <i>Junco</i>	91
Javier Sala, Borja Milá	
Whole Genome Sequencing reveals population structure of the deep-sea sponge <i>Phakellia ventilabrum</i> in the Northeast Atlantic and Mediterranean Sea.....	92
Gracia-Sancha, Carlota, Galià-Camps, Carles, Manousaki, Tereza, Riesgo, Ana, Díez-Vives, Cristina, Díaz, Julio, De la Torriente, Ana, Serrano, Alberto., Ana, Xavier, Joana R., Cárdenas, Paco, Martín, Alejandro, & Taboada, Sergi	
Population genetics reveals a new conservation approach for the white-foot limpet in the Canary Islands	93
Aliende-Hernández, Marina, Martín-Huete, Marta, Alfonso, Beatriz, Hernández, José Carlos, Pérez-Portela, Rocío	
Genetic structure of <i>Bittium reticulatum</i> (da Costa, 1778) across the Strait of Gibraltar	94
Casado-Vadillo, Alberto, Pizarro-Borrull, Maria, Recuero, Ernesto, Moreno, Diego, Templado, José & Machordom, Annie	
Dealing with uncertainty in biogeographic status: Case studies in cryptogenic Asteraceae in the Canary Islands	95
Jay-García, Louis S., Arjona, Yurena, Caujapé-Castells, Juli, Calleja, Juan A., Mirolo, Sebastien, Morente-López, Javier, Msanda, Fouad, Harrouni, Cherif, Naranjo Cigala, Agustín, Orihuela-Rivero, Raúl, Padrón-Mederos, Miguel A., Reyes-Betancort, J. Alfredo, Salas-Pascual, Marcos, Sicilia-Pasos, Guillermo, Wegmann, Daniel, Wietlisbach, Xenia, Fernández-Palacios, José María, & Patiño, Jairo	
Genomic population structure and connectivity of the endemic reef-builder <i>Cladocora caespitosa</i> in the Balearic Sea	96
Padua, Claudio, Sastraprawira, Shantika Maylana, de Oliveira Magalhães, Carolina, Schöninger Almaraz, Karen, Pons, Joan, Capa, Maria & Bassitta, Marta	
From Genomes to Venomes: Multi-Omic Insights into Iberian Snake Evolution.....	97
Sergi Tulloch Jiménez, Maria Estarellas, Bernat Burriel, Gabriel Mochales, Daniel Fernández-Guiberteau, Laura Blasón, Andrea Jhulyana López-Caro, Davinia Pla, Tyler Alioto, Juan José Calvete, Salvador Carranza	
Persistence despite isolation: Temporal genomic structure in the endemic and endangered cyprinodontiform fish <i>Aphanius baeticus</i> (Doadrio, Carmona & Fernández-Delgado, 2002)	98
López-Solano, Alfonso, Perea, Silvia, Nester, Tessa L., Ghanavi, Hamid & Doadrio, Ignacio	

Reassessing *Phoenix atlantica* from Cape Verde: genetic evidence of its relationship with *Phoenix dactylifera*..... 99

Sarmiento-Cabello, Sonia, Rodríguez-Rodríguez, Priscila, Arbelo Ramírez, Guacimara, Naranjo-Cigala, Agustín, Curbelo, Leticia, Monte da Graca Gomes, Maria, Brito, Juliana, Aberlenc, Frederique, Zehdi-Azouzi-Salwa, Sosa, Pedro A.

POSTERS 100

Comparative Analysis of BOLD and GenBank Databases during DNA Barcoding: an example of Wild Bees from La Palma..... 101

Carrasco-Palomo, Alfonso, Urueña, Álvaro, Lugo, David, Ruiz, Carlos, De la Rúa, Pilar

Updating the distribution of the threatened *Parachondrostoma* (Teleostei: Leuciscidae) and assessing co-occurring species using environmental DNA..... 102

Duque-Amado, Carmen, Perea, Silvia, Doadrio, Ignacio.

Impact of fire on flying insects and soil arthropods: Insights from fire-adapted and fire-sensitive forests across the temperate and subtropical regions 103

Moro, Gioele, Sucháčková, Alena, Čížek, Lukáš, Šebek, Pavel, Lanta, Vojtech, Emerson, Brent, Arribas, Paula, Andújar, Carmelo

Application of Molecular Tools in Forensic Identification and Traceability of Protected Species: Implications for CITES Implementation 104

Mas-Peinado, Paloma, Villegas, Belén, García, Sergio, Fernández, Andrea & Doadrio, Ignacio

DNA barcode reference library for European ants: a roadmap for phylogeography and species discovery 105

Mattia Menchetti, Enrico Schifani, Fede García, Sämi Schär, Elisabetta Sbrega, Nikola Balević, Bonnie B. Blaimer, Lech Borowiec, Dario Cioppa, Cecilia Corbella, Vlad Dincă, Vincenzo Gentile, Irakleitos Giotis, Kiko Gómez, José María Gómez Durán, Konstantinos Kalaentzis, Albenia Lapeva-Gjonova, Emiliano Mori, Gerard Talavera, Alberto Tinaut, Francisca Ruano, Sebastian Salata, Eduardo Sequeira, Maria Serracanta, Tomasz Suchan, Paul DN Hebert, Leonardo Dapporto, Roger Vila

Environmental DNA Monitoring for the Conservation of Native Fish in the Urban Manzanares River (Madrid, Spain)..... 107

Ortiz-Blanco, Paula, López-Solano, Alfonso, Alcaraz, Lourdes, Doadrio, Ignacio & Perea, Silvia

Diversity of old canary *Coffea* plants 108

Pérez, Verónica; Marante, J. Antonio; González-Díaz, A. Javier; Sosa, José Manuel; García, Santiago; Moreno, Javier; Ríos-Mesa, Domingo; Cubas, Pedro; Reyes-Betancort, J. Alfredo

Taxonomic composition of microfauna associated with macroalgal assemblages of Tenerife island..... 109

Ugena, Aitor, Alfonso, Beatriz & Hernández, José Carlos

BioMonI-Genes: Advancing DNA-Based biodiversity monitoring on oceanic islands.. 110

Paloma Martínez-Boix, Brent C. Emerson, Abraham Padilla, Javier Tuero-Septién, Agustín Naranjo-Cigala, Nereida M. Rancel-Rodríguez, Ana Losada-Lima, Lucía Bernardos-Concepción, Carmen Balibrea-Escobar, Raúl Orihuela-Rivero, Óscar Castillo-Agudo & Jairo Patiño

Digging into the entry point: assessing and monitoring the role of imported vegetation trade in introducing non-native soil species (<i>POLIZON</i>).....	111
Borrallo-Solís, María; Vega-Pita, Nira; Santos-Perdomo, Irene; Nieto-Cabrera, Victoria; Falcón-López, Lorenzo; Balibrea-Escobar, Carmen; Andújar, Carmelo & Arribas, Paula	
Evaluating variations of the Flotation-Berlese-Flotation approach for wocDNA metabarcoding of soil mesofauna	112
Nieto-Cabrera, Victoria, Falcón-López, Lorenzo, Santos-Perdomo, Irene, Moro, Gioele, Vega-Pita, Nira, Balibrea-Escobar, Carmen, Borrallo-Solís, María, Arribas, Paula & Andújar, Carmelo	
Retinoic Acid Pathway Conservation in Evolution: Insights from Planarians	113
Cuadrado, Daniel	
A First Glimpse into DNA Methylation in the Mediterranean Earthworm <i>Carpetania matritensis</i>	114
Tilikj, Natasha, Fernández Marchán, Daniel & Novo, Marta	
Host plant-driven physiological variation in a polyphagous migratory butterfly	115
Díaz-Martínez, Gemma, Vicelja, Mara, Vilaseca, Iu, Valenzuela, Laura, Sbrega, Elisabetta, Peraki, Danai, Temes, Javier, Talavera, Gerard	
The Secret relationships within Syllidae: disentangling their microbiota.....	116
Víctor Ruiz-López, Cristina Díez-Vives, Elena Andrés, Ana Riesgo, Patricia Álvarez-Campos	
The nuclear and mitochondrial genomes of the lined rockskipper, <i>Istiblennius lineatus</i> (Teleostei: Blennidae).....	117
Víctor M. Valencia-Cárdenas, Nikita Kulikov, Francisco J. Ruiz-Ruano, Alexander Ben Hamadou, Carola Greve, Diego F. B. Vaz, Terry J. Ord, Iker Irisarri	
Exploring genomic signatures of adaptation in South American populations of <i>Drosophila melanogaster</i> and <i>D. simulans</i>	118
Carlos Tinedo, Carlos E. Arboleda, Eduardo Amat, Dorcas Orengo, Andrea Barrio, Alejandro Sánchez-Gracia	
Across the hemispheres: a roadmap to understand genome evolution in migratory butterflies	119
Cavalcanti, Clara, García-Berro, Aurora, Talavera, Gerard	
Population genetics and gene flow in coastal fragmented habitats: a study of western Mediterranean supratidal rockpool beetles	120
García-Meseguer, Antonio José, Muñoz, Irene, Abellán, Pedro, Villastrigo, Adrián, Mirón-Gatón, Juana María, Millán, Andrés & Velasco, Josefa	
Preliminary molecular insights into Moroccan termites, based on mitochondrial DNA analysis.....	121
Najjari, Aya, Hernández-Teixidor, David, & Taheri, Ahmed	
Genomic insights on the laurel forest tree species of Tenerife.....	122
Tuero-Septién, Javier, Padilla, Abraham, López-González, Mercedes, García-Monzón, Irma, López-Soria, Juan Miguel, Sinka, Victoria, Padrón, Juan I. & Patiño, Jairo	

Taxonomic Review of the Genus <i>Urtica</i> L. (<i>Urticaceae</i>) in the Canary Islands: Morphological Description and Dichotomous Key	123
Agraso San Narciso, Sofía, González-Montelongo, Cristina, Reyes-Betancort, J. Alfredo & Padrón-Mederos, Miguel A.	
One Thousand Reasons to Explore the Deep-sea	124
González-Casarrubios, Alberto, Sánchez, Nuria, & Martínez Arbizu, Pedro	
Morphology-Based Phylogeny of the Genus <i>Dendrophyllia</i> (<i>Scleractinia</i>: <i>Dendrophylliidae</i>) from the Canary Islands	125
González-Porto, M. , A. Jurado-Ruzafa, J.E. Rodríguez-Riesco, S. Domínguez-Guerra, B. García-Mañé, Y. González-Rodríguez, C. Hernández-González, S. Jiménez-Navarro, L. Martín-García, J.C. Mendoza, S. Oliva and P. Martín-Sosa	
Morphological revision of the genus <i>Stichopathes</i> (<i>Antipatharia</i>, <i>Antipathidae</i>) in the Canary Islands	126
Martín-García, Laura, González-Porto, Marcos, Jurado-Ruzafa, Alba, Rodríguez-Barreto, Deiene, Dionis-Insensé, Noemi, Rodríguez-Valdez, Génesis, García-Mañé, Bertín, Villafranca-Sánchez, Pablo, Orozco-Borgas, Alejandro, Cruz-Delgado, Paula, Mendoza, José Carlos, Oliva, Silvia & Martín-Sosa, Pablo	
First record of the genus <i>Victorgorgia</i> (<i>Cnidaria</i>, <i>Octocorallia</i>) in the Canary Islands SW seamounts: expanding biodiversity insights	127
González-Porto, Marcos, Jurado-Ruzafa, Alba, Oliva, Silvia, Taboada, Sergi, Alonso Hartyanyi, Teresa, Boza, Cristina, Campillo, Sara, Dionis-Insensé, Noemi, García-Mañé, Bertín, Jiménez-Navarro, Sebastián, Mendoza, José Carlos, Martín-Sosa, Pablo & Martín-García, Laura	
Rediscovery and phylogenetic placement of <i>Allodessus skottsbergi</i> (<i>Coleoptera</i>: <i>Dytiscidae</i>) from Rapa Nui.....	128
Villastrigo, Adrián, Cotoras, Darko D., Edmunds, Merahi, Pakarati, Sebastián, Edmunds, Tahira & Balke, Michael	
Integrative taxonomy reveals cryptic species within the Canary Island endemic longhorn genus <i>Lepromoris</i> (<i>Coleoptera</i>; <i>Cerambycidae</i>)	129
Jiménez-García, Eduardo, Nogueras, Víctor, López, Heriberto & Emerson, Brent	
Exploring the Terrestrial Isopods of the Canary Islands: From Historical Records to Future Perspectives.....	130
Orihuela-Rivero, Raúl, Bernardos, Lucía, García del Real García, Eduardo, López, Heriberto, Macías-Hernández, Nuria, Hernández-Teixidor, David, Pérez-Delgado, Antonio José, García, Rafael, Balibrea, Carmen, & Oromí, Pedro	
First Genomic Insights into the Endangered Iberian Endemic <i>Squalius palaciosi</i>: Evidence of Hybridogenetic Origins	131
Perea, Silvia, Ghanavi, Hamid, & Doadrio, Ignacio	
Integrative revision of <i>Codium</i> (<i>Chlorophyta</i>, <i>Bryopsidales</i>) in the Canary Islands: combining morphology and molecular data.....	132
Rancel-Rodríguez, Nereida M.; Álvarez-Canali, Daniel; Roger-Baynat, Belén; Sansón, Marta & Sangil, Carlos	

Phylogenetic and genomic insights into a new syllid polychaete species from the Canary Islands with evidence of trans-Atlantic connectivity 133

Ruiz, Víctor, Martín-Hervás, M.Rosario, Moreno-Martín, Paula, Del Olmo, Irene, Taboada, Sergi & Álvarez-Campos, Patricia

Island isolation drives genetic divergence in the Canarian camel spider *Eusimonia wunderlich* (Solifugae) 134

Ariemma Cecilia, Lugo David, Robla Jairo, Pertegal Cristian, Oromí Pedro & Macías-Hernández Nuria

SPONSORSHIP 135





Welcome to CISA 2025!

Welcome to CISA 2025 (VI Iberian Congress of Biological Systematics), held from 27 to 31 October 2025 in Tenerife, at the Museum of Science and the Cosmos (MCC, Museos de Tenerife, S.C. La Laguna).

The congress is organised by the Institute of Natural Products and Agrobiology (IPNA-CSIC) and the University of La Laguna (ULL), two institutions deeply engaged in biodiversity and evolutionary research.

Hosting CISA in Tenerife and the Canary Islands offers a unique opportunity to merge cutting-edge biodiversity science with the archipelago's exceptional biological, geological, and historical richness.

Over these days, we will explore and exchange the latest advances in systematics and evolutionary biology, encompassing taxonomy, phylogenetics, phylogeography, biogeography, and adaptation in animals, plants, fungi, and unicellular organisms. Our aim is to encourage debate, collaboration, and new connections across the Ibero-Macaronesian research community.

Since its first edition, CISA has proven to be an outstanding meeting point for scientists in evolutionary biology. This sixth edition seeks to reinforce that spirit, with an engaging programme that welcomes the participation of young researchers and strengthens scientific networks across generations.

We are truly delighted to reunite in this inspiring setting: Tenerife, a crossroads of continents and cultures where science meets nature. We invite you to enjoy the talks, the discussions, the social events, and the magnificent environment and hospitality of the Canary Islands.

Welcome to CISA 2025. May these days be as stimulating as they are fruitful!

With our warmest regards,

Scientific and Local Committees

THE ORGANISING COMMITTEE CISA 2025

Carmelo Andújar (chair, IPNA-CSIC)
Paula Arribas (chair, IPNA-CSIC)
Nuria Macías Hernández (ULL)
Brent Emerson (IPNA-CSIC)
Jairo Patiño (IPNA-CSIC)
Manuel Nogales (IPNA-CSIC)
Alfredo Valido (IPNA-CSIC)
Heriberto López (IPNA-CSIC)
Marius Eisele (IPNA-CSIC)
Antonia Sacas-Castellano (IPNA-CSIC)
Irene Santos-Perdomo (IPNA-CSIC)
Nira Vega (IPNA-CSIC)
Lorenzo Falcón (IPNA-CSIC)
Victoria Nieto (IPNA-CSIC)
María Borrallo (IPNA-CSIC)
Carmen Balibrea (IPNA-CSIC)
Antonio Pérez (IPNA-CSIC)
Louis Steven Jay (IPNA-CSIC)
Raúl Orihuela (IPNA-CSIC)
Oscar Castillo (IPNA-CSIC)
Lucía Belén Bernardos (IPNA-CSIC)
Carlos Ruiz Carreira (ULL)
Miguel Ángel Zarzosa (IPNA-CSIC)
Gioele Moro (IPNA-CSIC & Biology Centre CAS)

SCIENTIFIC COMMITTEE CISA 2025

We would like to express our deepest gratitude to the Scientific Committee of CISA 2025, composed of renowned researchers who have generously contributed their time and expertise to evaluate the submitted works and advise on the scientific programme. Their commitment has been essential to ensuring the quality and diversity of the conference's scientific content.

Miquel Àngel Arnedo (Universitat de Barcelona)

Rafael Zardoya (MNCN-CSIC)

Mario García Paris (MNCN-CSIC)

Marta Novo (Universidad Complutense de Madrid)

Ana Riesgo (MNCN-CSIC)

Rosa Fernández (IBE-CSIC)

Sergi Taboada (MNCN-CSIC)

Lisa Pokorny (Real Jardín Botánico-CSIC)

Xavier Turón (CEAB-CSIC)

Paulo Borges (Universidade dos Açores)

Gerard Talavera (IBB-CSIC)

Jesús Gómez-Zurita (IBB-CSIC)

Yurena Arjona (Universidad de La Laguna)

Isabel Sanmartín (Real Jardín Botánico-CSIC)

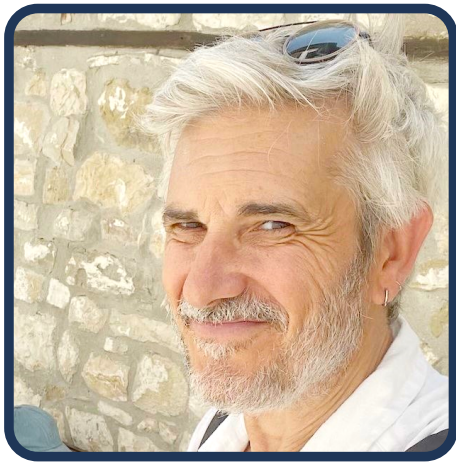
Alfredo Reyes (JAO-ICIA)

CODE OF CONDUCT IN THE CISA 2025

CISA 2025 is an inclusive event. Professional and respectful behaviour is expected. Harassment or discrimination of any kind will not be tolerated. If you need assistance, please contact the organisers or any identified staff member.



PLENARY TALKS



PLENARY TALK

**“Devils, Wolves, and Cannibals:
Evolutionary Tales of Island Spiders”**

Prof. Miquel Arnedo

Universitat de Barcelona (UB), Spain

Dr. Miquel Arnedo is Professor of Evolutionary Biology at the Universitat de Barcelona (UB), where he leads the Arthropod Systematics and Evolution Laboratory, and currently serves as Director of the Institut de Recerca de la Biodiversitat (IRBio-UB). His research centres on the evolutionary diversification, systematics, and biogeography of arachnids, with a particular focus on spiders. Throughout his career, Dr. Arnedo has made significant contributions to spider phylogenetics and adaptive radiations, particularly in Mediterranean and island ecosystems. His studies on the red devil spiders (*Dysdera*) have shed light on speciation, ecological diversification, and evolutionary processes in the Canary Islands. By integrating fieldwork, morphology, and cutting-edge molecular tools, he has published extensively on global spider evolution and the mechanisms shaping diversification in insular and subterranean faunas. More recently, he has expanded his research interests to the application of molecular methods for accelerating biodiversity inventorying and monitoring in hyperdiverse groups such as arthropods, with a growing focus on community ecology. At CISA 2025, Prof. Arnedo will present a plenary lecture on the evolution and diversification of spiders across island archipelagos. Drawing on striking examples of adaptive radiations in different spider lineages, his talk will explore the Macaronesian and other oceanic islands as natural laboratories for understanding the dynamics of adaptive diversification. His talk will showcase both his pioneering contributions to spider systematics and evolution, as well as their broader significance for island biodiversity and conservation.



PLENARY TALK

**“Secretos del mar: reproducción,
regeneración y células madre en
nuestros océanos”**

Dr. Patricia Álvarez-Campos

Department of Biology, Universidad Autónoma de Madrid, Spain

Dr. Patricia Álvarez-Campos is an evolutionary biologist and zoologist specializing in the developmental biology, regeneration, and reproductive mechanisms of annelid worms. She is currently a tenured professor at the Universidad Autónoma de Madrid (UAM), where she conducts research on the biodiversity, systematics, and evolution of marine annelids, particularly within the family Syllidae. Her work integrates various methodologies, including morphological studies, molecular phylogenetics, and cutting-edge techniques such as single-cell transcriptomics, to explore the processes of reproduction and tissue regeneration in these organisms. At CISA 2025, Dra. Álvarez-Campos will deliver a special plenary talk aimed at the general public, where she will discuss the most striking aspects of her research and the fascinating biology of her target organisms. This presentation will offer attendees a unique insight into the world of annelid worms, highlighting their remarkable regenerative abilities and the evolutionary significance of these processes.



PLENARY TALK

“Insects and Their Interactions: Tales from Nanopore Sequencing of Flies and Their Poop”

Dr. Amrita Srivathsan

Museum für Naturkunde, Berlin

Dr. Amrita Srivathsan is a molecular ecologist specializing in biodiversity discovery and species interactions. She is currently a researcher at the Museum für Naturkunde, Berlin, where she develops innovative bioinformatics tools and applies cutting-edge sequencing technologies, such as Nanopore sequencing, to advance integrative taxonomy and our knowledge of species interactions. Her research focuses on integrating modern molecular tools to facilitate traditional taxonomic research and studying trace DNA to understand biology of discovered species. She has contributed significantly to large-scale DNA barcoding and metagenomic techniques, particularly in understudied and highly diverse ecosystems. At CISA 2025, Dr. Srivathsan will share insights from her groundbreaking work on understudied taxa, highlighting the potential of next-generation sequencing to revolutionize systematics and natural history research.



PLENARY TALK

**“Linking Micro- and
Macroevolutionary Perspectives in
Eco-Evolutionary Research”**

Dr. Lisa Pokorny

Royal Botanic Garden (RJB), Spanish National Research Council (CSIC), Madrid

Dr. Lisa Pokorny is an evolutionary biologist and botanist specializing in macroevolutionary patterns of land plants. She is currently a researcher at the Royal Botanic Garden (RJB), part of the Spanish National Research Council (CSIC) in Madrid. Her research focuses on unraveling macroevolutionary patterns, particularly in land plants. She implements target capture sequencing approaches, such as Hyb-Seq, and utilizes high-performance computing (HPC) phylogenomic workflows to investigate plant evolution. Dra. Pokorny has contributed significantly to our understanding of plant diversification and evolutionary history, with numerous publications in leading scientific journals. At CISA 2025, she will share insights from her extensive research on plant macroevolution, highlighting the application of genomic tools in understanding plant diversity and evolution.



TALKS & SPEED TALKS

TAXONOMY, PHYLOGENY & SYSTEMATICS

BIODIVERSITY MONITORING & COMMUNITY ECOLOGY

EVOLUTIONARY BIOLOGY

PHYLOGEOGRAPHY AND POPULATION GENETICS



TAXONOMY, PHYLOGENY & SYSTEMATICS

Unravelling a pseudo-cryptic species complex in *Lewinskya* (Orthotrichaceae, Bryophyta) across the Mediterranean–Macaronesian islands

¹*Aguado-Ramsay, Pablo, Draper, Isabel, ²Patiño, Jairo, ¹Calleja, Juan Antonio, ³Garilleti, Ricardo & ¹Lara, Francisco

*lead presenter: pablo.aguador@uam.es

¹ Universidad Autónoma de Madrid, Spain

² Instituto de Productos Naturales y Agrobiología, Spain

³ Universidad de Valencia, Spain

Lewinskya F.Lara, Garilleti & Goffinet is a moss genus comprising about 80 species, widely distributed across temperate regions of both hemispheres. In the Macaronesian archipelagos its representation was thought to be limited, with only a few species recorded. For a long time, one of the most frequent species was considered to be *L. affinis* (Brid.) F. Lara, Garilleti & Goffinet, characterized by immersed capsules and peristomes with paired, recurved teeth when dry. However, Vigalondo et al. (2019) demonstrated that *L. affinis* is in fact absent from the Canary Islands, and that a phylogenetically close but a new distinct species, *L. scissa* Vigalondo, F. Lara & Garilleti, occurs instead, which has since been regarded as a local endemic. Moreover, extensive sampling campaigns across the Macaronesian archipelago have revealed previously overlooked morphological variability. Together, these findings suggest that the diversity of the Mediterranean–Macaronesian islands may be considerably underestimated. The present study applies an integrative approach, combining detailed morphological analyses with the NGS technique Genotyping-by-Sequencing, to examine all Macaronesian *Lewinskya* taxa displaying the above referred sporophytic features.

Our results reveal the existence of several distinct species belonging to different phylogenetic lineages. Two of them are new species, one from the Canary Islands and another morphologically similar but unrelated one from Crete. In addition, we expand the known distributions of two species previously regarded as narrowly endemic: *Lewinskya scissa*, until now reported only from Gran Canaria, is here documented from La Palma and Madeira; and *L. lamyana*, previously known solely from a single locality in southern Spain—where it is listed as Critically Endangered—is now also reported from Madeira, Gran Canaria, El Hierro, and La Palma. Despite being among the most intensively studied archipelagos for bryophytes, our findings underscore the ongoing need for basic taxonomic research, highlighting that even well-explored regions may still harbor undescribed species and unrecognized distribution patterns.

Reference:

Vigalondo B, Garilleti R, Vanderpoorten A, Patiño J, Draper I, Calleja JA, Mazimpaka V, Lara F. 2019. Do mosses really exhibit so large distribution ranges? Insights from the integrative taxonomic study of the *Lewinskya affinis* complex (Orthotrichaceae, Bryopsida). *Molecular Phylogenetics and Evolution* 140: 106598.

***Syllis prolifera* species complex: new data from the Eastern Mediterranean Sea**

¹*Belvis, Fernando, ²Martín-Hervás, M. Rosario, ²Ruiz, Víctor, ²del Olmo, Irene & ²Álvarez-Campos, Patricia

*lead presenter: fernando.belvis@estudiante.uam.es

¹ Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM) & Departamento de Biología (Zoología), Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain.

²Centro de Investigación en Biodiversidad y Cambio Global (CIBC- UAM) & Departamento de Biología (Zoología), Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain.

An increase in cryptic and pseudocryptic speciation have been detected among marine invertebrates in the last decade thanks to the use of integrative taxonomy that combines all available data sources to frame species. This approach has enhanced our understanding of the real biodiversity of a given area, which has fundamental implications for conservation and management of marine ecosystems. Within the family Syllidae Grube, 1850, *Syllis prolifera* Krohn, 1852 —traditionally regarded as a widespread, cosmopolitan species—has recently been recognized as a pseudocryptic species complex in the western Mediterranean Sea. However, its broader distribution suggests that additional pseudocryptic lineages may exist in other regions of this highly diverse area. In this study, we incorporate newly collected specimens from the Greek islands of Crete and Mykonos with all previously published data on the *S. prolifera* complex, aiming to assess the existence of more mediterranean putative species. Combining morphological, biogeographical, and molecular data (*COI*, *16S rRNA*, *18S rRNA*, and *28S rRNA* markers) we revealed the presence of at least three more novel lineages for the eastern Mediterranean Sea. However, unlike previous studies, no consistent diagnostic morphological characters were found across all lineages, suggesting that the complex includes both pseudocryptic and cryptic potential new species. Our results further support the view that species diversity within the family Syllidae remains underestimated and highlight the necessity of integrative studies for accurately assessing marine invertebrate biodiversity.

Vanishing of giant ecomorphs of chaffinches in the Azores revealed by ancient DNA

^{1*}Illera, Juan Carlos; ²Rando, Juan Carlos; ³Alcover, Josep Antoni; ¹Montero, Karina; ⁴Lalueza-Fox, Carles; ⁵Stervander, Martin; ⁶Irestedt, Martin; ⁷Ravinet Mark & ⁸Bover, Pere

*lead presenter: illerajuan@uniovi.es

¹ IMIB, Spain

² ULL, Spain

³ IMEDEA, Spain

⁴ IBE, Spain

⁵ NMS, UK

⁶ SMNH, Sweden

⁷ UO, Norway

⁸ IUCA, Spain

Islands are well known for hosting a high diversity of unique organisms. However, paleontological, archaeological, and historical records provide compelling evidence of significant disruptions to island biotas and community composition following human colonization. In fact, human activities have resulted in the extinction of numerous species and evolutionary lineages.

The Azores Islands exemplify how insular landscapes have undergone dramatic transformations since the relatively recent arrival of humans (ca. 15th century). Habitat deforestation, combined with hunting and the introduction of invasive mammalian species (e.g., rats, mice, and cats), had devastating consequences for native animal communities. These findings indicate that, prior to European colonization, the Azores supported more diverse avian assemblages than those observed today. This suggests that the disruption of key ecological processes led to both primary and secondary extinctions, with cascading effects on Azorean ecosystems. A compelling question arises from the discovery of fossil remains that resemble extant taxa but differ markedly in size: when do such morphological differences justify the designation of a novel taxon? In these cases, ancient DNA (aDNA) techniques are essential for resolving the evolutionary history of fossil specimens.

During several paleontological expeditions conducted in the Azores between 2011 and 2018, we recovered cranial and postcranial bird remains from Pico, Terceira, São Miguel, and Graciosa. Some of these bones were visually and unambiguously assigned to the genus *Fringilla*, but exhibited significantly larger cranial morphology compared to the extant Azorean common chaffinch (*Fringilla moreletti*). Notably, the skull and beak dimensions closely resembled those of the blue chaffinches (*F. teydea* and *F. polatzeki*), which are endemic to the Canary Islands. This observation raised the possibility that the fossil remains could represent a common ancestor of the Canarian blue chaffinches. By extracting endogenous DNA from these fossil remains, we successfully retrieved complete mitochondrial genomes from five individuals. Phylogenetic analyses incorporating both extinct and extant individuals clearly positioned the extinct birds within the clade of extant Azorean common chaffinches (*Fringilla moreletti*). These findings underscore the importance of integrating multiple lines of evidence—beyond morphology alone—to accurately resolve the evolutionary relationships of fossil taxa and to detect morphological shifts potentially driven by recent anthropogenic changes in island ecosystems.

Stitch or cluster? A comparison of alternative phylogenomic dataset assembly strategies for blenny fish

¹Muñoz-Sánchez, Álvaro, ^{2,3}Kulikov, Nikita & ^{2,3*}Irisarri, Iker

*lead presenter: iker.irisarri@mncn.csic.es

¹ Universidad Autónoma de Madrid, Spain

² Leibniz Institute for the Analysis of Biodiversity Change (LIB), Museum of Nature, Hamburg, Germany

³ Museo Nacional de Ciencias Naturales (MNCN-CSIC), Spain

Phylogenomics has revolutionized the way we infer evolutionary relationships. Several bioinformatic pipelines have been developed for assembling phylogenomic datasets, in which orthology inference is a key step. We compared two alternative dataset assembly strategies: sequence clustering (Orthofinder) and a new similarity-based approach that enriches a predefined set of BUSCO genes (Patchwork). With data reuse in mind, we downloaded all publicly available genomic data for the fish family Blenniidae, which is a typical scenario of heterogeneous source data (genome skimming, transcriptomes, genomes) obtained by different sequencing technologies (Illumina short reads, long Nanopore reads, 454 pyrosequencing). These data are characterized by various levels of read length, sequencing depth and per-base accuracies, which allowed us to benchmark the power and limitations of the two assembly pipelines and establish minimum quality standards on various sequencing data types. Our study is the first attempt to test the evolutionary relationships among combtooth blenny fish with phylogenomic data. We also explore two approaches to combine marker-rich phylogenomic data with taxonomically broad legacy multi-locus markers.

Testing the adequacy of amino acid substitution models across different timescales

¹*Giacomelli, Mattia, ¹Domènech, Marc, ¹Galán-Luque, Inés, ¹Suresh, Megha, ¹Arañó-Ansola, Javier, ²Pisani, Davide & ¹Lozano-Fernández, Jesús

*lead presenter: mattia.giacomelli@ub.edu

¹ Department of Genetics, Microbiology and Statistic & Institut de Recerca de la Biodiversitat – IRBio, University of Barcelona, Spain

² University of Bristol, United Kingdom

Amino-acid substitution models are central to phylogenomic inference, yet their adequacy—whether they realistically describe features of real datasets—remains insufficiently tested. Here, we evaluated six widely used substitution models across empirical datasets spanning diverse evolutionary timescales, using complementary metrics that quantify both site-level diversity and residue-frequency spectrum. Site-homogeneous models (represented by LG) performed worst, whereas site-heterogeneous mixtures provided better fits, with Poisson+CAT achieving the best overall adequacy. Other finite-mixture models showed intermediate or mixed behavior, with performance varying by dataset and by metric. Our results demonstrate also that model adequacy is both dataset- and feature-dependent: models may capture some aspects of the data while failing in others. Routine adequacy testing is therefore essential for identifying model limitations and ensuring accurate phylogenomic inference.

The imaginable, the possible and the recognisable: modelling morphospace under biological and taxonomic constraints in Kinorhyncha

*González-Casarrubios, Alberto

*lead presenter: albert23@ucm.es

Universidad Complutense de Madrid, Faculty of Biological Sciences, Department of Biodiversity, Ecology and Evolution. Madrid, Spain.

Systematics faces the challenge of cataloguing biological diversity in the most accurate and parsimonious way possible. However, both phylogeny and taxonomy rely on diagnostic criteria which, although consensual, have a direct but rarely quantified impact on the number of species we recognise. The concept of morphospace, the universe of anatomically possible forms for a given taxon, offers a quantitative framework to measure this impact. Due to its standardised taxonomy and segmented body plan, the phylum Kinorhyncha provides an ideal model system for this approach.

In this study, a formal mathematical model is presented in which different levels of morphological diversity are defined by a hierarchy of filters or constraints. A theoretical morphospace is first generated by combining all possible positions, segments, and characters. Biological restrictions are then applied to reflect the real body plan, producing a biological morphospace of anatomically viable morphotypes. On this basis, epistemological restrictions based on current taxonomic diagnostic criteria are introduced, delimiting the set of species that can be theoretically recognised. The complexity of each space is measured using Hartley entropy.

This framework makes it possible to measure the potential morphological diversity of the group and to quantify the impact of taxonomic criteria, whether lumpers or splitters. Thus, it is quantitatively shown that a single lumpers rule can collapse up to 90% of the morphospace. It also provides a virtual laboratory where hypothetical scenarios such as the origin of new characters or the loss of conserved patterns can be tested, showing their impact on both the number of morphotypes or species and the overall system complexity.

It is concluded that this formal framework can be used as a tool to assess objectively the consequences of taxonomic decisions. It also provides new opportunities to explore why some morphological traits have been favoured by evolution and sets the basis for the development of new identification keys capable of handling taxonomic information and complexity more efficiently.

Patterns of evolution within Tardigrada unveiled by time-calibrated multilocus phylogeny

^{1*}López-López, Alejandro, ¹Gąsiorek, Piotr, ^{1,2}Morek, Witold & ¹Michalczyk, Łukasz

*lead presenter: alejandro.lopez-lopez@uj.edu.pl

¹ Jagiellonian University, Poland

² Wellcome Sanger Institute, United Kingdom

Tardigrades, also known as “water bears” or “moss piglets”, most known due to their outstanding capabilities for withstand extreme environmental conditions, constitute a micrometazoan phylum with a global distribution, both in marine and terrestrial habitats. While numerous studies have explored the phylogenetic relationships within specific groups of tardigrades, only a few works have addressed the systematics and evolution of the phylum, albeit using incomplete or flawed matrices or unreliable methods and models.

In this work, we carry out a phylogenetic analysis of the phylum Tardigrada using a carefully assembled matrix composed of four nuclear and mitochondrial DNA fragments, from species from all groups of tardigrades for which reliable molecular data is available, including newly sequenced taxa. We calibrated out tree using known ages for some nodes inferred from phylogenies for closely related taxa.

Our analysis recovers the classic relationships between the main groups of tardigrades, but also reconstructs the timeline of major events of morphological and ecological evolution in this phylum. It shows how the acquisition of new characters, shifts in their lifestyles, or acquisition of cryptobiotic capabilities can be correlated to major events in the history of Earth, such as the formation of Pangaea and its subsequent changes in environmental conditions and extension of ecosystems.

Non-biting midge that lived alongside Australian dinosaurs held for dear life in the Jurassic Lake

^{1*}Viktor Baranov, ^{2,3}Matthew R. McCurry, ⁴André P. Amaral, ²Robert Beattie, ⁵Steven A. Trewick

**lead presenter*

¹ Doñana Biological Station-CSIC, Spain

² Australian Museum Research Institute, Australia

³ Earth and Sustainability Science Research Centre, School of Biological, Earth and Environmental Sciences (BEES), University of New South Wales, Australia

⁴ Faculty of Biology, Biocenter, Ludwig-Maximilians-Universität München (LMU Munich), Germany

⁵ Wildlife and Ecology, Massey University, New Zealand

Non-biting midges (Diptera, Chironomidae) have served as extremely important model organisms for the development of modern phylogenetic systematics. Brundin (1966) used Chironomidae material from Southern Hemisphere to apply Hennig's newly published methods of phylogeny reconstruction to the biogeographical history and evolutionary relationships of this group. His findings were seminal for our modern understanding of historical biogeography.

The most important group in Brundin's study was the Podonominae, a clade of non-biting midges within the Chironomidae family, distributed predominantly, though not exclusively, in the Southern Hemisphere. For a long time, it was believed that Podonominae originated in northern Gondwana and later spread to Laurasia. However, because the oldest known fossils of this group come from the Jurassic of Eurasia, more recent interpretations have suggested a Laurasian origin.

Here, we present the oldest record of Podonominae from Gondwana, specifically from the Tithonian age (Jurassic) in Australia. This discovery also represents the oldest Chironomidae fossil found in the Southern Hemisphere and suggests (when placed in historical biogeography analysis) that Podonominae likely originated in Gondwana. The new fossil represents a highly specialized form of Podonominae, adapted to living in the littoral zones of large lakes. It exhibits adaptations to this environment that are unique among Podonominae, and largely among the insects – its pupa had a terminal suction disc and robust body adapted for survival in the intertidal zone. The only similar adaptations are found in a scant few extant marine insects.

***Divide et vinctes*. Taxonomical advances and challenges of the *Andricus* oak gall wasp genus (Hymenoptera: Cynipidae: Cynipini).**

^{1*}Cuesta-Porta, Víctor, ²Nicholls, James A., ³Stone, Graham N., ³Tang, Chang-Ti, ⁴Melika, George & ¹Pujade-Villar, Juli.

*lead presenter: victorcp93@gmail.com

¹ Universitat de Barcelona, Facultat de Biologia, Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Avda. Diagonal, 645, 08028-Barcelona, Spain.

² Royal Botanic Garden Edinburgh, Edinburgh EH3 5NZ, Scotland, U.K.

³Institute of Evolutionary Ecology, University of Edinburgh, King's Buildings, Charlotte Auerbach Road, Edinburgh EH9 3FL, Scotland, U.K.

⁴ Retired entomologist, Budapest, Hungary.

Cynipini wasps (commonly called oak gallwasps, though they feed on a wider range of Fagaceae trees) offer an excellent opportunity to study evolutionary dynamics processes due to their intimate ecological relationships with host plants, high species richness spanning the Northern Hemisphere, and roles as keystone species supporting rich communities of associated parasitoids and herbivorous inquilines. They develop within structurally complex and species-specific galls that serve as both nurseries and defensive structures, though the adaptive significance of many gall phenotypes remains unclear. To answer these evolutionary questions an update on the classification of oak gall wasps is needed. Part of the outdated and erroneous genus-level boundaries have been re-defined for the last 10 years, yet the most complex genera remain unresolved. The greatest challenge of this revisionary process is tackling the *Andricus* Hartig, 1840 genus. With around 400 species accumulates 1/3 of the Cynipini tribe richness and is, by far, the largest genus in the superfamily Cynipoidea. The morphological and biological features of *Andricus* have become enormously diverse and the synapomorphies of the genus are unclear.

Several phylogenetic studies have shown the polyphyly of *Andricus*, and part of my Ph.D. has transferred some of the independent lineages into new genera (*Striatoandricus*; *Disholandricus*) and re-established valid genera (*Druon*; *Feron*). These revisions are based on the most comprehensive phylogeny of the tribe produced so far with six molecular markers. We follow an integrative approach to identify candidate genera in which each monophyletic group must be paired with morphological or biological distinctiveness. The gall morphology and the host-plant association can be reliable tools to define the limits of genera. However, the major conundrum we are facing is where the genus *Andricus* limits should be drawn. The type species of *Andricus* is placed within a major monophyletic clade containing several lineages from different biogeographic regions and remarkable morphological diversity. We propose several hypotheses on how to resolve the *Andricus* classification including the options of re-establishing the genus *Adleria* in the Western Palearctic or removing *Andricus* from the Nearctic and Neotropical fauna. The morphological synapomorphies, distribution, and biological features of this genus will vary accordingly with the strictness of its delimitation.

Phylogenetic relationships and species synonymization of cetacean parasites of the genus *Bolbosoma* Porta, 1908 (Acanthocephala: Polymorphidae)

^{1*}García-Gallego, Alicia, ¹Aznar, Francisco J., ^{2,3}Hernández-Orts, Jesús S., ⁴Davison, Nicholas J., ²Briscoe, Andrew G., ⁵Loizaga, Rocío, ²Littlewood, D. Timothy J., ^{1,2}Fraija-Fernández, Natalia

*lead presenter: alicia.garcia-gallego@uv.es

¹ Marine Zoology Unit, Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain

² Natural History Museum, London, United Kingdom

³ Institute of Parasitology, Biology Centre, Czech Academy of Sciences, České Budějovice, Czech Republic

⁴ Scottish Marine Animal Stranding Scheme, School of Biodiversity, One Health and Veterinary Medicine College of Medical, Veterinary & Life Sciences University of Glasgow, Glasgow G12 8QQ, UK

⁵ Centro para el Estudio de Sistemas Marinos-Consejo Nacional de Investigaciones Científicas y Técnicas, Puerto Madryn, Argentina

Acanthocephalans of the genus *Bolbosoma* Porta, 1908 are trophically-transmitted parasites that infect marine mammals worldwide. There are 12 species currently considered as valid; however, there is scarce information available on their phylogeny, taxonomy and evolutionary history. A particularly intriguing case is that of *Bolbosoma vasculosum* (Rudolphi, 1819), which has been frequently reported in toothed whales but rarely as adult, having been suggested to be synonymous with *Bolbosoma capitatum* (von Linstow, 1880). To shed light on these questions, we characterized the complete mitochondrial genome of *Bolbosoma balaenae* (Gmelin, 1790), *Bolbosoma turbinella* (Diesing, 1851), *B. capitatum* and *B. vasculosum*. Then, we reconstructed the phylogenetic relationships of *Bolbosoma* spp. and related taxa using mitochondrial genomes (or only *cox1* when full mitogenomes were unavailable) and nuclear ribosomal genes (18S and 28S). We paid particular attention to *B. vasculosum*, using morphological and molecular analyses to compare it with *B. capitatum*. Maximum likelihood and Bayesian inference analyses showed strong support for the monophyly of *Bolbosoma* spp. The resulting topology revealed two distinct clades for species infecting toothed whales and baleen whales, respectively. The complete mitochondrial genomes of *B. vasculosum* and *B. capitatum* (14,313 and 14,319 bp, respectively) showed a high pairwise identity for all protein-coding genes (>97.8 %) which, together with morphological evidence, suggests these two species are conspecific. The phylogenetic relationships obtained support the hypothesis that the association of *Bolbosoma* spp. with cetaceans originated through a host-switching event from aquatic birds.

*Supported by projects AICO2021/022 and CETABIOENA (CISEJI/2022/5), Generalitat Valenciana; and VARACOMVAL, Biodiversity Foundation, under the NextGenerationEU PRTR.

Multiple matrices to disentangle signals at the root of Metazoa

¹*Galán-Luque, Inés, ¹Giacomelli, Mattia, ¹Domènech, Marc, ¹Arañó-Ansola, Javier & ¹Lozano-Fernández, Jesús

*lead presenter: inesgalanluque@ub.edu

¹ Department of Genetics, Microbiology and Statistic & Institut de Recerca de la Biodiversitat – IRBio, University of Barcelona, Spain

The phylogenetic root of Metazoa has been one of the most debated questions in evolutionary biology over the past two decades, with different studies alternatively suggesting ctenophores or sponges as the earliest-branching animal lineage. Sponges lack nervous and digestive systems and so these features likely had only a single origin if they branched first. However, ctenophores have all these features, which may have evolved multiple times if they are the most ancient animal lineage. These conflicting results often depend on factors such as which species are included, the genes analyzed, and the evolutionary models applied. Additional challenges arise from methodological artifacts and the computational demands of complex models, making it difficult to confidently resolve early animal evolution.

We propose a workflow to assess the robustness of phylogenetic results using multi-protein, clade-specific matrices containing different taxa and different genes. This included reducing the number of species per lineage to allow the use of complex mixture models. Furthermore, we tested multiple strategies to explore how dataset composition and analytical choices affect results, such as the effect of outgroup selection and applying amino acid recoding to reduce noise. By comparing outcomes across these approaches, we evaluated how phylogenetic topology and support values change under different conditions, providing a framework for assessing the robustness of competing hypotheses about the early evolution of animals.

Hidden Diversity in Island Pollinators: Insights from *Osmia submicans* in the Canary Islands

¹*Patiño-Sauma, Diego, ²Lugo, David & ²Ruiz, Carlos

*lead presenter: diegopsauma@gmail.com

¹ University of La Laguna, Spain

² Department of Animal Biology, Edaphology and Geology, University of La Laguna, San Cristobal de la Laguna, Canary Islands, Spain

Bees constitute the most functionally important group of pollinators, underpinning the reproduction and maintenance of a substantial proportion of global plant diversity. However, a decline of the group has been reported worldwide during the last decades. Therefore, improving taxonomic knowledge is essential in order to preserve existing species. This is determinant in highly vulnerable ecosystems such as oceanic islands, where cryptic species may increase current estimates of biodiversity.

Osmia submicans Morawitz (1870) is widely distributed across the Western Palearctic, comprising five subspecies: one occurring in southern Europe, another in North Africa and the Mediterranean Levant, and three restricted to the Canary Islands. Recent molecular studies have found high genetic variability among populations from the different islands, suggesting cryptic speciation in the archipelago.

The present study combines morphological and molecular data in an integrative approach to characterize the cryptic diversity within *O. submicans*. Geometric morphometrics of the forewings and four mitochondrial and nuclear markers (*cox1*, *28S*, *ITS2*, *anonymous*) were analyzed in 39 specimens from populations of different islands and Morocco.

Both morphological and molecular data revealed significant differences between the majority of island and continental populations except for the oriental islands, supporting the existence of at least five endemic cryptic species in the Canary Islands. Moreover, haplotype composition in the easternmost islands suggests a complex pattern of colonization from the mainland.

The delimitation of distinct endemic lineages with a restricted distribution range highlights the need for a thorough re-assessment of their conservation status, as well as the urgency of developing species-specific conservation strategies to ensure the persistence of these insular endemic species.

Taxonomic challenges of Rajidae for conservation and management

¹*Pérez, Trinidad, ¹Piedrafíta Clara, ¹Gómez-Lobo Daniel, ¹Borrell, Yaisel J., ¹Miralles Laura,

*lead presenter: pereztrinidad@uniovi.es

¹ Dpto Biología Funcional, Genética, Universidad de Oviedo, Spain.

Skates (Rajidae) are among the most vulnerable groups of elasmobranchs due to their life history traits such as low fecundity, slow growth and late maturity. In the context of increasing fishing pressure and limited species-specific management accurate species identification is essential for effective conservation, since misidentification and mislabeling lead to critical gaps in fisheries data. Misidentification distorts the true catch composition and makes accurate stock assessments more difficult undermining efforts to implement effective conservation measures. Although in some cases economic benefits could be behind mislabeling of skates in Spanish fish markets, unintentional mislabeling rates cannot be ruled out due to the difficulties in species identification. Both, high phenotypic plasticity of some species and high morphological similarities between different species have been documented in scientific literature, as well as local morphotypes. For example, it is difficult to distinguish between *Raja brachyura* Fowler 1910 and *Raja montagui* Fowler 1910 due to their similar pattern. Meanwhile *Raja clavata* Linnaeus 1758, exhibits a large number of different phenotypes which has led to uncertainty about whether those differences represent variation within a single species or the presence of more than one, closely related species. Another example is *Raja maderensis* Lowe 1838 that has been described as a different species from *R. clavata*, however recent studies failed to support the genetic differentiation between both species and morphological differences are likewise unclear. In fact, genetics has long been recognized as valuable tool in fisheries management, particularly for species identification, stock structure definition, and the prevention of species misidentification. Specifically, DNA barcoding using the mitochondrial cytochrome c oxidase subunit I (COI) gene, is a powerful tool for genetically identifying elasmobranch species and has been widely used in studies addressing mislabeling skates.

This study aimed to identify species identification conflicts in the *Raja* genus and to assess the extent of species mislabeling and the genetic diversity of skates landed in the biggest primary fish market of Asturias (Avilés, Cantabrian Sea). Sampling was conducted between November 2024 and March 2025. A total of 413 individuals were sampled and genetically identified. Skate and ray species found within the sampling period in the landings included *R. clavata* (63.9%), *R. montagui* (11.4%), *L. naevus* (8.0%), *R. microocellata* (7.3%), *R. undulata* (5.3%), *R. brachyura* (3.4%). The global level of mislabeling was above 20%. These high levels of mislabeling highlight the need for urgent sustainable management of skate fisheries in northern Spain. The study emphasizes the need for implementing consistent species-specific labeling, personnel training, and integrating genetic tools into fisheries monitoring to improve traceability, conservation, and policy enforcement.

Biogeodynamics of orogenic arcs and their biodiversity hotspots in the Western Mediterranean

^{1,2*}Mas-Peinado, Paloma, ³Jiménez-Robles, Octavio, ⁴Galve,- J.P., & ⁴Booth-Rea, Guillermo

*lead presenter: p.mas@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, España.

² Departamento de Biología (C. D. Zoología), Facultad de Ciencias, Universidad Autónoma de Madrid (UAM), Madrid, España

³ Institut Natura e Teoria en Pirinèus, France

⁴ Departamento de Geodinámica, Universidad de Granada, España. gbooth@go.ugr.es

Many of the world's biodiversity hotspots are hosted in Orogenic Arcs (OA), like the Caribbean, Indonesian or Mediterranean subduction arcs. The tectonic evolution of these OA could have been a major driver of these regions' exceptional biodiversity. Here we focus on the Western Mediterranean OAs, formed through lithospheric slab rollback and oblique plate convergence. These tectonic mechanisms drove shallow-mantle flow, landmass displacements, archipelago fragmentation, crustal growth at volcanic arcs and high-elevation mountain building. Processes that triggered significant paleogeographic and ecological shifts that shaped evolutionary trajectories and biodiversity hotspot development.

This study examines how these changing configurations acted as barriers or temporary corridors, promoting allopatric and peripatric speciation, particularly in low-dispersal organisms. Repeated fragmentation and reconnection of landmasses, river systems, and marine basins created dynamic spatial discontinuities that fostered both divergence and diversification and also acted as dynamic stepping stones that favoured intercontinental dispersal. The westward migration of the Betic-Rif OA, along with the middle Miocene opening of the Algero-Balearic basin, the growth of the Alboran volcanic arc landbridge between SE Iberia and the eastern Rif, and closure of the Rif Strait in the late Messinian repeatedly redefined dispersal routes and biogeographic boundaries, which followed the westward direction of arc propagation. These transitions led to pulses of diversification and endemism, especially in taxa with limited dispersal ability.

Middle Miocene species radiated in the Alboran archipelago dispersed into Iberia in the late Miocene. Young MCRA are found towards the west, around the Gibraltar straits and the Guadalquivir lowlands, regions that emerged through ongoing crustal thickening in the late Pliocene. This study proposes a refined evolutionary framework for several groups of invertebrates and vertebrates that present speciation patterns that closely follow the evolution of the Betics-Rif orogen. By integrating geological (stratigraphy, tectonics, paleomagnetism) and biological data (biogeography, phylogenetics, fossil records) we highlight the central role of orogenic arc dynamics in shaping speciation, emphasizing the need to incorporate geodynamic history into models of diversification and dispersal of life in orogenic arcs like the Betics-Rif.

Updating of the taxonomy and systematics of the Iberian freshwater fish based on genomic and morphological data

¹*Perea, Silvia, ²Sousa-Santos, Carla, ²Robalo, Joana, ¹López-Solano, Alfonso, ¹Casal-López, Miriam, ³Mendes, Sofia, ³Sousa, Vitor & ¹Doadrio, Ignacio

*lead presenter: sperea@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales – CSIC, Madrid, España

² MARE-ISPA, Lisbon, Portugal

³ Faculdade de Ciências da Universidade de Lisboa, Lisbon, Portugal

The ichthyofauna of the Iberian Peninsula is characterized by a high degree of isolation from the rest of the European and North African fish faunas, at least since the Miocene, when the uplift of the Pyrenees and the opening of the Strait of Gibraltar conferred strong insularity to the region. As a result of this long-term isolation, Iberian freshwater fishes comprise relatively few but very ancient evolutionary lineages that have diversified into a large number of species. However, their morphological diversification has not paralleled the extent of their molecular differentiation. Consequently, advances in molecular techniques have revealed cryptic diversity in several genera, particularly those widely distributed across the peninsula, such as *Achondrostoma* and *Squalius* (Leuciscidae) and *Cobitis* (Cobitidae). In this study, we integrated morphometric and CT-scan data with molecular evidence (including mitochondrial and nuclear DNA sequences, as well as genome-wide SNPs) to evaluate inter- and intraspecific diversity within these three genera. Our analyses identified distinct evolutionary lineages for each genus which, when combined with morphological data, have led to the description of new species in the last two years (three in *Achondrostoma*, three in *Squalius*, and three in *Cobitis*), as well as the recognition of additional divergent lineages. The relevance of this study lies in the revision and updating of the taxonomy and systematics of the Iberian ichthyofauna, which represents a key component of the Mediterranean biodiversity hotspot. Furthermore, we identified intraspecific diversity within each of these three genera, which appears to be strongly shaped by the complex paleogeographic history of the Iberian Peninsula.

Keywords: systematics, taxonomy, Iberian ichthyofauna, genomics, new species.

Application of MALDI-TOF to Kinorhyncha identification: a combined morphological, genetic and proteomic approach

¹*Sánchez, Nuria, ¹González-Casarrubios, Alberto, ²Rossel, Sven, ²Khodami, Sahar & ²Martínez Arbizu, Pedro

*lead presenter: nurisanca@ucm.es

¹ Universidad Complutense de Madrid, Faculty of Biological Sciences, Department of Biodiversity, Ecology and Evolution. Madrid, Spain.

² Senckenberg am Meer, German Centre for Marine Biodiversity Research (DZMB). Wilhelmshaven, Germany.

The identification of meiobenthic organisms such as kinorhynchs remains a major challenge due to their minute size and the difficulties associated with morphological interpretation. Here we explore, for the first time, the applicability of MALDI-TOF mass spectrometry (Matrix Assisted Laser Desorption/Ionization - Time of Flight) to the discrimination of kinorhynch species. A total of 96 specimens belonging to the orders Anomoirhaga, Kentrorhagata, and Echinorhagata were analyzed. Each specimen was sequentially subjected to (1) MALDI-TOF analysis, (2) DNA barcoding (18S and COI), and (3) morphological examination. This workflow enabled a direct comparison of proteomic, molecular, and morphological data for the same specimen, maximizing the information obtained.

Preliminary results show that MALDI-TOF generates consistent proteomic fingerprints that allow clear separation of species belonging to different orders and even to different genera within the same Kinorhyncha family, in agreement with molecular and morphological identifications. In some cases, clusters may indicate intraspecific variability or sexual dimorphism, rather than evolutionary relationships.

MALDI-TOF was successfully applied to the identification of several macrofaunal and megafaunal groups; however, within meiofauna, copepods have so far represented the only taxon where this technique had been tested with success. Our results not only highlight the MALDI-TOF potential for advancing the taxonomy of Kinorhyncha, but also suggests that this technique may be broadly applicable to other meiofaunal groups, offering a rapid, sensitive and cost-effective tool, with the added benefit of preserving specimens for subsequent DNA and morphological analyses.

A new system classification of the current *Gibbula* concept (Vetigastropoda, Trochidae, Cantharidininae) based on integrative taxonomy

^{1*}Templado, ^{1,2,3}José; ⁴Uribe, Juan E.; ²Herbert, David G. & ¹Zardoya, Rafael

*lead presenter: templado@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain

² National Museum of Wales, Cardiff, U.K.

³ National Museum of Natural History, Smithsonian Institution, Washington, USA

⁴ Department of Bioscience, University of Milano, Italy

The subfamily Cantharidininae (Trochoidea: Trochidae) includes 26 recognized extant genera with *circa* 200 known species. Marine top shell snails of this family are microphagous grazers that generally live in shallow rocky shores or associated to seaweeds and seagrass beds in sub-tropical and temperate waters in the Indo-Pacific and the Eastern Atlantic Ocean, including the Mediterranean Sea and South African coasts. Our previous phylogenetic analyses suggested that the northeastern Atlantic/Mediterranean genera *Gibbula*, *Steromphala*, *Jujubinus*, *Phorcus* and *Clelandella* belong to the same natural lineage originated upon the closure of the Tethys. Among these, the most controversial genus is *Gibbula* s.l., which holds around 50 extant nominal species with a wide distribution. The present study is based on previous scalable phylogenetic hypotheses (nuclear and mitochondrial) and now focused on species from the Mediterranean and NE Atlantic, along with South African species ascribed to the genera *Gibbula* and *Oxystele*. The relative position of the genera *Phorcus* and *Jujubinus* in the phylogenies rendered *Gibbula* non-monophyletic. Its species were grouped in two independent major lineages, divided into three and two clades. Respectively. The first lineage included: 1) *Gibbula turbinoides* and *G. drepanensis*, as a sister group to the remaining, for which the genus name *Glomulus* (type species *Trochus turbinoides*), is restored from the synonymy; 2) *Steromphala* was recovered as monophyletic but divided into two subclades, one of them comprising the type species and the other one that including *S. umbilicalis* and *S. varia*. This clear-cut division justifies raising both subclades to the genus level. The clade that includes the type species of the genus *Steromphala* (*Trochus cinerarius*) would retain this generic name, whereas 3) the name *Gibbulastra* can be resurrected from synonymy for the other species (type species *Trochus divaricatus*). The second recovered lineage included the South African species ascribed to *Oxystele* and *Gibbula* and some European species of *Gibbula*, including the type species (*Trochus magus*). Therefore, 4) the true genus *Gibbula* s.s. should be restricted to these species, whereas 5) the South African ones require a new genus from which no name is available. Once the previous genetic clades were detected, phenotypic characters (from the shell and head-foot), were re-examined 'a posteriori' to formally delineate the W Atlantic/Mediterranean genera *Phorcus*, *Jujubinus*, *Clelandella*, *Steromphala* and *Gibbula* s.s., along with the new genera here proposed: *Gibbulastra* and *Glomulus*. Furthermore, the geographic distribution, habitat and data on the reproductive biology of the species included within each of these genera are provided.

Genomic analysis of *Plebejus* Kluk (Lycaenidae: Polyommatainae) clarifies taxonomy within Europe

^{1,2*}Toro-Delgado, Eric, ³Gauthier, Jérémy, ¹Hinojosa, Joan C., ^{4,5}Dincă, Vlad, ⁶Dapporto, Leonardo, ⁷Talavera, Gerard, ³Álvarez, Nadir & ¹Vila, Roger

*lead presenter: eric.toro@ibe.upf-csic.es

¹ Institut de Biologia Evolutiva, CSIC - Universitat Pompeu Fabra, Passeig Marítim de la Barceloneta, 37-49, 08003, Barcelona, Spain

² Universitat de Barcelona, Av. Diagonal, 643, 08028 Barcelona, Spain

³ Naturéum - State Museum of Natural Sciences, Palais de Rumine, Place de la Riponne 6, 1005 Lausanne, Switzerland

⁴ "Grigore Antipa" National Museum of Natural History, Șos. Kiseleff no. 1, R0-011341, Bucharest, Romania

⁵ Ecology and Genetics Research Unit, PO BOX 3000, FI-90014 University of Oulu, Finland

⁶ Dipartimento di Biologia dell'Università degli studi di Firenze, 50019 Sesto Fiorentino, Florence, Italy

⁷ Institut Botànic de Barcelona (IBB), CSIC-CMCNB, Barcelona 08038 Catalonia, Spain

Despite the need to describe Earth's biodiversity, some species groups are notoriously challenging to classify. One example is the genus *Plebejus* Kluk (Lycaenidae: Polyommatainae), which has been the subject of taxonomic debate for decades. Numerous studies have been conducted in North America, but European taxa remain underexplored at the genomic level. To fill this gap we analysed a ddRAD sequencing dataset comprising all European *Plebejus* taxa and a selection of Asian and North American ones. *Plebejus argus* (Linnaeus), *Plebejus argyrognomon* (Bergsträsser), and *Plebejus bellieri* (Oberthür) are each recovered as monophyletic with limited gene flow, supporting their species status. *Plebejus idas* (Linnaeus) is paraphyletic, highlighting the need for a revision of the genus at the Holarctic level. *Plebejus corsicus* (Bellier) presents clear but limited genetic divergence and should be considered a subspecies of *Pl. argus*, whereas *Plebejus villai* (Jutzeler, Leigheb, Manil, Villa & Volpe) is not divergent from *Pl. bellieri* and should be considered a population of the latter. *Pl. argus* and *Pl. idas* present geographic structure following the southern peninsulas, with central and northern European populations clustering with the Balkans, consistent with a scenario of southern glacial refugia and posterior range expansion. We also find widespread *Wolbachia* infection across all species except for *Pl. argus*, with low variation levels in the *Wolbachia* loci. Lastly, we also find evidence of increasing inbreeding levels in mainland *Plebejus* populations, especially in Eastern Europe, which may be due to land abandonment and agricultural intensification.

Widespread but not uniform: cryptic diversity in the cave-adapted pseudoscorpion *Troglobisium racovitzai* (Ellingsen, 1912)

Domènech, Marc^{1*}, Hlebec, Dora^{2,3,4}, Giacomelli, Mattia¹, Ribera, Carles² & Lozano-Fernandez, Jesus¹

*lead presenter: mdomenan@gmail.com

¹ Department of Genetics, Microbiology and Statistics & Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Avinguda Diagonal 643, 08028 Barcelona, Spain.

² Department of Evolutionary Biology, Ecology and Environmental Sciences & Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Avinguda Diagonal 643, 08028 Barcelona, Spain.

³ University of Zagreb, Faculty of Science, Department of Biology, Horvatovac 102a, 10000 Zagreb, Croatia.

⁴ Croatian Biospeleological Society, Rooseveltov trg 5, 10000 Zagreb, Croatia.

Subterranean habitats are extreme environments, found just a few kilometers from urban areas. Species inhabiting them typically have extremely restricted distributions, largely due to limited dispersal abilities. However, some display unexpectedly broad ranges, which may result from enhanced dispersal, underground connectivity, or overlooked cryptic diversity.

The highly cave-adapted pseudoscorpion *Troglobisium racovitzai*, the sole representative of its genus, is known only from caves in eastern Spain. Its distribution spans around 300km north to south and can be divided into three geographically separated regions—northern, central, and southern—each isolated by natural barriers like the Ebre river. Given that many troglobionts exhibit strong genetic structuring across even short distances, we hypothesized that *T. racovitzai* may comprise multiple distinct evolutionary lineages. To test this, we analyzed both museum specimens (14) and recently collected material (5), using an integrative approach that combines morphological data (27 characters) and four molecular markers (three nuclear and one mitochondrial).

The first three principal components accounted for 62% of the total morphological variation, with the three populations being sorted along the PC1, primarily influenced by leg IV tarsus, and pedipalpal patella and pedipalpal femur ratios. PC2 captured variation in pedipalpal hand morphology, with the highest contributions from pedipalpal hand and movable finger.

A phylogenetic analysis recovered three monophyletic lineages, with high mean COI pairwise distances between them (15.9–20.8% North-South). These results, together with morphological data, support the distinctiveness of the southern population as a potential new species, while additional material is needed to clarify species boundaries in the central region.

Species boundaries and phylogenetic relationships within Iberian *Alzoniella* Giusti & Bodon, 1984 (Gastropoda: Hydrobiidae): An integrative taxonomic approach

^{1,2*}García Guerrero, Fernando, ¹Miller, Jonathan P., ² Novo, Marta & ¹Delicado, Diana

*lead presenter f.garciaquerrero@mncn.csic.es

¹ National Museum of Natural Sciences (MNCN-CSIC), Spain

² Faculty of Biological Sciences, Complutense University of Madrid, Spain

The Iberian Peninsula is a crucial biodiversity hotspot for freshwater gastropods, particularly those belonging to the family Hydrobiidae W. Stimpson, 1865, which comprises numerous endemic and threatened species. These minute organisms (0.5–5 mm), predominantly found in isolated headwater springs, exhibit restricted dispersal. The morphological simplicity of hydrobiids has historically complicated species delimitation, which in turn has hampered systematic efforts within the group. However, recent molecular phylogenetic analyses suggest that some Iberian representatives of widespread Mediterranean genera form distinct, narrow-range lineages that may warrant recognition as separate genera. Given that accurate systematics is essential for effective conservation, our research focuses on *Alzoniella*, a widespread hydrobiid genus with over 40 nominal species, including 13 morphologically identified Iberian species.

To establish robust species hypotheses within Iberian *Alzoniella*, resolve lineage relationships and determine the group's biogeographic history, we sampled 11 of the 13 known Iberian taxa across 41 springs. Multilocus phylogenetic analyses based on five loci (mitochondrial COI, 16S; nuclear H3, 18S, 28S) identified three distinct clades and two independent lineages, with significant interspecific COI divergences (3–21%). Species delimitation methods (i.e., ABGD, bPTP, mPTP, and st-GMYC), particularly bPTP, largely corroborated the existence of the 11 morphologically described species, and three additional putative species. Geometric morphometrics analysis of 373 shells revealed distinctive clade-specific shell profiles despite intraspecific variability in shell shape (cylindrical vs. ovate-conic). Divergence dating and ancestral-area reconstructions suggest that *Alzoniella* originated in Iberia during the late Oligocene–Miocene, with subsequent founder-event speciation shaping their current microendemic distributions.

This systematic revision confirms that the Iberian *Alzoniella* complex encompasses at least six distinct genera and three previously undescribed species, each defined by a unique combination of molecular and morphological traits. This taxonomic reorganization aligns phylogenetic relationships with morphological diagnostics and underscores the importance of allopatric and peripatric speciation in spring habitats. By clarifying species boundaries and evolutionary lineages, our results provide a crucial framework to inform conservation efforts for these highly vulnerable and often overlooked freshwater gastropods.

Unravelling hidden lineages and ecological preferences of the *Allolobophora chlorotica* species complex in the western Mediterranean

¹*Piris, Alberto, ¹Martínez Navarro, Alejandro, ¹Tilikj, Natasha, ²Dupont, Lise, ¹Marchán, Daniel F., & ¹Novo, Marta

*lead presenter: alpiris@ucm.es

¹ Departamento de Biodiversidad, Ecología y Evolución. Universidad Complutense de Madrid, Spain

² Université Paris-Est Créteil, Créteil, France

Allolobophora chlorotica (Savigny, 1826) (Lumbricidae) is an endogeic earthworm widespread in Europe, with numerous introductions reported outside its native range. This species exhibits color dimorphism, with green and pink morphs normally associated with different ecological preferences: the green morph is more common in moist soils, while the pink is often found in drier environments. Previous studies have shown that these morphs are linked to distinct mitochondrial lineages, namely L1-L5, possibly reflecting the existence of different cryptic species. Some subspecies have also been described based on morphological differences (e.g., *A. chlorotica postepheba*, *A. chlorotica waldensis*...). Moreover, mitonuclear discordance and reproductive isolation have been detected between some of the lineages, pointing to historical hybridization or incomplete reproductive isolation within the complex.

In this work, we barcoded ~250 individuals of this species complex across the western Mediterranean, complemented with additional sequences retrieved from public databases. Multilocus data (COI, 12S, 16S, ND1 and 28S) were also generated for representatives of each lineage to refine their phylogenetic relationships and assess their taxonomic status. Some morphological traits were assessed to test for congruence with the molecular results (difference in clitellum position, length, weight, internal characters...). Together, these analyses support a clear separation between lineage L5 and the rest of the lineages (L1-L4), as well as for *A. c. waldensis*, and *A. c. postepheba* (the latter appears as a sister taxon to an outgroup species, *A. burgondiae*).

To explore ecological preferences, we carried out Species Distribution Models under both present and future climate scenarios. Models were constructed both separately for each lineage, giving special attention to those present in the Iberian Peninsula (L2 and L5) and jointly for the entire complex, using different modelling methods. Results highlight distinct ecological niches and potential shifts under climate change for the different lineages, indicating that cryptic taxa might be differentially vulnerable.

Our results comprise an integrative taxonomic revision of the *A. chlorotica* species complex, combining genetic, ecological, and morphological data. To understand the evolutionary history of the complex and develop adequate conservation strategies in a rapidly changing environment, it is essential to understand its hidden diversity.

Studying host diversification and habitat specialization in squat lobsters from vulnerable mesophotic and deep-sea ecosystems through ultra-conserved elements

*Paula C. Rodríguez-Flores

*lead presenter: paularodriguezflores@gmail.com
Muséum national d'Histoire naturelle, Paris, France

Target enrichment sequencing of ultraconserved genomic elements (UCEs) is increasingly being used to address evolutionary questions across multiple scales, from population genetics to phylogenetics. Probe sets have already been developed for several major groups, including corals, mollusks, and arthropods. Here, I present a case study demonstrating how UCEs can leverage material from museum collections, reducing the need for costly and logistically challenging deep-sea sampling. I use a probe set specifically designed for Decapoda capturing up to 1,384 loci, to study host diversification and habitat specialization in squat lobsters (Galatheaidea, Chirostyloidea) from vulnerable mesophotic and deep-sea ecosystems. Squat lobsters constitute a highly diversified group of marine decapods, including nearly 2,000 species described and about a third waiting to be discovered. Species in the family Munidopsidae inhabit vulnerable marine ecosystems such as hydrothermal vents and cold seeps, whereas species in the families Chirostylidae and Sternostylidae are symbiotic species on deep-sea corals (Scleractinia, Octocorallia and Antipatharia). Sequencing on legacy museum material collected since 1885 reveal high efficacy of target capture of UCEs, recovering from 10s to about 100s loci. Preliminary results show complex evolutionary history and rapid diversification on chemosynthetic environments in munidopsids squat lobsters, whereas polyphyly, hidden diversity, host-dependent diversification in chirostyloid squat lobsters from deep-sea corals. Ongoing work will expand these preliminary findings and clarify the role of host associations and habitat specialization in shaping diversification.



BIODIVERSITY MONITORING & COMMUNITY ECOLOGY

Improving the reliability of metabarcode inventory and monitoring of arthropod communities

^{1,2*}Eisele, Marius, ¹Emerson, Brent C. & ¹Andújar, Carmelo

*lead presenter: marius.eisele@ipna.csic.es

¹ Instituto de Productos Naturales y Agrobiología, Tenerife, Islas Canarias, España

² Department of Genetics and Microbiology Genomics, Bioinformatics and Evolution, Universitat Autònoma de Barcelona

This study evaluates the effectiveness of denoising tools, which are used to clean up noisy data from bulk sample DNA metabarcoding. Bulk sample DNA metabarcoding is a technique that can rapidly identify many different species from a single sample, such as complex mixtures of arthropods sample with Malaise traps. While denoising tools are designed to remove errors and noise to provide accurate species inventories, their ability to remove non-target sequences while retaining true mtDNA sequences derived from sampled individuals has not been well-studied.

Our research shows that current denoising tools often fail to remove all non-target sequences, leading to inaccurate species inventories and biased estimates of mtDNA variation within species. This is a significant limitation for biodiversity inventory and monitoring, as well as the study of community ecology and biodiversity. To address this, we evaluated the performance of several common denoising tools using real-world Malaise trap data.

We reveal that while denoising tools are useful, they often fail to remove a significant amount of noise. We find that two additional tools, LULU and metaMATE, are very effective at removing noise, but this unavoidably results in the collateral removal of a non-trivial proportion of target sequences. Based on our findings, we recommend using a specific workflow that combines one of the better-performing denoising tools, like DADA2 or UNOISE3, together with either LULU or metaMATE. This approach provides a balance between removing noise and retaining target sequences.

Our results reveal substantial limitations remain for reliable bulk sample metabarcoding. In this presentation I will also discuss the potential for deep learning models to further filter out remaining noise, particularly nuclear copies of the mtDNA (NUMTs), to improve accuracy (signal to noise ratio) and thus reliability of bulk sample metabarcoding.

Island-like environments through the lens of meiofaunal diversity: a metabarcoding approach

^{1,2*}García-Cobo, Marta, ³Cattano, Petra, ²Fontaneto, Diego, ²Di Nezio, Francesco, ¹Pardos, Fernando, ¹Sánchez, Nuria & ²Martínez, Alejandro.

*lead presenter: martag49@ucm.es

¹ Universidad Complutense de Madrid, Spain

² Molecular Ecology Group, IRSA-CNR, Italy

³ Management Authority for Parks and Biodiversity – Romagna, Italy

Island systems have long served as natural laboratories for ecology and evolution, enabling the development of theories of broad significance. Beyond actual islands, isolated habitats such as alpine lakes, caves, or deep-sea trenches function as “island-like environments”, offering to study processes of adaptation, speciation, and community assembly at multiple temporal and spatial scales.

Problematically, most island biogeography research is biased towards a narrow set of organisms, predominantly vertebrates and hexapods, whereas meiofauna—remarkably rich in taxonomic, functional and phylogenetic diversity—remains unexplored as a model. Despite their richness and diversity, unbiased assessments of meiofaunal biodiversity patterns remain challenging.

Metabarcoding provides a powerful entry point for studying meiofaunal diversity across habitats, producing large datasets efficiently. However, incomplete reference libraries and lack of trait annotation restrict taxonomic resolution and limit ecological inference. To mitigate this, we have developed a pipeline that places “unclassified” sequences within a reference tree, improving taxonomic assignment, retaining more sequence information, and enabling the calculation of functional and phylogenetic diversity metrics. Ultimately, the full potential of metabarcoding depends on integrative approaches: linking molecular surveys with traditional taxonomy and trait-based data.

Here we propose a conceptual synthesis: using meiofaunal metabarcoding as a rapid, broad-scale entry point into meiofaunal diversity across island-like environments, followed by morphological and functional analyses to infer causal processes. We illustrate this approach with case studies from terrestrial gypsum caves from (Vena del Gesso, Italy), marine benthic samples from Antarctica and freshwater samples from an alpine lake (Lake Cadagno, Switzerland).

Is it me or my circumstances? A study of oligochaete microbiome

¹*de Sosa, Irene, ¹Taboada, Sergi & ¹Riesgo, Ana

*lead presenter: irene.desosa@mncn.csic.es

¹ National Museum of Natural Science, Madrid, Spain

Oligochaetes (Annelida, Clitellata) have massively diversified across aquatic and terrestrial habitats. Terrestrial oligochaetes are known for their crucial modification of soil during their intestinal transit, a process in which their microbiome has a fundamental role. Since there is little information on the microbiome of a few oligochaetes, there are fundamental questions about the role of the oligochaete microbiome in their adaptation to the different habitats.

Here, our aim was to explore the microbial composition of eight oligochaetes species. Three of them (*Amyntas corticis*, *Eiseniella tetraedra* and *Eiseniella neapolitana*) were collected freshwater habitats, while the other five were sampled in terrestrial habitats (*Aporrectodea trapezoides*, *Aporrectodea rosea*, *Dendrobaena octaedra*, *Microscolex dubius* and *Octolasion cyaneum*). We extracted DNA from the gut of 96 specimen and we amplified a fragment of the V4 region of the 16S rRNA gene.

We identified a total of 49,131 ZOTUs in the sequenced samples. Among freshwater species, *Gammaproteobacteria* was the most abundant class (22.75%), followed by Actinobacteria (12.43%) and *Bacteroidia* (10.10%). In contrast, in terrestrial species the most abundant classes were *Actinobacteria* (22.87%), *Alphaproteobacteria* (13.74%) and *Bacilli* (11.89%). We found significant differences at species and habitat level in beta diversity. Also, we calculated the core microbiome of each habitat and species (present in at least 80% of samples). Despite species-specific differences, a common pattern emerged within freshwater and terrestrial habitats. This pattern was mainly driven by the high abundance of the class *Gammaproteobacteria* in freshwater species, whereas it was nearly absent in terrestrial ones.

We conclude that earthworms harbor different gut microbiome according to habitat. We hypothesized that it could be due to digestion of the available resources. In terrestrial habitats, we detected members of the orders *Burkholderiales*, *Sphingomonadales* and *Steroidobacterales*, specialized in degrading complex molecules, like cellulose and lignin, mostly present in soil. In contrast, in freshwater habitats orders such as *Pelagibacterales*, *Rhodobacterales* and *Methylococcales* prevailed, associated with the metabolism of dissolved carbon and methane, simple compounds that are more abundant in freshwater habitats, and that the earthworms' gut microbiota enables them to metabolize and exploit them. In addition, the presence of a stable core microbiome, such as the genera *Pseudomonadales* or *Hyphomicrobiales*, may ensure the performance of basic digestive functions that are shared across species.

This core provides metabolic resilience, enabling earthworms to adapt to environmental changes without compromising intestinal performance.

Biodiversity drivers and community assembly on islands and continents

^{1,2*}Macías-Hernández, N.; ^{3,4}Domènech, M. ^{2,5}Ramos C.; ³Arnedo M. ⁶Emerson B., ⁵Borges, P.A.V.; ^{2,7}Cardoso, P.

*lead presenter: nemacias@ull.edu.es

¹ Department of Animal Biology, Edaphology and Geology, University of La Laguna, La Laguna, Spain.

² LIBRe – Laboratory for Integrative Biodiversity Research, Finnish Museum of Natural History, University of Helsinki, Finland.

³ Department of Evolutionary Biology, Ecology & Environmental Sciences, & Biodiversity Research institute (IRBio), Universitat de Barcelona, Spain.

⁴ Department of Genetics, Microbiology and Statistics, Universitat de Barcelona, Spain.

⁵ cE3c - Centre for Ecology Evolution and Environmental Changes / Azorean Biodiversity Group / CHANGE - Global Change and Sustainability Institute and Universidade dos Açores, Terceira, Açores, Portugal.

⁶ Island Ecology and Evolution Research Group, IPNA-CSIC, Tenerife, Canary Islands, Spain.

⁷ Centre for Ecology, Evolution and Environmental Changes, CHANGE—Global Change and Sustainability Institute, Faculty of Sciences, University of Lisbon, 1749-016 Lisbon, Portugal.

One of the main aspects in the study of global patterns of biodiversity is understanding how communities assemble, and the evolutionary and ecological consequences of it. In this study we use spiders as model organisms and multiple island and continent datasets (Macaronesian archipelagoes and Iberian Peninsula) to compare taxonomic (TD), phylogenetic (PD) and functional (FD) diversity drivers between systems where distinct processes have shaped the current species composition. A phylogenetic tree with 492 taxa and 2 genes (mitochondrial and nuclear) was reconstructed to calculate PD indices. A functional database that includes life history traits (morphology, dispersal abilities, circadian activity, foraging strategy, prey range and vertical stratification) was used to build a global functional space and calculate FD indices.

Our preliminary results showed that, due to the differing ecological and evolutionary characteristics of islands and continent, contrasting patterns of phylogenetic and functional community structure were observed between both ecosystems. As expected, the number of species and the functional and phylogenetic diversity was higher in the continent compared to the islands. However, when corrected by species richness, the functional diversity was similar in both ecosystems, suggesting that the ecological role of many species from the continent not present in the the archipelagoes is being replaced by lineages occupying broader vacant niches on islands. Furthermore, we were able to detect both competitive exclusion and environmental filtering in the assembly of island communities.

Discovering animal diversity through phylogenetic placement of 18S metabarcoding data

^{1*}Arañó-Ansola, Javier,¹Lozano-Fernandez, Jesus, ¹Giacomelli, Mattia

**lead presenter: javierarano@ub.edu*

¹ *Department of Genetics, Microbiology and Statistics, University of Barcelona, Spain*

The small subunit ribosomal RNA (SSU rRNA) –18S in eukaryotes– is a universally present gene across the Tree of Life that has been instrumental to solve the most ancient relationships. Traditionally, 18S sequences are used to identify species or taxa. As a result, it serves as a molecular identifier of biodiversity in environmental DNA studies. Multiple methodologies have been proposed to identify known and novel biodiversity from environmental fragments of the 18S. One of those approaches, phylogenetic placement, arranges metabarcoding sequences into a phylogenetic context using a set of known reference sequences, the backbone tree. Despite its significance, specialised 18S databases still contain errors, which hinders the assembly of reliable reference phylogenetic trees needed to identify novel environmental 18S sequences.

We curated the most comprehensive 18S dataset of non-bilaterian animals in the Protist Ribosomal Reference Database. Using reliably identified sequences, we generated the largest backbone tree for non-bilaterians, essential for the taxonomic identification of molecular diversity within this group. Through phylogenetic placement, we are currently using our recently assembled backbone tree to analyse the avalanche of metabarcoding data generated by recent global expeditions such as Tara Oceans. With this approach, we mainly aim to unravel new diversity among non-bilaterian animals and to identify diversity patterns for such organisms. We also used this opportunity to study the suitability of the most common 18S-based barcodes, targeting their V4 and V9 regions, to phylogenetic placement.

Challenges and Opportunities in the Generation of Reference Genomes: Experiences from the Centre Balear de Biodiversitat

¹*Arboleda, Enrique, ¹de Oliveira Magalhães, Carolina, ¹Moragues-Solanas, Lluís, ¹Oliver-Riera, Bartomeu, ¹Perez, Rafaela, ¹Schöninger-Almaraz, Karen D., ¹Triginer-Llabrés, Laura, & ¹Capa, Maria.

*lead presenter: enrique.arboleda@uib.es

¹ Centre Balear de Biodiversitat (CBB-CMBB), Universitat de les Illes Balears (UIB), Spain.

Whole-genome sequencing under international standards, such as those established by the European Reference Genome Atlas (ERGA) and Biodiversity Genomics Europe (BGE), represents a fundamental step in comparative biology, systematics, and biodiversity conservation. At the Centre Balear de Biodiversitat, University of the Balearic Islands, we have undertaken the generation of reference genomes across a broad taxonomic range of marine and terrestrial plants and animals. This work has involved multiple technical challenges, including the extraction of high-molecular-weight DNA, the sequencing of long fragments across different platforms, and the application of Hi-C technologies for chromosome-level assemblies. These challenges highlight the inherent complexity of producing high-quality genomes, particularly in non-model organisms.

In this contribution, we share our experience, propose potential solutions to address some of these obstacles, and underscore the importance of network-based collaboration as a key strategy for standardizing protocols, optimizing resources, and advancing the generation of reference genomes. Although no single approach can resolve all difficulties, we aim to provide practical insights that may prove valuable to others embarking on similar endeavors. Finally, we stress the importance of depositing sample processing data and results in open platforms, thereby promoting global access to critical information for systematics and conservation.

Integrating megabarcoding and metabarcoding to unlock hidden biodiversity and overcome data shortfalls

^{1,2*}Santos-Perdomo, Irene, ³Salces-Castellano, A., ⁴Moraza, M. L., ^{5,6}Mateos, E., ⁷Muñoz-Barrera, A., ⁷González-Montelongo, R., ⁸Suárez, D., ^{1,2}Vega-Pita, N., ¹Falcón-López, L., ⁷Lorenzo-Salazar, J. M., ⁷Flores, C., ¹Arribas, P., ¹Andújar, C.

*lead presenter: isanper@ipna.csic.es

¹ Island Ecology and Evolution Research Group, Institute of Natural Products and Agrobiology (IPA-CSIC), 38206, La Laguna, Spain

² School of Doctoral and Postgraduate Studies, University of La Laguna, 38206, La Laguna, Spain

³ Department of Biology, University of Cádiz, Cádiz, Spain

⁴ Universidad de Navarra, Instituto de Biodiversidad y Medioambiente BIOMA, Irúnlarrea 1, 31008, Pamplona, Spain

⁵ Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals. Facultat de Biologia, Universitat de Barcelona, Barcelona, Spain

⁶ Institut de Recerca de la Biodiversitat. Facultat de Biologia, Universitat de Barcelona, Barcelona, Spain

⁷ Genomics Division, Instituto Tecnológico y de Energías Renovables S.A. (ITER), Santa Cruz de Tenerife, Spain

⁸ Department of Animal Biology, Edaphology and Geology, University of Laguna, La Laguna, Canary Islands, Spain

Soil mesofauna, comprising small invertebrates such as mites and springtails, are key contributors to ecosystem functioning but remain severely understudied, particularly within biodiversity hotspots. This knowledge gap is especially striking in the Canary Islands, a volcanic archipelago of exceptional conservation importance where soil mesofauna diversity has received little attention despite decades of ecological research. Here, we present an integrative workflow designed to accelerate regional biodiversity inventories of soil mesofauna by combining (i) megabarcoding, (ii) taxonomic identification, and (iii) metabarcoding. In the first step, megabarcoding of selected specimens from community soil samples generates a regional reference barcode database, enabling molecular taxonomic assignments and reducing the need for extensive morphological inspections. In the second step, this barcode inventory is cross-referenced with community DNA metabarcoding data to detect and map the presence of inventoried species across bulk samples. Applying this workflow in the Canary Islands led to the detection of 141 species of mites and springtails, 48 of which were recorded for the first time in the archipelago. Cross-checking the presence of these barcoded species across 168 metabarcoding samples of laurel forest from the Canaries provided 1,442 new distribution records (distributions assigned to 500 × 500 m grids), and for 30 species doubled the extent of their known distribution within the archipelago. This two-step workflow maximizes the strengths of both specimen-based and community-based approaches, providing a scalable framework for documenting dark taxa in soil ecosystems and advancing biodiversity assessments in megadiverse regions.

Testing island biogeography theory belowground: soil mesofauna on islands of contrasting age

^{1,2}Salces-Castellano, Antonia; ^{1,3*}Vega-Pita, Nira; ^{1,3}Santos-Perdomo, Irene; ¹López, Heriberto; ⁴González-Montelongo, Rafaela; ⁴Rubio-Rodríguez, Luís A.; ¹Emerson, Brent C.; ¹Andújar, Carmelo; ¹Arribas, Paula.

*lead presenter: nira.vega@csic.es

¹ Instituto de Productos Naturales y Agrobiología (IPNA – CSIC), 38206, La Laguna, Tenerife, Canary Islands, Spain

² Department of Biology, University of Cádiz, Cádiz, Spain

³ School of Doctoral and Postgraduate Studies, University of La Laguna, 38206, La Laguna, Tenerife, Canary Islands, Spain

⁴ Genomics Division, Instituto Tecnológico y de Energías Renovables S.A. (ITER), Santa Cruz de Tenerife, Spain

Island biogeography theory predicts that geological age plays a central role in shaping biodiversity patterns, yet most evidence comes from aboveground systems. In contrast, belowground diversity remains poorly characterised, despite its ecological importance and high levels of endemism. Soil mesofauna, in particular, combine limited active dispersal with high abundances that may promote passive long-distance transport, raising questions about how colonisation, diversification, and habitat specialisation unfold in island ecosystems. To address these gaps, we investigated soil mesofaunal communities across two Canary Islands of contrasting ages, Tenerife (~9 Ma) and El Hierro (~1 Ma), using whole organism community DNA (wocDNA) metabarcoding of the mtDNA COI gene from soil samples spanning four dominant habitats in these islands.

Our results revealed that both total and local species richness were higher in the soils of Tenerife than in those from El Hierro, consistent with predictions of greater accumulation on older (but also larger) islands. These differences were consistent across habitats, except in laurel forest communities, which harbour comparable local species richness of soil mesofauna. Community composition analyses indicated differentiated assemblages in soils from both islands, with only 17% of species shared overall. However, in El Hierro, these shared species represented more than 40% of its fauna, while in Tenerife, they accounted for only ~20%, with nearly 80% being exclusive to the older island. Within islands, communities were strongly structured by habitat and geographic distance, with stronger patterns in Tenerife. Tenerife communities also showed a higher prevalence of endemic, low-dispersive and specialist taxa, suggesting greater intra-island diversification than in El Hierro. Finally, while Tenerife hosted more introduced species in absolute terms, the relative contribution of introduced taxa to communities was similar across both islands, with ~25% of the species in local soil communities identified as potentially introduced. By integrating haplotype-level genetic data with ecological comparisons, this study provides one of the first empirical tests of island biogeographic predictions in soil systems.

Tiny consumers, big insights: uncovering kinorhynch diets with metabarcoding

¹*Khodami, Sahar, ²Sánchez, Nuria, ²González-Casarrubios, Alberto & ¹Martínez Arbizu, Pedro

*lead presenter: sahar.khodami@senckenberg.de

¹ Senckenberg am Meer, German Centre for Marine Biodiversity Research (DZMB). Wilhelmshaven, Germany.

² Universidad Complutense de Madrid, Faculty of Biological Sciences, Department of Biodiversity, Ecology and Evolution. Madrid, Spain.

Kinorhynchs are tiny meiofaunal invertebrates that inhabit marine sediments, yet almost nothing is known about their feeding ecology. Here we apply a multi-marker metabarcoding approach (18S and COI for eukaryotes and 16S for bacteria) to explore the dietary components of several kinorhynch species collected in the NW Mediterranean (Santa Pola, Spain) across two sampling periods.

The first dataset includes both adults and juveniles of *Echinoderes*, together with paired sediment and water samples. This unique design allows us to compare the dietary DNA signals of kinorhynchs with that of their surrounding habitat, providing insights into potential food sources and patterns of resource use. Differences between juveniles and adults may reflect a division in resource use that reduces competition and facilitates coexistence within the same habitat.

A second dataset complements this environmental framework by enabling direct comparisons among co-occurring consumers collected at the same time and place. We compare kinorhynchs with copepods, and also explore possible dietary differences between kinorhynch orders. Although no community samples from the surrounding environment were available for this dataset, such pairwise contrasts shed light on how meiofaunal groups, and particularly Kinorhyncha, may exploit different resources under similar environmental conditions.

Taken together, our study represents the first metabarcoding assessment of dietary patterns in kinorhynchs. It highlights the potential of molecular tools to unravel the feeding ecology of tiny animals and contributes new perspectives on their interactions with benthic microbial and protistan communities.

One Phylum, Two Worlds: Microbiome Contrasts in Freshwater and Marine Sponges

^{1*}Álvarez-Fernández, Almudena, ¹Corral, Andrea, ¹Gracia Sancha, Carlota, ¹Lorente-Sorolla, Jose, ¹Conejero, María, ¹Turon, Marta, ¹Taboada, Sergio, ²Díez-Vives, Cristina & ¹Riesgo Gil, Ana

*lead presenter: almudena.alvarez@mncn.csic.es

¹ National Museum of Natural Sciences (MNCN), Spain

² National Center for Biotechnology (CNB), Spain

Sponges occupy a unique position among invertebrates due to their intricate symbiotic relationships, hosting thousands of bacterial, archaeal, fungal, and viral taxa within their tissues. While most research until now has targeted marine sponges, the microbial community of freshwater sponges remains largely understudied, representing a potentially rich but overlooked reservoir of diversity and metabolic capabilities. Using 16S rRNA gene amplicon sequencing, we have characterized the microbiome of 15 species of freshwater sponges (order Spongillida) that are considered low microbial abundance (LMA) species and were collected from a variety of locations around the world. We compared their microbiome to those associated to marine sponge species belonging to the orders Scopalinida, Poecilosclerida and Haplosclerida, including both high microbial abundance (HMA) and LMA species, collected across various oceanic regions. The selection of marine sponges with varying degrees of phylogenetic relatedness to freshwater sponges, allows us to investigate the role of evolutionary history in shaping microbial community composition.

The microbiome of LMA freshwater sponges was found to be richer than both LMA and HMA marine sponges, and close in diversity to HMA sponge species. Microbiomes clustered strongly by habitat (marine vs. freshwater), with a clear separation of the freshwater order Spongillida from the marine orders, which showed considerable overlapping among themselves. Notably, the microbial community of freshwater species shared less than 0.02% of ASVs, in contrast to findings from other recent publications that compared at higher taxonomic levels. Moreover, the few symbionts shared between habitats were present at low relative abundances in marine sponges (mean 11.3%), and were minimally represented in freshwater sponges (mean 1.6%), suggesting diminished ecological role of these common microorganisms during adaptation to freshwater environments. Our results allow us to understand how the symbiotic interactions could have been affected during the transition from marine to freshwater environments, indicating a shift in the symbiotic communities, that might confer novel metabolic functions. This shift may be linked to increased plasticity in microbe recognition systems, facilitating the establishment of new symbiotic partnerships in freshwater habitats.

eDNA reveals multifaceted impacts of invasive *Gambusia holbrooki* on endangered killifish populations of the Iberian Peninsula

¹*Nester, Tessa Lynn, ¹López-Solano, Alfonso, ¹Perea, Silvia & ¹Doadrio, Ignacio

*lead presenter: tessa@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales, Madrid, Spain

The invasive Eastern mosquitofish (*Gambusia holbrooki*) poses a serious threat to the native ichthyofauna of the Iberian Peninsula, particularly two endangered and endemic killifish species: the Baetican toothcarp (*Aphanius baeticus*) and the Spanish toothcarp (*Aphanius iberus*). Since the introduction of *G. holbrooki* into their native habitats, these two species have experienced significant declines or local extinctions, although the underlying mechanisms remain unclear. In this study, we used environmental DNA (eDNA) to investigate whether this decline is due primarily to resource competition or predation. Over a three-year period, fecal and gut content samples were collected from co-occurring populations of *A. baeticus* and *G. holbrooki* in the San Pedro Stream (Cádiz), and over two years from coastal lagoons in Baix Empordà (Girona), where *A. iberus* and *G. holbrooki* coexist. Additionally, a controlled mesocosm experiment was conducted to further assess interspecific interactions. This experiment consisted of three treatments: the species maintained separately, coexisting freely, and coexisting but separated by a physical barrier that allowed only the passage of zooplankton, enabling assessment of resource competition without direct contact.

Our study reveals that *G. holbrooki* significantly impacts *Aphanius* populations through a complex interaction of interspecific effects, including resource competition, agonistic behavior, and predation. These findings were consistent for both *A. baeticus* and *A. iberus*, suggesting that *G. holbrooki* represents a widespread and analogous threat. These findings underscore the urgent need for targeted management aimed at mitigating the negative impact of invasive mosquitofish on toothcarp populations, especially since *G. holbrooki* has been detected at all known extant sites of *A. baeticus* and *A. iberus*. Given the multifaceted pressures exerted by invasive mosquitofish, its continued presence poses a significant threat to the viability of these two endemic and endangered species. Implementing effective conservation strategies for invasive species management is therefore essential to safeguard the remaining populations of *A. baeticus* and *A. iberus*, and to ensure their long-term persistence within their native habitats.

Spatio-temporal metabarcoding surveys in ports reveal homogenised communities with high genetic diversity of non-indigenous species

^{1*}Zarcero, Jesús, ¹Antich, Adrià, ²Fernández-Tejedor, Margarita, ³Palacin, Cruz, ³Wangensteen, Owen S., ¹Rius, Marc & ¹Turon, Xavier

*lead presenter: jzarcero@ceab.csic.es

¹ Department of Marine Ecology, Centre for Advanced Studies of Blanes (CEAB), CSIC, 17300 Blanes, Catalonia, Spain

² Institute of Agrifood Research and Technology (IRTA), La Ràpita, Catalonia, Spain

³ Department of Evolutionary Biology, Ecology and Environmental Sciences and Biodiversity Research Institute (IRBio), University of Barcelona, 08028 Barcelona, Catalonia, Spain

Large commercial ports introduce non-indigenous species (NIS), while smaller harbours and marinas facilitate their regional spread. Despite extensive research, genetic connectivity among harbour communities has not been assessed at the whole-community level. This study investigated metazoan communities over one year across four medium-sized harbours in the NW Mediterranean. Using COI metabarcoding, we identified 1,800 metazoan molecular operational taxonomic units (MOTUs), including 85 NIS via a custom Mediterranean NIS database. Harbours exhibited lower species richness, yet NIS comprised 34–75% of relative abundance. The southernmost harbour showed the highest NIS abundance, likely influenced by nearby aquaculture. While overall community structure varied among harbours, NIS were more homogeneous, sharing more MOTUs across sites. Notably, NIS also displayed higher haplotype diversity and lower genetic differentiation than native species, suggesting more effective regional dispersal via local boating. These results highlight distinct NIS dynamics in artificial environments and emphasize the importance of continued monitoring to manage coastal NIS spread.

Genomic monitoring of biodiversity in the Canary Islands

¹López Delgado, Julia, ¹Zurita Pérez, Nieves, ¹Arechavaleta Hernández, Manuel & ¹Delgado Lu-zardo, Asunción.

**lead presenter*

¹*Servicio de Biodiversidad, Gobierno de Canarias, España*

We present a new strategy for the genomic monitoring of biodiversity in the Canary Islands, designed to integrate molecular data into existing biodiversity assessment frameworks and conservation policy. The strategy combines genetic indicators and genomic studies to provide complementary and distinct information for guiding biodiversity management.

Genetic indicators, derived from non-genetic datasets such as ecological studies, enable large-scale and rapid evaluations of genetic diversity status and trends when molecular data are unavailable. These indicators support policymakers in prioritising management actions and identifying key populations in need of further investigation. In parallel, genomic data provide detailed information about conservation status, including population differentiation or barriers to gene flow, demographic patterns, inbreeding, hybridisation, genetic load, and adaptive potential. Together, these approaches offer a comprehensive framework for species and ecosystem management.

The strategy builds upon established infrastructures in the archipelago, including the Natural Inventory Bank (BIOCAN) and the Biodiversity Bank (BIOTA), and introduces a new molecular data platform to connect ecological and genomic datasets. In addition, the establishment of a consortium will consolidate a collaborative network among stakeholders and partners for the integration of biodiversity genomics with policy and practitioner needs. Collectively, these efforts harness recent advances in genomics and biotechnology to ensure long-term monitoring and conservation of the Canary Islands' unique biota.

How many samples do I need to take for community studies?

¹*Martinez Arbizu, Pedro

*lead presenter: pmartinez@senckenberg.de

¹ Senckenberg am Meer, Germany

The number of samples (replicates) taken and analyzed in ecological studies is rarely based on statistical principles but constrained by the available time and budget. Optimizing resources is crucial, but the number of replicates should still be enough to be able to detect the differences under studied. Reducing the number of replicates may result in loss of statistical power. In other words, reducing the number of samples reduces the probability of finding a difference (effect) that really exists. Statistical power is not only dependent on the number of replicates, but also on the magnitude of the difference (effect size) and the variance of the data (standard deviation of the observed distributions). Rawly speaking, the greater the difference and smaller the variance the less replicates will be necessary to guarantee statistical power.

Statistical significance is mostly based on the probability that two (or more) datasets belong to the same distribution or on the probability that the observed differences between datasets can be due to chance. Biological communities, having as attributes species composition and their abundances are multivariate in nature. It is common to compare multivariate communities by using synoptic values derived from similarity or distance indices. To my knowledge there is no established method to assess statistical power in biological community studies.

PERMANOVA has become a standard tool to assess the significance of observed community differences. In PERMANOVA the similarity between the replicates belonging to same groups is compared to the similarities to the members of foreign groups to calculate a ratio called F-value. In a second step, the labels of the group-memberships are shuffled by chance, and the resulting F-value is recorded during several permutations to produce an empirical null distribution of meaningless random F-values. The probability that the observed (true) difference could be reproduced by random shuffling is used to determine statistical significance.

In this talk I present a method to determine the statistical power of PERMANOVA (adonis in R) by rarefying the replicates of the groups and observing the behavior of the resulting F-values across multiple permutations. The F-value is used as effect size and knowing the variance of its distribution allows to calculate the statistical power. Finally, knowing the power and effect size allows us to estimate the number of replicates needed to achieve a desired significance level.

The method is as versatile as PERMANOVA itself and can be applied to any quantitative or binary similarity/distance index like Bray-Curtis, Jaccard, Hellinger etc.

Results of simulations are presented as well as some examples with true field macrofauna data.

Tracking marine invasive species with marine sponges, possibilities and future directions

^{1*}Gallego, Ramón, ²Corral-Lou, Andrea, ³Ramón-Laca, Ana, ³Alcaraz, Lourdes, ³Taboada, Sergi, ⁴Lanna, Emilio, ⁴Cavalcanti, Fernanda & ³Riesgo Gil, Ana

*lead presenter: ramon.gallego@uam.es

¹ Universidad Autónoma de Madrid, Spain

² Interdisciplinary Centre of Marine and Environmental Research, Portugal

³ Museo Nacional de Ciencias Naturales, Spain

⁴ Federal University of Bahia, Brazil

The early detection of marine non-indigenous species (NIS) is a critical step for marine conservation and biosecurity. Human-mediated transport remains the primary vector for the introduction of NIS, with ports acting as major gateways for the arrival and potential establishment of new taxa (Aglieri et al., 2023; Tempesti et al., 2020). Innovative molecular approaches are increasingly required to monitor these environments effectively and at scale.

Here we aim to detect NIS with the application of environmental DNA from natural samplers (nsDNA). With this technique, we use small pieces of tissue from filter feeders (phylum Porifera) and apply metabarcoding sequencing of the Cytochrome Oxidase Subunit I (COI) gene (Leray, 2013) to obtain a list of species detected in 17 ports from six countries, using 14 different sponge taxa as accumulators.

The potential for detection of multiple species is hampered by two main factors: the affinity of the primers to the host species, and the proportion of target DNA of NIS origin. Our analysis offers clues for optimizing this protocol, pointing at the most advantageous host for increased nsDNA detection.

Bridging Scales in Plant-Animal Interactions: Integrating Citizen Science with Field Data in the Pyrenees

¹*Platania, Leonardo, ¹Pérez-Lorenzo, Iván, , ²Palazzesi, Luis, & ¹Hidalgo Oriane

*lead presenter: leonardo.platania@gmail.com

¹ Institut Botànic de Barcelona (CSIC-CMCNB), Catalonia, Spain.

² Museo Argentino de Ciencias Naturales, CONICET, División paleobotánica, Buenos Aires, Argentina.

Plant-animal interactions are one of the most common examples of interdependence in biological communities and represent a fundamental pillar of ecological systems. In the Mediterranean, invertebrates mediate most interactions, including pollination, herbivory, seed predation and seed dispersal, among others. The complexity of the phenomenon and the large number of taxa involved make its understanding challenging, requiring a balance between rigour and scale that constrains the studies in terms of time and space. Conversely, wide-scale studies are usually dependent on literature-derived data, which in many cases have incomplete, outdated, anecdotal, or taxonomically heterogeneous information. In addition, low attention has been paid to the plant perspective, especially the influence of interactions on their reproductive biology. Citizen science platforms can help address these gaps by providing large volumes of spatially and temporally informed observations over extended periods and across various spatial scales. Focusing on Asteraceae (Compositae), a megadiverse family of plants with worldwide distribution across environmental gradients, we assembled a curated dataset of plant–animal interactions in the Pyrenees by combining records from iNaturalist with targeted field observations and sampling.

At this stage of the ongoing study, which has so far yielded over 12,000 curated observations, we present a synthesis of preliminary results, focusing on their relevance for two potential applications: (1) building a reference list of invertebrate species to support the training of AI-based identification tools, and (2) developing plant–animal interaction networks. We describe the dataset's structure and taxonomic coverage, assess systematic biases and identification uncertainty, and discuss the types of questions it enables. We finally compare citizen science data with and without the observations collected during our fieldwork at monitored stations, to evaluate the added value of expert input. We argue that integrating reviewed citizen-science records with targeted field studies provides an efficient and scalable pathway for biodiversity monitoring and for plant-centred analyses of interaction networks across local to regional scales.

Increased fish detection sensitivity with environmental RNA

^{1,2*}Ramón-Laca, Ana, ³Gallego, Ramón, ¹Duque, Carmen, ¹Doadrio, Ignacio ⁴Parsons, Kim M.,
⁴Nichols, Krista M., ⁴Engster, Samantha, ⁴Wells, Abigail, & ¹Riesgo, Ana

*lead presenter: analaca@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales - CSIC, Spain

² Escuela de Doctorado, Universidad Autónoma de Madrid, Spain

³ Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain

⁴ Northwestern Fisheries Science Center, National Marine Fisheries Service (NOAA), United States

Environmental RNA (eRNA), the traces of RNA from the living organisms shed in an environment, can potentially augment or add to the biological monitoring ability of the established environmental DNA (eDNA) applications in conservation. Environmental RNA offers unique advantages: it can differentiate living from deceased organisms, potentially yield insights regarding physiological conditions via gene transcription, and potentially offer higher detection sensitivity due to its inherent amplified nature for certain genes depending on the physiology and the environmental conditions despite faster degradation.

This study focused on the attainability and sensitivity of eRNA for detecting fish in real-life environments: an endangered freshwater fish in a seasonal stream throughout the year and a pelagic fish of commercial interest in the ocean. We developed field sampling and laboratory protocols for eRNA preservation and extraction, addressing the challenges of its natural instability and making its use achievable. We compared the detection sensitivity of eDNA and eRNA using species-specific digital PCR (dPCR) assays targeting mitochondrial cytochrome b and 12S ribosomal RNA genes, which are messenger RNA (mRNA) and ribosomal RNA (rRNA), respectively.

The results showed consistent higher concentrations of rRNA compared to mRNA, suggesting their superior utility for detecting low-abundance organisms while providing information regarding the expected amounts of mRNA genes for the basic cellular pathway. Importantly, in the freshwater system, the eRNA and eDNA concentrations followed the same trend, which was consistent with the varying hydrological conditions.

These results highlight the importance of marker choice in eRNA studies. This research provides insights into sampling strategies and molecular targets for eRNA-based biomonitoring, demonstrating its potential to improve the detection of endangered species and inform conservation efforts by providing a more accurate snapshot of extant biological communities.



EVOLUTIONARY BIOLOGY

Independent genomic trajectories shape adaptation to life on land across animal lineages

^{1,2*}Martínez-Redondo, Gemma I., ^{1*}Eleftheriadi, Klara, ¹Salces-Ortiz, Judit, Escudero, ¹Nuria, ^{3,4}Fernández-Álvarez, Fernando Ángel, ¹Carbonetto, Belén, ¹Vargas-Chávez, Carlos, ¹García-Vernet, Raquel, ^{1,5}Palma-Guerrero, Javier, ¹Rentería, Libe, ⁶Rojo, Iñaki, ^{7,8}Chiva, Cristina, ^{7,8}Sabidó, Eduard, ⁹Bombarely, Aureliano & ¹Fernández, Rosa

**lead presenters:* gemma.martinez@ibe.upf-csic.es, klara.eleftheriadi@ibe.upf-csic.es

¹ Metazoa Phylogenomics and Genome Evolution Lab, Institute of Evolutionary Biology (CSIC-UPF), Barcelona (Spain)

² Universitat de Barcelona, Barcelona (Spain)

³ Centro Oceanográfico de Gijón, Instituto Español de Oceanografía, Gijón (Spain)

⁴ Institut de Ciències del Mar (ICM-CSIC), Barcelona (Spain)

⁵ Current address: Research Institute of Organic Agriculture (FiBL), Aargau (Switzerland)

⁶ Citizen scientist, Sopelana (Spain)

⁷ Centre for Genomic Regulation (CRG), Barcelona Institute of Science and Technology (BIST), Barcelona (Spain)

⁸ Universitat Pompeu Fabra (UPF), Barcelona (Spain)

⁹ Instituto de Biología Molecular y Celular de Plantas, Valencia (Spain)

How animals repeatedly adapted to life on land is a central question in evolutionary biology. While terrestrialisation occurred independently across animal phyla, it remains unclear whether shared genomic mechanisms underlie these transitions. We combined large-scale comparative genomics, machine learning, and multi-omics data—including proteomics and transcriptomics from stress experiments in 17 species—to investigate the genomic basis of terrestrial adaptation. Gene co-expression networks revealed that stress-response hubs were largely lineage-specific, yet converged in function through the co-option of ancient gene families. Phylogenomic and machine learning analyses supported a dominant role for early-evolving genes, enriched in stress-related functions, with extensive gene loss at terrestrialisation nodes. Our findings support a model of functional convergence via lineage-specific repurposing of conserved genomic elements.

Evolution and diversity of venom-producing cells in ribbon worms

^{1*}Verdes, Aida, ²Álvarez-Campos, Patricia, ²del Olmo, Irene, ³Emili, Elena, ¹Koutsouveli, Vassiliki, ¹Cuesta-Martín, David, ⁵Solana, Jordi & ⁴Bermúdez-Díaz, Isabel

*lead presenter: aida.verdes@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales (MNCN-CSIC), Spain

² Universidad Autónoma de Madrid, Spain

³ University of Rome Tor Vergata, Italy

⁴ Oxford Brookes University, United Kingdom

⁵ University of Exeter, United Kingdom

Venoms are key evolutionary innovations that have convergently evolved in more than 100 lineages across the tree of life. Specialized venom glands and delivery systems have evolved from diverse developmental tissues across different venomous lineages, and thus venomous animals offer unique opportunities to examine the processes underlying the convergence of adaptive traits and the origin of novel genes, cells and organs. However, the diversity of toxin genes, venom producing cell types and tissues, as well as the genetic mechanisms underlying how venom systems originate and evolve is not well understood in most taxa.

Ribbon worms (phylum Nemertea) are a poorly known venomous lineage of active predators that use an eversible proboscis to inject toxins into prey and secrete an epidermal toxic mucus for defense. Nemerteans do not have distinct multicellular venom glands like snakes or spiders; instead, toxins are secreted by different types of glandular cells lining the body wall and the proboscis epithelia, making them an ideal system to study the cellular basis of venom production.

Here, we explore cell type diversity in the bootlace worm *Lineus longissimus* using a single-cell RNA sequencing (scRNA-seq) pipeline that combines ACME dissociation with the SPLiT-seq combinatorial cell barcoding protocol. Following this approach, we generated a comprehensive cell atlas with 37 distinct cell types, including toxin-producing cell populations. Within this atlas, we identified different secretory clusters with enriched expression of toxin-related transcripts, including toxin families that are conserved in other animal venoms (e.g., pore-forming proteins, neurotoxins, metalloproteases) as well as novel nemertean toxins. Differential expression analyses showed divergent transcriptional profiles between epidermal and proboscis secretory cells, suggesting tissue-specific functional specialization for defense and predation. Together, these results provide the first single-cell characterization of venom production in a nemertean, offering new insights into the cellular and molecular origins of venom systems.

The first chromosome-scale assemblies of *Dugesia* shed light on the genome size evolution in flatworms

^{1,2*}Daniel Dols-Serrate, ^{1,2}Ignacio Tenaguillo-Arriola, ^{1,2}Vadim A. Pisarenco, ^{1,2}Marta Olivé-Muñiz, ^{1,2}Julio Rozas & ^{1,2}Marta Riutort

*lead presenter: bcn27101993@gmail.com

¹ Departament de Genètica, Microbiologia i Estadística, Universitat de Barcelona. Avinguda Diagonal 643, 08028, Barcelona, Catalonia, Spain.

² Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Catalonia, Spain.

Genomes are an indispensable source of information for understanding the processes underpinning life on Earth. Knowing their sequences not only empowers scientific discovery for the focal species, but also related taxa. Planarian flatworms (Platyhelminthes, Tricladida) constitute a diverse taxonomic group comprising hundreds to thousands of species distributed globally that exhibit a broad spectrum of phenotypic diversity and have colonized terrestrial, marine, and freshwater environments. However, this wealth of diversity contrasts with the almost complete lack of genomic resources for this taxonomic group. Here, we present the chromosome-scale genome assemblies of *Dugesia etrusca*, *Dugesia hepta*, *Dugesia liguriensis* and *Dugesia xeropotamica*, which constitute the firsts of their kind for the longstanding genus of freshwater planarians, *Dugesia*. These new assemblies represent a significant improvement in contiguity, exceeding 200 times the level achieved by the single available genome of the genus up to the present day, which is that of the model species *Dugesia japonica*. We performed macrosynteny comparative analyses among our chromosome-scale genomes and that of *Schmidtea mediterranea*, that belongs to *Dugesia*'s sister genus. We found a substantial lack of synteny conservation between both genera. Furthermore, our analyses revealed an expansion of DNA transposable elements in *Dugesia* not present in *Schmidtea*, and discarded the hypothesis of a whole-genome duplication as the underlying cause for the differences in genome size between both genera. In addition, our analyses shed light on the chromosomal rearrangements underlying the uncommon chromosomal complement of *D. hepta* ($n = 7$), unique among its Western Palearctic congeners, wherein $n = 8$ is the most prevalent chromosomal complement.

Comparative genomics of conotoxin gene organization in cone snails

¹Herráez-Pérez, Ana, ¹Pardos-Blas, José Ramón, ²Jiménez Tenorio, Manuel & ¹Zardoya, Rafa

*lead presenter: anaherraez.p@gmail.com

¹ Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales (MNCN-CSIC), José Gutiérrez Abascal 2, 28006 Madrid, Spain.

² Departamento CMIM y Q. Inorgánica-INBIO, Facultad de Ciencias, Universidad de Cádiz, 11510 Puerto Real, Cádiz, Spain.

Cone snails (Caenogastropoda: Conidae) are predatory venomous marine snails with more than 900 described species distributed across tropical and subtropical seas. They produce complex venoms composed of hundreds of short peptides, named conotoxins, which they use for predation and defense. Conotoxins represent not only valuable tools for neuroscience and drug discovery, but also an exceptional model for investigating evolutionary mechanisms of molecular diversification.

Here, we present the first comparative genomic analysis of conotoxin gene organization (synteny) in the only two available high-quality cone snail genomes, *Kalloconus canariensis* and *Lautoconus ventricosus*. We identified a total of 233 conotoxin genes in *L. ventricosus* and 154 in *K. canariensis*, of which 109 are orthologous between the two species (identity >80%). Among these orthologs, 94 are located in homologous chromosomes, while 15 are found in different chromosomes in each species. In addition, we investigated syntenic regions surrounding conotoxin genes present in one species but absent in the other, using ± 200 kb windows and defining synteny as identity >80% and coverage >50%. Most of these regions were found in homologous chromosomes; however, in a few cases syntenic regions mapped to non-homologous chromosomes, suggesting chromosomal rearrangements.

These results reveal both gene-level and chromosome-level evolutionary dynamics shaping conotoxin gene repertoires, providing new insights into the origin and diversification of cone snail venoms.

Conserved and lineage-specific mechanisms underlying regeneration in the annelid *Ophryotrocha labronica*

^{1*}Del Olmo, Irene, ²Herranz, María, ³Worsaae, Katrine, ⁴Verdes, Aida, & ¹Álvarez-Campos, Patricia

*lead presenter: irene.olmo@uam.es

¹ Department of Biology (Zoology), Universidad Autónoma de Madrid, Spain

² Department of Biology and Geology, Physics and Inorganic Chemistry, Universidad Rey Juan Carlos, Madrid, Spain

³ Marine Biological Section, Department of Biology, University of Copenhagen, Universitetsparken 4, 2100 Copenhagen, Denmark

⁴ Department of Biodiversity and Evolutionary Biology, Museo Nacional de Ciencias Naturales de Madrid, Spain.

Regeneration, understood as the ability to replace or restore lost body parts, is a widespread post-embryonic phenomenon across metazoans. Specifically, annelids or segmented worms represent a remarkable group for investigating this process, as they show extensive and variable regenerative abilities. Although both anterior and posterior regeneration are considered ancestral traits in annelids, the extent of this capacity varies greatly across lineages, and most have lost the ability to restore anterior segments.

Molecular and developmental studies of annelid regeneration have rocketed in recent years, paving the way for comparative studies of the molecular basis underlying regeneration. However, our understanding of how these processes evolved throughout annelid evolutionary history and the factors driving this regenerative capacity remains incomplete.

In this work, we investigate posterior regeneration in the dorvilleid annelid *Ophryotrocha labronica* La Greca & Bacci, 1962, by integrating morphological staging with transcriptomic analysis. We define four distinct morphological phases of posterior regeneration, spanning from wound healing to the re-establishment of the posterior growth zone within five days. Using acetylated α -tubulin immunoreactivity, we also describe the general neuroanatomy and provide a detailed characterization of nerve regeneration. We further assess cell proliferation dynamics via 5-ethynyl-2'-deoxyuridine (EdU) labelling, revealing intense cell division during blastema development. Finally, through bulk RNA sequencing we identify stage-specific transcriptional profiles driving each phase of regeneration. While several genes are reported here for the first time, others belong to a conserved set of regeneration-associated genes shared among annelids and other metazoans with varying regenerative capacities.

Our results highlight both the novelty and the conservation of regenerative mechanisms in annelids, pointing to evolutionary convergence in core molecular pathways but also lineage-specific mechanisms underlying this fundamental biological process.

Evolutionary consequences of hybridisation: genomic evidence of hybrid speciation in insular beetles

^{1,2*}Noguerales, Víctor, ¹Eisele, Marius, ¹Andújar, Carmelo & ¹Emerson, Brent.

* lead presenter: victornoguerales@gmail.com

¹ Instituto de Productos Naturales y Agrobiología, Tenerife, Islas Canarias, España

² Current address: Universidad de la Laguna, Tenerife, Islas Canarias, España

Our view of the role of hybridisation in speciation dynamics is being revolutionized with the increasing availability of genome-wide data from non-model organisms and their integration into approaches combining population genetic and phylogenomic tools. Gene flow among species has historically been viewed as a mere inhibitor of genomic divergence, through its homogenising effect on gene pools, but has been documented more recently as a driver of a number of creative evolutionary outcomes. These may range from the allele exchange across species boundaries (*i.e.* introgression), potentially facilitating the acquisition of adaptive traits, to the recombination of differentiated genomes leading to the formation of new species (*i.e.* hybrid speciation). While introgression has been found to be frequent across numerous organismal groups, hybrid speciation is thought to be relatively rare in nature. However, its actual importance may be artificially underestimated due to the strict criteria to define a hybrid species, according to some authors.

Beyond the controversial definition of a hybrid species, a major challenge in hybrid speciation is to understand the mode, pace, and geographical context in which recombinant populations can establish initial reproductive barriers against parental species (*i.e.* escaping from the homogenising effects of gene flow with their sympatric progenitors). In this work, we present a case of hybrid speciation in a hidden snout weevil (Coleoptera: Cryptorhynchinae) endemic to the Canary Island of Tenerife, within which the hybrid lineage and both parental species are sympatrically distributed in a geographically limited cloud forest formation. Here, we first assessed the species boundaries within the target species and identified that the previously recorded single taxon is actually composed of three cryptic species, with well-segregated nuclear genomes. Further analyses provide unequivocal support for an ancestral divergence event leading to the formation of two species, followed by the hybridization event between these two parental species, from which the third species was derived. We discuss the spatio-temporal dynamics of species ranges within the focal habitat, and their potential for these to have catalysed these speciation events. We argue for a hybrid speciation model where the interplay of geographical isolation and genetic drift within an early-stage hybrid swarm may promote a pathway for reproductive isolation to evolve against parental forms.

Functional specialization and lineage-specificity shape the evolution of ribbon worm venoms

^{1,2*}Andrés, Elena, ² Muñoz-Santiago, José, ¹ Koutsouveli, Vassiliki, ¹ Verdes, Aida

*lead presenter: elena.andres@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales, Spain

² Universidad de Alcalá, Spain

Ribbon worms (Nemertea) are understudied active predators that employ an eversible proboscis to inject toxins into their prey and ecrete a toxic epidermal mucus for defense. There are three main lineages of ribbon worms—Hoplonemertea, Palaeonemertea, and Pilidiophora—characterized by differences in the proboscis morphology, hunting strategies, and dietary niches. Previous studies have identified lineage-specific toxins, suggesting that venom evolution in nemerteans is highly divergent and may be associated with different ecological and functional pressures. Here, we explore toxin diversity and venom evolution across the phylum, characterizing the predatory and defensive cocktails of 14 species representing all major nemertean clades. We used RNA-seq-based differential gene expression analyses to investigate toxin gene diversity and expression patterns in the proboscis and epidermis, the two main toxin-producing tissues.

Our analyses reveal that both tissues produce compositionally distinct venoms, highlighting clear functional specialization between predation and defense. The proboscis toxins show functions related to paralysis and digestion, whereas epidermal toxins included compounds potentially involved in pain and defense mechanisms. Our results also reveal lineage-specific differences in toxin composition, with particular toxins restricted to different lineages. We further explored venom composition and lineage-specificity across the phylum by searching for homologs of the putative defensive and predatory toxins in the transcriptomes 16 of additional species. We used OrthoFinder, which allowed us to delineate lineage-specific toxin sets and classify them into functional groups, potentially reflecting functional convergence or specialization. This comparative framework allowed us to detect patterns of diversification across the phylogeny and functional partitioning between predatory and defensive ribbon worm venoms.

This study provides the first large-scale comparative analysis of venom composition in nemerteans, integrating transcriptomic and phylogenomic approaches to shed light into how lineage history and functional specialization shape the evolution of animal venoms.

FANTASIA: user-friendly pipeline based on Natural Language Processing models illuminates the dark proteome across the Eukaryote Tree of Life

^{1*}Belén Carbonetto, ¹Gemma I. Martínez-Redondo, ²Francisco M. Perez-Canales, ²Ildefonso Cases, ³Iñigo de Martín-Agirre, ^{3*}Aureliano Bombarely, ²⁺Ana M. Rojas & ¹⁺Rosa Fernández

*lead presenter: belen.carbonetto.metazomics@gmail.com

¹ Metazoa Phylogenomics and Genome Evolution Lab, Institute of Evolutionary Biology (CSIC-UPF), Passeig marítim de la Barceloneta 37-49, 08003 Barcelona, Spain.

² Computational Biology and Bioinformatics, Andalusian Center for Developmental Biology (CABD-CSIC), 41013 Sevilla, Spain.

³ Bioinformatics and Evolutionary Genomics, Institute of Molecular and Cellular Biology of Plants (CSIC-UPV), Valencia, Spain

+ Co-senior authors

Protein functional annotation is crucial in biology, but many protein-coding genes remain uncharacterized, especially in non-model organisms. Traditional annotation methods primarily rely on function transference via sequence similarity, which limits their effectiveness for annotating highly divergent or fast-evolving proteins. Many genes remain undetected or uncharacterized due to rapid evolution, orphan status, or intrinsic disorder, making their functional classification particularly challenging. Incomplete or inaccurate functional annotations can lead to biased biological interpretations, impairing enrichment analyses, network inference, and comparative genomics. More importantly, poorly characterized genes may also be linked to important evolutionary innovations, and their omission from analyses can result in incomplete or misleading models of evolutionary change. This highlights the imperative necessity of novel methodologies able to unlock the ‘hidden biology’ behind these genes. In order to tackle this, we present FANTASIA (Functional ANnoTation based on embedding space SImilarity) a user-friendly pipeline which integrates protein language models (pLMS) and embedding similarity for large-scale functional annotation ready for downstream functional genomics and comparative genomics analyses. Applied to ~1,000 animal proteomes, FANTASIA predicted functions to virtually all proteins, including up to 50% that remained unannotated by traditional homology-based methods. We will show how the tool is performing equally well in diverse lineages such as plants and apicomplexan protists, highlighting its potential to shed light on the ‘dark proteome’ across the Eukaryote Tree of Life. For example, the annotation of 200 plant proteomes delivered 100% of proteins annotated and important differential functional patterns were observed for each plant lineage. We will also showcase the new options implemented in FANTASIA v3, including the ability to control the lookup-table for benchmarking, and choice of different protein language models and two distance metrics if a direct comparison between model performance is desired. All in all, FANTASIA holds great promise for functional discovery in non-model organisms, offering advantages over homology-based tools in sensitivity and generalizability. FANTASIA is open access and available at <https://github.com/CBBIO/FANTASIA>.

Evolution for Everyone: Integrating Palaeontology, DNA, and Ecosystems in the Casa de la Ciencia Sevilla (CSIC) Science Outreach Centre

¹*Inshyna, Valentyna, Pérez Gutiérrez, ¹Clara Elena, ¹Ferreira Palomo, Ismael

*lead presenter: valentyna.inshyna@csic.es

¹ Delegation of the Spanish National Research Council (CSIC) in Andalusia, Spain

Understanding evolutionary biology is essential for developing scientific literacy and equipping societies to confront biodiversity loss and environmental change. In Spain, as elsewhere, education in evolution is strengthened by complementary initiatives beyond formal schooling that engage learners of all ages and backgrounds. Through close collaboration with researchers, science outreach centres broaden the reach of scientific knowledge and make it accessible to wider audiences.

At the Casa de la Ciencia in Seville, a leading science outreach centre, a wide programme of workshops is offered to schools and the general public, engaging participants from preschool to adults. Between 1 October 2024 and 8 July 2025, approximately 15,000 people from 340 educational centres – including preschools, primary and secondary schools, adult education centres, vocational schools, universities, and special education classrooms – participated in these activities. Within this framework, a set of workshops focuses specifically on evolution, using fossils, trait-based analysis, ecological networks, and simulations of DNA and molecular methods to make evolutionary mechanisms tangible and accessible to learners of all ages.

The activities are organized into four thematic areas. Fossils, palaeontology, and deep time cover macroevolution, extinction, and geological change. Anatomy, traits, and adaptation explore convergent evolution, morphological innovation, coloration, and arthropod diversification. Development, DNA, and variation address Evo-Devo, genetic control of form, ecological networks, and diet reconstruction. Finally, dispersal, interactions, and ecosystems examine coevolution, seed dispersal, endemic species, and rapid anthropogenic selection.

This work demonstrates the value of integrating research expertise with educational practice. By combining scientific accuracy with innovative outreach methods – such as games, simulations, reconstructions, and 3D models – and incorporating real data provided by scientists, including field samples, videos, and other research materials, the programme makes evolutionary concepts tangible and engaging for diverse audiences. These approaches extend the reach of evolutionary biology beyond traditional classrooms, foster lifelong learning, and strengthen public engagement with science in Spain and beyond, highlighting the importance of sustained collaboration between scientists and outreach centres.

Transcriptomic insights into early developmental stages of a marine gastropod

¹Paula Moreno-Martín, ²Ana Herráez-Pérez, ¹Patricia Álvarez-Campos, ¹Cristina Grande, & ²Rafael Zardoya

*lead presenters: paula.moreno@uam.es; paula.moreno@uam.es; patricia.alvarez@uam.es; cristina.grande@uam.es; rafaz@mncn.csic.es; ana.herraez@mncn.es

¹ Centro de Investigación en Biodiversidad y Cambio global (CIBC-UAM), Departamento de Biología (Zoología), Facultad de Ciencias, Universidad Autónoma de Madrid, Spain.

² Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales de Madrid, Consejo Superior de Investigaciones Científicas, MNCN-CSIC, Spain.

Venomous snails are a fascinating group of marine gastropods in which developmental studies can shed light on evolutionary trajectories and the origin of complex adaptations such as toxin production. *Conus guanche*, a species endemic to the Canary Islands and the adjacent Northwest African coasts, is one such example. Like other marine gastropods, it passes through a typical sequence of embryonic stages before reaching a free-swimming larval stage, during which key regulatory genes guide body asymmetry and organ formation. At the same time, the species develops the ability to produce a diverse venom repertoire that supports prey capture and defense.

To explore the molecular basis of early development, we performed RNA sequencing across five stages—cleavage, blastula, gastrula, organogenesis, and larva. Biological replicates from each stage were used to generate a de novo transcriptome assembly, followed by differential expression analyses. Pairwise comparisons identified sets of transcripts with stage-specific regulation, which were then annotated against the SwissProt database and the genome of the closely related *Lautoconus ventricosus*. Special focus was placed on genes involved in left–right asymmetry, including *Nodal*, *Inversin*, and *BMP2/4*, whose expression patterns were examined across development. In parallel, candidate toxin-related genes were analyzed to investigate possible links between developmental processes and venom evolution.

Overall, this study provides one of the first transcriptomic resources for a non-model marine gastropod, offering new insights into the genetic regulation of early development and the diversification of venom systems.

Chemosensory gene family diversity and evolution in red devil *Dysdera* spiders

^{1,2}*Pisarenco, Vadim A., ^{1,2}Olivé-Muñiz, Marta, ^{1,2}Sánchez-Gracia, Alejandro, ^{1,2}Guirao-Rico, Sara and ^{1,2}Rozas, Julio

*lead presenter: v.pisarenco@ub.edu

¹ Departament de Genètica, Microbiologia i Estadística, Universitat de Barcelona, Barcelona, Spain.

² Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Barcelona, Spain.

Advances in sequencing technologies have enabled the generation of high-quality genome assemblies, opening new opportunities to address previously unfeasible evolutionary questions. In this study, we studied the major chemosensory (CS) gene families (ionotropic and gustatory receptors) in genome assemblies of *Dysdera* spiders. Our work is set within the context of the recent discovery of a pronounced genome size reduction (GSR) in Canary Island species, while still preserving a conserved macrosynteny with their continental relatives. We comprehensively characterised the gene family size and the genomic organisation of the main chemoreceptor gene families in six *Dysdera* genome assemblies.

Our analyses revealed the following key findings: (i) Continental species harbour larger CS repertoire, organised in larger genomic clusters (up to 125 genes and spanning ~24 Mb) in comparison with insular species; (ii) The X chromosome consistently harbours fewer CS genes, which are minimally clustered; (iii) A considerable fraction of members are classified as partial and/or included in minor scaffolds; (iv) The phylogenetic analysis reveals that chromosomal clustering reflects evolutionary relatedness, indicating a strong link between a gene's physical location and its phylogenetic history. Our findings suggest that these gene families originated through duplication by unequal crossing-over, and their subsequent evolution is consistent with a birth-and-death model. Overall, our results reveal a drastic reduction in the size of the CS gene families in the Canary Island *Dysdera* species, likely associated with GSR. The study also stresses the importance of the use of standardised methods for the annotation of multigene families, and demonstrates the utility of reference-guided scaffolding strategy for comparative genomic studies.

Adaptive Radiation and Trophic Specialization in *Dysdera* Spiders: A Genomic Perspective

^{1,2*}Olivé-Muñiz, Marta, ^{1,2}García-Juan, Silvia, ^{1,2,3}Escuer, Paula, ^{1,2}Pisarenco, Vadim A., ⁴Macías-Hernández, Nuria, ^{2,5}Arnedo, Miquel A., ^{1,2}Sánchez-Gracia, Alejandro, ^{1,2}Guirao-Rico, Sara and ^{1,2}Rozas, Julio

*lead presenter: molive@ub.edu

¹ Departament de Genètica, Microbiologia i Estadística, Universitat de Barcelona, Barcelona, Spain.

² Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Barcelona, Spain.

³ Institute of Biology, University of Neuchâtel, Neuchâtel, Switzerland.

⁴ Departamento de Biología Animal, Edafología y Geología, Universidad de La Laguna (Tenerife), Canary Islands, Spain.

⁵ Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Universitat de Barcelona, Barcelona, Spain.

Island radiations provide a powerful framework to study the molecular basis of adaptation, with archipelagos offering multiple independent evolutionary replicates to test for molecular parallelism behind convergent phenotypes. Here, we study the remarkable diversification of the *Dysdera* red devil spiders in the Canary Islands. This radiation has involved dietary shifts, including morphological, metabolic and behavioural specialisations for feeding on woodlice (Isopoda), which bioaccumulate exceptionally high concentrations of heavy metals from the soil. Hence, these endemic spiders represent an excellent model for investigating the evolutionary drivers and genomic factors underlying dietary convergence and adaptive radiations.

Here, we investigate the genomic basis of this dietary specialisation at short- and mid-term evolutionary timescales integrating population and comparative genomics data. In particular, we generated high-quality chromosome-level genome-assemblies and performed low-coverage whole-genome resequencing of multiple individuals from natural populations of five endemic *Dysdera* species from the Canary Islands. The species were selected to represent two independent shifts of dietary specialisation, each occurring in distinct evolutionary and geographic contexts. Our analyses identified candidate genes under distinctive selective constraints in specialist lineages, including genes associated with detoxification and homeostasis. Notably, specialist species exhibit a twofold increase in gene death rates, suggesting accelerated gene loss related to stenophagy. We also detected exceptionally high levels of nucleotide diversity reflecting historical large effective population sizes, and identified genomic signatures of recent selective sweeps, uncovering potential targets of adaptive evolution. Together, these findings reveal key genomic changes associated with dietary specialization, contributing to our understanding of diversification in island radiations.

Sex Chromosomes and Polygenic Sex Determination Systems in Sponges

¹Lorente-Sorolla, Jose, ¹Verdes, Aida, ¹de Sosa, Irene, ¹Galiá-Camps, Carles, ¹Tonzo, Vanina, ¹Turon, Marta, ²Rossi, Eleonora, ¹Conejero, María, ¹Koutsouveli, Vasiliki, ³Leiva, Carlos, ⁴Díez-Vives, Cristina, ⁵Álvarez-Presas, Marta, ⁶Grau-Bové, Xavier, ⁷Hermoso, Juan Antonio, ⁸El Hilali, Sami, ¹Taboada, Sergi, ⁹Álvarez-Campos, Patricia, ¹⁰Alison Wright, & ^{1*}Riesgo, Ana

*lead presenter: anariesgogil@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales (CSIC), Spain

² University of Galway, Ireland

³ Estación Biológica Doñana (CSIC), Spain

⁴ Centro Nacional de Biotecnología (CSIC), Spain

⁵ Universitat de Barcelona, Spain

⁶ Centre for Genomic Regulation (CRG), Spain

⁷ Instituto de Química-Física Blas Cabrera (CSIC), Spain

⁸ Ludwig-Maximilians-Universität, Germany

⁹ Universidad Autónoma de Madrid, Spain

¹⁰ University of Sheffield, United Kingdom

Sex is a widespread biological feature that provides advantages at multiple evolutionary levels. In animals, sex determination can be either genetic (GSD) or environmental (ESD), with a wide variety of mechanisms described across metazoans. However, the mechanisms of sex determination of most metazoans are not discovered yet, especially those of early-splitting lineages, like sponges. Due to the remarkable diversity and plasticity of sexual reproduction in sponges, it has long assumed that sex is environmentally determined. Here, we used whole genome sequencing, ddRADseq, and RNAseq to investigate sex determination systems in eight gonochoristic sponge species. We identified sex chromosomes in two species, as well as hundreds of genes with sex-specific loci across the different species surveyed, pointing to a polygenic system that was either XX/XY or ZZ/ZW. Interestingly, sex determination pathways appear to converge on a common set of genetic regulators involved in DNA repair, meiosis and gonad fate maintenance and transposable element control. Among the 2895 genes with sex loci detected across all species, only 65 were found in synteny, most of them those of *Chondrosia reniformis* located in the sex chromosome. Evolutionary analysis of sex-related genes revealed that most have ancient origins, with many tracing back to early lineages such as cellular organisms and Eukaryota. Nonetheless, we found notable variation in species-specific sex genes, suggesting a combination of ancient retention and lineage-specific divergence in the evolution of sex-determining gene families. Our analysis reveals an ancient, conserved sex-determining molecular machinery that has been finely tuned in each species to produce female or male phenotypes.

Decoding Earthworms' Slumber: An Interdisciplinary Perspective at the Tissue Level

^{1*}Tilikj, Natasha, ²Conejero, María, ²Riesgo, Ana, ¹Fernandez Marchán, Daniel, ³Świątek, Piotr, ¹Díaz Cosín, Darío J & ¹Novo, Marta

*lead presenter: ntilikj@ucm.es

¹ Biodiversity, Ecology and Evolution Department, Faculty of Biological Sciences, Complutense University of Madrid, Madrid, Spain

² Department of Biodiversity and Evolutionary Biology, National Museum of Natural Sciences (CSIC), c/ José Gutiérrez Abascal 2, 28006 Madrid, Spain.

³ Institute of Biology, Biotechnology and Environmental Protection, Faculty of Natural Sciences, University of Silesia, ul. Jagiellońska 28, Katowice, Poland.

Earthworms are highly sensitive to climate change due to their dependence on stable environmental conditions which is essential for biodiversity conservation. RNA-Seq and DNA methylation analysis reveal how environmental stress shapes gene regulation and metabolism. *Carpetania matritensis* is an earthworm species endemic to central Spain and an ideal model for multiomics research, as it can survive desiccation for up to a year within its aestivation chamber.

DNA methylation and gene expression were profiled across six tissues: digestive, posterior segments, tegument, nephridia, nervous, and circulatory, enabling the capture of organ-specific regulatory dynamics. In earthworms most differential methylation events occurred at CpG sites, consistent with invertebrate methylation landscapes.

Transcriptomic analysis showed widespread downregulation of digestive processes and metabolic suppression, coupled with upregulation of genes linked to oxidative stress response, DNA repair, telomere maintenance, and cell cycle regulation. Notably, posterior segments and circulatory tissues displayed distinct methylation-driven remodeling signatures associated with regenerative processes. Nervous tissue analysis revealed differential expression of circadian rhythm and sleep-related genes, hypermethylation of genes involved in intracellular transport, and histological evidence of oxidative stress. In the nephridia of aestivating earthworms, differential expression analysis revealed downregulation hinted at reduced ion transport, which triggered hyperosmotic response pathways supported by increased heat shock protein expression and morphological changes in the basal folds. These processes may be regulated by methylation-linked G protein signaling.

These findings demonstrate the interplay between epigenetic modifications and transcriptional regulation during aestivation, advancing our understanding of invertebrate physiological plasticity and highlighting potential vulnerabilities and adaptive capacities under projected climate change scenarios.

Transcriptomic responses to dietary plasticity in the migratory painted lady butterfly (*Vanessa cardui*)

¹*Mara Vicelja, ¹Gemma Díaz, ¹Aurora García-Berro, ¹Javier Temes, ¹Gerard Talavera

*lead presenter: maravicelja@gmail.com

¹ Institut Botànic de Barcelona (IBB, CSIC), Spain

Dietary shifts shape the ecology and evolution of herbivorous insects, yet most species remain restricted to closely related host plants due to physiological constraints. In contrast, generalists such as the migratory painted lady butterfly (*Vanessa cardui*) feed on plants spanning multiple phylogenetic lineages. This extraordinary breadth raises key questions about how such insects overcome diverse plant defenses and nutritional challenges. For wide-ranging migrants encountering shifting plant communities along seasonal routes, dietary plasticity is crucial for survival and ecological success. Here, we investigated the transcriptional mechanisms enabling polyphagy in *V. cardui* by rearing larvae on 14 phylogenetically and chemically diverse host plants, combining RNA sequencing of gut tissues with larval performance metrics. Our analysis addressed two complementary scales: (1) an evolutionary scale, examining whether gene expression diverges more on novel hosts compared to ancestral hosts, and (2) an ecological scale, testing whether diet-induced gene expression differences correlate with larval performance. We found that host shifts trigger widespread transcriptional reprogramming, with hundreds of genes involved in digestion, detoxification, and stress responses differentially expressed across diets. On favorable hosts like *Silybum marianum* (Asteraceae) and *Echium vulgare* (Boraginaceae), larvae showed rapid development, high growth, and strong upregulation of digestive and nutrient storage genes. In contrast, on suboptimal hosts like *Centaurea dealbata* (Asteraceae) and *Forsskaolea tenacissima* (Urticaceae), larvae activated stress-response and gut-maintenance pathways, reflecting physiological adjustments to challenging diets. Strikingly, while some transcriptomic patterns reflected evolutionary history, others were shaped by host-specific chemical and nutritional properties. Across non-Asteraceae diets, common upregulation of lipid catabolism genes indicated a shared metabolic shift meeting energetic demands. Yet, most responses were host-specific, demonstrating a modular, flexible transcriptional toolkit. Our findings reveal that *V. cardui* balances evolutionarily conserved responses with host-specific plasticity, a dual strategy that likely underpins its ecological success as a migratory generalist across diverse and unpredictable environments.

Water vs. Land: Gene Battles in the Evolution of Arthropod Respiration via a scRNA Perspective

¹*Tatsis, Polychronis, ¹Salces, Judit, ²Solana, Jordi, ²Salamanca-Diaz, David, ¹Fernández, Rosa

*lead presenter: polychronis.tatsis@ibe.upf-csic.es

¹ Metazoa Phylogenomics & Genome Evolution Lab, IBE (Instituto de Biología Evolutiva), Spain

² Solana Lab, Living Systems Institute, University of Exeter, UK

The conquest of land represents one of the most dramatic evolutionary transitions, demanding for new solutions to the fundamental problem of breathing. Arthropods represent a striking case study: while grouped in the same phylum, they evolved highly dissimilar respiratory organs, from gills and book gills in aquatic animals to tracheae and book lungs in terrestrial ones. What remains unclear is whether these diverse morphologies are underpinned by conserved genetic programs or by lineage-specific innovations. To address this, I present the first single-cell RNA-sequencing (scRNA-seq) analyses of respiratory organs in three arthropods: a horseshoe crab (with book gills), a scorpion (with book lungs), and a terrestrial crab (with gills), focusing entirely on respiration. By resolving transcriptional profiles at single-cell resolution, this study seeks to identify the existence of shared and non-shared gene expression patterns in all the representative cell types of the respiratory organs under investigation. Beyond generating the first single-cell atlases of these non-model arthropods for the core function of respiration, this work aims to contribute to the understanding of the gene-level basis of a fundamental macroevolutionary transition: the shift from aquatic to terrestrial respiration.

An asexual scandal! Genomic consequences of long-term asexuality in freshwater planarians

¹*Tenaguillo-Arriola, Ignacio, ¹Riutort, M.

*lead presenter: itenaguillo6@ub.edu,

¹ Departament de Genètica, Microbiologia i Estadística and Institut de Recerca de la Biodiversitat (IRBio),
Universitat de Barcelona. Avinguda Diagonal 643, 08028, Barcelona, Catalonia, Spain

Long-term asexuality has been considered an evolutionary dead-end, due to reduced genetic diversity and weakened purifying selection, as deleterious mutations cannot be purged through recombination. As such, it is expected that asexual individuals from the same population should be clonal presenting low levels of genetic diversity and a loss of heterozygosity. Freshwater planarians of the genus *Dugesia* can reproduce sexually or asexually by fission, meaning that an individual divides itself into two bodies that fully regenerate the missing parts. In a recent biogeographic study of the genus, asexual populations of the Iberia-Apennines-Alps clade (conformed by *D. etrusca*, *D. liguriensis* and *D. ilvana*) showed an unusual phylogenetic pattern, which was associated with long-term asexuality. This hypothesis was tested through an extensive workflow, showing that this pattern was not a methodological artifact, but a genetic footprint of ancient asexuality, and these asexual populations were proposed as a new asexual scandal, being the first not presenting parthenogenetic asexuality but agametic, which implies the inheritance of somatic mutations. However, little is known about the genomic consequences of long-term asexuality in this type of asexuality and how it can affect the success of the species presenting it.

To investigate this, we obtained chromosome-level genome assemblies for sexual representatives of *D. etrusca* and *D. liguriensis*, and SNP data were generated by mapping transcriptome reads from sexual and asexual populations to both genomes. Multidimensional scaling plots revealed less differentiation among asexual populations. Interestingly, at intraindividual level, heterozygosity was higher in asexual than in sexual individuals, a clear sign of Meselson effect. Density plots showed a more uniform distributions of SNPs across the genomes in asexual individuals than in sexual ones, where some regions were identified to present significantly more SNPs. We will discuss the potential adaptive nature of the increment of intraindividual diversity in asexuals, as well as how our results fit the expectations under an asexual scenario under fissiparity, in contrast with the more studied consequences of asexuality under parthenogenesis.



PHYLOGEOGRAPHY AND POPULATION GENETICS

Population connectivity and adaptation patterns of the deep-sea sponge ground forming *Geodia hentscheli* across its geographic range

^{1,2*}Taboada, Sergi, ¹Turon, Marta, ³Díez-Vives, Cristina, ²Arias, María Belén, ¹Galià-Camps, Carles, ⁴Martín Huete, Marta, ¹Riesgo, Ana

*lead presenter: sergio.taboada@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, Spain

² Natural History Museum of London, London, UK

³ Centro Nacional de Biotecnología (CNB-CSIC), Madrid, Spain

⁴ Universitat de Barcelona, Barcelona, Spain

Geodia hentscheli sponge grounds are common deep-sea ecosystems in the North Atlantic and Arctic playing a fundamental role in the formation of biogenic habitat. However, little is known about the gene flow and adaptation patterns of this sponge, crucial information to develop effective management/conservation plans under current global change scenarios.

Here, we used ddRADseq on 110 specimens of *G. hentscheli*, together with microbial profiling, transcriptomics and metatranscriptomics for a selection of specimens to investigate their genetic diversity, molecular connectivity and adaptation. Sampling covered the species' entire distribution spanning ca. 6,000 km, from nine geographic regions within a wide bathymetric range (from 160 to more than 3,500 m depth). We obtained 1,115 neutral SNPs identifying a long-distance genetic connectivity among regions separated 1,000s of km, and a strong genetic structure segregating populations by depth at ca. 1,300 m, in line with our microbial analyses. Our coalescent analyses inferred the split of these depth-related genetic entities ca. 10,000 ya, coincident with the last post-glacial maximum. Our analyses of SNPs under selection, combined with transcriptomic and metatranscriptomic data highlighted the presence of several sponge genes and microbial metabolic pathways involved in adaptation to depth including heat shock proteins and fatty acids, amongst others.

Our study provides a paradigmatic example of a phenomenon known as Depth Differentiation Hypothesis mainly caused by changes in environmental conditions at different depths producing an effect on local adaptation.

Effect of land-use heterogeneity on fairy-shrimps (Anostraca) dispersal across human-modified landscapes

^{1,2}Sainz-Escudero, Lucía, ³Rosas-Ramos, Natalia, ⁴Gutiérrez-Rodríguez, Jorge, ²Perea, Silvia & ^{2*}García-París, Mario

*lead presenter: mparis@mncn.csic.es

¹ Genomics Division, Faculty of Bioscience and Aquaculture, Nord University, Norway

² Museo Nacional de Ciencias Naturales (MNCN-CSIC), Spain

³ Department of Zoology, Universidad de Salamanca, Spain

⁴ Estación Biológica de Doñana (EBD-CSIC), Spain

Population connectivity and gene flow can be severely altered in fragmented human-managed landscapes, disrupting metapopulation dynamics and reducing the genetic diversity that sustains species adaptability, resilience and long-term survival. In these situations, designing precise and impactful strategies for conservation management, requires a thorough understanding of the environmental and landscape features that facilitate species dispersal. Landscape genomics provides a powerful framework for uncovering these relationships by correlating genetic patterns with environmental variation. Most studies to date have been centred in the effect of landscape heterogeneity on genetic connectivity in species with different active dispersal abilities, but its effect on passively dispersers have not been discussed.

Most species of fairy shrimps (Anostraca, Crustacea) inhabit very small and unpredictable temporary pools, that might change from year to year. Population survival is based on resistance eggs, able to survive on dry mud for a few years. Dispersal of resistance eggs in Anostraca relies on external biotic agents, such as mammals, birds, and amphibians, but also abiotic agents as wind, or even motorised vehicles that run through the pools. Some species of fairy shrimps inhabit very particular environments (as salt lakes or rock pools), but a few other are able to colonize strongly modified agricultural landscapes and are often found within landscape matrices dominated by agricultural fields interspersed with (semi)natural shrub-land. We are intrigued on the effect that such landscape composition might have on the genetic connectivity and genetic diversity between populations located in agricultural landscapes with different cover of natural areas, and if any of these land uses is effectively promoting dispersal and gene flow.

In this study, we focus on *Chirocephalus diaphanus*, a widespread species across the Western Palearctic region. We applied landscape genomics (using SNPs) on a nested designed sampling matrix of fairy shrimp populations embedded in agricultural landscapes in the Iberian Peninsula to evaluate the effect of land cover density in the genetic structuring of Anostraca across landscapes with different composition. Our findings aim to provide useful conservation strategies for species in similar ecological contexts.

Genomic insights into the montane lizards of the genus *Iberolacerta* (Lacertidae, Squamata)

^{1,2}Talavera, A., ^{1,3}Burriel-Carranza, Bernat*, ^{1,4}Mochales-Riaño, Gabriel, ¹Estorellas, Maria, ⁵Arribas, Oscar, ^{6,7}Tejero-Cicuéndez, Héctor, ¹Salces-Ortiz, Judit, ⁸Fernández-Guiberteau, Daniel, ⁹Amat, Fèlix, ¹⁰Niell, Manel, ¹Fernández, Rosa, ¹¹S. Mikheyev, Alexander, ¹Carranza Salvador

+ Authors contributed equally

*lead presenter: bburriel@bcn.cat

¹ Institute of Evolutionary Biology (CSIC-Universitat Pompeu Fabra), Barcelona, Spain

² CREAF, Cerdanyola del Vallès, Catalonia, Spain

³ Museu de Ciències Naturals de Barcelona, P^o Picasso s/n, Parc Ciutadella, 08003, Barcelona, Spain

⁴ New York University Abu Dhabi, Abu Dhabi, United Arab Emirates

⁵ IES Castilla, Junta de Castilla, Castilla y León, 42003 Soria, Spain

⁶ Department of Biodiversity, Ecology and Evolution, Faculty of Biology, Universidad Complutense de Madrid, 28040, Madrid, Spain

⁷ Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany

⁸ Centre de Recerca i Educació Ambiental de Calafell (CREAC-GRENPAjuntament de Calafell), Spain

⁹ Àrea d'Herpetologia, BiBIO, Museu de Granollers – Ciències Naturals. Palau d'Àrea 102, Granollers, Catalonia, Spain

¹⁰ Andorra Recerca + Innovació, Av. Rocafort 21-23, AD600 - Sant Julià de Lòria, Principat d'Andorra. Research School of Biology, Australian National University, Canberra, ACT 26000, Australia.

Distributed across the massifs of the Iberian Peninsula, and with an isolated species in the Alps, the eight species from the *Iberolacerta* genus constitute a small group of range-restricted, montane-adapted lizards. Given their small distribution and general confinement to high elevations, the ongoing trends of global warming can pose an imminent threat to the survival of this genus. Here, we present a comprehensive genomic study aimed at characterizing *Iberolacerta* lizards, investigating their evolutionary and demographic histories, genomic diversity, and the adaptations that have led this group of ectotherms to thrive in low-temperature, high elevations. We assembled and annotated a chromosome-level reference genome for *Iberolacerta aurelioi*. Macrosynteny comparisons revealed deep chromosomal rearrangements compared to the closely-related lacertids of the genera *Podarcis*, *Zootoca*, and *Lacerta*. Furthermore, we generated whole genomes for 13 samples, including representatives from each *Iberolacerta* subspecies, as well as representatives from the aforementioned genera, to explore the evolutionary history, genomic variability, and demographic history of the group. Phylogenomic reconstructions supported *Lacerta* as the sister genus to *Iberolacerta*, with *Zootoca* unexpectedly recovered as the deepest split among the studied taxa. Within *Iberolacerta*, most species exhibited low diversity and small effective population sizes over the last 100,000 years, aligning with their restricted distributions. Finally, we investigated the hemoglobin gene clusters as candidates for adaptation to relatively hypoxic high-altitude environments. Although we did not find variation in the number of gene copies of these clusters, we found higher expression and stronger purifying selection in an isoform of enhanced oxygen affinity, but, in theory, minor in reptiles. Thus, *Iberolacerta* species might cope with hypoxia by directly relying on a once-minor isoform, already present in the genomes of other lacertids. Altogether, our findings underscore the unique adaptations of *Iberolacerta* lizards, while highlighting the importance of their protection in the face of impending temperature increases.

Deciphering genomic signatures of climatic adaptation and phenotypic diversity in a polyploid earthworm species complex

^{1*}Martínez Navarro, Alejandro, ²Caproni, Leonardo, ²Dell'Acqua, Matteo, ²Mager, Svenja, ³Gracia, Carlota, ³Taboada, Sergi, ¹Trigo, Dolores, ¹Marchán, Daniel F., ¹Novo, Marta

*lead presenter: alejma21@ucm.es

¹ Faculty of Biological Sciences, Complutense University of Madrid, Spain.

² Institute of Plant Sciences, Scuola Superiore Sant'Anna, Pisa, Italy.

³ Department of Biodiversity and Evolutionary Biology, Museo Nacional de Ciencias Naturales, CSIC, Madrid, Spain.

Earthworms are pivotal components of terrestrial ecosystems. Their long-term adaptation to life in soil has resulted in a simplified body plan shared across species, leading to the emergence of numerous cryptic species and species complexes. The *Allolobophora molleri* complex comprises five green-pigmented, mixed-ploidy species whose differences are primarily based on a single morphological trait: the position of the clitellum. Prior phylogenetic studies have supported the synonymy of this complex into a single species, pointing to unusually high phenotypic plasticity in a key morphological trait.

This study aims to investigate the interplay between genotype, phenotype, and environment within this species complex. To this end, 192 individuals from 43 populations across the Iberian Peninsula and northern Morocco were genotyped using double-digest RAD sequencing. Genomic diversity was analyzed both via de novo assembly and against the reference genome of the close relative *Allolobophora icterica*, using tools to account for polyploidy. The analyses revealed geographically coherent genetic clusters at broad and regional scales; within the Iberian Peninsula, the obtained genetic clusters followed a latitudinal gradient, contradicting the currently described species.

Furthermore, genomic associations with climatic and phenotypic variation in terms of the position of the clitellum were explored using Gradient Forest (GF), Redundancy Analysis (RDA), and Genome-Wide Association Studies (GWAS). GF projected genomic composition across the distribution range and highlighted three main geographic zones shaped by precipitation and temperature. RDA showed that population structure, geography, and climate significantly explain genomic variance and flagged SNPs associated with climatic variation. GWAS under a mixed linear model identified SNPs with additive effects on clitellum position, revealing a molecular basis for this phenotypic variation with important consequences for molecular systematics. These findings advance our understanding of earthworm adaptation to climate and provide insights into their resilience under changing climatic conditions.

Dissecting the genomics of migration in the Painted Lady butterfly

^{1,2*}García-Berro, Aurora, ³Shipilina, Daria, ³Backström, Niclas, ⁴Suchan, Tomasz, ^{1,3}Palahí, Aleix, ⁵Collins C., Steve, ^{6,7}Martins J., Dino, ⁸Pierce E., Naomi, ⁹Vila, Roger & ¹Talavera, Gerard

*lead presenter: auroragbn@gmail.com

¹ Institut Botànic de Barcelona (IBB), CSIC-CMCNB, Spain

² Departament de Genètica, Microbiologia i Estadística, Universitat de Barcelona, Spain

³ Evolutionary Biology Program, Department of Ecology and Genetics, Uppsala University, Sweden

⁴ W. Szafer Institute of Botany, Polish Academy of Sciences, Kraków, Poland

⁵ African Butterfly Research Institution (ABRI) Box 14308, 0800 Nairobi, Kenya

⁶ Mpala Research Centre, P.O. Box 555, Nanyuki, Kenya

⁷ Turkana Basin Institute, Stony Brook University NY, Stony Brook, New York, USA

⁸ Museum of Comparative Zoology, Harvard University, 26 Oxford Street, Cambridge, USA

⁹ Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Barcelona, Spain

Insect migration is a multifaceted trait encompassing morphological, behavioural and physiological adaptations to environmental seasonality. While such complex traits are often underpinned by highly polygenic architectures with numerous variants distributed across the genome, some are shaped by discrete genomic regions with large effects. The migratory Painted Lady butterfly (*Vanessa cardui*) exhibits differences in migratory timing, orientation, and potential migratory loss in some populations, providing a valuable framework to investigate the genomic basis of migration.

In this study, we examine how migratory dynamics shape genetic variation across the nearly global distribution of *V. cardui*. By analysing 358 genomes, we test whether populations from two tropical island archipelagos—Indonesia and Hawaii—have independently adapted to a sedentary lifestyle, a phenomenon known as “migratory drop-off.” In contrast, we also investigate whether populations in the Northern and Southern Hemispheres have evolved distinct migratory strategies in the light of opposing seasonal regimes, a mechanism we term “hemisphericity.”

Our results reveal widespread genomic signatures associated with migration loss in island populations, consistent with polygenic selection acting on numerous small-effect variants. Conversely, we uncover a 9 Mb chromosomal inversion differentiating mainland Northern and Southern hemisphere populations, pointing to a modular genomic architecture underpinning alternative migratory strategies at each hemisphere. Finally, we characterize genes and regulatory pathways linked to migration, including loci related to neuronal and hormonal regulation. Together, our findings illuminate the diversity of genetic architectures of insect migration and offer insights into the evolution of complex adaptive traits in natural populations.

Spatial patterns of phylogenetic diversity in the Asteraceae across the Canary Islands

^{1,2,*}Jairo Patiño, ^{1,2}Louis S. Jay-García, ^{1,2}Oscar Castillo, ³J. Alfredo Reyes-Betancort, ¹Javier Morante-López, ⁴Marcos Salas-Pascual, ⁵Agustín Naranjo-Cigala, ^{1,2}Guillermo Sicilia-Pasos, ³Miguel A. Padrón-Mederos, ^{1,2}Raúl Orihuela-Rivero, ⁶Rafaela González-Montelongo and ^{1,2}Yurena Arjona

**lead presenter*

¹ Island Ecology and Evolution Research Group, Instituto de Productos Naturales y Agrobiología, Consejo Superior de Investigaciones Científicas (IPNA-CSIC), Tenerife, Spain.

² Department of Botany, Ecology and Plant Physiology, University of La Laguna (ULL), Tenerife, Spain.

³ Jardín de Aclimatación de La Orotava, Instituto Canario de Investigaciones Agrarias (ICIA), Tenerife, Spain.

⁴ Instituto de Estudios Ambientales y Recursos Naturales (IUNAT), University of Las Palmas de Gran Canaria (ULPGC), Gran Canaria, Spain.

⁵ Department of Geography, University of Las Palmas de Gran Canaria (ULPGC), Gran Canaria, Spain.

⁶ Genomics Division, Instituto Tecnológico y de Energías Renovables (ITER). Plataforma genómica de alto rendimiento para el estudio de la biodiversidad, ITER, Unidad Asociada al CSIC por el IPNA-CSIC, ITER, Polígono Industrial de Granadilla, 38600. Santa Cruz de Tenerife, Spain.

Understanding the spatial and evolutionary dimensions of biodiversity is fundamental for effective conservation and management, particularly in insular systems that face accelerating habitat degradation, biological invasions, and climate change. Traditional assessments of species richness and endemism, while valuable, capture only part of biodiversity's complexity. Phylogenetic approaches add a temporal and evolutionary perspective, offering key insights into the origins, persistence, and vulnerability of lineages. Here, we focus on the Asteraceae family of the Canary Islands, one of the archipelago's most diverse and ecologically influential plant groups. Using a HybSeq-based multilocus phylogeny as a framework, we integrate species distribution data with measures of phylogenetic diversity and endemism, and apply categorical analysis of neo- and paleo-endemism (CANAPE) to identify evolutionary hotspots of native taxa. By contrasting spatial phylogenetic patterns of native and alien species, we further provide a refined basis for conservation prioritization that highlights not only areas rich in evolutionary novelty and persistence but also regions particularly vulnerable to invasion. This phylogenetically informed approach underscores the need to safeguard unique evolutionary lineages while addressing invasion risks, thereby guiding more integrative strategies for biodiversity conservation and management in oceanic islands.

Second chance speciation in the clouded Apollo butterfly (*Parnassius mnemosyne*)

^{1,2*}J. Lancho-Silva, ^{1,2}L. Spilani, ¹V. Marques, ⁵C. Bruschini, ³V. Dinca, ³M. Mutanen, ⁴M. Franzén, ⁶D. Adams, ⁵L. Dapporto, ¹R. Vila

*lead presenter: josep.lancho@ibe.upf-csic.es

¹ Institut de Biologia Evolutiva (CSIC-UPF), Barcelona, Spain

² Facultat de Biologia, Universitat de Barcelona, Barcelona, Spain

³ Ecology and Genetics Research Unit, University of Oulu, Oulu, Finland

⁴ Faculty of Science & Engineering, Linnaeus University, Sweden

⁵ Department of Biology, University of Florence, Florence, Italy

⁶ Department of Ecology, Evolution, and Organismal Biology, Iowa State University, USA

Secondary contact zones are powerful natural laboratories to explore the dynamics of speciation. In the case of the clouded Apollo butterfly (*Parnassius mnemosyne*), a charismatic and protected species traditionally considered widespread and uniform, we present evidence of a cryptic species complex using a comprehensive integrative approach. Through genome-wide ddRAD-seq (PCA, STRUCTURE, phylogenetic analysis), demographic modeling (DADI), ABBA-BABA tests, ecological niche modeling (ENM), geometric morphometrics, and chemical analysis of cuticular hydrocarbons (CHCs), we confirm the presence of a Western Mediterranean lineage (*P. turatii*) that diverged from *P. mnemosyne* over 800,000 years ago. Around 154,000 years ago, a secondary contact with admixture occurred in Western Europe, giving rise to the current Pyrenean populations—at that time, reproductive isolation had not yet evolved. In contrast, present-day populations in a narrow alpine contact zone (~40 km) show strong genomic integrity and no detectable gene flow, indicating that reproductive barriers have since emerged. Therefore, speciation must have occurred between the time of the last admixture event (~154 kya) and the present, providing a rare example of “second chance speciation.” Morphological data show no differentiation in the contact zone highlighting the complexity of current reproductive isolation. Our findings confirm a previously unrecognized European endemic and highlight the need for urgent reevaluation of conservation strategies for *P. mnemosyne*. This study not only advances our understanding of speciation dynamics but also underscores the importance of revising conservation frameworks to account for cryptic biodiversity.

Genome architecture and photo-symbiont flexibility underpin colonization success of the small giant clam *Tridacna maxima* across the Indo-Pacific

^{1,2,*}Leiva, Carlos, ³Fauvelot, Cecile, ⁴Neo, Mei Lin, ^{4,5}Lee, Li Keat, ⁶Reimer, James, ⁷Conaco, Cecilia, ^{2,8}Torrado, Héctor, ²Combosch, David, ^{2,8}Lemer, Sarah

*lead presenter: cleivama@gmail.com

¹ Estación Biológica de Doñana (EBD-CSIC), Spain

² University of Guam, Marine Laboratory, Guam, USA

³ Institut de Recherche pour le Développement, France

⁴ Tropical Marine Science Institute, National University of Singapore, Singapore

⁵ Institute of Ocean and Earth Sciences, Universiti Malaya, Malaysia

⁶ University of the Ryukyus, Japan

⁷ Marine Science Institute, University of the Philippines, Diliman, Philippines

⁸ Museum of Nature Hamburg, Leibniz Institute for the Analyses of Diversity Change, Germany

The small giant clam, *Tridacna maxima*, is the most common and widely distributed giant clam species, ranking among the bivalves with the broadest natural ranges. It thrives across contrasting environments, from the hypersaline Red Sea to the seasonally cold waters of Okinawa, the tropical warm pool in Papua New Guinea, and the oligotrophic atolls of French Polynesia. Deciphering the molecular mechanisms that underpin the remarkable ecological breadth in a species like *T. maxima* is key to advancing our understanding of adaptation, symbiosis, and resilience. To address this, we integrated whole-genome resequencing of 196 individuals, spanning the species' range, with analyses of transposable elements (TEs), structural variation, and symbiont community composition.

We identified pronounced population structure, partitioned into seven regional genetic clusters with little gene flow across open-ocean barriers. Despite overfishing driving local extinctions in certain parts of its range, our results indicated historically stable populations characterized by large effective population sizes, high standing genetic variation, and low inbreeding—features that may buffer *T. maxima* against ongoing environmental changes. We also uncovered a flexible genome architecture, shaped by haploblock polymorphisms from putative chromosomal inversions, population-specific TE dynamics, and ancient selective sweeps that contributed to local adaptations. In parallel, a remarkable symbiont flexibility was detected across the species' range, with distinct stress-resistant Symbiodiniaceae lineages occurring in extreme environments such as the Red Sea and Papua New Guinea. This suggests that symbiont community contribute to local adaptation alongside host genomic plasticity.

Together, our findings revealed that the interaction between genome architecture and holobiont flexibility is key to the ecological success of *T. maxima* across the Indo-Pacific. Our results also suggest that adaptation and resilience are emergent properties of multiple interacting mechanisms that can only be captured through an integrative approach, bridging population genomics, structural variation, and symbiont community composition.

Phylogeography and colonization history of cryptic *Poecilia* species in the Nicaraguan lakes

¹*Barluenga, Marta, ¹*Perea, Silvia, ²Garita-Alvarado, Carlos & ²Ornelas-García, Claudia Patricia

*lead presenter: Marta.Barluenga@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales, CSIC, Spain

² UNAM, México

The colonization of isolated lakes, like the colonization of archipelagos, opens up new opportunities for the emergence of evolutionary processes related to isolation and local adaptation. Nicaraguan crater lakes are a very young archipelago of terrestrial islands (ca. 50000 years) arising as an excellent model for the study of recent speciation and adaptive radiation. Among the native ichthyofauna of these lakes, thoroughly studied cichlids stand out as particularly diverse. In contrast, the very abundant, relatively old and widespread poeciliids are typically phenotypically cryptic and much less studied in the area. Fish from the genus *Poecilia* have recently revealed more diversified than previously thought. Two widely distributed species (belonging to the *P. mexicana* complex) have been found in the lakes, and more recently an endemic species (*P. sp. tipitapa*) was described. In this study, a combination of mitochondrial genes and whole genome data were used with the aim of reconstructing the phylogeography and colonization history of *Poecilia* in this region, and to investigate their evolutionary processes and potential recent hybridization among species. Our results will contribute to our understanding the evolutionary processes related to the colonization of isolated island-like environments.

Evolutionary history of a rapid post glacial radiation in the songbird genus *Junco*

¹*Javier Sala, Borja Milá

*lead presenter: b.mila@csic.es

¹ Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid

Recent post glacial radiations provide an exclusive window into speciation dynamics following abrupt climate shifts. The radiation of dark-eyed juncos (*Junco hyemalis*) across North America following the Last Glacial Maximum provide a unique system to understand the relative roles of selective and neutral factors involved in rapid speciation. Here we investigate the role of post LGM range shifts, local adaptation, sexual selection, and demographic factors in driving the rapid diversification of dark-eyed juncos. We performed genome resequencing of 225 birds covering 19 junco taxa and paired these data with paleoclimatic niche models. Coalescent species tree analyses recover a ladder like topology that tracks latitude and points to a single north bound colonization ~18 kya from a Mesoamerican refugium. Principal components and ADMIXTURE analyses delineate a shallow genomic cline punctuated by sky island breaks and the low elevation desert basins separating them, while D statistics reveal distance decaying bidirectional gene flow culminating in a recent admixture hotspot in the northern Rocky Mts. Fastsimcoal2 analyses favor divergence with gene flow over strict isolation and, together with SMC++, identify serial founder bottlenecks followed by a five-fold increase in effective population size between 17 and 9 kya. Ecological niche models reconstruct a continuous montane corridor from Mexico's Sierra Madre to the Madrean Sky Islands of the SW USA throughout the late glacial, neatly predicting genomic contact zones. Our results portray the *Junco* radiation as a climate driven serial founder cascade, with limited but persistent introgression, rapid demographic growth, with important roles for both local adaptation and sexual selection.

Whole Genome Sequencing reveals population structure of the deep-sea sponge *Phakellia ventilabrum* in the Northeast Atlantic and Mediterranean Sea

^{1,2*}Gracia-Sancha, Carlota, ¹Galià-Camps, Carles, ³Manousaki, Tereza, ¹Riesgo, Ana, ¹Díez-Vives, Cristina, ⁴Díaz, Julio, ⁵De la Torriente, Ana, ⁵Serrano, Alberto., Ana, ⁶Xavier, Joana R., ⁴Cárdenas, Paco, ⁷Martín, Alejandro, & ¹Taboada, Sergi

*lead presenter: carlotagrsa@gmail.com

¹ Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, Spain

² Universidad Complutense de Madrid (UCM), Madrid, Spain

³ Hellenic Center for Marine Research, (HCMR), Heraklion, Greece

⁴ Museum of Evolution, Uppsala University, Uppsala, Sweden

⁵ Instituto Español de Oceanografía (IEO-CSIC), Santander, Spain

⁶ Interdisciplinary Centre of Marine and Environmental Research (CIIMAR), Porto, Portugal

⁷ Instituto Español de Oceanografía (IEO-CSIC), Málaga, Spain

Deep-water sponge grounds are crucial ecosystem engineers, shaping biodiversity in benthic habitats worldwide. Because of their ecological importance and sensitivity to bottom trawling, they are classified as Vulnerable Marine Ecosystems (VMEs). To improve conservation strategies, recent studies have focused on the genetic diversity and connectivity of deep-sea sponges of the genus *Phakellia*. However, these studies have relied on ddRADseq, a method with limited resolution for detecting selection and local adaptation. Whole Genome Sequencing provides finer-scale genetic insights, allowing deeper understanding of variation, selection, and evolutionary patterns. For the first time, low coverage Whole Genome Sequencing ($\approx 10X$) was performed for 150 samples of the deep-sea sponge *Phakellia ventilabrum* from the NE Atlantic and the Mediterranean Sea (30–900 m depth) to assess genetic variation and connectivity. After mapping the sequences to the reference genome, variant calling and filtering, a total of 1.5 M SNPs were found. By examining patterns of genetic variation across the entire genome the molecular data reflected four genetically distinct groups across all sampling sites including a group of samples from the Iberian Peninsula (comprising samples from the Cantabrian Sea, Portugal and Cadiz), another group from the British Islands, Norway and Iceland, a distinct one in Roscoff, and another in Mallorca, supporting the presence of a structured pattern of genetic diversity in the species. The genetic break detected at the Iberian Peninsula and the long-distance genetic connectivity present in the northern samples are mainly explained by prevalent oceanographic currents existing in the study area. A strong genetic difference is observed in some samples from Iceland which were collected at 700 m. Apart from the genetic connectivity patterns, we also provide insights on the adaptation patterns for *P. ventilabrum* specimens living in contrasting environmental conditions. Our results provide a solid foundation for future conservation actions for this common species forming VMEs in the NE Atlantic and Mediterranean Sea.

Population genetics reveals a new conservation approach for the white-foot limpet in the Canary Islands

¹*Aliende-Hernández, Marina, ²Martín-Huete, Marta, ³Alfonso, Beatriz, ¹Hernández, José Carlos, ²Pérez-Portela, Rocío

*lead presenter: maliende@ull.edu.es,

¹ Departamento de Biología Animal, Edafología y Geología, Universidad de La Laguna, Tenerife, Canary Islands, Spain.

² Departamento de Biología Evolutiva, Ecología i Ciències Ambientals, Facultat de Biologia & Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Spain

³ Departamento de Botánica, Ecología y Fisiología Vegetal. Universidad de La Laguna, Tenerife, Canary Islands, Spain.

Limpets of the genus *Patella* are keystone species in rocky shore communities of the Northeast Atlantic and Mediterranean Sea. In the Macaronesian archipelagos, limpets have been collected for human consumption since colonization, and their harvest continues today, making them a crucial resource for small-scale fisheries in the Canary Islands.

Given their ecological and economic importance of this species, its conservation is a priority. This study investigates the genetic connectivity of *Patella aspera* populations across the Canarian archipelago to understand gene flow and its relevance for managing and conservation planning. In this study, we isolated 13,286 single nucleotide polymorphisms (SNPs) to assess the genetic structure and connectivity of the populations.

Our findings reveal marked genetic homogeneity and high connectivity throughout the archipelago, indicating robust gene flow that appears unrestricted by oceanographic distance. This connectivity may enhance the resilience of limpet populations, helping them to mitigate the effects of over-exploitation. However, we have detected genetic differences between the populations on the eastern islands (Lanzarote, Fuerteventura and Lobos islet) and those on the rest of the archipelago. These results underscore the need for establishing separate conservation strategies among the eastern and western part of the archipelagos, considering the singularity of these two identified genetic clusters.

Genetic structure of *Bittium reticulatum* (da Costa, 1778) across the Strait of Gibraltar

¹*Casado-Vadillo, Alberto, ²Pizarro-Borrull, Maria, ²Recuero, Ernesto, ³Moreno, Diego, ²Templado, José & ²Machordom, Annie.

*lead presenter: acasadovadillo@gmail.com

¹ UIMP-CSIC, Spain

² Museo Nacional de Ciencias Naturales (MNCN-CSIC), Spain

³ Agencia de Medio Ambiente y Agua, Junta de Andalucía

Marine biogeographic barriers play a crucial role in shaping ocean biodiversity by limiting gene flow between populations, favoring genetic differentiation, and promoting speciation processes that result in complex and highly structured biogeographic patterns. The Strait of Gibraltar constitutes a multidimensional biogeographic barrier, integrating oceanographic, bathymetric, and historical events (e.g., Messinian Salinity Crisis, MSC) components that influence the connectivity and distribution of marine species. In the case of marine invertebrates, the Strait of Gibraltar, or the associated Almería-Oran Front, frequently affects gene flow patterns between Atlantic and Mediterranean populations, promoting many instances of genetic differentiation, endemism, and even cryptic speciation events.

We focused on populations of *Bittium reticulatum* (da Costa, 1778), a marine gastropod that is widely distributed along the Atlantic and Mediterranean coasts of Europe and North Africa. It is a ubiquitous species that lives in different rocky infralittoral communities, especially in photophilous algae, and in seagrass meadows, and has populations both in the open waters and in coastal lagoons. We implemented fieldwork and also used previously collected material of *Bittium reticulatum* individuals.

This study investigates the phylogeographic and population genetic structure of this species using mitochondrial (COI, 16S rRNA) and nuclear (28S rRNA) markers to assess connectivity between Atlantic and Mediterranean populations. As an innovation, these markers were sequenced using a MinION device from Oxford Nanopore Technologies (ONT) using indexed primers to allow demultiplexing.

Our goals are to characterize population genetic diversity and geographic patterns of genetic divergence, in order to explore the influence of geological and climatic history on the evolutionary history of *Bittium reticulatum* and evaluate the potential presence of cryptic lineages. We anticipate significant genetic structuring across the Strait of Gibraltar and evidence of historical demographic events, such as recolonization processes following the MSC. The results will contribute to a deeper understanding of the evolutionary history of *Bittium reticulatum* and inform broader biogeographic and conservation frameworks for coastal marine invertebrates.

Dealing with uncertainty in biogeographic status: Case studies in cryptogenic Asteraceae in the Canary Islands

^{1,2*}Jay-García, Louis S., ^{1,2}Arjona, Yurena, ³Caujapé-Castells, Juli, ⁴Calleja, Juan A., ^{1,5}Miroló Sebastian, ⁶Morente-López, Javier, ⁷Msanda, Fouad, ⁸Harrouni, Cherif, ⁹Naranjo Cigala, Agustín, ^{1,2}Orihuela-Rivero, Raúl, ¹⁰Padrón-Mederos, Miguel A., ¹⁰Reyes-Betancort, J. Alfredo, ⁹Salas-Pascual, Marcos, ^{1,2}Sicilia-Pasos, Guillermo, ^{11,12}Wegmann, Daniel, ^{11,12}Wietlisbach, Xenia, ¹Fernández-Palcios, José María, & ^{1,2}Patiño, Jairo

* lead presenter: louissjaygarcia@gmail.com

¹ Universidad de La Laguna (ULL), Spain.

² Instituto de Productos Naturales y Agrobiología (IPNA-CSIC), Spain.

³ Jardín Botánico Canario "Viera y Clavijo" - Unidad Asociada de I+D+i al CSIC, Cabildo de Gran Canaria, Spain.

⁴ Universidad Autónoma de Madrid, Madrid, Spain.

⁵ University of Liège (ULiège), Liège, Belgium.

⁶ Goethe-University Frankfurt, Frankfurt am Main, Germany

⁷ Hassan II Institute of Agronomy and Veterinary Sciences, Agadir, Morocco.

⁸ Ibn Zohr University, Agadir, Morocco.

⁹ Universidad de Las Palmas de Gran Canaria, (ULPGC), Las Palmas de Gran Canaria, Spain.

¹⁰ Jardín de Aclimatación de la Orotava - Instituto Canario de Investigaciones Agrarias (JAO - ICIA), Puerto de la Cruz, Tenerife, Spain.

¹¹ University of Fribourg, Fribourg, Switzerland.

¹² Swiss Institute of Bioinformatics, Fribourg, Switzerland.

Species can be described as cryptogenic when there is no conclusive evidence to determine their native or nonnative status. This type of biogeographic status uncertainty is among the most understudied shortfalls and is particularly problematic for the study of island floras, such as the Canary Islands. These species are found throughout the tree of life but are more commonly categorized as such when: 1) long-distance dispersal mechanisms are (putatively) present; 2) they are native in adjacent continental areas; and/or 3) the taxonomic groups are understudied. The inability to distinguish between these two scenarios has significant implications for conservation and management, as the lack of evidence often blurs the lines between natural colonization and human-mediated introduction, hindering effective action. Despite proposed methodologies, a widely applicable framework for accurately assessing the status of cryptogenic plant species has been notably absent from the scientific literature.

To fill this critical gap, we propose the application of well-known genomics-based approaches. We combined ddRAD sequencing in population genomics and demographic modeling to assess the cryptogenic status of several vascular plant species within the Asteraceae family, a well-represented taxonomic group in the Canarian flora. Our sampling design included populations from all major islands of the archipelago, as well as continental populations from two adjacent areas, namely Morocco and the Iberian Peninsula. Our primary goal was to test which of several competing demographic scenarios best explained the observed spatial distribution of genomic variation. Our testing scenarios ranged from ancient, single colonization events to recent, multiple introductions. The methodology also allowed us to estimate the approximate timing of each species' colonization of the archipelago, providing a temporal context for their presence.

Our findings revealed two contrasting patterns among the examined species: Several cases displayed genomic signatures consistent with ancient colonization events, compatible with natural colonization scenarios. In contrast, other species exhibited clear evidence of very recent introductions, compatible with human-aided naturalization scenarios. By providing genomics-based evidence of identifying human-introduced species, this framework empowers conservation managers to better prioritize limited resources while also providing a valuable model that can be readily applied to reduce biogeographic status uncertainty in other study systems and regions.

Genomic population structure and connectivity of the endemic reef-builder *Cladocora caespitosa* in the Balearic Sea

¹*Padua, Claudio, ¹Sastraprawira, Shantika Maylana, ¹de Oliveira Magalhães, Carolina, ¹Schöninger Almaraz, Karen, ²Pons, Joan, ¹Capa, Maria & ³Bassitta, Marta

*lead presenter: claudio.padua@uib.es

¹ Balearic Biodiversity Centre (CBB-CMB), University of the Balearic Islands, Palma, Spain

² Mediterranean Institute for Advanced Studies (IMEDEA, CSIC-UIB), Esporles, Spain

³ Grup de Genètica Humana i Evolutiva (HEGEN-IUNICS), University of the Balearic Islands, Palma, Spain

Coral reefs worldwide are rapidly deteriorating due to global change and rising sea temperatures. *Cladocora caespitosa*, the only zooxanthellate, endemic reef-building coral in the Mediterranean, is a long-lived, slow-growing ecosystem engineer that plays a key role in sustaining biodiversity in shallow habitats. However, its life-history traits make it particularly vulnerable to multiple anthropogenic stressors. Rising sea temperatures have additionally triggered recurrent bleaching and mortality events, causing severe declines in the extent of local populations. Consequently, *C. caespitosa* is currently listed as Endangered on the IUCN Red List.

Because isolated populations of vulnerable species may exhibit reduced resilience, understanding patterns of connectivity and gene flow is crucial for conservation strategies. Genomic approaches such as double-digest restriction-site-associated DNA sequencing (ddRAD-seq) enable the discovery of thousands of single nucleotide polymorphism (SNP) markers across the genome, providing powerful insights into effective population size, gene flow, demographic history, and adaptive potential.

Here, we apply ddRAD-seq to investigate the fine-scale population genetic structure and connectivity of *C. caespitosa* in the Balearic Sea. We analysed 96 individuals from populations throughout the coastal areas of the Balearic archipelago and along the Spanish mainland coast, aiming to assess whether oceanographic features act as barriers to dispersal, both between and within populations, and how gene flow shapes the population structure of this coral species. The results provide useful insights into the genetic patterns of *C. caespitosa* across populations in the Balearic Sea, informing effective conservation and management strategies for this endangered Mediterranean coral.

From Genomes to Venomes: Multi-Omic Insights into Iberian Snake Evolution

^{1*}Sergi Tulloch Jiménez, ¹Maria Estarellas, ^{1,2}Bernat Burriel, ^{1,3}Gabriel Mochales, ⁴Daniel Fernández-Guiberteau, ⁴Laura Blasón, ⁴Andrea Jhulyana López-Caro, ⁵Davinia Pla, ^{6,7}Tyler Alioto, ⁵Juan José Calvete, ¹Salvador Carranza

*lead presenter: sergi.tulloch@ibe.upf-csic.es

¹ Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Spain

² Museu de Ciències Naturals de Barcelona, Spain

³ New York University Abu Dhabi, United Arab Emirates.

⁴ CREAC, Centre de Recerca i Educació Ambiental de Calafell (GRENPAjuntament de Calafell), Spain

⁵ Evolutionary and Translational Venomics Laboratory, Instituto de Biomedicina de Valencia, Consejo Superior de Investigaciones Científicas (CSIC), Spain

⁶ Centro Nacional de Análisis Genómico (CNAG), Spain

⁷ Universitat de Barcelona, Spain

Venom is a complex and fascinating evolutionary trait that has independently emerged multiple times across the animal kingdom. In snakes, venom is synthesized in specialized glands – venom glands – and serves primarily for predation or self-defensive purposes, reflecting intense ecological pressures and offering a unique window into evolutionary innovation. Despite advances in molecular systematics, many phylogenetic relationships –particularly among colubroid snakes – remain ambiguous or contested, limiting our understanding of venom evolution in its broader genomic context.

The overall aim of the project is to investigate the evolution and diversity of venom in Iberian snakes through an integrative multi-omics approach. Specifically, we are generating and analysing high-quality reference genomes, venom-gland transcriptomes, and proteomic profiles for all snake genera native to the Iberian Peninsula. This effort will allow us to compile comprehensive catalogues of venom-gland-specific toxin genes—the so-called venom-ome—representing the functional core effector proteins of envenomation.

Simultaneously, population genomic analyses will be carried out using whole-genome resequencing data to explore phylogenetic relationships, demographic history, inbreeding, and population structure across species and subspecies. These analyses will help resolve long-standing taxonomic uncertainties and provide new insight into the evolutionary processes shaping snake diversity in the region.

As a proof of concept, we present the assembly of five high-quality genomes and preliminary results from the population genomics of *Malpolon monspessulanus*. Ultimately, this project will produce valuable genomic resources, refine the phylogenetic framework of Iberian snakes, and deepen our understanding of venom evolution—contributing to both biodiversity conservation and potential biomedical applications.

Persistence despite isolation: Temporal genomic structure in the endemic and endangered cyprinodontiform fish *Aphanius baeticus* (Doadrio, Carmona & Fernández-Delgado, 2002)

¹*López-Solano, Alfonso, ²Perea, Silvia, ²Nester, Tessa L., ³Ghanavi, Hamid & ²Doadrio, Ignacio

* lead presenter: alfonso.lopez@mncn.csic.es

¹ National Museum of Natural Sciences – CSIC, Spain

² National Museum of Natural Sciences – CSIC, Spain

³ Lund University, Sweden

Many conservation efforts remain disproportionately focused on emblematic species, leaving most threatened biodiversity, particularly freshwater fishes, largely overlooked. In the Iberian Peninsula many fish species face conservation concern, yet habitat degradation, invasive species, and unsustainable water use continue to drive severe declines. Among the most threatened is the Baetican toothcarp *Aphanius baeticus* (Doadrio, Carmona & Fernández-Delgado, 2002), an endangered endemic small fish restricted to a few fragmented populations along Spain's southwestern Atlantic coast.

We investigated population structure and temporal change in *A. baeticus* by analyzing genome-wide SNPs from low-coverage whole-genome sequencing of 54 individuals sampled in two campaigns separated by 14 years (2008 vs. 2022). We quantified structure with different genomic approaches and estimated diversity and divergence. Mitochondrial CytB haplotypes and genome-wide analyses consistently recovered four conservation genetic units covering (i) Doñana coastal wetlands, (ii) inland Guadalquivir (Lebrija–Montero), (iii) the Guadalete/San Pedro drainage, and (iv) the Iro–Conil system. While some populations matched previously hypothesized human-mediated translocations, others had disappeared by the second survey.

Between 2008 and 2022 we detected increased differentiation and a pronounced decline in nucleotide diversity across all reassessed populations, consistent with fragmentation, reduced connectivity, and demographic contraction. Analyses supported historical gene exchange among nearby coastal systems, compatible with episodic dispersal during extreme hydrological events, but contemporary patterns indicate erosion of that connectivity. Our results provide a replicated temporal framework showing that a formerly metapopulation-like network has transitioned toward more isolated, erosion-prone units within just ~10–14 generations. This temporal genomic baseline offers an early-warning system and a transferable template for other fishes facing analogous conservation pressures.

Reassessing *Phoenix atlantica* from Cape Verde: genetic evidence of its relationship with *Phoenix dactylifera*

^{1*}Sarmiento-Cabello, Sonia, ¹Rodríguez-Rodríguez, Priscila, ¹Arbelo Ramírez, Guacimara, ¹Naranjo-Cigala, Agustín, ¹Curbelo, Leticia, ²Monte da Graca Gomes, Maria, ²Brito, Juliana, ³Aberlenc, Frederique, ⁴Zehdi-Azouzi-Salwa, ¹Sosa, Pedro A.

*lead presenter: sonia.sarmiento@ulpgc.es

¹ Instituto Universitario de Estudios Ambientales y Recursos Naturales (IUNAT), Universidad de Las Palmas, España

² Direcao Geral Da Agricultura Silvicultura e Pecuaria e Delegacao do Ministerio da Agricultura e Ambiente do Sal e da Boavista, Praia, Cabo Verde.

³ Plant Diversity, Adaptation and Development, Universite de Montpellier, Institut de Recherche pour Developpement, Centre de Cooperation Internationale en Recherche Agronomique pour le Developpement, 911 Av. Agropolis, BP 64501, 34394 Montpellier CEDEX 5, France

⁴ Laboratoire de Genetique Moleculaire, Faculte des Sciences de Tunis, Immunologie et Biotechnologie (LR99ES12), Universite de Tunis El Manar, Campus Universitaire Farhat Hached, Tunis

The Cape Verde palm tree, *Phoenix atlantica*, holds a high ecological and cultural importance within Cape Verde archipelago ecosystem. However, recent studies have raised questions about its distinctiveness, due to its close relationship with and potential origin from its relative, the date palm (*Phoenix dactylifera*). In this study, employing an expanded sample set and a diverse array of molecular markers, we characterized *P. atlantica* in Cape Verde and investigate its relationship with other *Phoenix* species. Our findings reveal genetic markers responsible for the differentiation of a *P. atlantica* genetic pool. Additionally, we uncover evidence of the recent divergence of *P. atlantica* from northern African date palm populations, suggesting a relatively recent colonization in Cape Verde. These results pose a significant advancement in elucidating the enigma the provenance of *P. atlantica* and its connection to *P. dactylifera*, representing a crucial step forward for Cape Verde nature conservation. Furthermore, our study reveals distinct genetic patterns across various islands in the archipelago. Overall, our results contribute to the intricate historical trajectories and characterization of palm trees in Africa.

Keywords: *Phoenix atlantica*, *Arecaceae*, Cape Verde, population genetics, oceanic islands



POSTERS

Comparative Analysis of BOLD and GenBank Databases during DNA Barcoding: an example of Wild Bees from La Palma

¹Carrasco-Palomo, Alfonso, ¹Urueña, Álvaro, ²Lugo, David, ^{2*}Ruiz, Carlos, ¹De la Rúa, Pilar

*lead presenter: cruizcar@ull.edu.es

¹ Area of Animal Biology, Faculty of Veterinary Medicine, University of Murcia, Spain

² Department of Animal Biology, Soil Science and Geology, Faculty of Science, University of La Laguna, Spain

Bees, especially wild species, hold unparalleled value in both scientific research and society, primarily due to their unique biology, and the ecosystem services they offer, particularly pollination. For this reason, proper taxonomic identification of bee populations and species is essential for assessing their conservation status and the ecological roles they fulfil. The BOLD (Barcode of Life Data Systems) and GenBank integrated in NCBI (National Centre for Biotechnology Information) are among the most widely used databases for comparing sequences and identifying taxa at the genus and species levels across different animal groups. In this study, both databases were employed for the taxonomic identification of wild bees collected on the island of La Palma (Canary Islands), in order to evaluate the effectiveness of these identification tools. As part of the APISALUS project*, a total of 90 individuals were collected in 2024 using pan traps in two high-altitude shrubland locations. DNA was extracted from each individual, and the mitochondrial cytochrome c oxidase subunit I (Cox1) gene was PCR-amplified. After Sanger-sequencing, sequences were edited and aligned using MEGA X software (version 11, 64-bit) and then compared against the BOLD and GenBank databases using the Bold id engine v4 and the BLAST tool. According to the similarity thresholds established by Hebert et al. (2003), BOLD yielded higher identity percentages (100% and 40% at the genus and species levels respectively, 97.7% and 23.3% with Genbank). Fifty-four individuals were identified to genus level, while 36 could only be assigned to species level using both databases. The most represented genus (80%) was *Lasioglossum* Curtis, 1833, with the species *L. villosulum* (Kirby, 1802) particularly frequent. Of those identified only to the genus level, 57% corresponded to *Lasioglossum* sp. and 2% to *Hylaeus* sp., suggesting the presence at least of two new undescribed species for Canary Islands.

In this work, the DNA barcoding technique in conjunction with the public databases available (BOLD and Genbank), has yielded partial taxonomic identification of the sampled bees. Discrepancies were observed when both databases were used simultaneously, likely attributable to delays in updating and the complementarity of the sequences they contain. Additionally, reference sequences for numerous wild bee species are still lacking, a limitation that must be addressed to ensure accurate identifications in future biodiversity studies.

*Project TED2021-131316B-I00 financed by MCIN/AEI /10.13039/501100011033 and by the European Union NextGenerationEU/ PRTR

Updating the distribution of the threatened *Parachondrostoma* (Teleostei: Leuciscidae) and assessing co-occurring species using environmental DNA

¹*Duque-Amado, Carmen, ¹Perea, Silvia, ¹Doadrio, Ignacio.

*lead presenter: carmen.duque@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales, Spain

Human population growth and the increasing demand for resources have extensively degraded Mediterranean freshwater habitats where high endemism levels exacerbate the critical situation. One of this endemic genera is the cyprinid genus *Parachondrostoma* Robalo, Almada, Levy & Doadrio, 2007, which comprises three Iberian species inhabiting eastern Spain, one of the most impacted areas by anthropogenic pressures in the region. Two of them species, the loína (*Parachondrostoma arrigonis* (Steindachner, 1866)), endemic to the Júcar Basin, and the Turia nase (*Parachondrostoma turiense* (Elvira, 1987)), endemic to the Turia and Mijares basins, are endangered; in particular the loína has undergone a marked population decline over the last three decades (80% in abundance and range). The loína has disappeared from the main river course and persists only in a few fragmented tributaries. This regression is mainly due to river channelization, dam regulation, water pollution, and severe habitat degradation in the middle and lower Júcar. Moreover, alien species have worsened its status by competition with the translocated *Pseudochondrostoma polylepis* and predation by *Micropterus salmoides* and *Esox lucius* have led to local extinctions.

Similarly, the Turia nase populations are in alarming decline, threatened by exotic species, nutrient pollution from agriculture and industry, habitat fragmentation from dams and canals, and water or gravel extraction that degrades spawning grounds.

This study evaluates the potential of environmental DNA (eDNA) to update the distribution of *P. arrigonis* and *P. turiense*, and to explore the composition of cohabitant fish species. Water samples were collected both from sites where the loína and the Turia nase are still present and from localities with no records in the past decades. Metabarcoding analyses using a fragment of the mitochondrial 12S rRNA gene allowed us to detect *Parachondrostoma* species and to characterize the accompanying fish assemblages. Our results highlight the sensitivity of eDNA-based approaches for monitoring freshwater biodiversity. Beyond providing updated information on the conservation status of *P. arrigonis* and *P. turiense*, this methodology offers valuable insights into community structure and invasive species interactions, reinforcing its role as an essential tool for the conservation of threatened Iberian freshwater fish endemic species.

Keywords: conservation, cyprinids, distribution range, eDNA, metabarcoding, *Parachondrostoma arrigonis*, *Parachondrostoma turiense*.

Impact of fire on flying insects and soil arthropods: Insights from fire-adapted and fire-sensitive forests across the temperate and subtropical regions

^{1,2*}Moro, Gioele, ^{1,3}Sucháčková, Alena, ^{1,2}Čížek, Lukáš, ¹Šebek, Pavel, ⁴Lanta, Vojtech, ⁵Emerson, Brent, ⁵Arribas, Paula, ⁵Andújar, Carmelo

*lead presenter: gioele.moro@outlook.com

¹ Institute of Entomology, Biology Centre CAS, Czech Republic

² Faculty of Science, University of South Bohemia, Czech Republic

³ Senckenberg German Entomological Institute, Germany

⁴ Department of Functional Ecology, Institute of Botany CAS, Czech Republic

⁵ Consejo Superior de Investigaciones Científicas IPNA-CSIC, Spain

This project investigates flying insect and soil arthropod communities across sites with contrasting fire impact (severely burnt, weakly burnt, and unburnt) in temperate and subtropical forests. In each of the two regions, we apply a factorial design with 6 replicates of 3 fire treatments across 2 forest types, totalling 72 plots. In temperate forests (Bohemian and Saxon Switzerland National Parks, Czechia and Germany), plots are located in pine (fire-prone) and beech (fire-sensitive) stands. In subtropical forests (Las Lagunetas, Tenerife, Spain), plots are in pine (fire-prone) and laurel (fire-sensitive) stands. Flying insects are sampled with Malaise traps, and soil arthropods via the flotation-berlese-flotation method. Bulk samples are analyzed with DNA metabarcoding. We test four hypotheses: (i) fire enhances beta diversity of flying insects; (ii) soil arthropods in fire-prone forests are more fire-resilient; (iii) deeper soil layers host more resilient arthropod communities; (iv) active dispersal drive faster post-fire recolonization by flying insects than by soil arthropods. Our preliminary metabarcoding results from Malaise trap samples collected in Czechia and Germany (2023–2024) show a strong association of species composition with burnt treatment, while species richness remains stable. These findings suggest that forest fires may have an ecological role in maintaining forest communities' biodiversity.

This project was financed with the state support of the Technology Agency of the Czech Republic within the Environment for Life Programme (SS06010261) and by the Ramón y Cajal program by the AEI (Spain/FEDER, EU, ID RyC2021-034291-I).

Application of Molecular Tools in Forensic Identification and Traceability of Protected Species: Implications for CITES Implementation

^{1*}Mas-Peinado, Paloma, ¹Villegas, Belén, ¹García, Sergio, ¹Fernández, Andrea & ¹Doadrio, Ignacio

*lead presenter: p.mas@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, España.

The international trade of wild species regulated under the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) poses a growing challenge for biodiversity conservation, particularly due to the illegal trafficking of specimens and derived products. In this context, molecular methodologies applied to systematics, phylogeny, and forensic identification have become essential tools for the effective implementation of CITES.

This study synthesises current and emerging approaches, including molecular phylogenetics, DNA barcoding, and genomics, used for the authentication and traceability of traded or seized specimens. It highlights cases where morphological ambiguity, evolutionary convergence, or product processing hinders accurate identification, emphasizing the need for standardized and validated molecular protocols.

Case studies include the genetic traceability of *Prionace glauca* (blue shark), often mislabeled in trade; African raptors, as well as other taxidermied animals and processed products, which are often challenging to identify; processed dehydrated holothurians (sea cucumbers), where morphological traits are obscured; Genetic analysis of a confiscated Galápagos giant tortoise; and hybrids between domestic cats (*Felis catus*) and wild felids such as *Leptailurus serval* or *Caracal caracal*, for which the degree of hybridization confirmed genetically determines their legal status.

DNA barcoding (COI, cyt b), Sanger sequencing, and phylogenetic analyses enabled the confirmation of species identities and, through low-coverage genome sequencing, the identification of hybrids. These results emphasize the critical role of validated genetic databases and standardized forensic workflows for reliable species determination.

These examples reinforce the role of molecular systematics in supporting precise, evidence-based, and legally robust biodiversity management under CITES. They also contribute to understanding evolutionary and phylogenetic patterns in high-value taxa and offer practical applications for authorities, enforcement agencies, and forensic laboratories. This integrative approach promotes resilient, taxonomically informed decision-making that support CITES conservation goals.

DNA barcode reference library for European ants: a roadmap for phylogeography and species discovery

^{1,2*}Mattia Menchetti, ^{1,3}Enrico Schifani, ⁴Fede García, ⁵Sämi Schär, ^{1,6}Elisabetta Sbrega, ⁷Nikola Balević, ²Bonnie B. Blaimer, ⁸Lech Borowiec, ⁹Dario Cioppa, ¹Cecilia Corbella, ^{10,11}Vlad Dincă, ¹²Vincenzo Gentile, ¹³Irakleitos Giotis, ¹⁴Kiko Gómez, ¹⁵José María Gómez Durán, ^{16,17}Konstantinos Kalaentzis, ¹⁸Albena Lapeva-Gjonova, ^{19,20}Emiliano Mori, ⁶Gerard Talavera, ²¹Alberto Tinaut, ²¹Francisca Ruano, ⁸Sebastian Salata, ²²Eduardo Sequeira, ^{1,23}Maria Serracanta, ²⁴Tomasz Suchan, ²⁵Paul DN Hebert, ²⁶Leonardo Dapporto, ¹Roger Vila

**lead presenter*

¹ *Institut de Biologia Evolutiva (CSIC-Univ. Pompeu Fabra), Barcelona, Spain*

² *Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Center for Integrative Biodiversity Discovery, Invalidenstraße 43, Berlin, Germany*

³ *Department of Chemistry, Life Sciences, and Environmental Sustainability, University of Parma, Parma, Italy*

⁴ *Barcelona, Spain*

⁵ *Dietikon, Zürich, Switzerland*

⁶ *Institut Botànic de Barcelona (IBB), CSIC-CMCNB, Barcelona 08038 Catalonia, Spain*

⁷ *University of Montenegro, Department of Biology, Podgorica, Montenegro*

⁸ *Department of Biodiversity and Evolutionary Taxonomy, Myrmecological Laboratory, University of Wrocław, Wrocław, Poland*

⁹ *Department of Biological, Geological and Environmental Sciences, University of Bologna, Bologna, Italy*

¹⁰ *"Grigore Antipa" National Museum of Natural History, Bucharest, Romania*

¹¹ *Ecology and Genetics Research Unit, University of Oulu, Oulu, Finland*

¹² *C.so Umberto I, 301, Torre Annunziata 80058 Naples, Italy*

¹³ *Division of Bioscience, University College, London, United Kingdom*

¹⁴ *Garraf, Barcelona, Spain*

¹⁵ *Madrid, Spain*

¹⁶ *Department of Genetics, Development & Molecular Biology, School of Biology, Faculty of Science, Aristotle University of Thessaloniki, Greece*

¹⁷ *Hydrobiological Station of Rhodes, Hellenic Centre for Marine Research, Rhodes, Greece*

¹⁸ *Department of Zoology and Anthropology, Faculty of Biology, Sofia University, Sofia, Bulgaria*

¹⁹ *Consiglio Nazionale Delle Ricerche, Istituto di Ricerca sugli Ecosistemi Terrestri, Via Madonna del Piano 10, 50019, Sesto Fiorentino, Italy*

²⁰ *National Biodiversity Future Center, 90133, Palermo, Italy*

²¹ *Department of Zoology, University of Granada, Campus de Fuentenueva s/n, Granada, Spain*

²² *Peral, Lisbon, Portugal*

²³ *Facultat de Biociències, Universitat Autònoma de Barcelona, Barcelona, Spain*

²⁴ *W. Szafer Institute of Botany, Polish Academy 1057 of Sciences, Kraków, Poland*

²⁵ *Centre for Biodiversity Genomics, University of Guelph, Guelph, Canada*

²⁶ *ZEN Lab, Department of Biology, University of Florence, Sesto Fiorentino, Florence, Italy*

Comprehensive sequencing of mtDNA and construction of reference DNA barcode libraries provide useful tools for specimen identification, highlighting potential new species and detecting introduced ones. This is particularly important in diverse and ecologically relevant groups, such as ants.

We present a comprehensive DNA barcode library for European ants with the aim of tackling the Linnean, Wallacean, and Darwinian shortfalls by providing an updated checklist, updated distributional ranges, genetic diversity maps, and mitochondrial gene trees.

The European ant fauna is here estimated to include 650 species, including one species reported for the first time from the continent and 24 species for the first time from 11 countries. Our genetic dataset covers 77.8% of this fauna (506 species), with 6,512 georeferenced COI sequences of which 62.3% are newly generated. We calculated intra- and inter-specific genetic distances and generated a total of 52 genus-level trees, genetic diversity, and specimen maps for 490 species, and haplotype networks for 288 species, all available in the Supplementary file as the atlas “The Genetic Diversity Maps of European Ants”.

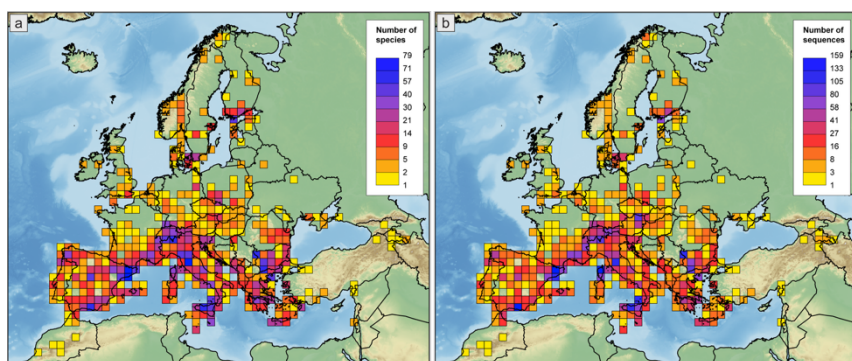


Figure: Number of species (a) and COI sequences (b) for each 100x100 km cell. Sequences from outside the study area were included only when they were not available from within it, for taxa described elsewhere, or for non-native species.

DNA barcoding performance largely varies among genera and species groups, likely reflecting biological (e.g., hybridisation, incomplete lineage sorting) and operational factors (e.g., taxonomy), and highlights the existence of potential cryptic taxa and the need for taxonomic revisions.

The intraspecific genetic maps we have generated provide insights into the mtDNA phylogeographic structure of European ants. The degree and patterns of population differentiation observed may be linked to species traits, human introductions, and genetic differentiation in glacial refugia and islands.

The data produced in this study offer a significant contribution to the evolving understanding of the biogeography of European ants, aiming to facilitate future research and species discovery.

Environmental DNA Monitoring for the Conservation of Native Fish in the Urban Manzanares River (Madrid, Spain)

¹*Ortiz-Blanco, Paula, ¹López-Solano, Alfonso, ¹Alcaraz, Lourdes, ¹Doadrio, Ignacio & ¹Perea, Silvia

*lead presenter: paula.ortiz@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales - CSIC

The Manzanares River constitutes the main hydrological artery flowing through the city of Madrid. This tributary of the Jarama River (Tagus Basin) was channelized in 1924, a modification that profoundly altered its natural flow and morphology, with major repercussions for its fish fauna. Today, it represents a highly transformed urban river ecosystem, heavily impacted by hydrological regulation, pollution, and the spread of exotic species, factors that have driven to the decline or local extinction of much of its native ichthyofauna. In recent years, a renaturalization plan has been developed in the Manzanares River, aiming to restore its ecosystems so they can once again support native fish species such as the bermejuela (*Achondrostoma numantinum*), the Iberian straight-mouth nase (*Pseudochondrostoma polylepis*), the Iberian chub (*Squalius pyrenaicus*), and the southern Iberian spined loach (*Cobitis paludica*). To this end, a captive breeding and release program is underway at several sites along the river where these species historically occurred. To evaluate the success of these reintroductions, a monitoring strategy based on environmental DNA (eDNA) has been implemented over the past two years. eDNA has emerged as an effective and non-invasive tool for biodiversity monitoring in conservation contexts. This methodology enables the simultaneous detection of multiple taxa through DNA fragments present in the water (metabarcoding), and it is particularly useful in urban ecosystems where traditional sampling methods present limitations. Water samples were collected from four sites in 2023 and five sites in 2024, covering urban and peri-urban stretches of the river across all four seasons, and were analyzed using the universal mitochondrial 12S rRNA *MyFish* marker. The analyses detected the presence of some reintroduced native species at various sites, as well as a diverse group of invasive species commonly found in Iberian rivers, whose spread poses a major challenge to the conservation of native ichthyofauna. Furthermore, this approach functions as an early warning system for the detection of new invaders, such as *Pseudorasbora parva*, a species of particular concern in Europe. This project exemplifies the application of advanced molecular techniques to the conservation of critically endangered native species in urban river ecosystems. eDNA-based monitoring offers robust, low-impact data that complements captive breeding and population reinforcement efforts, providing a key tool for the adaptive management of the Manzanares River and other Mediterranean rivers under similar environmental pressures.

Keywords: environmental DNA, Manzanares River, native ichthyofauna, invasive species, ex situ conservation.

Diversity of old canary *Coffea* plants

^{1,2},*Pérez, Verónica; ³Marante, J. Antonio; ³González-Díaz, A. Javier; ⁴Sosa, José Manuel; ⁴García, Santiago; ¹Moreno, Javier; ⁵Ríos-Mesa, Domingo; ⁶Cubas, Pedro; ¹Reyes-Betancort, J. Alfredo

*lead presenter: vperez@icia.es

¹ Jardín de Aclimatación de La Orotava, Instituto Canario de Investigaciones Agrarias, Spain.

² Laboratorio de Agrobiología Juan José Bravo Rodríguez (Cabildo de La Palma), Unidad Técnica del Instituto de Productos Naturales y Agrobiología (IPNA-CSIC), Spain

³ Cabildo Insular de La Palma, Servicio de Agricultura, Santa Cruz de La Palma, Spain.

⁴ Cabildo Insular de Gran Canaria, Servicio de Agricultura, Las Palmas de Gran Canaria, Spain.

⁵ Departamento de Ingeniería Agrícola y Medio Natural, Universidad de La Laguna, La Laguna, Spain

⁶ Cabildo Insular de La Gomera, Servicio de Agricultura, San Sebastián de La Gomera, Spain.

Coffee is one of the most important commodities worldwide, with an estimated annual production of 11 million tons. The coffee we consume comes mainly from two species: *Coffea arabica*, appreciated for its high quality and aroma, and *Coffea canephora* (commonly known as Robusta), which is more productive but considered of lower quality. Both species are native to Africa, where there are other *Coffea* species. Currently, 131 *Coffea* species are accepted, distributed in Africa, Asia and Oceania. The commercial coffee species were introduced and expanded across the world, mainly in South America. In the Canary Islands, coffee has been known for many years, and probably introduced like other tropical species through trade with American regions. In the archipelago, coffee has traditionally remained in family gardens, and the seeds of the cherry fruits were roasted and ground coffee at home. Coffee cultivation and production require significant labor, making it unprofitable at low production scale. However, in recent years, a market to select coffees, produce in unique environments, is having high prices. In this context, small scale production has gained relevance. The isolated trees that still remain in some gardens were used for propagation and the establishment of commercial coffee orchards, first in Gran Canaria and later in La Palma, La Gomera, and Tenerife. This coffee is sold as brewed coffee to tourist or in small gourmet bag packages. Canarian coffee plants are free from the main diseases that affect major production areas, and the cultivated plants are not part of recent breeding programs that generate resistant plants. In this study, we analysed isolated old coffee trees from Gran Canaria, La Palma, La Gomera, and some plants from Tenerife using SSR molecular markers to assess the genetic diversity among them. We also included specimens from the Jardín de Aclimatación de La Orotava (Tenerife), a botanical garden founded in 1788 that received early introductions of tropical species, including coffee, to evaluate whether the cultivated plant could descend from these introductions or have a different origin. Preliminary analysis indicated a high degree of similarity among numerous samples from the four islands, predominantly corresponding to *Coffea arabica* var. *Typica*. Nonetheless, additional genetic profiles were identified, associated with varieties such as 'Bourbon', 'Castilla' or 'Gehisa', likely reflecting both historical and more recent introductions.

Taxonomic composition of microfauna associated with macroalgal assemblages of Tenerife island

^{1*}Ugena, Aitor, ^{1,2}Alfonso, Beatriz & ^{1,2}Hernández, José Carlos.

*lead presenter: a.ugena2001@gmail.com

¹ Marine Community Ecology and Conservation. Dpto. Biología Animal, Edafología y Geología. Universidad de La Laguna, Tenerife, Canary Islands, Spain

² Marine Community Ecology and Conservation. Dpto. Botánica, Ecología y Fisiología Vegetal. Universidad de La Laguna, Tenerife, Canary Islands, Spain

Marine benthic microinvertebrates play a key role in coastal ecosystem functioning, yet their associations with specific macroalgal communities remain poorly understood, particularly in subtropical island environments. Macroalgae not only provide food, but other important features of the ecological niche, such as habitat complexity for shelter, proper environmental chemical composition, etc. Understanding how microinvertebrate assemblages vary across algal communities is therefore essential to uncover patterns of habitat preference, ecological specialization, and potential bioindication of certain environmental features.

In this study, we characterized the structure and taxonomic composition (at phylum, family, and species levels) of microinvertebrates associated with four dominant macroalgal assemblages in Tenerife (Canary Islands): *Dictyota* spp., *Asparagopsis* spp., *Lobophora* spp., and a consortium of red algae. These macroalgal groups differ markedly in morphology and ecological traits, offering an ideal environmental spectrum to explore benthic associations in detail.

Sampling was performed at the two main sea seasons for the archipelago, with thermocline-warm season (23,5°) and without thermocline-cold season (18,5°), allowing us to capture the temporal variability for the benthic community composition. Our results provide a valuable reference point for identifying habitat preferences of specific taxa and can serve as a practical tool for researchers working on microinvertebrate groups, helping them to locate target species more efficiently based on their algal affinities. This kind of data is currently lacking for the region and represents a significant contribution to the understanding of benthic biodiversity and systematics of the Macaronesian coastal marine ecosystem.

Analyses has revealed clear differences in community composition across algal types and between seasons, in all the taxonomic levels that we have studied. For instance, the *Dictyota* community hosted a broader range of phyla in warmer months, when *Asparagopsis* and *Lobophora* were associated with specific groups such as arthropods or annelids. In contrast, The red algae consortium and *Lobophora* showed the lowest number of phyla, but contained some unique ones.

BioMonI-Genes: Advancing DNA-Based biodiversity monitoring on oceanic islands

¹*Paloma Martínez-Boix, ¹Brent C. Emerson, ¹Abraham Padilla, ¹Javier Tuero-Septién, ²Agustín Naranjo-Cigala, ³Nereida M. Rancel-Rodríguez, ³Ana Losada-Lima, ¹Lucía Bernardos-Concepción, ¹Carmen Balibrea-Escobar, ¹Raúl Orihuela-Rivero, ¹Óscar Castillo-Agudo & ¹Jairo Patiño

*lead presenter: paloma.boix@ipna.csic.es

¹ Island Ecology and Evolution Research Group, Instituto de Productos Naturales y Agrobiología, Consejo Superior de Investigaciones Científicas (IPNA-CSIC), Tenerife, Spain.

² Department of Geography, University of Las Palmas de Gran Canaria, Las Palmas de Gran Canaria, Spain.

³ Department of Botany, Ecology and Plant Physiology, University of La Laguna, Tenerife, Spain.

Within this framework, the work package led by the Spanish National Research Council (CSIC) targets overlooked aspects of biodiversity in oceanic island flora and invertebrate communities, with a special focus on the Canary Islands. Using DNA-based monitoring approaches, the project seeks to enhance our understanding of phylogenetic diversity and community structure.

To achieve this, we are employing a combination of Sanger and high-throughput sequencing (HTS) technologies to identify effective strategies for characterizing phylogenetic diversity and community composition across spatial scales and habitat types. This dual approach balances resolution and coverage, enabling extensive molecular sampling.

Four permanent 50 × 50 m plots have been established in the laurel forest of Anaga Rural Park (Tenerife), a biodiversity-rich ecosystem. Samples were collected across major plant lineages (including vascular plants, ferns, bryophytes, and green microalgae) with the goal of constructing a representative, DNA-based framework for assessing phylogenetic diversity at multiple taxonomic and ecological levels. Complementary passive trapping and barcode sequencing of flighted invertebrates is also being implemented to (i) assess the scalability of such approaches within insular forest ecosystems, and (ii) better characterise the less understood “dark taxa” within such ecosystems.

This integrative effort supports long-term biodiversity monitoring and provides essential tools to detect shifts in ecosystem composition and function, particularly on vulnerable oceanic islands facing the accelerating impacts of global change.

Digging into the entry point: assessing and monitoring the role of imported vegetation trade in introducing non-native soil species (*POLIZON*)

^{1*}Borrallo-Solís, María; ^{1,2}Vega-Pita, Nira; ^{1,2}Santos-Perdomo, Irene; ^{1,2}Nieto-Cabrera, Victoria;
¹Falcón-López, Lorenzo; ¹Balibrea-Escobar, Carmen; ¹Andújar, Carmelo & ¹Arribas, Paula

*lead presenter: mborrallosolis@ipna.csic.es

¹ Instituto de Productos Naturales y Agrobiología (IPNA – CSIC), 38206, La Laguna, Tenerife, Canary Islands, Spain

² School of Doctoral and Postgraduate Studies, University of La Laguna, 38206, La Laguna, Tenerife, Canary Islands, Spain

Globalisation, driven by the increasing economic, technological, cultural, political, and environmental exchanges worldwide, entails a variety of risks that humanity currently faces. One of these, in the context of environmental conservation, is the rise of non-native species introductions, both intentional and unintentional, which can threaten native biodiversity. In many cases, such impacts are easily perceived, e.g., when involving larger species with high adaptability and proliferation rates, which produce direct effects on the economy and society of the colonised areas. However, there are other scenarios in which such impacts are not immediately evident, and their study can be considerably complex.

In the context of soil biodiversity, the effects of introduced species on native biodiversity remain largely unexplored. Nevertheless, the import and export of seedlings or saplings is particularly concerning due to the potential unintentional co-introduction of soil mesofauna that travel in the substrate as “stowaways”. While EU and national legislation on vegetation trade and import/export activities mainly focus on quarantine species (specific priority plant pests), the quantification and management of soil mesofauna (not considered quarantine species) that could be co-introduced through vegetation trade appears to be the “elephant in the room”, an overlooked problem.

Here, we introduce the POLIZON project, whose main objectives are: (i) to provide the first quantitative measures of co-introduced soil mesofauna species in the imported vegetation trade, and (ii) to design and evaluate an early detection tool for introduced species in substrates using eDNA metabarcoding. To achieve these goals, POLIZON employs wocDNA metabarcoding as an innovative approach to detect and characterize introduced species in soils and substrates associated with the ornamental plant trade in Tenerife. To date, we have processed 248 community samples from nursery facilities across the island. Preliminary results from the project reveal a high occurrence of soil mesofauna in soils and nursery pot substrates. Further steps will focus on identifying the drivers of the prevalence of introduced species and evaluating simplified eDNA approaches for detecting introduced mesofauna using reduced soil volumes, as a potential biosecurity tool.

Evaluating variations of the Flotation-Berlese-Flotation approach for wocDNA metabarcoding of soil mesofauna

^{1,2*}Nieto-Cabrera, Victoria, ¹Falcón-López, Lorenzo, ^{1,2}Santos-Perdomo, Irene, ³Moro, Gioele, ^{1,2}Vega-Pita, Nira, ¹Balibrea-Escobar, Carmen, ¹Borrallo-Solís, María, ¹Arribas, Paula & ¹Andújar, Carmelo

*lead presenter: v.nieto@ipna.csic.es

¹ Instituto de Productos Naturales y Agrobiología (IPNA-CSIC), Tenerife, Canary Islands, Spain

² School of Doctoral and Postgraduate Studies, University of La Laguna (ULL), Tenerife, Canary Islands, Spain

³ Institute of Entomology, Biology Centre CAS, České Budějovice, Czech Republic

Soil mesofauna plays a fundamental role in ecosystem functioning and yet remains one of the frontiers of scientific knowledge. Advances in *high-throughput sequencing* (HTS) techniques and the adoption of novel approaches, such as the use of *whole organism community* DNA (wocDNA) metabarcoding, are enabling deeper insights into these communities. An efficient extraction of soil mesofauna is a key first step for their study through this framework.

One of the methods used for mesofauna extraction is the Flotation–Berlese–Flotation (FBF) protocol. In this study, surface and deep soil samples were collected from pine and laurel forests on the island of Tenerife (Canary Islands, Spain) to evaluate, from the perspective of wocDNA metabarcoding, the performance of different modifications to the FBF protocol: one consisting of omitting the initial flotation step, and another involving the use of modified Berlese extraction devices instead of standard funnels. Additionally, we compared the effect of sonication versus mechanical homogenization (grinding) on the extracted communities.

Analysis of haplotype and 3% lineage richness for mites (Acari), springtails (Collembola), and beetles (Coleoptera) showed that performing the initial flotation step, using unmodified Berlese funnels, and applying mechanical homogenization all resulted in significantly higher richness compared to treatments without flotation, with modified extraction devices, or using sonication. At the taxonomic order level, the initial flotation step enabled significantly higher haplotype and 3% lineage richness for mites and beetles. Similarly, the use of unmodified Berlese funnels and grinding of extracted communities yielded greater richness for mites and springtails, compared to their respective alternatives.

Retinoic Acid Pathway Conservation in Evolution: Insights from Planarians

¹*Cuadrado, Daniel

*lead presenter: cuadradopm@hotmail.com

¹ Department of Genetics, Microbiology and Statistics, University of Barcelona, Spain

Retinoic acid (RA), a metabolite of vitamin A (retinol), is one of the most conserved morphogens across Metazoa and plays a crucial role in embryonic development, body axis patterning, and organogenesis. The RA signaling pathway has shaped key developmental processes by regulating gene transcription through nuclear receptors, forming a fundamental axis for morphological innovation and tissue plasticity.

The origin of the RA pathway traces back to the common ancestor of bilaterians and relies on a tightly regulated sequence of metabolic conversions, transforming dietary β -carotenes and retinal esters into retinal, then into retinol and finally into retinoic acid (through enzymes including carotene oxygenases, BCO1/BCO2; retinol dehydrogenases, RDH; aldehyde dehydrogenases, ALDH1; among others).

Orthologs of these key metabolic enzymes and the nuclear receptors, retinoic acid receptors (RARs) and retinoid X receptors (RXRs), have been identified in deuterostomes (including vertebrates, urochordates, cephalochordates and ambulacrarians) and also in several protostome lineages, such as annelids, mollusks and some ecdysozoans like arthropods. However, this toolkit displays an uneven distribution today, with multiple independent losses of RAR documented in ecdysozoans (arthropods, nematodes) and in flatworms. While chordates have retained a well-conserved RAR/RXR module, many non-chordates rely on RXR and alternative co-regulators to maintain RA sensitivity, underlining the flexibility and evolutionary plasticity of this ancestral signaling system.

Planarians (flatworms), provide an exceptional model to study the link between RA signaling, development and regeneration. In *Schmidtea mediterranea*, no RAR genes have been detected, consistent with the gene losses observed in other protostomes such as arthropods and nematodes. However, RXR homologs with conserved DNA and ligand-binding domains are present and likely functional. Recent genomic analyses suggest that RXR, together with co-regulators like the RERE complex, may compensate for the absence of RAR and mediate RA-dependent transcriptional control. Experiments in *S. mediterranea* have shown that physiological concentrations of RA can modulate neoblast proliferation. These findings raise new questions about how RA pathway components diverge and adapt in different lineages, and about their implications in developmental processes and regenerative capacities.

A First Glimpse into DNA Methylation in the Mediterranean Earthworm *Carpetania matritensis*

^{1*}Tilikj, Natasha, ¹Fernández Marchán, Daniel & ¹Novo, Marta

*lead presenter: ntilikj@ucm.es

¹ Biodiversity, Ecology and Evolution Department, Faculty of Biological Sciences, Complutense University of Madrid, Madrid, Spain

DNA methylation is a key epigenetic mechanism largely unexplored in invertebrates, including earthworms, which play a vital role in soil ecosystems. Methylation patterns were analyzed across key tissues involved in fundamental earthworm physiological processes. To link epigenetic regulation with physiology, tissue pairings with complementary functions were compared: anterior digestive tissue versus posterior segment tissue for distinct phases of digestion, nephridia versus tegument for coordinated excretion and osmoregulation, nervous tissue versus tegument for sensory perception and motor control, and pseudohearts versus tegument for circulation and cutaneous respiration. Using a bioinformatic approach, key differentially methylated genes (DMGs) associated with essential biological processes were identified, providing insights into how methylation regulates core earthworm functions.

Digestion-related tissues showed the highest number of DMGs, particularly in hypomethylated regions, while sensory perception tissues exhibited fewest DMGs overall. Most genes showed no direct link between differential methylation and gene expression, with over 80% remaining unchanged and only a small proportion being up- or downregulated across all comparisons.

Digestion is characterized by methylation differences affecting microvilli organization and signaling pathways involved in cell differentiation and homeostasis. In excretion, methylation appears to regulate filtration through channels and transporters as well as ciliogenesis. Sensory perception was influenced to a lesser extent, with the nervous vs. tegument pairing primarily defined by methylation changes in genes related to axon homeostasis. Finally, methylation also impacts regulatory pathways involved in circulatory system maintenance, potentially enabling rapid adaptations to fluctuating blood pressure. These findings offer the first insight into tissue-specific methylation in earthworms, opening new avenues for epigenetic research in invertebrates.

Host plant-driven physiological variation in a polyphagous migratory butterfly

¹*Díaz-Martínez, Gemma, ¹Vicelja, Mara, ¹Vilaseca, Iu, ¹Valenzuela, Laura, ¹Sbrega, Elisabetta, ¹Peraki, Danai, ¹Temes, Javier, ¹Talavera, Gerard

*lead presenter: gemma.diaz@ibb.csic.es

¹ Institut Botànic de Barcelona (IBB, CSIC), Spain

Migratory behaviour is a response to ecological heterogeneity. In Lepidoptera, the evolution of migration is often linked to polyphagy – the adaptation of immatures to develop on multiple hostplants. This adaptive strategy broadens biogeographic potential and buffers populations against environmental variability. Moreover, the use of different host plants across regions may shape physiological capacity and influence migratory decisions. Yet, the physiological implications of larval host breadth for traits underpinning migration remain poorly understood. Here, we take an integrative approach to explore how larval diet influences migration-relevant physiology in the painted lady butterfly (*Vanessa cardui*), a cosmopolitan, polyphagous migrant. We reared ~300 individuals on 14 host plants and quantified developmental, metabolic rate, morphological, energetic and gut microbiome traits across stages. Diet most strongly affected developmental timing: hosts differed markedly in the growth rate–development time trade-off, whereas adult body mass largely converged across diets. Metabolic effects were stage-dependent—pronounced in early larvae and attenuated by pupation. Adults exhibited a >18-fold increase from resting to flight metabolic rate irrespective of sex; mean fat stores were broadly similar among diets, but resting metabolic rate scaled with fat in a host-specific manner, indicating that fuel economy, not fuel amount alone, differentiates phenotypes. Wing size was also different across hosts, though shape remained largely buffered. Gut communities tracked host identity in larvae but were more homogeneous in adults, consistent with transient, diet-linked microbiota and partial reset across metamorphosis. Together, these results show that no host plant maximises all traits simultaneously. Instead, larval diet influences migration-relevant physiology through allocation trade-offs, with early nutritional effects later reshaped by metamorphosis. By providing the first integrative map of diet–migration trade-offs in *V. cardui*, this study advances our understanding of how polyphagy constrains and modulates migratory capacity in insects.

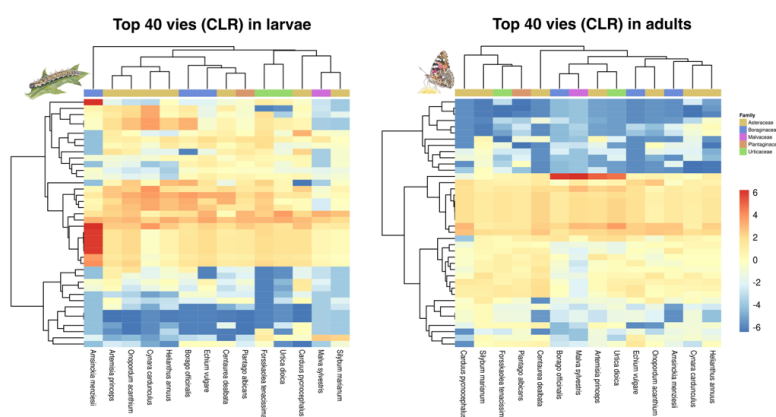


Fig.1. Heatmap for top 40 microbial metabolic routes in gut's larvae and adult

The Secret relationships within Syllidae: disentangling their microbiota

¹*Víctor Ruiz-López , ²Cristina Díez-Vives, ³Elena Andrés, ³Ana Riesgo, ¹Patricia Álvarez-Campos

**lead presenter*

¹ Dpto. Biología & Centro de Investigación en Biodiversidad y Cambio Global (UAM, Madrid, España)

² Centro Nacional de Biotecnología (CSIC, Madrid, España)

³ Museo Nacional de Ciencias Naturales (CSIC, Madrid, España)

Although the microbiome is increasingly acknowledged as a key factor in the evolutionary success of marine invertebrates, the microbial symbionts associated with Syllidae polychaete annelids remain largely unexplored, even though their ecological significance as one of the main components of the oceanic benthos. Moreover, the genetic and environmental drivers shaping microbial communities at the intraspecific level have not yet been investigated in this family.

To address this gap of knowledge, we have analyzed the microbiomes of multiple syllid species collected in Mediterranean Sea, Pacific and Atlantic Oceans using 16S rRNA gene amplicon sequencing. Furthermore, we have examined whether geographic location or genetic structure of conspecific syllids mainly collected in the Canary Islands, influences their microbial assembly. In contrast to what was previously suggested in a genus within this family, our results show the microbiome is not species-specific. However, a certain degree of specificity was observed at the genus level. In addition, we have identified that widely distributed genus *Syllis*, harbors a great diversity of microbiota. Finally, we found that microbiome seems to be more strongly influenced by geographical factors than by genetic factors, at least at the genus level.

Overall, our findings indicate that, in syllid species exhibiting high gene flow, microbial community composition appeared to be shaped more by geographic location than by host genetic divergence.

The nuclear and mitochondrial genomes of the lined rockskipper, *Istiblennius lineatus* (Teleostei: Blennidae)

^{1*}Víctor M. Valencia-Cárdenas, ^{1,2}Nikita Kulikov, ³Francisco J. Ruiz-Ruano, ⁴Alexander Ben Hamadou, ⁴Carola Greve, ⁵Diego F. B. Vaz, ⁶Terry J. Ord, ^{1,2}Iker Irisarri

**lead presenter*

¹ *Department of Biodiversity and Evolutionary Biology, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, Spain*

² *Leibniz Institute for the Analysis of Biodiversity Change, Museum of Nature Hamburg, Hamburg, Germany*

³ *Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig Bonn, Bonn, Germany*

⁴ *Senckenberg Research Institute and Natural History Museum Frankfurt, Frankfurt am Main, Germany*

⁵ *Natural History Museum, London, UK*

⁶ *Evolution and Ecology Research Centre, and the School of Biological, Earth and Environmental Sciences, University of New South Wales, Kensington, New South Wales, Australia*

The family Blenniidae (combtooth blennies) comprises cryptobenthic fishes of high ecological relevance in coastal and reef ecosystems. Despite their evolutionary diversity and importance, genomic resources for this group remain limited. Here, we report the nuclear chromosome-scale and mitochondrial genome assemblies for the lined rockskipper, *Istiblennius lineatus* (Valenciennes 1836). The assemblies were produced using PacBio HiFi long-read sequencing and Arima Hi-C scaffolding technology. The assembled genome is 643.3 Mb in size, with a scaffold N50 of 23.5 Mb, a contig N50 of 9.23 Mb and a GC content of 43.34 %, consistent with other combtooth blenny genomes. We reconstruct the 24 pseudochromosomes expected from karyotype studies, which account for 83% of the genome assembly. The genome is highly complete (>97% BUSCO completeness) and free of haplotypic duplication and contaminations. The genome is annotated using direct RNAseq and protein homology evidence. We analyze the macro-synteny against other available combtooth blenny genomes. The mitochondrial genome is 16.5 kb in length and has the genome content and order expected for the family. Both genome assemblies, mitochondrial and nuclear contribute to addressing the current paucity of genomic data in the Blenniidae and supports future research into the evolution and ecology of this intertidal species.

Exploring genomic signatures of adaptation in South American populations of *Drosophila melanogaster* and *D. simulans*

^{1*}Carlos Tinedo, ²Carlos E. Arboleda, ³Eduardo Amat, ^{1,4}Dorcas Orengo, ¹Andrea Barrio, ^{1,4}Alejandro Sánchez-Gracia

*lead presenter: carlosmunyoztinedo@gmail.com

¹ Departament de Genètica, Microbiologia i Estadística, Universitat de Barcelona, Barcelona, Spain

² Neuroscience Group, Genetics Institute, Universidad Nacional de Colombia, Bogotá, Colombia.

³ Faculty of Law and Forensic Sciences, Tecnológico de Antioquia, Institución Universitaria, Medellín, Colombia

⁴ Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Barcelona, Spain

The worldwide expansion of *Drosophila melanogaster* and its sibling species *D. simulans* from their ancestral range in Africa provides an exceptional framework to investigate the genomic basis of adaptation. In *D. melanogaster*, several comprehensive population genomic studies have revealed numerous genes and genomic regions targeted by positive selection in natural populations from different continents. A striking and controversial observation emerging from this work is the geographic heterogeneity of selective signatures: while European and African populations show frequent evidence of hard sweeps, in North American populations, signals of recent selection appear more consistent with soft sweeps. By contrast, genomic studies in *D. simulans* remain scarce, leaving important gaps in our knowledge of its adaptive history. Another important limitation is the complete absence of population genomic studies on these two species in South America, a region with considerable geographic and environmental variation where potential adaptive responses remain unexplored. In this study, we use Pool-Seq data, probabilistic models, and various summary statistics of nucleotide variation to perform genome-wide scans for selection in a large set of natural populations of both *D. melanogaster* and *D. simulans* sampled across Colombia. Our aim is to characterize the contribution of hard and soft sweeps to the adaptation history of these species in South America in order to compare their adaptive architectures. This approach offers the opportunity to study both shared and species-specific genomic responses to selection and to better understand how demography, local environmental pressures, and genome architecture, determine the tempo and mode of adaptation.

Across the hemispheres: a roadmap to understand genome evolution in migratory butterflies

¹*Cavalcanti, Clara, ¹García-Berro, Aurora, ¹Talavera, Gerard

*lead presenter: clara.cavalcanti@ibb.csic.es,

¹ Botanical Institute of Barcelona (IBB-CSIC), Spain

Animal migration is a key behavioral adaptation to seasonally variable resources. In insects, the vast scale and ecological importance of seasonal migrations are increasingly recognized, yet knowledge about the phylogeography and genome evolution of migratory insects is limited. The concept of migratory divides, i.e. geographic boundaries where neighboring populations adopt divergent migratory routes, is well established in vertebrates but largely unexplored in insects. Recent work on the painted lady (*Vanessa cardui*), the most cosmopolitan migratory butterfly, revealed that distinct migratory phenotypes in the hemispheres are associated with strong intraspecific genetic differentiation. This discovery raises the possibility that hemispheric asymmetries, driven by inverted seasonal regimes, may promote diversification in highly mobile insects. Here, we explore whether other migratory lineages are similarly segregated across the equator and investigate their genomic architectures. At the interspecific level, several pairs of migratory sister species occur in opposite hemispheres, sometimes meeting only in narrow contact zones around the equator. While iconic species such as the painted lady and the monarch (*Danaus plexippus*) have yielded key genomic insights, progress across other migratory butterflies has been hindered by the lack of reference genomes and population genomic data. To fill this gap, we generate PacBio and Omni-C chromosome-level genome assemblies for six species/populations and compare with their close relatives in the opposite hemisphere, including *Danaus erippus* (the South American sister of the monarch), the African *Belenois aurota* (showing marked hemispheric genetic differentiation) and its Australian sister *B. java*, and a southern representative of *V. cardui*, characterized by a large chromosomal inversion underlying the hemispheric migratory divide. Our assemblies are highly contiguous (<70 contigs, N50>8Mb) and complete (BUSCO >97.3%). We also report the smallest known butterfly genome to date (*Belenois java*, 197 Mb). We then combine ab initio and homology-based annotation with whole-genome alignments to characterize synteny, structural rearrangements, repeat landscapes, and gene family evolution between sister species. Together, our incipient results start illuminating how large-scale migratory behavior influences genome evolution in butterflies, highlighting contrasting hemispheric cues as potential drivers of diversification and offering new insights into the evolutionary significance of migration.

Population genetics and gene flow in coastal fragmented habitats: a study of western Mediterranean supratidal rockpool beetles

^{1*}García-Meseguer, Antonio José, ²Muñoz, Irene, ³Abellán, Pedro, ^{4,5}Villastrigo, Adrián, ¹Mirón-Gatón, Juana María, ¹Millán, Andrés & ¹Velasco, Josefa

*lead presenter: aj.garciameseguer@um.es

¹ University of Murcia, Spain

² Complutense University of Madrid, Spain

³ University of Seville, Spain

⁴ SNSB-Zoologische Staatssammlung, Germany

⁵ University of León, Spain

Supratidal rockpools, located at the interface between land and sea, are highly fragmented habitats characterized by extreme and fluctuating environmental conditions and hosting unique species such as *Ochthebius* beetles. These beetles, which exhibit broad geographical ranges and cryptic lineages in the western Palaearctic, represent valuable models for studying population genetic processes in coastal ecotones.

This study investigates the impact of geographic and environmental distances, coastal features, and marine barriers on the genetic structure and connectivity of three co-occurring species in the western Mediterranean. Across species, we observed consistently low genetic diversity and comparable levels of heterozygosity. However, *Ochthebius quadricollis* exhibited higher diversity and notable population variations, standing out as the only species with significant genetic structure. AMOVA indicated substantial genetic variation among predefined groups within this species, for which an association was found between genetic differentiation and geographical distances.

Our research highlights generally high levels of connectivity and gene flow among supratidal rockpool populations, likely driven by passive dispersal mechanisms. Nonetheless, the three species exhibit distinct spatial genetic patterns along the Iberian coast. While our findings broadly align with previous large-scale studies using less sensitive markers, important discrepancies emerged, especially regarding the role of the Ibiza Channel as a barrier. Finally, our data suggest that marine currents contribute little to recent gene flow, probably due to the stochastic nature of passive dispersal events.

Preliminary molecular insights into Moroccan termites, based on mitochondrial DNA analysis

^{1,3*}Najjari, Aya, ²Hernández-Teixidor, David, & ¹Taheri, Ahmed

*lead presenter: najjari.a@ucd.ac.ma

¹ LESCOB URL-CNRST N° 18, FS, Abdelmalek Essaadi University, Tetouan, Morocco.

² Island Ecology and Evolution Research Group, Instituto de Productos Naturales y Agrobiología (IPNA-CSIC), 38206 La Laguna, Tenerife, Canary Islands, Spain.

³ LP2E, FS, Chouaib Doukkali University, El Jadida, Morocco.

Termites are key ecosystem engineers, yet their molecular diversity in North Africa remains poorly documented. To address this gap, we generated the first molecular dataset of Moroccan termites using the mitochondrial DNA. Samples were collected from multiple regions across Morocco, covering diverse habitats and termite lineages. Specimens were sequenced and analyzed through maximum-likelihood phylogenetic reconstruction.

A total of 399 mitochondrial sequences were obtained, revealing well-defined genetic structuring among the principal families (Hodotermitidae, Kalotermitidae, Psammotermitidae, Termitidae). Populations from different Moroccan localities showed clear genetic signals, highlighting the role of geography in shaping termite diversity.

These findings provide the first molecular framework for Moroccan termites and a basis for understanding their evolutionary history and biogeographic patterns in Morocco. Ongoing work will incorporate new genetic markers and morphological data to refine species delimitation, resolve ambiguous placements, and achieve a more detailed understanding of termite diversity and biogeography in the region.

Genomic insights on the laurel forest tree species of Tenerife

¹*Tuero-Septién, Javier, ¹*Padilla, Abraham, ¹*López-González, Mercedes, ¹García-Monzón, Irma, ¹López-Soria, Juan Miguel, ¹Sinka, Victoria, ¹Padrón, Juan I. & ¹Patiño, Jairo.

*lead presenters: jturo@ipna.csic.es, abraham.padilla@csic.es & m.lopez@csic.es.

¹ Institute of Natural Products and Agrobiology, National Spanish Research Center (IPNA-CSIC), Tenerife, Canary Islands.

The Macaronesian laurel forest represents one of the last remnants of the Palaeotropical–Tethyan Geoflora, once widespread across Europe and North Africa but today confined to the northern Macaronesian archipelagos (Azores, Madeira, and the Canary Islands). Despite its role as a biodiversity hotspot, this forest is highly vulnerable due to its reduced and fragmented distribution, largely driven by centuries of human disturbance. In Tenerife, the laurel forest is structured by c. 20 tree species spanning diverse families, phylogenetic lineages, and biogeographical origins, many of which exhibit contrasting levels of conservation concern. To disentangle their evolutionary history and clarify taxonomic relationships, integrative approaches combining DNA barcoding, next-generation sequencing (NGS), and classical systematics are essential. Such studies provide critical insights into inter- and intraspecific dynamics, with implications for both evolutionary biology and conservation management.

Building on this evolutionary and conservation framework, the “*Librería de Productos Naturales de Tenerife (LiPNaT)*” project, funded by the Cabildo de Tenerife, leverages the unique biodiversity of Tenerife’s laurel forest to explore links between species’ evolutionary identities and their phytochemical profiles. Using a Hyb-Seq, hybridization-based approach targeting universal nuclear loci, we first confirm the taxonomic identity of each lineage and generate a comprehensive repository of DNA and genomic information. This framework enables the exploration of potential correspondences between individual specimens, their natural products, and underlying genomic variation. In parallel, we develop protocols to create and preserve herbarium vouchers digitally linked to representative specimens, capturing all diagnostic morphological characters. Together, these approaches provide an integrative platform connecting systematics, genomics, and phytochemistry, advancing both evolutionary studies and the sustainable utilization of native plant diversity on Tenerife island.

Taxonomic Review of the Genus *Urtica* L. (*Urticaceae*) in the Canary Islands: Morphological Description and Dichotomous Key

¹*Agraso San Narciso, Sofía, ¹*González-Montelongo, Cristina, ²Reyes-Betancort, J. Alfredo &
²Padrón-Mederos, Miguel A.

*lead presenter: alu0101328539@ull.edu.es

¹ Universidad de La Laguna, Spain

² Jardín de Aclimatación de La Orotava (JAO, ICIA), Spain

In the Canary Islands, the genus *Urtica* L. is represented by four species; *Urtica membranacea* Poir., *U. morifolia* Poir. —a Macaronesian endemic—, *U. stachyoides* Webb & Berthel. —a Canarian endemic—, and *U. urens* L. Although some of them play an important ecological role in the islands, their taxonomic identification remains challenging due to the limited morphological differentiation among some of the aforementioned taxa. Within the framework of this study, a taxonomic revision of the *Urtica* species present in the Canary Islands was carried out, describing their morphological, ecological, phenological characters, and conservation status based on fresh and herbarium material (deposited in the ORT and TFC Herbaria). These descriptions were compared with the consulted literature. Finally, an identification key adapted to the four species recorded in the archipelago is proposed.

One Thousand Reasons to Explore the Deep-sea

^{1*}González-Casarrubios, Alberto, ²Sánchez, Nuria, & ³Martínez Arbizu, Pedro

*lead presenter: albert23@ucm.es,

¹ Universidad Complutense de Madrid, Faculty of Biological Sciences, Department of Biodiversity, Ecology and Evolution. Madrid, Spain.

² Universidad Complutense de Madrid, Faculty of Biological Sciences, Department of Biodiversity, Ecology and Evolution. Madrid, Spain.

³ Senckenberg am Meer, German Centre for Marine Biodiversity Research (DZMB). Wilhelmshaven, Germany.

The deep ocean remains one of the least explored frontiers of biodiversity on Earth. Despite being the largest ecosystem on the planet, only an estimated 24–34% of animal diversity is formally described, with taxonomic gaps being particularly acute in deep-sea environments and for microscopic taxonomic groups. Among the most neglected animal phyla are Kinorhyncha and Loricifera, for which current estimates suggest that only 20% and 5% of their global diversity, respectively, are known. In response to this knowledge deficit, the Sustainable Seabed Knowledge Initiative (SSKI), and its program “One Thousand Reasons”, was launched by the International Seabed Authority to promote the discovery and description of at least 1.000 new deep-sea species from areas beyond national jurisdiction by 2030, in line with the United Nations 2030 Agenda for Sustainable Development. Within this framework, our project aims to advance the systematic study and formal description of deep-sea Kinorhyncha and Loricifera across a truly global scale, encompassing samples from oceans and regions spanning pole to pole.

Since the project’s inception, substantial progress has been achieved. In total, five new species of Kinorhyncha and one of Loricifera have been identified so far, with several more under investigation. Remarkably, one of these Kinorhyncha species shows morphological characteristics never observed in adults of its order, challenging long-held assumptions in kinorhynch taxonomy. Their formal descriptions are being developed through an integrative approach that combines LM, SEM, CLSM, and molecular data.

This contribution highlights the first outcomes of an ongoing effort to bridge the deep-sea taxonomic gap in meiofaunal biodiversity. At a time when species are going extinct before they are even discovered, taxonomy remains a cornerstone for understanding and preserving life on Earth. Moreover, documenting hidden biodiversity in the deep sea provides essential baselines for responsible management of seabed ecosystems in the context of increasing human activities, including prospective mining, offshore energy infrastructure, or submarine cables.

Morphology-Based Phylogeny of the Genus *Dendrophyllia* (Scleractinia: Dendrophylliidae) from the Canary Islands

*González-Porto, M. , A. Jurado-Ruzafa, J.E. Rodríguez-Riesco, S. Domínguez-Guerra, B. García-Mañé, Y. González-Rodríguez, C. Hernández-González, S. Jiménez-Navarro, L. Martín-García, J.C. Mendoza, S. Oliva and P. Martín-Sosa

*lead presenter, gonzalez@ieo.csic.es

Oceanographic Center of the Canary Islands (COC), Spanish Institute of Oceanography (IEO-CSIC), Spain

The genus *Dendrophyllia* de Blainville, 1830 (Scleractinia: Dendrophylliidae) comprises a group of azooxanthellate corals with a broad distribution in deep-sea environments. Despite their ecological relevance, phylogenetic relationships within this genus remain insufficiently resolved, particularly in the northeastern Atlantic. This study presents a morphology-based phylogenetic analysis of *Dendrophyllia* specimens collected during oceanographic campaigns in the waters surrounding the Canary Islands, conducted by the Oceanographic Centre of the Canary Islands within the framework of the EU Marine Strategy Framework Directive (MSFD). Morphometric analyses were conducted under stereomicroscope on four species (*D. alternata* Pourtalès, 1880, *D. laboreli* Zibrowius & Brito, 1984, *D. ramea* (Linnaeus, 1758) and *D. cornigera* (Lamarck, 1816)), focusing on key skeletal features traditionally used in scleractinian taxonomy. The results support clear morphological differentiation among species and reveal trait-based affinities that may reflect underlying evolutionary relationships. These findings offer a regional baseline for future integrative studies combining morphological and molecular data and underscore the biogeographic importance of the Canary Islands as a transition zone for Atlantic deep-sea coral fauna. Improved understanding of *Dendrophyllia* phylogeny will contribute to conservation strategies aimed at protecting vulnerable coral ecosystems in the face of increasing climatic and anthropogenic pressures.

Morphological revision of the genus *Stichopathes* (Antipatharia, Antipathidae) in the Canary Islands

¹Martín-García, Laura, ^{1*}González-Porto, Marcos, ¹Jurado-Ruzafa, Alba, ²Rodríguez-Barreto, Deienne, ¹Dionis-Insensé, Noemi, ¹Rodríguez-Valdez, Génesis, ¹García-Mañé, Bertín, ³Villafranca-Sánchez, Pablo, ¹Orozco-Borgas, Alejandro, ¹Cruz-Delgado, Paula, ¹Mendoza, José Carlos, ¹Oliva, Silvia & ¹Martín-Sosa, Pablo.

*lead presenter: marcos.gonzalez@ieo.csic.es

¹ Oceanographic Center of the Canary Islands (COC), Spanish Institute of Oceanography (IEO-CSIC), Spain

² Department of Chemical Engineering and Pharmaceutical Technology, University of La Laguna, Spain

³ Department of Animal Biology, Soil and Geological Sciences, University of La Laguna, Spain

Black corals of the genus *Stichopathes* are widely distributed in the circalittoral and bathyal bottoms of the Canary Islands, where they act as structural species within vulnerable marine habitats. Despite their ecological importance, the taxonomy of this genus remains problematic due to its high morphological variability and its recognition as a polyphyletic group. Previous molecular analyses conducted in the region have proven inconclusive, further highlighting the need for comprehensive morphological assessments to refine species delimitation.

In this study, we present a morphological revision of *Stichopathes* specimens collected across the archipelago during oceanographic surveys and ROV operations at depths between 150 and 1,200 m. Diagnostic characters of the colonies—including polyp size and arrangement, corallum characteristics, and spine morphology—were examined and compared with previous descriptions of Atlantic taxa. Our revision confirms the widespread presence of *Stichopathes gracilis*, the occurrence of *S. gravieri*, and a series of morphotypes provisionally classified as *Stichopathes* sp. Recent collections revealed more than ten distinct morphospecies based on external features, suggesting a higher diversity than previously reported.

This work advances ongoing efforts to clarify the taxonomy of *Stichopathes* in the Canary Islands and provides a robust baseline for biodiversity assessments. Moreover, it underlines the importance of these black coral assemblages as part of Habitat 1170 “Reefs” under the European Habitats Directive, a habitat recognized as highly vulnerable and requiring specific conservation measures.

First record of the genus *Victorgorgia* (Cnidaria, Octocorallia) in the Canary Islands SW seamounts: expanding biodiversity insights

^{1*}González-Porto, Marcos, ¹Jurado-Ruzafa, Alba, ¹Oliva, Silvia, ²Taboada, Sergi, ²Alonso Hartyan-yi, Teresa, ³Boza, Cristina, ¹Campillo, Sara, ¹Dionis-Insensé, Noemi, ¹García-Mañé, Bertín, ¹Jiménez-Navarro, Sebastián, ¹Mendoza, José Carlos, ¹Martín-Sosa, Pablo & ¹Martín-García, Laura

*lead presenter: marcos.gonzalez@ieo.csic.es

¹ Oceanographic Center of the Canary Islands (COC), Spanish Institute of Oceanography (IEO-CSIC), Spain

² Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Spain

³ Oceanographic Center of Gijón (COG), Spanish Institute of Oceanography (IEO-CSIC), Spain

Within the framework of the EU Marine Strategy Framework Directive (MSFD), we conducted a scientific survey on the southwestern seamounts off the Canary Islands (NW Africa) during the summer of 2024, with the aim of identifying and characterizing the existing mesophotic and deep-sea communities included in Habitat 1170-Reefs of the European Habitats Directive. Sampling of the lower bathyal zone consisted on transects of georeferenced video recording, by means of a semi-autonomous video camera wired to the vessel, and rock dredging. During sampling we observed purple gorgonian colonies between 1119 and 1387 m depth never observed before. In order to identify them, molecular analyses and morphological study of its sclerites were conducted on a collected specimen.

Our analyses on the purple gorgonian indicate that it is a species of the genus *Victorgorgia* López-González & Briand, 2002, constituting the first record of this genus and its family –Victorgorgiidae– in the study area. The presence of the genus *Victorgorgia* in the region is consistent with its previous description on another seamount located northwards the archipelago that fall within the Canary Current of the North Atlantic Gyre, which flows southwest. Yet further exploration is needed to properly identify this species and to describe the extent and abundance of this gorgonian in the Canarian region lower bathyal zone. This discovery supports the necessity of protecting these areas, given the highly unknown biodiversity that may harbour.

Rediscovery and phylogenetic placement of *Allodessus skottsbergi* (Coleoptera: Dytiscidae) from Rapa Nui

^{1*}Villastrigo, Adrián, ^{2,3}Cotoras, Darko D., ⁴Edmunds, Merahi, ⁴Pakarati, Sebastián, ⁴Edmunds, Tahira & ⁵Balke, Michael

*lead presenter: avillc@unileon.es,

¹ University of León, Spain

² Pontificia Universidad Católica de Chile, Chile

³ California Academy of Sciences, USA

⁴ Proyecto "Estudio Territorial Bio/Socio Ambiental de los humedales de Rapa Nui"

⁵ SNSB-Zoologische Staatssammlung München, Germany

The diving beetle genus *Allodessus* Guignot, 1953 comprises five species distributed across the Pacific, inhabiting freshwater environments such as temporary and semi-permanent pools. One of these, *Allodessus skottsbergi* Zimmerman, 1924, is endemic to Rapa Nui (Easter Island, Chile) and has not been recorded since its original description. Its presumed extinction, due to habitat degradation and the introduction of predatory fish into Rano Kau crater lake (its type locality), left its phylogenetic position unresolved and molecular data unavailable.

We report the rediscovery of *A. skottsbergi* from a temporary pond inside the crater of Rano Kau. Low-coverage whole-genome sequencing was performed, allowing assembly of its mitochondrial genome and recovery of key nuclear markers. A comprehensive phylogenetic analysis using Maximum Likelihood methods, incorporating all described *Allodessus* species and relevant outgroups was conducted.

Contrary to previous hypotheses, *A. skottsbergi* is not the most basal member of the genus but is phylogenetically nested within *Allodessus*, confirming its placement in the genus. The analysis identified *A. megacephalus* as sister to all other species. Furthermore, we observed minimal genetic divergence among *A. bistrigatus*, *A. thienemanni* and *A. oliveri*, supporting the hypothesis that these taxa may represent a single widespread species.

These results refine the evolutionary framework of *Allodessus* and underscore the conservation value of remnant aquatic habitats on Rapa Nui. The rediscovery of *A. skottsbergi*, combined with new phylogenetic insights, highlights the importance of integrating field surveys with genomic data in resolving systematic questions in remote island faunas.

Integrative taxonomy reveals cryptic species within the Canary Island endemic longhorn genus *Lepromoris* (Coleoptera; Cerambycidae)

^{1*}Jiménez-García, Eduardo, ²Noguerales, Víctor, ¹López, Heriberto & ¹Emerson, Brent.

*lead presenter: e.jimenezgarcia@ipna.csic.es

¹ Institute of Natural Products and Agrobiology (IPNA-CSIC), San Cristóbal de La Laguna, Tenerife, Canary Islands, 38206, Spain

² Departamento de Biología Animal, Edafología y Geología, Facultad de Ciencias, Universidad de La Laguna, San Cristóbal de La Laguna, Tenerife, Canary Islands, 38206, Spain

The monotypic genus *Lepromoris* is distributed throughout the archipelago of the Canary Islands, with its constituent species *Lepromoris gibba* being apterous and associated with *Euphorbia* shrublands. Here we undertake a comprehensive geographic sampling for an integrative taxonomic revision of the genus that incorporates mitochondrial and genome-wide nuclear genomic markers together with morphological data. Our analyses reveal the existence of cryptic species within the genus, with the only diagnostic morphological character being the curvature of the eye. The new species, ***Lepromoris exophthalmus* Jiménez-García & López sp. nov.** occurs on the islands of Fuerteventura, Lanzarote, Gran Canaria and El Hierro, while the known *Lepromoris gibba* is found on the islands of Tenerife, La Gomera, La Palma and El Hierro. Thus, both species are sympatric on the island of El Hierro. We also describe genetic differentiation within *Lepromoris gibba* on the island of El Hierro that is suggestive of a possible third species, but for which further sampling would be needed to clarify this.

Exploring the Terrestrial Isopods of the Canary Islands: From Historical Records to Future Perspectives

^{1,2}Orihuela-Rivero, Raúl, ^{1*}Bernardos, Lucía, ^{3,4}García del Real García, Eduardo, ¹López, Heriberto, ³Macías-Hernández, Nuria, ¹Hernández-Teixidor, David, ¹Pérez-Delgado, Antonio José, ⁵García, Rafael, ¹Balibrea, Carmen, & ³Oromí, Pedro

*lead presenter: lbernardos@ipna.csic.es,

¹ Instituto de Productos Naturales y Agrobiología (IPNA-CSIC), Tenerife, Spain

² School of Doctoral and Graduate Studies, University of La Laguna, Tenerife, Spain

³ Department of Animal Biology, Edaphology and Geology, University of La Laguna, Tenerife, Spain

⁴ University of Valencia, Valencia, Spain

⁵ C/. El Pilar 8, 3^opta. 1. 38700 Santa Cruz de La Palma, La Palma, Spain

Oceanic archipelagos are hotspots of biodiversity and endemism, offering natural laboratories for the study of colonization and speciation. Terrestrial isopods (Oniscidea) are particularly informative in this context due to their limited dispersal abilities and frequent island radiations. Despite more than a century of records, knowledge of the Canarian fauna has long remained fragmented and outdated. Here we present an updated review of terrestrial isopods from the Canary Islands. We compiled and cross-validated information from the literature, examined material in the main institutional collections of the archipelago (DZUL, IPNA-CSIC, TFMC), and incorporated records from GBIF and iNaturalist up to December 2024, which were carefully filtered and, when possible, verified in the field.

Our synthesis documents 71 species in 25 genera and 11 families. Compared with previous lists, we recover overlooked taxa, add higher-level elements including the family Detonidae and the genus *Buchnerillo* (incertae sedis), and discard or question several names that were erroneously reported. Nearly a third of the fauna corresponds to endemic species, largely concentrated in the western islands, with most taxa occurring on only one or a few islands. Biogeographic affinities are heterogeneous, dominated by Mediterranean and Atlantic elements. Patterns of beta-diversity reveal a marked east–west structuring: the western islands are characterized by high turnover driven by endemic replacements, whereas the eastern group shows stronger nestedness, with local faunas representing subsets of the regional pool. Introduced species are emerging as major drivers of change, reshaping the functional trait composition of isopod communities and potentially reducing the distinctiveness of native assemblages.

This synthesis consolidates more than a century of scattered information and provides a baseline for monitoring and conservation. It also highlights research priorities, including integrative taxonomy, phylogeographic analyses to clarify species origins, and biosecurity measures to limit invasive spread. The Canary Islands thus emerge as a model system for studying the drivers of diversity and vulnerability in insular Oniscidea.

First Genomic Insights into the Endangered Iberian Endemic *Squalius palaciosi*: Evidence of Hybridogenetic Origins

¹*Perea, Silvia, ²Ghanavi, Hamid, & ¹Doadrio, Ignacio

*lead presenter: sperea@mncn.csic.es

¹ Museo Nacional de Ciencias Naturales – CSIC, Madrid, España

² Lund University, Sweden

The species *Squalius palaciosi* (Doadrio, 1980; Leuciscidae) is highly threatened. This species has a very restricted distribution area, limited to a few tributaries on the right bank of the Guadalquivir basin. Its populations were very abundant during the 1980s, constituting one of the main species within the fish community of the rivers it inhabited. However, they underwent a drastic decline due to pollution and dam regulation, leading the species to near-total extinction. One of the most remarkable features of *S. palaciosi* from an evolutionary perspective is its polyploid condition and its potential membership in hybridogenetic complexes, a rare phenomenon in the Iberian Peninsula that has been described for its congeners *Squalius alburnoides*, distributed across several Iberian river basins, and *Squalius* sp., restricted to a few rivers in the Guadiana basin. While numerous molecular studies exist for *S. alburnoides* describing reproductive modes and genomic functioning within the complex, knowledge is scarce for *Squalius* sp. and completely absent for *S. palaciosi*. In this study, we obtained genomic sequences for the first time from bone fragments of skeletons of *S. palaciosi* deposited in the fish collection of the MNCN, sequenced using Illumina short reads. After quality filtering and the removal of contaminant reads (bacteria, etc.), we reconstructed the complete mitochondrial genome of the species, which was then incorporated into the phylogenetic context of the genus *Squalius* in the Iberian Peninsula. The results corroborate the close relationship of the mitochondrial genome of *S. palaciosi* with *S. alburnoides* and *S. tartessicus*, with strong bootstrap support (maximum likelihood) and posterior probability (Bayesian inference). The next steps of this project will focus on analysing the nuclear genome of the species in order to identify the paternal genome that gave rise to this hybridogenetic species within a spatiotemporal evolutionary framework. This study is relevant as it contributes to describing and understanding a process as complex as hybridogenetic speciation in freshwater fishes, a phenomenon with only a few known examples worldwide, among which those described for the genus *Squalius* in the Iberian Peninsula are particularly notable.

Keywords: *Squalius*, hybridogenetic complexes, Iberian ichthyofauna, Museomics, genomic short reads

Integrative revision of *Codium* (Chlorophyta, Bryopsidales) in the Canary Islands: combining morphology and molecular data

¹*Rancel-Rodríguez, Nereida M.; ¹Álvarez-Canali, Daniel; ¹Roger-Baynat, Belén; ¹Sansón, Marta & ¹Sangil, Carlos

*lead presenter: nrrodri@ull.edu.es

¹ Departamento de Botánica, Ecología y Fisiología Vegetal, Universidad de La Laguna, España

The genus *Codium* (Bryopsidales, Codiaceae) includes more than 130 taxa worldwide and shows high morphological variability despite its simple siphonous structure. This variability has complicated species delimitation, especially in the Canary Islands, where identifications based only on morphology have resulted in doubtful records and unresolved names.

We analyzed approximately 800 *Codium* specimens from regional herbaria (TFC, BCM, BOT-MAR-ULL), representing 16 nominal species, of which 14 are currently accepted for the archipelago (BIOTA database). Within the BRYOCAN project, DNA barcoding with chloroplast markers (*tufA* and *rbcl*) was applied to 10 species. Preliminary *tufA* results provide clear support for *C. intertextum*, *C. effusum*, and *C. decorticans*, while *C. vermilata* and *C. carolinianum* show promising patterns but require further sequencing to confirm species-level boundaries.

This ongoing work highlights the value of integrating morphology and molecular evidence to resolve taxonomic uncertainties in *Codium*. Continued sequencing will be necessary to complete the molecular characterization of the Canary Islands flora and to consolidate historical records. Future efforts should also include deep-water sampling, as several species (*C. elisabethiae*, *C. fragile*, *C. tomentosum*, *C. guineense*) remain rare or underrepresented in available collections.

Phylogenetic and genomic insights into a new syllid polychaete species from the Canary Islands with evidence of trans-Atlantic connectivity

¹Ruiz, Víctor, ^{1*}Martín-Hervás, M.Rosario, ²Moreno-Martín, Paula, ²Del Olmo, Irene, ³Taboada, Sergi & ²Álvarez-Campos, Patricia

*lead presenters: victor.ruiz@uam.es; maria.martin-hervas@uam.es

¹ Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM) & Departamento de Biología (Zoología), Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain.

² Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM) & Departamento de Biología (Zoología), Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain.

³ Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales (MNCN), CSIC, Madrid 28006, Spain.

In this study, the still largely unknown marine biodiversity of the Canary Islands and Bermuda—both recognized as hotspots of marine biodiversity—is explored through an integrative phylogenetic and population genomic analysis of polychaete worms from the genus *Megasyllis* San Martín, Hutchings & Aguado, 2008 (Annelida, Syllidae). While only a single species of this genus has previously been recorded in the Atlantic Ocean, numerous species are distributed throughout the Pacific. This research combines traditional morphological analyses with advanced molecular techniques, including sequencing of mitochondrial markers (COI, 16S rRNA) and nuclear genes (18S rRNA, 28S rRNA), together with genome-wide SNP data generated by ddRAD-seq from specimens collected across four Canary Islands.

We conducted extensive samplings in both archipelagos, collecting specimens from 12 localities across four Canary Islands (La Gomera, Tenerife, Gran Canaria and La Palma) and Bermuda locations. Our integrative approach combined traditional morphological analyses with advanced molecular techniques, including sequencing of mitochondrial markers (COI, 16S rRNA) and nuclear genes (18S rRNA, 28S rRNA), together with genome-wide SNP data generated by ddRAD-seq. Phylogenetic trees constructed using Maximum Likelihood and Bayesian inference methods identified two distinct species: one corresponding to the previously described species *M. procera* from Bermuda, and a second, *Megasyllis* sp. nov. occurring on both sides of the Atlantic.

Population genomic analyses of 83 individuals revealed high gene flow among Canary Island populations from La Gomera, Tenerife, Gran Canaria and La Palma but absence from Fuerteventura and Lanzarote. Shared haplotypes and phylogeographic patterns implicate transoceanic ballast water via Tenerife as the vector for initial colonization, representing the first confirmed case of amphi-Atlantic distribution in syllids. These findings not only expand the known diversity of *Megasyllis* in the Atlantic but also provide the first genetic assessment of connectivity and population structure in this genus, underscoring the roles of natural currents and anthropogenic transport in shaping marine invertebrate biogeography.

Island isolation drives genetic divergence in the Canarian camel spider *Eusimonia wunderlichi* (Solifugae)

¹Ariemma Cecilia, ¹Lugo David, ²Robla Jairo, ^{3,4}Pertegal Cristian, ¹Oromí Pedro & ^{1*}Macías-Hernández Nuria

*lead presenter: nemacias@ull.edu.es

¹ Departamento de Biología Animal, Edafología y Geología, Universidad de La Laguna, La Laguna, España.

² Departamento de Biología de la Conversación y Cambio Global, Estación Biológica de Doñana (CSIC), Sevilla.

³ Departamento de Biodiversidad, Ecología y Evolución. Universidad Complutense de Madrid. Avenida Séneca 2 - Madrid, España.

⁴ Departamento de Zoología, Universidad de Córdoba, Edificio C-1, Campus de Rabanales, 14071 Córdoba.

Solifugae are a poorly studied order of cursorial arachnids, with limited phylogenetic and taxonomic research, particularly in island systems. *Eusimonia wunderlichi* Pieper, 1977 (Karschiidae) is the only described solifugae species from the Canary Islands, yet its taxonomic status remains unresolved. Given the low dispersal ability of the group and the complex biogeographic history of the archipelago, it is plausible that *E. wunderlichi* constitutes a cryptic species complex. In this study, we present a preliminary taxonomic assessment of Canarian Solifugae, based on molecular evidence. A total of 75 specimens were sampled across the five islands where the species occurs (Lanzarote, Fuerteventura, Gran Canaria, Tenerife and La Gomera). Phylogenetic analyses were conducted using a multilocus dataset comprising mitochondrial (Cytochrome c Oxidase I, 16S rRNA) and nuclear (28S rRNA) markers. Phylogenies were inferred under Maximum Likelihood analyses and delimitation methods were performed with both distance-based approaches (ASAP & ABGD) as well as phylogeny-based methods (GMYC). Our results reveal significant inter-island genetic divergence (6-16%), suggesting the presence of previously unrecognized lineages in each island due to different inter-islands colonisation events. These findings underscore the necessity for additional morphological and ecological studies, but also highlight the role of island isolation and habitat heterogeneity in driving diversification in poorly dispersive arachnid taxa, and contribute novel insights into Solifugae systematics.

SPONSORSHIP

We gratefully acknowledge the support of our partner institutions:



DELEGACIÓN EN
CANARIAS

