UNIVERSITÀ DI PISA

bio
DIPARTIMENTO di BIOLOGIA

UZI SIP 2024

CONGRESSO CONGIUNTO

83° CONGRESSO
UNIONE ZOOLOGICA
ITALIANA

34° CONGRESSO
SOCIETÀ ITALIANA DI
PROTISTOLOGIA

BOOK OF ABSTRACTS
COMMUNICATIONS

11-14 settembre 2024 Pisa

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UNIVERSITÀ DI PISA
MUSEO DI STORIA NATURALE

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Il logo del Congresso UZI-SIP 2024 è stato ideato e realizzato da Alessandro Allievi, Tianshi Li e Giulio Petroni

Altri disegni a cura di Fosca Mastrandrea

INFORMAZIONI SUL CONGRESSO

Al Congresso congiunto UZI-SIP 2024 sono previsti più di **211 contributi** e **260 partecipanti** registrati.

Per questa edizione, si è cercato di ritagliare quanti più spazi possibili per la visibilità dei contributi scientifici, prevedendo due giornate con simposi in parallelo. Si è scelto di coinvolgere relatori e relatrici con diversi background, non solo dal punto di vista della formazione, ma anche delle diverse realtà sociali e nazionalità.

Molti simposi includono contributi sull'impiego di nuove tecnologie e approcci trasversali per far fronte alla rapidità con cui le discipline zoologiche stanno evolvendo, di pari passo con le esigenze della divulgazione scientifica, dalla didattica pura alla *Citizen Science*. Inoltre, si è scelto di introdurre tematiche quali la stesura e il coordinamento di **progetti internazionali**, così da fornire esempi pratici.

Per favorire il coinvolgimento delle nuove generazioni, gli organizzatori hanno aperto le porte agli studenti dell'Università di Pisa e non solo, offrendo loro la possibilità di assistere gratuitamente alle presentazioni. Questa iniziativa mira a ispirare i giovani studenti e a promuovere un maggiore interesse verso la ricerca scientifica.

Il Congresso e gli eventi sociali associati sono stati realizzati prestando attenzione alle esigenze dei partecipanti e, al contempo, cercando di garantire un'organizzazione rispettosa dell'ambiente. Ove possibile si è cercato di ridurre gli sprechi e l'impatto ambientale, scegliendo di utilizzare materiali riciclati per i gadget del Congresso e preferendo aziende e prodotti locali.

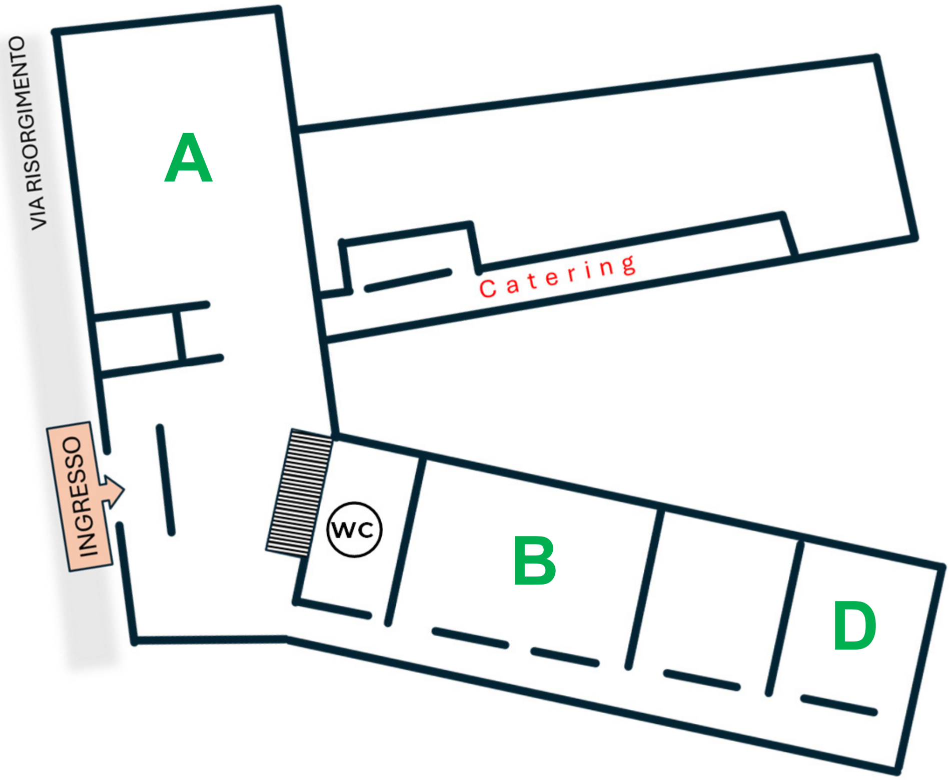
Un elemento centrale di questa edizione del congresso è stata **l'inclusività**. Tutti i membri dei comitati organizzativi e dello staff sono stati coinvolti attivamente nella pianificazione e nella gestione dell'evento, ricevendo il giusto riconoscimento.

In sintesi, il **Congresso UZI-SIP 2024** non vuole solamente essere un'opportunità per condividere conoscenze scientifiche, ma anche un evento che riflette un impegno concreto verso la sostenibilità, l'inclusione e la valorizzazione di ogni contributo

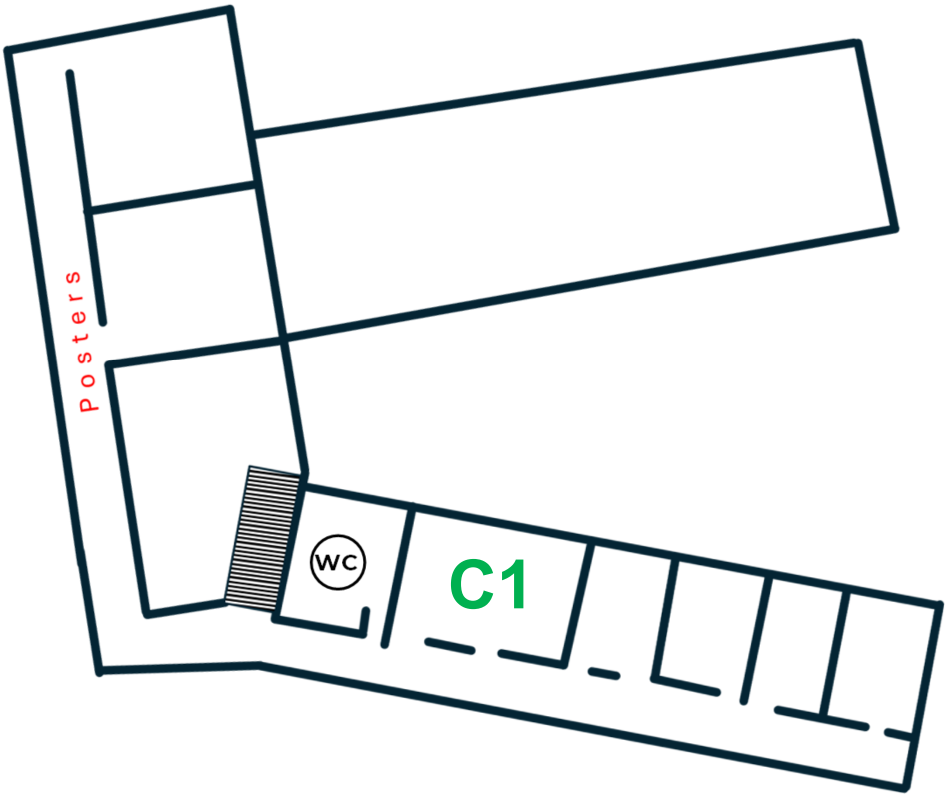
Sperando che le nostre iniziative vi siano gradite, auguriamo buon Congresso a tutte e a tutti.

AULE

PIANO TERRA



PRIMO PIANO



mercoledì 11 settembre

12:30 - 14:00	Registrazioni e affissione Poster -Polo Didattico di San Rossore
14:00 - 14:30	Saluti e Cerimonia di apertura – Aula A
SIMPOSIO 3 - Biodiversità del Territorio e Governance condivisa: monitoraggi e casi studio Coordinatori: Roberto Sandulli, Alessandro Cini, Andrea Gennai	
14:30 - 15:00	Invited speaker - Leonardo Dapporto Innovative strategies for monitoring pollinators in data-limited contexts
15:00 - 15:15	Challenges and opportunities of the ue agenda 2030: establishing a shared long-term animal monitoring scheme Simona Bonelli
15:15 - 15:30	Lo studio e la conservazione degli insetti protetti attraverso la *Citizen Science* Alessandro Campanaro, Silvia Gisondi, Alice Lenzi, Pio Federico Roversi
15:30 - 15:45	Transnational monitoring of wildlife populations: the experience of the European Observatory Of Wildlife (EOW) Massimo Scandura, Tancredi Guerrasio, Davide Carniato, Stefania Zanet, Alessandro Forti, Joaquin Vicente, Jose Antonio Blanco-aguiar, Pelayo Acevedo, Pablo Palencia, Jim Casaer, Yorick Liefting, Patrick Jansen, Marcus Rowcliffe, Marco Apollonio, Ezio Ferroglio
15:45 - 16:00	The alienfish project: integrating citizen science, morphological and molecular approaches to the study of mediterranean bioinvasions Alessandro Nota, Anna Olivieri, Antonio Torroni, Francesco Tiralongo
16:00 - 16:15	The forgotten *Posidonia oceanica* (L.) Delile detrital habitat: nematode community and two new species of *Echinoderes* (Kinorhyncha: Echinoderidae) inhabiting this neglected environment Adele Cocozza Di Montanara, Francesco Rendina, Federica Semprucci, Alberto González-casarrubios , Diego Cepeda, Luigia Donnarumma, Giovanni Fulvio Russo, Roberto Sandulli
16:15 - 16:30	Managing soil to support soil biodiversity in protected areas agroecosystems: the conero park case study Martina Coletta, Marco Monticelli, Celeste Gentili, Aldo D'alessandro, Antonietta La Terza
16:30 - 17:00	Coffee Break

mercoledì 11 settembre

SIMPOSIO 4 - Modelli animali utilizzati a fini scientifici

Coordinatori: Adriana Canapa, Federico Buonanno, Marco A. L. Zuffi

17:00 - 17:30	Invited speaker - Roberto Sacchi Evoluzione e mantenimento del polimorfismo cromatico nelle lucertole del genere *Podarcis*
17:30 - 17:45	The sipunculan *Phascolosoma stephensoni* (Annelida: Phascolosomatidae) as a new model for bioinspired robots Luigi Musco, Joachim Langeneck, Desirèe Dimichele, Alessandra Martines, Mariafrancesca Cascione, Rosaria Rinaldi, Kleoniki Keklikoglou, Linda Paternò, Antonio De Simone, Arianna Menciassi
17:45 - 18:00	Ciliated protozoa as models to study cellular and organismal responses to environmental changes: the case of the Antarctic ciliate *Euplotes focardii* treated with the pollutant bisphenol a Angela Piersanti, Alessandra Borghi, Sandra Pucciarelli, Matteo Mozzicafreddo , Cristina Miceli
18:00 - 18:15	Il baco da seta come modello di infezione alternativo per lo screening di antibiotici nanoconiugati Aurora Montali, Francesca Berini, Federica Gamberoni, Ilaria Armenia, Alessio Saviane, Silvia Cappellozza, Giovanni Bernardini, Rosalba Gornati, Flavia Marinelli, Gianluca Tettamanti
18:15 - 18:30	The emerging role of mitochondrially encoded small interfering RNAs to regulate nuclear gene expression Federico Plazzi, Diego Carli, Alessandro Formaggioni, Iuri Icaro, Youn Le Cras, Giovanni Marturano, Giorgio Muneretto, Francesco Nardi, Oscar Wallnoefer, Marco Passamonti
18:30 - 18:45	The brittle star *Ophiactis virens* (Echinodermata: Ophiuroidea) as non-conventional model organism for studing the effects of polyethylene terephthalate nanoplastics Maria Battistoni, Renato Bacchetta, Francesco Bonasoro, Paolo Tremolada, Davide Tessaro, Michela Sugni
18:45 - 19:00	Diving into diversity: fish models as powerful tools for biological discovery Elena Frigato, Elia Gatto, Tyrone Lucon-xiccato, Cristiano Bertolucci
19:00 - 20:45	Aperitivo di benvenuto

giovedì 12 settembre

Aula A

SIMPOSIO 5 - Le innovazioni in Zoologia: dal microscopio all'intelligenza artificiale

Coordinatori: Cristina Giacoma, Paolo Luschi

09:00 - 09:30	Invited speaker - Francesco Caruso Studying cetaceans using high-tech instruments and machine learning approaches
09:30 - 09:45	Genetic manipulation of the silkworm *Bombyx mori*: from basic science to biotechnological applications Daniel J. Brady, Alessio Saviane, Matteo Battistolli, Irene Varponi, Federica Barca, Silvia Cappellozza, Federica Sandrelli
09:45 - 10:00	Il microbioma intestinale delle larve di mosca soldato nera come strumento per lo sviluppo di strategie innovative di bioconversione Silvia Caccia, Morena Casartelli, Gianluca Tettamanti
10:00 - 10:15	Insect functional morphology: from basic research to biomimetics Manuela Rebora, Silvana Piersanti, Gianandrea Salerno, Stanislav Gorb
10:15 - 10:30	Nuove tecnologie a supporto della zoologia per il monitoraggio e lo studio del comportamento animale: dai droni e l'intelligenza artificiale alla stampa 3D Daniele Giannetti, Donato A. Grasso
10:30 - 10:45	The evolutionary neuroanatomy of blood feeding in mosquitoes revealed by X-ray tomography Paolo Gabrieli, Irene Arnoldi, Marta Villa, Soresinetti Laura, Leah Houri-zeevi
10:45 - 11:00	Machine learning applications for animal behavior studies: the case of automatic discrimination of voiced and unvoiced primate faces Filippo Carugati, Olivier Fiard, Elisa Protopapa, Camilla Mancassola, Emanuela Rabajoli, Chiara De Gregorio, Daria Valente, Valeria Torti, Teresa Raimondi, Valeria Ferrario, Walter Cristiano, Marco Gamba
11:00 - 11:30	Coffee Break

SIMPOSIO 6 - Oltre i confini della Zoologia: multi/inter/trans-disciplinarietà nella zoologia

Coordinatori: Biagio D'Aniello, Giovanni Boschian, Valentina Serra

11:30 - 12:00	Invited speaker - Antonio De Simone Motility from shape control: from biophysics to biorobotics

giovedì 12 settembre

12:00 - 12:15	The zoological contribution to the multidisciplinary study of two shipwrecks off Tuscany coasts (Italy, western mediterranean) Jonathan Tempesti, Domingo Belcari, Valeria Croce, Gabriella Caroti, Simonetta Menchelli, Ferruccio Maltagliati
12:15 - 12:30	*Crematogaster scutellaris* e *Vicia faba*: mutualismo manipolativo? Giulia Magoga, Giobbe Forni, Daniele Giannetti, Matteo Brunetti, Valentina Picchi, Elia Russo, Nadia Bazihizina, Morena Casartelli, Alberto Spada, Massimo Nepi, Stefano Mancuso, Franco Faoro, Donato Grasso, Matteo Montagna
12:30 - 12:45	Under pressure: understanding the impact of air pollution on pollinators and pollination Irene Piccini
12:45 - 13:00	Genomic investigations indicate a novel evolutionary scenario for a bacterial lineage associated with Ecdysozoa Michele Castelli, Leandro Gammuto, Diona Podushkina, Matteo Vecchi, Tiziana Altiero, Emanuela Clementi, Roberto Guidetti, Lorena Rebecchi, Davide Sassera
13:00 - 13:15	Impiego di una combinazione di tratti morfo-funzionali come metodo alternativo per l'analisi della struttura della nematofauna marina e terricola Federica Semprucci, Eleonora Grassi
13:15 - 13:30	From zoology to tissue engineering: the second life of sea urchin wastes Michela Sugni, Giordana Martinelli, Margherita Roncoroni, Tamara Chwojnik, Luca Melotti, Anna Carolo, Giulia Zivelonghi, Marco Patruno, Stefania Marzorati
13:30 - 15:00	Pranzo
15:00 - 17:00	Sessioni Parallele Simposi: 3 (Aula A) - 4 (Aula D) - 5 (Aula B) - 6 (Aula C1)
17:00 - 17:30	Coffee Break

17:30 -19:00	Sessione Poster	
19:00 - 19:45	Presentazione Libri	Augusto Foà: Colombi e binocoli, lucertole e cronometri Manuale di Zoologia a cura di Loriano Ballarin

18:15 - 21:45	Aperitivo Autogestito dagli Studenti

12 settembre - Sessioni Parallele

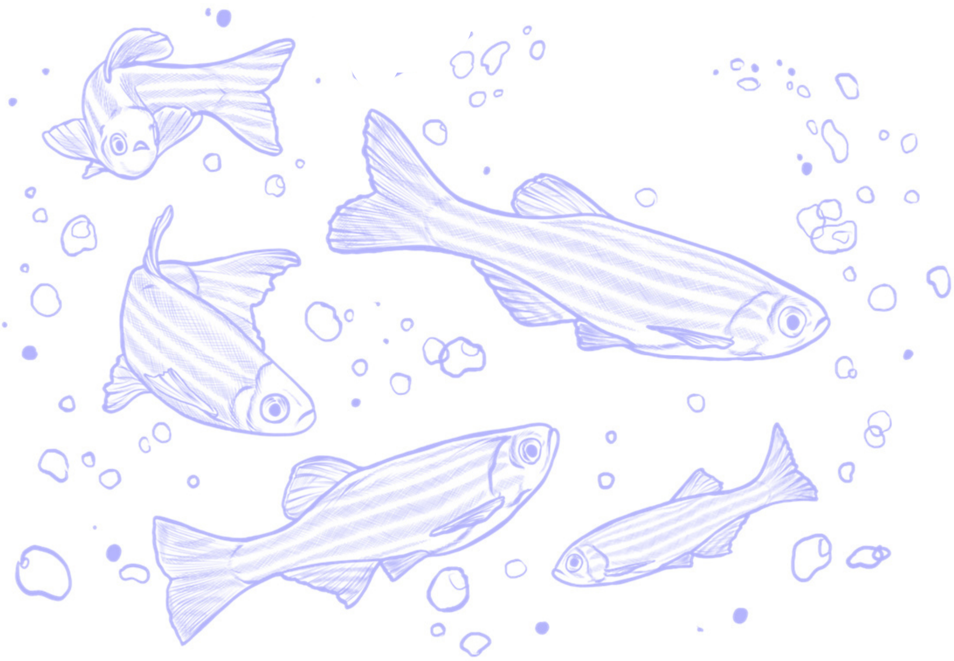
Parallela Simposio 3 - Biodiversità del Territorio e Governance condivisa: monitoraggi e casi studio
Aula A

15:00 - 15:15	Lo stato di conservazione del gambero nativo di fiume *Austropotamobius pallipes* complex (Decapoda: Astacidae) nel parco delle foreste Casentinesi Elena Tricarico, Sara Forni, Beatrice Melone, Matteo Orlando, Asia Rossi, Marco Morbidelli
15:15 - 15:30	Struttura genetica della trota fario (*S. ghigii* Pomini, 1941): nuove evidenze dalle popolazioni native sarde e peninsulari tramite approccio genomico (GBS) Tommaso Righi, Andrea Splendiani, Tatiana Fioravanti, Francesco Palmas, Andrea Sabatini, Diego Micheletti, Andrea Gandolfi, Vincenzo Caputo Barucchi
15:30 - 15:45	Do faunal bioinvasions pass trough marine litter pollution? the case of a brackish coastal lagoon in the central mediterranean sea Gioele Capillo, Claudio D’iglio, Dario Di Fresco, Nunziacarla Spano’, Marco Albano, Serena Savoca
15:45 - 16:00	Honeybees impacts on wild bees biodiversity in a small and protected island through exploitative competition: the case study of Giannutri Lorenzo Pasquali, Alessandro Cini, Giorgio Vicari,claudia Bruschini, Leonardo Dapporto
16:00 - 16:15	*Paraleucilla magna* (Porifera, Calcarea): il contributo di una spugna aliena in un mare di cambiamenti Roberta Trani, Caterina Longo
16:15 - 16:30	Bathymetric distribution and co-presence in coralligenous community of *Eunicella cavolini* (Koch, 1887) and *Paramuricea clavata* (Risso, 1827) Federica Ferrigno, Luca Appolloni, Luigia Donnarumma, Francesco Rendina, Roberto Sandulli, Giovanni F. Russo
16:30 - 16:45	Valutazione in campo dei possibili effetti dell'olio essenziale di *Ocimum basilicum* L. sulle comunità di nematodi a vita libera del suolo Eleonora Grassi, Linda Catani, Loretta Guidi, Priscilla Farina, Camilla Tani, Barbara Conti, Anna Annibaldi, Federico Girolametti, Roberta Ascrizzi, Guido Flamini, Luana Da Costa Monteiro, Federica Semprucci
16:45 - 17:00	QBS-ar VS QBS-e: a comparison of their performance on arable land under different management practices Marco Monticelli, Martina Coletta, Alessandro Mascaretti, Leonardo Salvatori, Aurora Torresi, Mario Marconi, Antonietta La Terza

12 settembre - Sessioni Parallele

Parallela Simposio 4 - Modelli animali utilizzati a fini scientifici
Aula D

15:00 - 15:15	Notes on the use of *Artemia salina* (Linnaeus, 1758) and congeners in scientific research Marco Albano, Claudio D'iglio, Serena Savoca, Nunziacarla Spano', Gioele Capillo
15:15 - 15:30	Histopathological abnormalities in zebrafish liver induced by dimoxystrobin, a synthetic strobilurin fungicide Rachele Macirella, Abdalmoiz I.M. Ahmed, Federica Talarico, Marcello Mezzasalma, Elvira Brunelli
15:30 - 15:45	Clearwing moths (Lepidoptera : Sesiidae) as effective models for studying the efficiency of mimicry in predator-prey interactions Marta Skowron Volponi, Leonardo Dapporto, Luca P. Casacci, Francesca Barbero, Elena Chiesa, Paolo Volponi
15:45 - 16:00	Genus *Lepidurus* (Crustacea, Notostraca) as a model for study the biological rhythms Vittorio Pasquali
16:00 - 16:15	Olfaction in the black soldier fly *Hermetia illucens* Silvana Piersanti, Manuela Rebora, Giorgia Carboni Marri, Gianandrea Salerno
16:15 - 16:30	Dall' etologia all'ecotossicologia: le vespe cartonaie come organismi modello nella ricerca scientifica Federico Cappa, Livia De Fazi, David Baracchi, Rita Cervo



12 settembre - Sessioni Parallele

Parallela Simposio 5 - Le innovazioni in Zoologia: dal microscopio all’intelligenza artificiale

Aula B

15:00 - 15:15	L’uso delle telecamere temporizzate nello studio della dimensione temporale delle comunità marine Marzia Bo, Federico Betti, Francesco Enrichetti, Andrea Rivela, Giorgio Bavestrello
15:15 - 15:30	Killer whales formation swimming: relative energetic costs and group geometry Federica Spina, Michael N. Weiss, Darren P. Croft, Paolo Luschi, Alessandro Massolo, Paolo Domenici
15:30 - 15:45	Yawn contagion in zebrafish (*Danio rerio*): preliminary data from a multidisciplinary approach Alice Galotti, Gianluca Manduca, Matteo Digregorio, Sara Ambrosini, Donato Romano, Massimiliano Andreazzoli, Elisabetta Palagi
15:45 - 16:00	Individual personality affects the behavioural response of free-flying homing pigeons to an artificial predator Luca Marinoni, Giulia Cerritelli, Claudio Carere, Robert Musters, Diego Rubolini, Irene Vertua, Lorenzo Vanni, Anna Gagliardo, Dimitri Giunchi
16:00 - 16:15	Qualitative and quantitative sampling of epigeal soil macroarthropods: different methods for different objectives Gianluca Polgar, Paolo Iezzi, Marzio Zapparoli, Romolo Fochetti, Anna Maria Fausto
16:15 - 16:30	Application of innovative imaging techniques to the study of the proboscis of *Aedes albopictus* (Culicidae) Irene Arnoldi, Marta Villa, Laura Soresinetti, Paolo Gabrieli
16:30 - 16:45	An ecologist-friendly R workflow for expediting species-level classification of camera trap images Luca Petroni, Luca Natucci, Alessandro Massolo
16:45 - 17:00	Integrating fossil data into ecological niche models to forecast the effect of climate change on mammal biodiversity Mirko Di Febbraro, Arianna Morena Belfiore, Silvia Castiglione, Marina Melchionna, Giorgia Girardi, Alessandro Mondanaro, Pasquale Raia

12 settembre - Sessioni Parallele

Parallela Simposio 6 - Oltre i confini della Zoologia: multi/inter/trans-disciplinarietà nella zoologia
Aula C1

15:00 - 15:15	Urban biodiversity and applied zoology: a marriage of forensic interest Paolo Bonivento, Emiliana Minenna
15:15 - 15:30	The Arthropod-based Biological Soil Quality index (QBS-Ar): three-year application in the Sentina reserve (Italy) Martina Coletta, Aurora Torresi, Marco Monticelli, Aldo D'alessandro, Antonietta La Terza
15:30 - 15:45	Symbiotic peritrichs (Ciliophora: Oligohymenophorea) of the okavango panhandle, Botswana Gerhard De Jager, Linda Basson, Liesl Van As, Valentina Serra, Giulio Petroni
15:45 - 16:00	Analisi del microbioma intestinale e dei parassiti gastrointestinali in *Lepus corsicanus* (De Winton, 1898) Martina Tenuzzo, Flavio Vallone, Claudia Vannini, Valter Trocchi, Giorgia Romeo, Fabio Macchioni
16:00 - 16:15	Playful packs: facial expressions and mimicry in wild *Canis lupus italicus* Veronica Maglieri, Alice Galotti, Alessio Garzelli, Marco Apollonio, Chiara Benedetta Boni, Nadia Cappai, Francesca Coppola, Marco Del Frate, Alessia Di Rosso, Arianna Dissegna, Paola Fazzi, Antonio Felicioli, Andrea Gennai, Marco Lucchesi, Alessandro Massolo, Luca Petroni, Elisabetta Palagi
16:15 - 16:30	Primates extract social information from vocal interactions: a playback experiment in wild geladas (*Theropithecus gelada*) Luca Pedruzzi, Martina Francesconi, Alice Galotti, Bezawork Afework Bogale, Elisabetta Palagi, Alban Lemasson
16:30 - 16:45	Can sea urchin waste be used as a valuable source of calcium for laying hens? Francesca Leone, Michela Sugni, Stefania Marzorati, Lorenzo Ferrari, Valentina Ferrante
16:45 - 17:00	When zoology meets design: the sea urchin as a model for biomimetics Sara Ignoto, Valentina Perricone, Renato Bacchetta, Ruben Marchesi, Morena Rocco, Serena Passaro, Assunta Venditto, Francesco Bonasoro, Carla Langella, Michela Sugni

venerdì 13 settembre

Aula A

Simposio 2 - Variabilità, Plasticità E Resilienza In Un Mondo In Rapido Cambiamento

Coordinatori: Piero Giulianini, Cristina Miceli, Alessandro Massolo

9:00 - 9:30	Invited speaker – Francesco Ferretti Plasticity in behavioural responses to predator recolonisation: ungulates, foxes *Vulpes vulpes* and wolves *Canis lupus* in a Mediterranean area
9:30 - 9:45	The selection of thermal refugia is the main driver of behavioural choices in alpine ibex *(Capra ibex*) responding to global warming Stefano Grignolio, Francesca Brivio, Francesco Sganzerla, Bruno Bassano, Cristiano Bertolucci, Marco Apollonio
9:45 - 10:00	On the wings through the streets: a solitary bee shows morphological, physiological and behavioural shifts in heavily urbanised area Carlo Polidori, Andrea Ferrari
10:00 - 10:15	Effects of tire particles and associated-chemicals on the pacific oyster *Crassostrea gigas* physiology, reproduction and next-generation Bernardini Ilaria, Tallec Kevin,, Paul-Pont Ika, Peruzza Luca, Dalla Rovere Giulia, Huber Matthias, Di Poi Carole, Koechlin Hugo, Quéré Claudie, Quillien Virgile, Le Grand Jacqueline, Le Goïc Nelly, Lambert Christophe, Lagarde Fabienne, Détrée Camille, Rafael Trevisan, Charlotte Corporeau, Tomaso Patarnello, Huvet Arnaud, Milan Massimo
10:15 - 10:30	Ecotoxicological effects of tyre wear road particles: metal accumulation and physiological response in *Tenebrio molitor* Maria Luigia Vommaro, Attilio Naccarato, Rosangela Elliani, Piero Giulio Giulianini, Antonio Tagarelli, Anita Giglio
10:30 - 10:45	A multidisciplinary approach unveils the resilient behavior of *Chamelea gallina,* a case study Federica Carducci, Elisa Carotti, Maria Assunta Biscotti, Adriana Canapa, Marco Barucca
10:45 - 11:00	Living in a contaminated environment: the role of the midgut in black soldier fly larvae Daniele Bruno, Jeroen De Smet, Martina Marzari, Dries Vandeweyer, Dario Lachi, Morena Casartelli, Gianluca Tettamanti
11:00 - 11:30	Coffee Break

venerdì 13 settembre

Simposio 7 - Premio UTET: Didattica, Divulgazione e Social Media in Zoologia

Coordinatori: Graziano Di Giuseppe, Elisabetta Palagi

11:30 - 12:00	Invited speaker – Nicla Panciera Giornalismo scientifico: sfide vecchie e nuove
12:00 - 12:30	Invited speaker – Willy Guasti Bestie del Web: social e zoologia
12:30 - 13:30	Tavola rotonda con Associazione Nazionale Musei Scientifici: didattica, educazione, divulgazione della zoologia: il ruolo delle associazioni e dei musei naturalistici Coordinatori: Alberto Ugolini, Fausto Barbagli
13:30 - 15:00	Pranzo

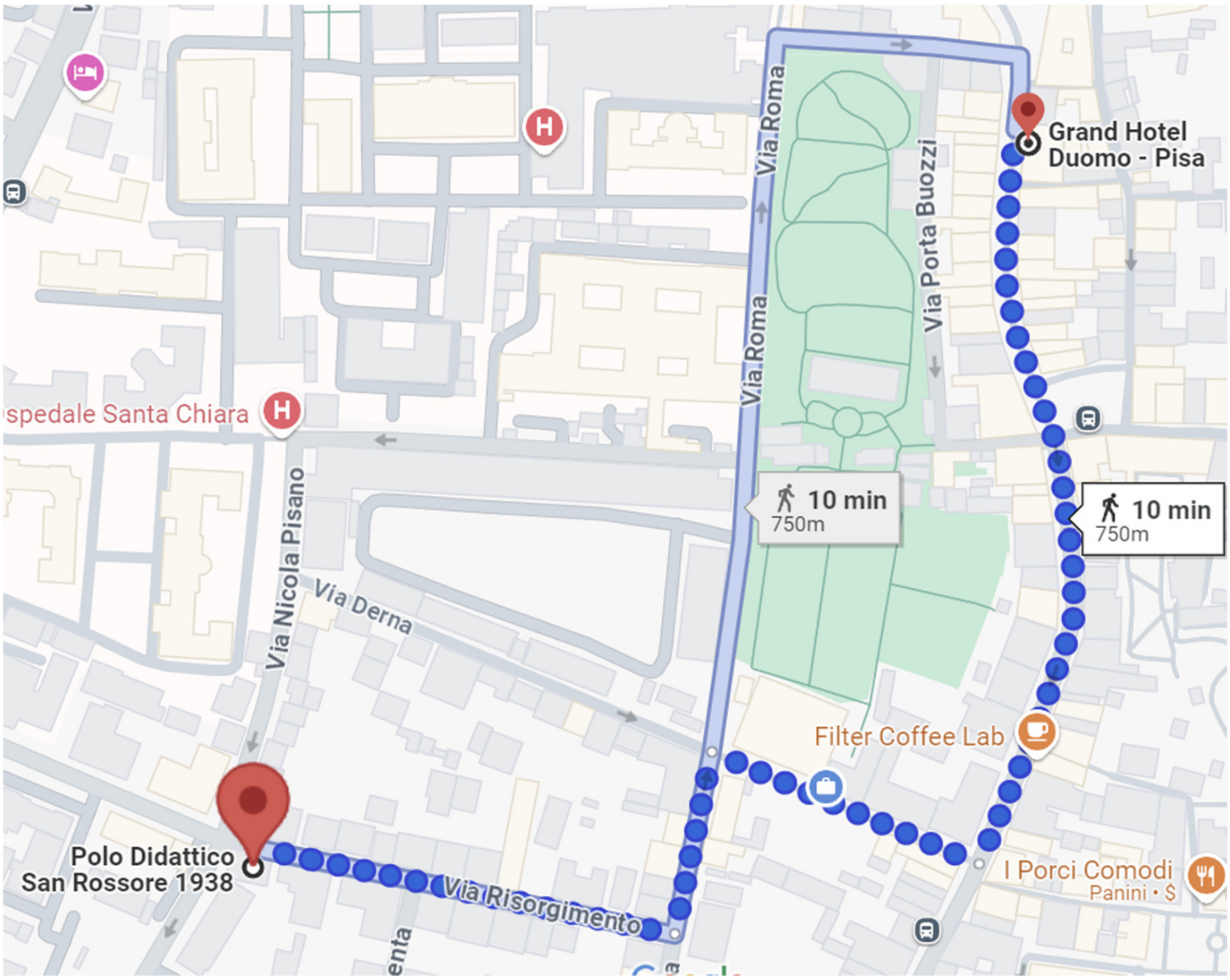
Simposio Satellite: Esperienze di progettazione internazionale in zoologia per Junior and Senior Investigators

Coordinatori: Cristina Giacoma, Giulio Petroni

15:00 - 15:10	An Italian zoologist abroad: personal experience, myths and reality Marco Musiani
15:10 - 15:20	The role of zoologists in INTEREG projects through selected examples Manuela Mauro, Hornsby Lucie Branwen, Francesco Longo, Aiti Vizzini, Claudio Gargano, Mirella Vazzana, Vincenzo Arizza
15:20 - 15:30	MSCA Individual fellowships (and similar grants): a personal experience in “POLLINATORS ET AL.” project Irene Piccini
15:30 - 15:40	Mattei Plan and Institute of European Studies "De Gasperi" as new opportunities for international employment in training and applied research for young zoologists: the example in Angola and Mauritania with studies on *Hippotragus niger variani* (Thomas, 1916) for the management and protection of an important bioindicator of water and environmental quality Antonio Sabbatella, Francesco Napolitano, Emiliana Minenna, Edna Carmelino Do Nascimento, Paolo Bonivento
15:40 - 15:50	A zoologist in a multidisciplinary context of international cooperation: a personal experience Alessandra Bardi

venerdì 13 settembre

15:50 - 16:00	Behind the scenes: the evaluation steps for the advanced ERC projects Elisabetta Palagi
16:00 - 16:10	EU Project pitfalls: when everything goes wrong (not only) on Friday the 13th Mascha Stroobant
16:10 - 16:30	General concluding remarks and question time Cristina Giacoma, Giulio Petroni
16:30 - 17:00	Coffee Break
17:00 - 19:00	Presentazione Poster finalisti/selezionati
19:00 - 21:00	Assemblea UZI
21:00	Cena sociale UZI Presso: Grand Hotel Duomo (Via Santa Maria 94, Pisa)



sabato 14 settembre

Aula A

Premiazione Poster

Simposio 1 - Zoologia molecolare

Coordinatori: Marco Passamonti, Filippo Barbanera, Giulio Petroni

9:00 - 9:30	Invited speaker - Martin Kolisko Culturing, single cell sequencing and phylogenomics: advancing our understanding of the diversity and evolution of eukaryotes
9:30 - 9:45	We can’t change who they are: integrating public and new COI, NADH2 and 12S sequences to build reference libraries for cartilaginous fish species Simone Di Crescenzo, Cariani Alessia, Valentina Crobe, Alice Ferrari, Martina Spiga, Riccardo Melis, Andrea Bellodi, Antonello Mulas, Maria Cristina Follesa, Rita Cannas
9:45 - 10:00	Essere o non essere *Raja* L. 1758: quando e quanto tassonomia e sistematica molecolare sono necessarie per la biodiversitá delle razze Fausto Tinti, Alice Ferrari, Valentina Crobe, Alessia Cariani
10:00 - 10:15	Population genetics of a habitat-forming scleractinian coral in the mesophotic and deep-sea of the Red Sea Roberto Arrigoni, Tullia I Terraneo, Fabio Marchese, Chakkiath P Antony, Nicolas Oury, Federica Barreca, Silvia Vimercati, Giovanni Chimienti, Sam J Purkis, Carlos M Duarte, Mohammad A Qurban, Mattie Rodrigue, Ameer A Eweida, Francesca Benzoni
10:15 - 10:30	Pleiotropy drives the cryptic persistance of male reproduction in parthenogenetic stick insects Giobbe Forni, Barbara Mantovani, Alexander S. Mikheyev, Andrea Luchetti
10:30 - 10:45	Multiple receptors for multiple vitellogenin forms? Marco Barucca, Chiara Spinsante, Federica Carducci, Elisa Carotti, Adriana Canapa, Davide Bizzaro, Maria Assunta Biscotti
10:45 - 11:00	The water-borne protein pheromone families of the ciliate *Euplotes*: an improved view of their structural evolution Claudio Alimenti, Bill Pedrini, Pierangelo Luporini, Adriana Vallesi
11:00 - 11:30	Coffee Break
11:30 - 13:30	Sessioni Parallele simposi : 1 (Aula A) - 2 (Aula B)
13:30 - 15:00	Pranzo

sabato 14 settembre – Sessioni parallele

Parallela Simposio 1 – Zoologia molecolare
Aula A

11:30 - 11:45	Caratterizzazione molecolare delle risposte delle larve di zanzara *Aedes albopictus* all'entomopatogeno *Bacillus thuringiensis* Maria Carmen Valoroso, Monica Vaghi, Gaetano Aufiero, Nunzio D'agostino, Silvia Caccia
11:45 - 12:00	Genetic basis of reproductive host plant preferences in *Cacopsylla melanoneura* (Hemiptera, Psyllidae). Lapo Ragionieri,Erika Corretto, Christian Stauffer, Jeffrey Feder; Hannes Schuler
12:00-12:15	Rediscovering the *Alectoris partridges* (Phasianidae): advances and perspectives in the genomic era Giovanni Forcina, Kritika Garg, Balaji Chattopadhyay, Tang Qian, Abdellah Ichen, José Antonio Blanco-aguiar, Fabián Casas, Sen Song, Tamer Albayrak, Monica Guerrini, Frank Erwin Rheindt, José Antonio Davila, Filippo Barbanera
12:15 - 12:30	Evidence of convergent evolution in the nuclear and mitochondrial oxphos genes across Squamata deep lineages Oscar Wallnoefer, Alessandro Formaggioni, Federico Plazzi, Marco Passamonti
12:30 -12:45	Molecular architecture and gene rearrangement in the mitochondrial genomes of gastrotrichs Anush Kosakyan, Agata Cesaretti, Francesco Saponi, Leandro Gammuto, Valentina Serra, Giulio Petroni, M. Antonio Todaro
12:45 - 13:00	Advancing tardigrade biodiversity monitoring in leaf litter: the potential of eDNA metabarcoding Federica Frigieri, Elia Lo Parrino, Michele Cesari, Ilaria Giovannini, Elisa Vandelli, Gentile Francesco Ficetola, Lorena Rebecchi, Roberto Guidetti
13:00 – 13:15	Tardigrades biodiversity in Italian rock pools revealed trought metabarcoding Matteo Vecchi, Jakub Godziek, Claudio Ferrari, Diego Fontaneto, Daniel Stec
13:15 – 13:30	A full raft: the nudibranch fauna (Mollusca, Gastropoda) traveling on board the bryozoan *Amathia verticillata* (Delle Chiaje, 1822) Giulia Furfaro, Egidio Trainito, Michele Solca, Alessio Mauro, Emanuele Mancini

sabato 14 settembre – Sessioni parallele

Parallela Simposio 2 – Variabilità, Plasticità E Resilienza In Un Mondo In Rapido Cambiamento
Aula B

11:30 - 11:45	Il delfino comune del mediterraneo: ricostruzione della storia ecologica ed evolutiva attraverso i reperti osteologici Pasino Martina, Cilli Elisabetta, Gnone Guido, Iacovelli Maria Vittoria, Iacumin Paola, Podestà Michela, Tinti Fausto
11:45 - 12:00	Using thermal priming to mitigate the lethal effects of marine heatwaves on the manila clam *Ruditapes philippinarum* Luca Peruzza, Carmen Tucci, Giulia Dalla Rovere, Ilaria Bernardini, Serena Ferraresso, Rafaella Franch, Massimiliano Babbucci, Mattia Panin, Tomaso Patarnello, Massimo Milan, Luca Bargelloni
12:00-12:15	Cambiamenti climatici e variazioni nella diversità genetica della trota fario (*Salmo trutta* complex) in Italia meridionale: evidenze dal DNA antico (aDNA) Andrea Splendiani, Tatiana Fioravanti, Tommaso Righi, Daniele Albertini, Antonio Tagliacozzo, Vincenzo Caputo Barucchi
12:15 - 12:30	Comparative head morphology in adult of tiger beetles of the genus *Calomera* by geometric morphometrics Yavuz Koçak, Asli Doğan Sarikaya, Federica Talarico, Elvira Brunelli
12:30 -12:45	Chemical and vibrational cues involved in the host location of *Sclerodermus cereicollis* and *Sclerodermus domesticus* (Hymenoptera: Bethylidae) Paolo Masini, Lorenzo Austeri, Manuela Rebora, Silvana Piersanti, Gianandrea Salerno
12:45 - 13:00	Ibridazione naturale ed antropogenica, e potenziale adattativo nel caribù (*Rangifer tarandus*) e in altre specie Marco Musiani
13:00 – 13:15	Intra-guild competition and ecosystem services of mammal scavengers in a new colonized wolf landscape Rudy Brogi, Paolo Bongi, Marco Del Frate, Sara Sieni, Anna Cavallera, Marco Apollonio

sabato 14 settembre

Simposio della Società Italiana di Protistologia

Coordinatori: Anush Kosakyan, Adriana Vallesi

15:00 - 15:30	Invited speaker - Ewa Joachimiak Diversity and similarity of cilia tips across the evolution
15:30 - 16:00	Invited speaker - Estienne Swart An endosymbiosis that got stuck? observations of genome evolution in the mixotrophic ciliate *Mesodinium rubrum*
16:00 - 18:30	Sessioni Parallele simposi : 1 (Aula A) - 2 (Aula B) – SIP (Aula C1)
17:15 - 18:30	Assemblea Società Italiana di Protistologia
18:30	Saluti finali e chiusura del Congresso

sabato 14 settembre – Sessioni parallele

Parallela Simposio 1 – Zoologia molecolare
Aula A

16:00 - 16:15	Integrative taxonomy reveals multiple invasions of the Mediterranean Sea by indo-pacific *Dorvillea* (Annelida, Dorvilleidae) Joachim Langeneck, Matteo Putignano, Desirèe Dimichele, Chloé J. L. Fourreau, Georgios Chatzigeorgiou, Maria Rousou, Marcos A. L. Teixeira, Yann Toso, Andrea Toso, Susana Carvalho, Adriana Giangrande, Alberto Castelli, Luigi Musco
16:15 - 16:30	Molecular phylogeny and species delimitation reveal hidden diversity within the water beetle species of the *Ochthebius quadricollis* complex (Coleoptera: Hydraenidae) from Atlantic and W- Palaearctic marine rockpools Simone Sabatelli, Pietro Gardini, Paolo Audisio
16:30 - 16:45	La diversità cromatica e molecolare in *Scolopendra cingulata,* Latreille, 1829, rivela eventi multipli di colonizzazione in Sicilia Francesco Paolo Faraone, Luca Vecchioni, Gabriele Giacalone, Calogero Muscarella, Matteo Riccardo Di Nicola, Marco Arculeo, Federico Marrone
16:45 - 17:00	La presenza di *Pseudorca crassidens* (Odontoceti, Delphinidae) in Mediterraneo valutata tramite analisi genetica di campioni museali e moderni Tatiana Fioravanti, Lucrezia Latini, Giovanni Manetti, Nicola Maio, Michela Podestà, Andrea Splendiani, Vincenzo Caputo Barucchi

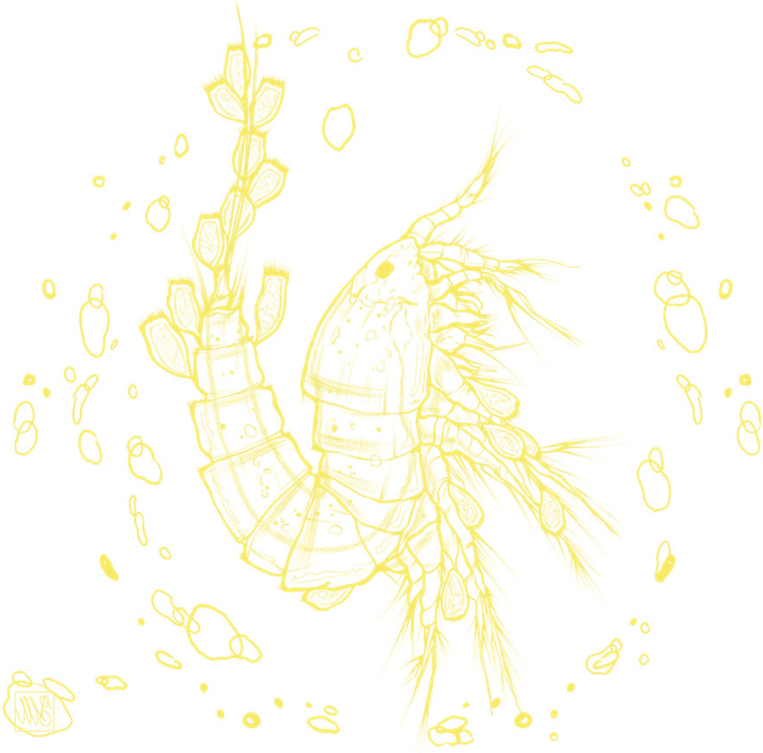
Parallela Simposio 2 – Variabilità, Plasticità E Resilienza In Un Mondo In Rapido Cambiamento
Aula B

17:15 - 17:30	Transcriptomic response to urbanization in two wild bee species, *Bombus pascuorum* (Scopoli, 1763) and *Osmia cornuta* (Latreille, 1805) Davide Maggioni, Nicola Tommasi, Beatrice Colombo, Andrea Galimberti
17:30 - 17:45	Honeybee pathogens: who wins in the city? Urbanisation affects pathogen transmission to wild bees and wasps Andrea Ferrari, Giovanni Cilia, Carlo Polidori

sabato 14 settembre – Sessioni parallele

Parallela Simposio della Società Italiana di Protistologia
Aula C1

16:00 - 16:15	Symbioses between prokaryotes and ciliates in the natural environment: distribution, patterns, and glimpses into evolutionary dynamics Vittorio Boscaro, Vittoria Manassero, Patrick J. Keeling, Claudia Vannini
16:15 - 16:30	Predator-prey interaction between the freshwater ciliated protist *Coleps hirtus* and the microturbellarian flatworm *Stenostomum sphagnetorum* Federico Buonanno, Gabriele Achille, Santosh Kumar, Daizy Bharti, Graziano Guella, Claudio Ortenzi
16:30 - 16:45	Understanding ecological adaptation in the ciliate *Tetrahymena pyriformis* through the lens of energy allocation Andrea Perna, Enrico Rivoli, Daniel Perkins
16:45 - 17:00	Systematic review of genus *Lacrymaria* with morphology-based identification key Alessandro Allievi, Giulio Petroni, Valentina Serra
17:00 - 17:15	Multidisciplinary description of a new species of ciliate, *Frontonia moderata* sp. nov. (Ciliophora, Oligohymenophorea) from Italy and South Africa Andrea Lenti, Alessandro Allievi, Giulio Petroni, Valentina Serra



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Simposio 3
Biodiversità del Territorio e Governance condivisa: monitoraggi e casi studio

coordinatori: Roberto Sandulli, Alessandro Cini, Andrea Gennai

Gli abstracts sono riportati seguendo l'ordine del programma del Congresso.

LEONARDO DAPPORTO[1]

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INNOVATIVE STRATEGIES FOR MONITORING POLLINATORS IN DATA-LIMITED CONTEXTS

Insects are declining globally, with evidence showing population decreases, local extinctions, and shifts to smaller areas at higher altitudes and latitudes. However, this evidence, although widespread, is often confined to a few regions where insect abundance data have been collected in recent decades. Without historical data, the impact of human activities on insect populations remains largely undetectable. In Italy, significant efforts over the past five years have established monitoring programs for pollinating insects, such as the Butterfly Monitoring Scheme, BeeNet, and the Pollinator Directive, to produce semi-quantitative data revealing population trends for the coming decades. Nonetheless, this data is limited in both duration (short time since initial collection) and spatial resolution (limited number of sites). Therefore, understanding environmental changes requires innovative solutions to assess pollinator conservation status in data-limited contexts. Assessing persistence or local extinctions in Italy can rely on exceptional past datasets or by aggregating presence data from diverse sources, including citizen science, into a common format for simple and robust statistical analysis. We recently developed the PETS algorithm, akin to the extinction rate formula, which uses the time elapsed since the last sighting of species to extrapolate an intuitive index of potential community-level species erosion. Applying this method, we found that, at least qualitatively, the butterfly communities in eight Apennines National Parks are largely intact. However, rarefaction has notably impacted generalist species and those thriving in cold climates. An alternative to traditional qualitative and quantitative monitoring is using behavioral markers. Defining potential behavioral responses to environmental stress will allow us to swiftly identify at-risk populations through ethological observations. We applied this approach on the model area of Giannutri Island to uncover competition between managed honey bees and feral bees. Combining these alternative methods with semi-quantitative assessments (transects) can help detect and address population declines quickly, aiming to implement conservation actions before local extinctions impact communities.

SIMONA BONELLI[1]

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CHALLENGES AND OPPORTUNITIES OF THE UE AGENDA 2030: ESTABLISHING A SHARED LONG-TERM ANIMAL MONITORING SCHEME

The ambitious EU Biodiversity Strategy 2030 implemented in the text of the European restoration Law recognises the scale and urgency of actions needed to halt and reverse declines in biodiversity. Declines in invertebrate diversity and abundance are well documented. Reports periodically drawn under the provisions of Article 17 of the Habitats Directive confirm that many species of European importance, listed in the HD appendixes, are in unfavourable status and many show declining trends. To fill this gap concretely, the availability of a representative, permanent monitoring network will be crucial to collect semi-quantitative data to plan and evaluate conservation actions. To date, only butterflies, among invertebrates, are monitored at EU level under a shared network.

Butterflies are taxonomically well-known and many of them are reasonably easy to identify in nature, a fact that has stimulated thousands of enthusiastic citizens to cooperate in recording observations of their occurrence. Such Citizen-science activities are run under the coordination by the European Butterfly Monitoring Schemes (eBMS), an international organisation currently active across 26 EU member States. More than 10000 transects are walked every year across Europe since 1990, for a total of 17600 km.

These data are the only available tool to evaluate numerical fluctuations of butterfly species along the years, and draw conservation programs reaching far beyond this specific case. Butterflies in fact include many “umbrella” species, so that acting for butterflies will benefit other wild pollinators, as well as many birds and even several habitats currently in poor conservation state.

The European Butterfly Monitoring Scheme (eBMS) is an initiative resulting from a collaboration between Butterfly Conservation Europe (BCE) and the British Centre for Ecology & Hydrology (CEH). It runs the Grassland Butterfly Indicator adopted by the EU commission and listed in art 9 of the Eu Restoration Law, to estimate supra-national population trends. The eBMS is active in Italy since 2019. Its National Committee includes the Universities of Turin and Florence, as well as the CREA Research Centre of Forestry and Wood of Cosenza. The eBMS experience demonstrates the importance of an European level monitoring scheme, the need of a national organisation capable of investing time and resources in the coordination of contributions offered by citizens, and the crucial role of scientific societies.

ALESSANDRO CAMPANARO[1,2], SILVIA GISONDI[1,2], ALICE LENZI[1,2,3], PIO FEDERICO ROVERSI[1,2]

1 CREA – Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Centro di ricerca Difesa e Certificazione, Firenze
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3 Università di Siena, Dipartimento Scienze della Vita

LO STUDIO E LA CONSERVAZIONE DEGLI INSETTI PROTETTI ATTRAVERSO LA *CITIZEN SCIENCE*

Un numero sempre crescente di ricerche scientifiche (KULLENBERG and KASPEROWSKI, 2016) dimostra come la *citizen science* abbia assunto un ruolo centrale nel monitoraggio della biodiversità, in particolar modo per studi a lungo termine e su ampia scala, o nei casi in cui essa può essere di supporto per gli adempimenti previsti dalle normative in materia ambientale (i.e. Direttiva Habitat). La ricca bibliografia oramai disponibile ha anche esaminato le potenzialità e le criticità di questo approccio, per sua natura multidisciplinare e dai diversi impatti (CHANDLER *et al.*, 2017).

Inoltre, il dipanarsi di iniziative e progetti ha generato negli ultimi anni la necessità di armonizzare i metodi, di raccogliere le buone pratiche e di riunire le iniziative nazionali: emblematico il caso italiano con la nascita, nel 2023, dell'associazione Citizen Science Italia e il suo primo convegno a Pisa.

Il CREA, in tale scenario, ha rivolto particolare attenzione agli insetti, gruppo spesso negletto, e in particolare ai coleotteri saproxilici, organismi che forniscono un contributo rilevante alla biodiversità degli ecosistemi forestali. A partire dal 2014, durante i progetti LIFE MIPP e InNat, i volontari coinvolti hanno fornito migliaia di dati relativi alla presenza di insetti protetti. Tali informazioni hanno permesso di accrescere la conoscenza di base sulla distribuzione delle specie selezionate (ZAPPONI *et al.*, 2017), propedeutica anche alla pianificazione di misure di conservazione idonee e piani di monitoraggio. I dati raccolti sono stati recentemente resi a libero accesso (CAMPANARO et al., 2024).

Una *citizen science* più "spinta" ha invece caratterizzato il progetto LIFE ESC360, in cui giovani volontari hanno partecipato attivamente al monitoraggio di specie e habitat protetti in Riserve dello Stato e contribuito alla disseminazione dei risultati, generando un'esperienza unica in Europa (BARDIANI *et al.*, 2023). Il progetto ha prodotto diverse tipologie di risultati: nuove indagini in siti non precedentemente attenzionati; la conferma della presenza di specie protette in aree Natura 2000; il rinvenimento di specie non precedentemente censite (LENZI *et al.*, 2022); l'individuazione di aree a tutela più rigorosa.

Il contributo proposto fornirà esemplificazioni degli aspetti sopracitati anche con l'intento di stimolare una discussione fra gli zoologi italiani sul punto di arrivo e sulle domande ancora aperte per un completo sviluppo della *citizen science* in Italia.

MASSIMO SCANDURA[1], TANCREDI GUERRASIO[1], DAVIDE CARNIATO[1], STEFANIA ZANET[2], ALESSANDRO FORTI[2], JOAQUIN VICENTE[3], JOSE ANTONIO BLANCO-AGUIAR[3], PELAYO ACEVEDO[3], PABLO PALENCIA[3,4], JIM CASAER[5], YORICK LIEFTING[6], PATRICK JANSEN[6], MARCUS ROWCLIFFE[7], MARCO APOLLONIO[1], EZIO FERROGLIO[2], THE ENETWILD CONSORTIUM

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3 Institute for Game and Wildlife Research (IREC) CSIC-UCLM-JCCM, Ciudad Real, Spain
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5 Research Institute for Nature and Forest,
6 Wildlife Ecology and Conservation, Wageningen University, Wageningen, Netherlands
7 Institute of Zoology, Zoological Society of London, London, UK

TRANSNATIONAL MONITORING OF WILDLIFE POPULATIONS: THE EXPERIENCE OF THE EUROPEAN OBSERVATORY OF WILDLIFE (EOW)

Global trends pose serious challenges to the human society, that are increasingly including its relationship with wildlife. In Europe, many species (e.g. large mammals) are increasing because of habitat recovery, some wild species approach cities and establish urban populations, introduced alien species spread and become invasive, pathogens hosted by wild animals are transmitted to livestock and pets and can represent a serious risk to their and human health. These situations require a transnational coordination and an evidence-based management, but quite often national/local authorities play their part alone. Hence, there is a growing need for coordinated initiatives enabling the monitoring and an informed management of wildlife populations.

In the last ten years some initiatives have been trying to fill this gap. In most cases international projects were launched either to merge data collected separately or to involve citizens in data collection (i.e. citizen science projects). A limited effort has been put in defining common standards to collect comparable data, necessary to produce trends data or spatial models at continental scale.

Here, a review of current initiatives is presented, remarking the different objectives, the role of new technologies, the involvement of non-professionals in data collection, and their main shortcomings and challenges.

In this frame, the creation of the European Observatory of Wildlife (EOW) represents a promising novelty. It was constituted by the ENETWILD consortium, a partnership of European institutions constituted in 2017 under commitment of the European Food Safety Authority (EFSA). The ratio of the EOW is the implementation of an ‘observatory’ approach to gather harmonized data across Europe, relying on an open network of monitoring sites where shared protocols are applied to collect comparable data on wildlife populations and their pathogens. The use of IT tools, including remote sensing, online applications, and artificial intelligence allows to reduce the effort and automatize data analysis. Since 2022 more than 45 participants in 27 European countries have adhered to the EOW, were trained and implemented, on an annual basis, a common protocol relying on camera trapping and the random encounter model (REM, Rowcliffe et al. 2008) to estimate the population density of multiple mammal species. The data gathered are made available to national and international authorities, contributing to the management of wildlife populations, human-beast interactions and health risks.

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2 Ente Fauna Marina Mediterranea, Scientific Organization for Research and Conservation of Marine Biodiversity, Avola, Italy
3 NBFC, National Biodiversity Future Center, Palermo, Italy
4 Department of Biological, Geological, and Environmental Sciences, University of Catania, Catania, Italy
5 National Research Council, Institute of Marine Biological Resources and Biotechnologies, Ancona, Italy

THE ALIENFISH PROJECT: INTEGRATING CITIZEN SCIENCE, MORPHOLOGICAL AND MOLECULAR APPROACHES TO THE STUDY OF MEDITERRANEAN BIOINVASIONS

The increasing presence of new thermophilic species in the Mediterranean Sea jeopardizes the rich and unique biodiversity of the basin. Many citizen science initiatives have been launched to monitor the arrival and expansion of these species. Among these, the AlienFish project aims to study the ecology and distribution of rare, thermophilic, and non-indigenous fishes in the Mediterranean. In this work, we studied the expansion of sea chubs (genus *Kyphosus*), aiming to address two main questions:
-which sea chub species is currently expanding in the basin?
-what is the phylogeographic origin of expanding populations?
In this study, three approaches have been employed to collect data on the presence of sea chubs in the Mediterranean: (i) citizen science, through the involvement of divers and fishermen; (ii) morphological/meristic and stomach content analyses on one collected specimen; (iii) molecular analyses on two specimens, i.e. sequencing their complete mitogenomes.
The three approaches yield complementary results which together provide a clear overview of the invasion dynamics of sea chubs. (i) Citizen involvement through fishing and marine biology Facebook groups allowed us to collect 13 new sea chub records from many localities, adding to the 26 previously published records. (ii) Morphological and meristic analyses of collected specimens allowed comparisons with historical literature and thus the species-level identification: our data evidenced that the sea chub currently expanding in the basin is *K. vaigiensis*. Besides, stomach content analyses confirmed the herbivorous nature of the fish. (iii) Molecular analyses confirmed the species-level identification and provided insights into the phylogeographic origin of the fish populations. The two sequenced individuals of *K. vaigiensis* cluster phylogenetically with Atlantic specimens, suggesting a natural expansion of the species through the Strait of Gibraltar.
In the study of biological invasions, each data collection method has its own advantages and limitations. For this reason, a multidisciplinary approach is essential to soundly shed light on the distribution, ecology, and population movements of expanding species. This research clarifies the invasion dynamics of sea chubs in the Mediterranean and provides a model for future studies on marine invasions, highlighting the critical role of a comprehensive approach.

ADELE COCOZZA DI MONTANARA[1], FRANCESCO RENDINA[1], FEDERICA SEMPRUCCI[2], ALBERTO GONZÁLEZ-CASARRUBIOS[3], DIEGO CEPEDA[4], LUIGIA DONNARUMMA[1], GIOVANNI FULVIO RUSSO[1], ROBERTO SANDULLI[1]

1 Department of Science and Technology (DiST), Parthenope University of Naples, ULR CoNISMa, Centro Direzionale, Italy
2 Department of Biomolecular Sciences (DiSB), University of Urbino 'Carlo Bo', loc. Crocicchia, Urbino, Italy
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THE FORGOTTEN *POSIDONIA OCEANICA* (L.) DELILE DETRITAL HABITAT: NEMATODE COMMUNITY AND TWO NEW SPECIES OF *ECHINODERES* (KINORHYNCHA: ECHINODERIDAE) INHABITING THIS NEGLECTED ENVIRONMENT

Seagrass beds are among the most important and studied marine vegetated habitats worldwide, Recently, the supra-littoral deposits of leaf litter (i.e., *banquettes*), have been investigated as part of the seagrass life cycle, in terms of their nutrients, biomass and associated community. Nevertheless, an overlooked fraction of the seagrass detritus never reaches the shore and sinks far away to deeper seafloor, but the destiny of the leaves transported to deep subtidal habitats remains unknown, even if they might host organisms consuming and processing seagrass carbon far away from the donor bed. Meiofauna is the most abundant and ubiquitous component of the benthos, which could be a useful tool to answer several ecological questions, since plays a key role enhancing energy flow from the microbial community to the entire food web. A huge issue related to meiofaunal research is the lack of information on both taxonomy and community structure, and despite recently this trend is changing, several habitats remain unexplored, such as the deep macerating *P. oceanica* detritus. This study investigated for the first time the meiofaunal community inhabiting sediments characterized by *P. oceanica* detritus in a deposit located at 65-80 m depth off Ischia Island (Gulf of Naples, Italy) in the zone D of the MPA "Regno di Nettuno". The results show that the meiofaunal community appears highly diversified and strongly dominated by nematodes (from 85% to 93%). The nematode community revealed a very high biodiversity (number of families and genera: 31 and 104, respectively), with a clear prevalence of selective and non-selective deposit feeders that suggest the key role of this habitat in the benthic detrital food web.

Additionally, two new species of *Echinoderes* are described: *Echinoderes semprucciae* sp. nov. and *Echinoderes sandullii* sp. nov. Both species can be easily distinguished from their congeners by their unique arrangement of cuticular structures and represent the first record of kinorhynchs inhabiting a macerating *P. oceanica* detrital habitat. This study will possibly draw attention to this peculiar environment that deserves to be deeply investigated given the strong connection to the much better-known living seagrass beds, which support incredibly diverse community, from tiny invertebrates to large fishes, providing important services to people as well, especially in the Mediterranean Sea.

MARTINA COLETTA[1], MARCO MONTICELLI[1], CELESTE GENTILI[1], ALDO D'ALESSANDRO[1], ANTONIETTA LA TERZA[1]

1 School of Biosciences and Veterinary Medicine, University of Camerino, Camerino (MC), Italy.

MANAGING SOIL TO SUPPORT SOIL BIODIVERSITY IN PROTECTED AREAS AGROECOSYSTEMS: THE CONERO PARK CASE STUDY

Sustainable soil management is fundamental to the conservation of soil biodiversity and the continued provision of vital ecosystem services that are essential to human life. The EU's Biodiversity Strategy for 2030 emphasizes the key role of organic farming and land protection in halting biodiversity loss, including the edaphic one. To assess the effectiveness of the proposed measures a study was conducted to assess and compare the soil health of different organic agroecosystems located within a protected area using the arthropod-based Biological Soil Quality Index (QBS-ar) over a two year period. Given the diverse agronomic practices employed across the different agroecosystems, a second objective was to establish soil quality benchmarks within each system and to identify the most effective agricultural practices for maintaining soil quality in an area of significant natural value.

Four arable lands, four olive groves, and four vineyards located within the Conero Regional Park (Italy) were examined. The QBS-ar Index, number of biological and euedaphic forms, density (ind/m^3) and abundance, Acari/Collembola ratio, and percentage of Oribatid mites out of total mites were determined. Ordination analysis was used to analyse soil microarthropod community composition among different agroecosystems.

The first-year results showed that organic farming in conjunction with land protection had a beneficial impact on soil quality. Most farms exhibited excellent soil quality, with the highest levels observed on arable land. This is consistent with the Intermediate Disturbance Hypothesis (IDH), which posits that non-intense disturbance within a habitat can have a beneficial effect on biodiversity, compared to predominantly stable conditions. Similarly, microarthropods community composition in arable land differed from those in the more stable arboreal crops. Nevertheless, olive groves exhibited a higher abundance and diversity of microarthropods compared to vineyards, which exhibited lower levels.

It is fundamental to regularly monitor soil health in protected areas to ascertain the condition of these valuable habitats over time and to ensure their continued protection. The application of different farming practices can lead to variations in soil health and soil community structure across agroecosystems. Thus, it is crucial to establish reliable benchmarks for different agroecosystems to facilitate prompt and effective intervention aimed at addressing degraded conditions.

mercoledì 11 settembre
ore 17:00 - 19:00

Simposio 4

Modelli animali utilizzati a fini scientifici

coordinatori: Adriana Canapa, Federico Buonanno, Marco Zuffi

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EVOLUZIONE E MANTENIMENTO DEL POLIMORFISMO CROMATICO NELLE LUCERTOLE DEL GENERE *PODARCIS*

Il polimorfismo cromatico può essere utilizzato per studiare i processi evolutivi fondamentali come la selezione correlativa per le combinazioni di caratteri adattativi e la selezione dipendente dalla frequenza per il mantenimento dei morfi entro una stessa popolazione. L'interesse nello studio del polimorfismo cromatico ha inoltre importanti conseguenze nella comprensione di meccanismi evolutivi di base come la fissazione morfica e la speciazione simpatrica. Le lucertole del genere *Podarcis* rappresentano un ottimo modello per lo studio del polimorfismo cromatico sia per quanto riguarda gli studi di campo sia per osservazioni comportamentali in laboratorio. Dal 2004 studiamo le cause che controllano l'evoluzione e il mantenimento del polimorfismo nella lucertola comune (*Podarcis muralis*), un lacertide europeo molto diffuso che presenta un marcato polimorfismo di colore in entrambi i sessi. Le nostre ricerche hanno studiato i modelli di variabilità delle frequenze dei morfi su base geografica e si sono concentrate sulla variabilità morfo-specifica in diversi tratti ecologici, fisiologici e comportamentali tra cui la territorialità, l'aggressività, l'immuno-competenza e l'ecologia termica. I risultati finora ottenuti suggeriscono che i morfi rappresentino strategie riproduttive alternative - optima alternativi - adattati localmente che possono essere alla radice dei processi di speciazione simpatrica attraverso la fissazione del morfo più adattato.

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THE SIPUNCULAN *PHASCOLOSOMA STEPHENSONI* (ANNELIDA: PHASCOLOSOMATIDAE) AS A NEW MODEL FOR BIOINSPIRED ROBOTS

Among the diverse array of marine invertebrates, annelids stand out as a fascinating source of bioinspiration in robotics, demonstrating how movement can be controlled through the mechanical reactions of entirely soft-bodied parts. The EIC Pathfinder Open project MAPWORMS (grant agreement N° 101046846; www.mapworms.eu) aims to use marine annelids as models for innovative soft robots capable of autonomously performing tasks and adapting to the environment through the exploitation of their smart materials. The project follows a multidisciplinary approach, integrating biological, chemical, physical, and mathematical data to inform the development of the final robot.

While the movement of typical segmented annelids is generally regulated by antagonistic interactions between circular and longitudinal muscles in different metameres, unsegmented annelids as Sipuncula and Echiura are characterised by peristaltic movements on a single chamber, and Sipuncula also show an interesting mechanism of eversion/retraction of the introvert modulated by circular muscles and specialised retractor muscles which are unique to this group of annelids.

Due to its anatomical and bio-mechanical traits combined with its hardiness, which makes it easy to maintain in laboratory conditions, *Phascolosoma stephensoni* Stephen, 1942 was selected as the main model for soft robots. Individuals of *P. stephensoni* sampled along the coastline of Salento were characterised from the morphological and behavioural point of view through high-quality footage obtained in experimental aquaria, and the anatomical structures underlying the eversion mechanism were studied through micro-CT scans performed on individuals fixed in different positions. Finally, structural properties of the body wall were characterised through stretch tests at the macroscopic scale, and using an atomic force microscope at the microscopic scale.

Morphological, anatomical, behavioural and structural data were then combined to develop a mathematical model of the shape-morphing and movement of *P. stephensoni*, which will be applied to mimic the characteristics of this species in a robot prototype.

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CILIATED PROTOZOA AS MODELS TO STUDY CELLULAR AND ORGANISMAL RESPONSES TO ENVIRONMENTAL CHANGES: THE CASE OF THE ANTARCTIC CILIATE *EUPLOTES FOCARDII* TREATED WITH THE POLLUTANT BISPHENOL A

Ciliated protozoa are cosmopolitan eukaryotic microorganisms well adapted to aquatic and marine ecosystems and play a crucial role in the microbial loop important to food webs. Some species are also well characterized by omics technologies and genetic manipulations, making them optimal models for studying cellular and organismal responses to environmental changes in temperature, salinity, and pollutants. Our approach combines morphological and molecular analyses, examining changes in ciliate phenotypes (e.g., cilia organization, structure, and motility) and gene expression.

Using a procedure where toxicity tests were followed by transcriptomic approaches and bioinformatic analyses, we identified biological processes and marker genes affected by environmental stresses in *Tetrahymena thermophila* exposed to silver and silver nanoparticles, which are increasingly used in industrial applications and are well known as biocides (Piersanti *et al.*, *Environ Pollut*, 2021). Currently, we are analyzing the response to plastic contamination in the ciliate *Euplotes focardii*, an Antarctic endemic species. Antarctica represents a unique natural laboratory for ecotoxicological studies due to its limited internal pollution but high external contamination levels.

Here, we report the response of *E. focardii* to the plastic derivative bisphenol A (BPA), identifying genes and biological processes involved. Transcriptome analysis revealed the participation of cellular motility pathways, with a downregulation of dynein and kinesin, which was also confirmed by changes in ciliary movements. Additionally, there was an overall upregulation in both autophagy pathways and xenobiotic metabolism involving cytochrome P450 and glutathione-S-transferase. The level of gene involvement was concentration dependent. Although *E. focardii* showed resistance to relatively high concentrations of BPA, this study raises a relevant research question. BPA is known to affect membrane fluidity, which is typically higher in Antarctic organisms. Could this adaptation strategy of *E. focardii* to the Antarctic environment increase its vulnerability to rapid environmental changes, such as the distribution of plastic pollution? We address this question by comparing the response of *E. focardii* to BPA with that of the closely related mesophilic species *E. crassus*. These comparative studies will help establish *Euplotes* as a new model for investigating plastics and their derivatives in marine environments.

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IL BACO DA SETA COME MODELLO DI INFEZIONE ALTERNATIVO PER LO SCREENING DI ANTIBIOTICI NANOCONIUGATI

L'uso improprio ed eccessivo degli antibiotici ha portato negli ultimi decenni a una rapida diffusione di batteri antibiotico-resistenti. Questi sono causa di circa 1 milione di morti all'anno. Di conseguenza, risulta indispensabile sviluppare nuove molecole con proprietà antimicrobiche e/o formulazioni alternative più efficaci. Una delle strategie più promettenti per superare la resistenza microbica si basa sull'utilizzo di nanoparticelle come sistema di delivery per gli antibiotici. In questo ambito, lo sviluppo di nuovi nanoantibiotici richiede test preclinici che vengono solitamente condotti *in vivo* su mammiferi, quali topi e ratti, sebbene le recenti direttive europee sull'utilizzo degli animali in laboratorio promuovano l'impiego di nuovi modelli animali quali gli invertebrati.

Il presente progetto ha lo scopo di validare l'utilizzo di larve di *Bombyx mori* come modello di infezione per lo screening di antibiotici nanoconiugati. A questo scopo, gli insetti sono stati infettati con un patogeno Gram-positivo (*Staphylococcus aureus* ATCC6538P) e trattati con teicoplanina coniugata a nanoparticelle di ossido di ferro. La sperimentazione è stata condotta a 37°C per cercare di riprodurre al meglio le condizioni fisiologiche umane. Oltre al tasso di sopravvivenza delle larve, sono stati valutati marcatori del sistema immunitario, umorali e cellulari, per avere un quadro completo sull'effettiva efficacia del formulato.

Il nanoantibiotico è risultato efficace nel curare le larve, incrementando la loro percentuale di sopravvivenza e inibendo l'attività dei marcatori immunitari.

In conclusione, i dati raccolti dimostrano l'utilità del baco da seta come modello di infezione per testare l'efficacia di molecole antimicrobiche nanoconiugate, ampliando la gamma di applicazioni per il quale questo insetto può essere utilizzato.

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THE EMERGING ROLE OF MITOCHONDRIALLY ENCODED SMALL INTERFERING RNAS TO REGULATE NUCLEAR GENE EXPRESSION

Mitochondria seem to be connected to many more cell functions than ATP production. The possibility that mitochondrial DNA (mtDNA) can act on nuclear gene expression has been suggested only recently: mtDNAs have been found to produce small noncoding RNAs (sncRNAs), long non-coding RNAs (lncRNAs) and peptides, all of them suggested or demonstrated to interact via different pathways with the nucleus. Our research aims at characterizing the retrograde mitochondrial-to-nucleus signaling by mitochondrially encoded small RNAs (called small mitochondrial highly transcribed RNAs, smithRNAs), in a comparative way. We have already predicted the presence of many and proved functionality of two smithRNAs in *Ruditapes philippinarum* (A. Adams & Reeve, 1850), in which they are likely involved in gonad formation and sex determination. While we have developed a bioinformatic pipeline to detect and analyze smithRNAs in metazoans, we present new data on: 1. their phylogenetic distribution among Metazoa; 2. their role in mito-nuclear incompatibilities and speciation; 3. their evolvability in the context of the polycistronic maturation of mtDNA; 4. their possible ways to escape mitochondria to deliver their function in the cytoplasm; and 5. their maturation processes, to understand whether they can be ascribed to the known classes of small interfering RNAs (i.e., miRNA, siRNA or piRNA), or to a new unknown one. Overall, smithRNAs are emerging as a fast-evolving generalized new form of retrograde signaling and, potentially, a common feature among metazoans, adding a brand-new functionality level of mitochondria in the eukaryotic cell.

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THE BRITTLE STAR *OPHIACTIS VIRENS* (ECHINODERMATA: OPHIUROIDEA) AS NON-CONVENTIONAL MODEL ORGANISM FOR STUDING THE EFFECTS OF POLYETHYLENE TEREPHTHALATE NANOPLASTICS

Invertebrates represent the majority of living animals in all the ecosystems and are increasingly used as sentinel organisms in ecotoxicological studies to expand our understanding of the potential adverse effects of new pollutants introduced in the environment.

In marine ecosystems, where plastic represents the dominant type of litter, echinoderms are considered excellent biological indicators of contamination thanks to their ecological role, abundance and wide distribution.

Therefore, aim of this work was to investigate the potential effects of polyethylene terephthalate nanoplastics (NPET) on the biology (including regeneration) of the brittle star *Ophiactis virens* (M. SARS, 1859), a small fissiparous ophiuroid and an emerging non-conventional animal model in ecotoxicology.

Individuals of *O. virens* were subjected to arm amputation and then exposed to three NPET concentrations (0.05, 0.5 and 5 µg/mL), to artificial seawater (ASW)(control), or ASW+ NPET solvent (solvent control) for two weeks in semi-static conditions. Three replicates per experimental condition were performed using 10 individuals/replicate.

At the end of the exposure period the surviving individuals were processed to assess the effects of NPET on different parameters at different levels of biological organization, including mortality, behavioural responses (righting time, moving distance), arm regeneration capacity (regenerate length, differentiation index), presence of anomalies in the external/internal anatomy.

Preliminary results showed no effects induced by NPET on righting time and moving distance as well as no presence of anomalies in the external and/or internal anatomy. In contrast, a significative increase in mortality was recorded at the higher tested doses, along with a significative reduction in arm regenerate length and a consequent increase of the differentiation index. Accumulation of NPET was also observed in the preoral cavity of the samples in a dose-related manner.

Overall, these preliminary results highlight the risk of ingestion of nanoplastic materials by *O. virens*, with a possible indirect dose-dependent impact on its physiology. In addition, our study confirms the reliability of echinoderms as non-conventional model organisms in ecotoxicology because of their sensitivity to contaminants, making further studies on risk assessment by nanoplastics necessary.

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DIVING INTO DIVERSITY: FISH MODELS AS POWERFUL TOOLS FOR BIOLOGICAL DISCOVERY

Fish are the most diverse group of vertebrates and offer research alternatives to endothermic animals. Fish 'simpler' systems provide unique insights into a remarkable range of complex biological processes, driving the surge in fish research in recent years. With examples from the research of our group, we underline the use of fish species to explore fundamental biological processes and address pressing environmental challenges. By analysing fish adapted to extreme environments, like the blind cavefish (*Phreatichthys andruzzii* and *Astyanax mexicanus*), we investigate the adaptive evolution of the biological clock. This line of research has revealed, for instance, that cavefish have a “blind” circadian clock, due to loss-of-function mutations in three, non-visual opsin genes and that feeding represents the strongest synchronizer for molecular and behavioural circadian clock. The range of molecular tools available in zebrafish (i.e., generation of null mutants and primary cell lines) offers an ideal platform to dissect the role of specific genes in behaviour and cognition. For example, we showed that the neurotrophin *bdnf* has a central role in learning: null *bdnf* mutants failed several visual colour and spatial discrimination tasks, and wild-type individuals displayed variation in *bdnf* expression that predicted learning. Zebrafish give us also the opportunity to study anthropogenic pollutants in aquatic environments. For instance, we showed that Artificial Light at Night (ALAN) affects behaviour, cognition and locomotor rhythmicity across developmental stages. ALAN-treated adult zebrafish lacked daily patterns of behavioural activity and brain transcriptomic analyses across the 24h revealed significant alterations in the expression of clock and clock-controlled genes like *per1*, *cry1* and *aanat2*, the key enzyme for the melatonin synthesis. Last, fish behavioural analysis holds great, yet underutilized, potential in aquaculture practices. By incorporating behavioural considerations, we can enhance production and welfare in sea bass, sea bream or tilapia. Particularly, environmental and cognitive enrichments promote natural behaviours, reduce stress, and improve overall fish health. The collective contributions of fish species to scientific research underscore their importance as model organisms. Their diverse characteristics, from genetic similarity to humans to their adaptability to various environments, offer scientists unique and valuable tools.

giovedì 12 settembre
ore 09:00 - 11:00

Simposio 5

Le innovazioni in Zoologia: dal microscopio all'intelligenza artificiale

coordinatori: Cristina Giacoma, Paolo Luschi

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STUDYING CETACEANS USING HIGH-TECH INSTRUMENTS AND MACHINE LEARNING APPROACHES

Cetaceans are large predators that influence their environment through enormous prey consumption, bypumping and recycling of nutrients, and by acting as “ecosystem engineers”. Living as apex predators in both polar and tropical regions, their evolutionary history explains significant parts of the ecological dynamics of the current oceans. As lung-breathing animals, they spend most of their time underwater, so monitoring them in the vast marine environment, especially in remote and deep offshore areas, is a significant challenge.

In recent decades, new technologies (e.g., autonomous vehicles, acoustic stations, satellite systems, bio- logging devices, aerial drones) have become available to the international scientific community, and are expanding our knowledge of cetacean behavior. In addition, with the development of automated data analysis techniques (e.g., signal and image processing, machine learning, artificial intelligence) large amounts of data can be quickly examined. Therefore, research on marine mammalsis rapidly innovating, following the global trend of using both high-tech tools and new computational approaches to gather important information about these elusive species. A global strategy requires the acquisition of reliable scientific data to better determine the taxonomy, population structure and habitat distribution of the numerous species around the world. Depending on local conditions, this data can then be used to promote actions to reduce human impact. Threats to cetaceans are largely human-caused, such as habitat degradation from pollutants, incidental capture in fishing gear, ship strikes, and other critical issues. Effective conservation measures to minimize risks and promote their recovery can only be implemented through improved scientific knowledge.

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GENETIC MANIPULATION OF THE SILKWORM *BOMBYX MORI*: FROM BASIC SCIENCE TO BIOTECHNOLOGICAL APPLICATIONS

The domestic silkworm *Bombyx mori* is extensively studied as a model organism for lepidopteran genetics and has an economic value in silk production. In recent years, the use of *B. mori* and its byproducts in cosmetics, biomedical products, and animal feed has also received considerable attention. In 2021, the European Commission approved the use of *B. mori*-derived proteins for animal feed, and in 2024, the first commercial pet food featuring silkworm proteins was released on the European market.

B. mori domestication occurred around 5,000 years ago and currently more than 4,000 silkworm strains are reared worldwide. Traditional genetic breeding methods have led to a massive diversification of silkworm lines and qualities, significantly contributing to the sericulture industry. However, modern biotechnology, particularly CRISPR/Cas9 genome editing technology, holds the potential to revolutionize this field by drastically improving efficiency.

One promising area of interest is the circadian clock, an internal timekeeping mechanism that regulates gene expression and numerous physiological and behavioral processes throughout the day. The circadian clock synchronizes physiological and behavioral activities with environmental cues, optimizing biological functions and enhancing fitness. In Lepidoptera, circadian rhythms influence egg hatching, adult eclosion, feeding, and metabolism, all of which are vital for their ecological roles and economic value.

Our study investigates the role of the circadian clock gene *Clock* in *B. mori* using CRISPR/Cas9-mediated mutagenesis to create a *Clk* null mutant strain ($\mathit{Clk}^{\Delta 29}$). We demonstrated a dysregulation of the circadian clock in $\mathit{Clk}^{\Delta 29}$ by detecting altered temporal transcriptional profiles of core circadian clock genes and observing disrupted circadian-controlled behaviors. Importantly, $\mathit{Clk}^{\Delta 29}$ mutants demonstrated significant increments in key economic traits, as silk production increased by up to 7%, and pupal weight increased by up to 25%, compared to wild-type controls. Future research will aim to elucidate the specific molecular mechanisms underlying these phenotypes and explore the impact of the $\mathit{Clk}^{\Delta 29}$ mutation in various genetic backgrounds used in commercial silk production. Taken together, these findings underscore the potential of genetic manipulation of circadian clock genes to improve sericultural productivity.

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IL MICROBIOMA INTESTINALE DELLE LARVE DI MOSCA SOLDATO NERA COME STRUMENTO PER LO SVILUPPO DI STRATEGIE INNOVATIVE DI BIOCONVERSIONE

La mosca soldato nera (*Hermetia illucens*, Linnaeus 1758) è un dittero cosmopolita appartenente alla famiglia Stratiomyidae. Negli ultimi anni l'interesse verso questo insetto è aumentato in modo esponenziale perché le sue larve saprofaghe sono in grado di bioconvertire in modo estremamente efficiente scarti organici e sottoprodotti della filiera agroalimentare. Dalla biomassa così ottenuta è possibile estrarre macromolecole di alto valore come proteine e lipidi da impiegare, rispettivamente, per la produzione di mangimi o bioplastiche, e di biocarburanti. I nostri studi hanno dimostrato che la grande adattabilità alimentare di queste larve, in grado di crescere su molteplici substrati organici, è dovuta alla plasticità morfofunzionale del loro complesso intestino e al microbiota ad esso associato.

Negli ultimi anni le nostre ricerche si sono concentrate sulla caratterizzazione del microbiota intestinale di queste larve con l'obiettivo di sviluppare nuove strategie di biodegradazione di macromolecole complesse e recalcitranti che sfruttino le potenzialità della comunità batterica che risiede nell'intestino di questi insetti. In particolare, le larve allevate su substrati contenenti polimeri complessi (come, ad esempio, lignina o plastiche) possono essere utilizzate come "bioincubatori" per la selezione di ceppi e geni microbici utili per la biodegradazione di queste macromolecole. Abbiamo infatti dimostrato che polietilene e polistirene ingeriti dalle larve vengono biodegradati grazie alla selezione di specifici ceppi e funzioni del microbioma intestinale. Un altro approccio interessante riguarda la possibilità di "insegnare" alle larve a bioconvertire polimeri complessi presenti nel loro substrato di crescita attraverso la colonizzazione dell'intestino da parte di microorganismi che possiedano i pathway di degradazione necessari.

Lo studio dell'interazione tra l'insetto e il suo microbiota intestinale rappresenta quindi la base per lo sviluppo di strategie innovative per la bioconversione e la biodegradazione di polimeri complessi naturali e sintetici e, in questo contesto, le larve di *H. illucens* sono uno strumento efficace e con grandi potenzialità ancora da esplorare.

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INSECT FUNCTIONAL MORPHOLOGY: FROM BASIC RESEARCH TO BIOMIMETICS

Understanding the basic structure and function of organisms is one of the oldest areas of research pertaining to the natural world. The study of the relationship between the structure and function of morphological features in the animal kingdom has always fascinated human beings, thus providing fundamental knowledge in an ecological and evolutionary perspective. Among animals, insects, with their extraordinary evolutionary success, show a remarkable variety of morphological features on their body surface to adapt to their environment. Indeed they exhibit a range of micro- and nanoarchitectures on their cuticle with different functions such as antiwetting, self-cleaning, antireflection, enhanced color, adhesion, antimicrobial properties, sensory. In this context, although the functional morphology of insects remains a basic science, insect structures offer a variety of existing and potential applications in biomedical, structural, mechanical and aerospace engineering. In the last twenty years, engineers, biologists, physicians and chemists come together with an interdisciplinary approach to answer important questions in functional morphology and biomechanics which led to the inspiration of engineering innovations.

The present talk aims to provide some examples of recent studies in the field of insect functional morphology investigating in detail the morphology and material properties of the nanostructures on insect cuticle involved in grooming behaviour, insect adhesion and structural colours in different insect species. Examples of data collected with the help of scanning and transmission electron microscopy, confocal laser scanning microscopy, Raman-Brillouin microscopy, spectroscopy, are provided to characterize with a multidisciplinary approach joining physics and biology skills insect cuticular surfaces. Understanding the structure-material-function relationship in insect cuticle can drive the development of new biomimetic surfaces.

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NUOVE TECNOLOGIE A SUPPORTO DELLA ZOOLOGIA PER IL MONITORAGGIO E LO STUDIO DEL COMPORTAMENTO ANIMALE: DAI DRONI E L'INTELLIGENZA ARTIFICIALE ALLA STAMPA 3D

La progressiva riduzione dei costi e dimensioni del materiale elettronico ha consentito uno sviluppo e disponibilità di nuovi strumenti tecnologici per il monitoraggio e lo studio della natura. I sistemi a pilotaggio remoto sia in aria che a terra come droni e rover hanno ottenuto una crescente attenzione e implementazione. In modo particolare i droni (UAV- *unmanned aerial vehicle*), grazie al miglioramento della avionica, dei sistemi di alimentazione, alla disponibilità di carico e il miglioramento dei sistemi di stabilizzazione in volo hanno consentito a operatori anche con ridotta esperienza di pilotaggio di utilizzare facilmente questi mezzi in campo. Inoltre, la possibilità di utilizzo integrato di differenti sistemi di acquisizione immagini e analisi ha consentito di incrementare i campi di utilizzo di questi mezzi per il monitoraggio del territorio e della fauna, finora particolarmente rivolta ai vertebrati. In questa presentazione introdurrò i principali campi di applicazione dei droni grazie alla presenza di differenti sistemi di acquisizione dati come termico, LIDAR e ottico. Tali sistemi applicabili assieme all'intelligenza artificiale possono consentire il monitoraggio su ampie superfici di terreno, l'individuazione in scarse condizioni di luce e lo studio del comportamento di differenti specie. Tuttavia in questo contesto, l'impiego di queste tecnologie nel monitoraggio e studio della fauna invertebrata è caratterizzata ancora da molti vuoti e poche applicazioni. A tale scopo da alcuni anni in collaborazione con differenti enti e istituti di ricerca stiamo sviluppando differenti attività di ricerca con l'utilizzo di sistemi UAV abbinati all'intelligenza artificiale come strumento per il riconoscimento e monitoraggio della fauna invertebrata e lo sviluppo di nuove trappole artificiali realizzate mediante stampa 3D. La produzione di prototipi ci ha consentito di brevettare e sperimentare nuove biostrutture funzionali all'implementazione della biodiversità e allo studio del comportamento sia in campo che in laboratorio.

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THE EVOLUTIONARY NEUROANATOMY OF BLOOD FEEDING IN MOSQUITOES REVEALED BY X-RAY TOMOGRAPHY

Background: Female mosquitoes feed on blood, which is a special behaviour that ensures the supply of amino acids needed to complete the oogenesis. Blood feeding is a complex behaviour that involves numerous physiological processes, and this strong need was lost in 3 branches of the mosquito phylogenetic tree and these mosquitoes found alternative solutions for providing amino acids for the egg development. This unique behavioural adaptation offers an excellent model to study the neuronal functions governing this process.

Methods: To gain insight into the evolutionary changes underlying the loss of blood feeding in the mosquito neuroanatomy, we used X-ray-based morphological examinations (X-ray tomography). We acquired datasets from four females and three males of each of the species. We selected 6 species feeding on humans or other warm-blooded animals (*Aedes aegypti, Aedes albopictus, Anopheles stephensi, Culex pipiens, Culiseta longiareolata* and *Sabethes cyaneus*), 1 feeding on amphibians (*Uranotaenia lowii*) and 3 non-blood feeding species (*Toxorhynchites rutilus*, *Malaya genurostris* and *Topomyia yanbarensis*). We also added nonblood feeding individuals from *Wyeomyia smithii*, whose population can display plastic feeding habits. The X-ray data were collected at the synchrotron facilities (European Synchrotron Radiation Facility, ESRF, and Elettra Sicrotrone Trieste), the datasets were reconstructed using in loco pipelines; the 3D rendering, segmentation and volume analysis were performed using Dragonfly software. The volumetric data were statistically analysed using R software using NMDS and Multivariate Generalised Linear Mixed Models using Markov chain Monte Carlo techniques to account for the phylogenetic relatedness of the examined species.

Results: The allometric relationship of the brain compared to the body size of the mosquitoes is different between blood feeding and non blood feeding mosquitoes. Comparing different brain regions (optical lobes, antennal lobes, mushroom bosies, central complex, etc.) and the pharyngeal pump and associated muscles, we revealed variation of the relative volume of head regions in response to the blood feeding behaviour.

Conclusions: Novel anatomical analysis, such as X-ray computed tomography, coupled to advanced genomic studies can help us to understand the biology and physiology of complex organs, such as brain, and to better understand the evolution of complex behaviours, such as blood feeding in mosquitoes.

FILIPPO CARUGATI[1], OLIVIER FIARD[1], ELISA PROTOPAPA[1], CAMILLA MANCASSOLA[1], EMANUELA RABAJOLI[1], CHIARA DE GREGORIO[1], DARIA VALENTE[1], VALERIA TORTI[1], TERESA RAIMONDI[1], VALERIA FERRARIO[1], WALTER CRISTIANO[1], MARCO GAMBA[1]

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MACHINE LEARNING APPLICATIONS FOR ANIMAL BEHAVIOR STUDIES: THE CASE OF AUTOMATIC DISCRIMINATION OF VOICED AND UNVOICED PRIMATE FACES

Recent technological advancements are essential for bridging the gap between the large volume of raw materials collected in wild and captive settings and the rapid extraction of meaningful information. Artificial intelligence (AI), especially deep learning, has displayed potential in various fields, including the study of animal behavior. Deep learning can revolutionize animal behavior research in visual tasks by effectively capturing postural and locomotor sequences across different species. Over the last years, markerless pose estimation techniques have significantly advanced, enabling the analysis of motions across a broad spectrum of species and providing insights into behavior associated with body configurations. This study employs pose estimation algorithms to analyze primate facial gestures, explicitly focusing on distinguishing between voiced and unvoiced facial configurations. Current methodologies for understanding animal facial expressions rely heavily on labor-intensive manual frame-by-frame methods, which are challenging for analyzing large datasets. To address this, we extracted and annotated 2355 frames of *Indri indri*, 5200 frames of *Propithecus diadema*, and 7180 frames of *Nomascus gabriellae*. Deep-learning models were developed to identify 13 key facial landmarks, and through measuring distances between these points, we summarized variations in facial configurations. Multiple classifiers, including multi-layer perception, support vector machine, and random forest, achieved over 90% accuracy in classifying vocalized versus non-vocalized frames. These findings demonstrate a novel application of pose estimation and underline the potential of deep learning in quantifying primate facial gestures. This approach facilitates intra-species investigations and advances comparative primate communication research significantly.

giovedì 12 settembre
ore 11:30 - 13:30

Simposio 6

Oltre i confini della Zoologia: multi/inter/trans-disciplinarietà nella zoologia

coordinatori: Biagio D’Aniello, Giovanni Boschian, Valentina Serra

ANTONIO DE SIMONE[1,2]

1 The BioRobotics Institute, Scuola Superiore Sant'Anna, Pisa
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MOTILITY FROM SHAPE CONTROL: FROM BIOPHYSICS TO BIOROBOTICS

In recent years we have studied a number of morphing related and shape control problems in the context of locomotion in robotic systems and of motility of biological systems. Our aim is to distill lessons from biology useful for the design of bio-inspired devices.

This has required the use of tools from theoretical/computational mechanics of solids and fluids, physical experimentation and manufacturing of prototypes, observations at the microscope of unicellular swimmers.

Applications range from novel morphing and shape-control mechanisms based on actuation with unlimited stroke, results and prototypes of low Reynolds number swimmers, environmental sensors inspired by dispersal strategies of natural seeds, surgical robotic tools inspired by marine Annelida.

MICHELA SUGNI[1], GIORDANA MARTINELLI[1], MARGHERITA RONCORONI[1], TAMARA CHWOJNIK[1], LUCA MELOTTI[2], ANNA CAROLO[2], GIULIA ZIVELONGHI[2], MARCO PATRUNO[2], STEFANIA MARZORATI[1]

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FROM ZOOLOGY TO TISSUE ENGINEERING: THE SECOND LIFE OF SEA URCHIN WASTES

Sea urchins are key players of marine ecosystems. Some species are a well-known food resource and they can also be a source of valuable biologically relevant molecules, which are the result of peculiar physiological/anatomical adaptations selected over their evolutionary history. These molecules can be profitably used in various applied human fields. Indeed we previously demonstrated that food wastes deriving from the processing of the mediterranean *Paracentrotus lividus* (more than 70% of the animal mass) can be sustainably used to extract fully native fibrillar collagen as well potent antioxidant pigments (polyhydroxynaphthoquinones-PHNQs).
The aim of this work is to provide an overview of the main results obtained after three years of RICCIcliamo, a research project addressed to the innovative valorization of sea urchin waste into novel products for biomedical applications.
A high-added value recycling pathway was addressed to a 100% by-product valorization through extraction of collagen (from the peristomial membrane) and PHNQs (from the remaining waste) and the development of a variety of biomaterials for future tissue engineering applications. These included simple collagen-made biomaterials as well PHNQ-collagen composite materials, the latter displaying synergic multifunctional features combining the properties of the single components (i.e. structural support and antioxidant activity). The obtained biomaterials were tested in several *in vitro* and *in vivo* (rat and sheep models) tests which indicated a good biocompatibility and regeneration efficacy. As a further technological upgrade, we recently developed novel highly biomimetic hydrogels, with improved structural and cell response performances, as well the first sea urchin-derived bio-ink (SeaUrch-Ink) which was used in 3D bioprinting techniques to create customized three-dimensional biomaterials (fiber-reinforced hydrogels) mimicking the structure and functions of the extracellular matrix.
Overall these results and valorization strategies underline the possibility to exploit sea urchin waste (and their biological features) for the development of eco-friendly and innovative products, perfectly matching the blue growth and circular economy directives. Furthermore, this project underlined the potentiality and productivity of an efficient cross-talk between zoology and other apparently distant disciplines such as tissue engineering.

GIULIA MAGOGA[1], GIOBBE FORNI[2], DANIELE GIANNETTI[3], MATTEO BRUNETTI[1],
VALENTINA PICCHI[4], ELIA RUSSO[1], NADIA BAZIHIZINA[5], MORENA CASARTELLI[6],
ALBERTO SPADA[7], MASSIMO NEPI[8], STEFANO MANCUSO[5], FRANCO FAORO[4,7],
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8 Dipartimento di Scienze della Vita, Università di Siena, Siena, Italia

CREMATOGASTER SCUTELLARIS E *VICIA FABA*: MUTUALISMO MANIPOLATIVO?

Le piante dotate di nettari extraflorali (NEF) sono attrattive per le formiche, in quanto il nettare zuccherino da loro prodotto rappresenta un'importante risorsa trofica. Allo stesso tempo, la presenza di formiche su queste piante comporta una riduzione dei danni causati da insetti fitofagi. Pertanto, la relazione tra formiche e piante con NEF è un classico esempio di mutualismo, nel quale la pianta offre una ricompensa alimentare in cambio di protezione. In questo studio, abbiamo analizzato la relazione tra *Vicia faba* e *Crematogaster scutellaris*, una formica visitatrice opportunista di NEF di diverse piante nell'area mediterranea, con lo scopo di analizzare i benefici ottenuti dai due partner adottando un approccio multidisciplinare (tecnologie omiche, microscopia, saggi comportamentali ed esperimenti fenotipici). I risultati ottenuti hanno confermato che *C. scutellaris* fornisce protezione a *V. faba* nei confronti di insetti fitofagi, ma anche di potenziali patogeni. Di conseguenza *V. faba* rialloca maggiori risorse verso processi come la fotosintesi e lo sviluppo, suggerendo un aumento della fitness. Dall'altra parte, *C. scutellaris* nutrendosi sui NEF ottiene un pasto ricco di zuccheri e lipidi, questi ultimi ricavati escidendo i tricomi dei NEF. Tuttavia, il nettare extrafiorale include anche L-DOPA, un amminoacido fenolico non proteico che *V. faba* produce come difesa chimica contro i fitofagi. La concentrazione di L-DOPA, oltre a quella di zuccheri, risulta essere maggiore nelle piante visitate dalle formiche, suggerendo che questo amminoacido possa avere un ruolo nell'interazione formica-pianta. Questa ipotesi è confermata dai risultati degli esperimenti comportamentali che hanno mostrato come L-DOPA sia responsabile di un aumento dell'aggressività delle formiche verso altri insetti. Inoltre, i risultati delle analisi trascrittomiche hanno suggerito che la formica aumenta la propria sensibilità a stimoli nocicettivi a seguito dell'ingestione di nettare extrafiorale. Questo studio mette in luce aspetti finora sconosciuti dell'interazione tra *V. faba* e *C. scutellaris*, in più mostra per la prima volta come un metabolita secondario presente nel nettare extrafiorale sia in grado di manipolare il comportamento delle formiche in modo da aumentare l'efficacia dei servizi protettivi offerti alla pianta partner. Si tratterebbe, quindi, di un ulteriore caso di sistema cooperativo non puramente mutualistico ma caratterizzato anche da elementi coercitivi.

IRENE PICCINI[1]

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POLLINATORS ET AL. – POLLINATOR STREET AS VITAL CONNECTION TO MAINTAIN FUNCTIONAL URBAN AREAS

In October 2023, I started my current truly international project POLLINATORS ET AL. at Poznan University of Life Sciences and in collaboration with 5 other Universities across Europe, spanning from Sweden to Italy. The project is co-funded by the Polish National Science Centre, the EU H2020 research and innovation program under the MSCA Grant Agreement. It aims to investigate mobility of pollinator, pollinator and vegetation communities, their interaction (e.g. pollination) and pollen transport along urban road verges across Europe. During the presentation, I will discuss my experience on applying to international calls, finding partners, consolidate networking, writing and developing an international project with specific attention to challenges and opportunities.

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3 Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Krakow, Poland
4 Dipartimento Educazione e Scienze Umane, Università degli Studi di Modena e Reggio Emilia, Italy
5 Fondazione IRCCS Policlinico San Matteo, Pavia, Italy

GENOMIC INVESTIGATIONS INDICATE A NOVEL EVOLUTIONARY SCENARIO FOR A BACTERIAL LINEAGE ASSOCIATED WITH ECDYSOZOA

Background Animals and other eukaryotes often engage in associations with prokaryotes, broadly defined as symbioses, which involve diverse interactions with deep physiological and evolutionary impacts. Certain bacterial lineages present evolutionarily conserved host-associations with wide range of hosts, hinting for evolutionary flexible adaptations. Among such bacteria, the *Holosporales* (*Alphaproteobacteria*) encompass multiple intracellular bacteria in unicellular eukaryotes, as well as the members of the family "*Candidatus* Hepatincolaceae", living in the gut lumen of Ecdysozoa. These associations and their evolution are still poorly understood.

Methods We sequenced the genome of a "*Candidatus* Hepatincolaceae" bacterium associated with the tardigrade *Richtersius coronifer*, and identified the genomes of further members of this bacterial lineage from published arthropod metagenomes. We inferred the phylogeny of these bacteria with up-to-date methods that account for sequence compositional biasses in host-associated bacteria. Then, we compared the respective functional gene repertoires in order to investigate the interactions with their hosts and the underlying evolutionary processes.

Results We revealed that the phylogenetic grouping of the "*Candidatus* Hepatincolaceae" with the protist-associated *Holosporales* was an artefact due to compositional biasses, with the former representing an independent lineage within the *Alphaproteobacteria*. The "*Candidatus* Hepatincolaceae" are nutritionally flexible, being able to get energy from a wide range of compounds taken from the host guts, and can also grow anaerobically. As compared to intracellular bacteria, they display a less rich apparatus involved in regulating the interaction with the hosts. On the other hand, we found indications of physiological adaptations to each specific host, both in terms of nutrient uptake and of environmental resistance. This is consistent with a probable competence for DNA uptake, hinting for a contribution of horizontal gene transfer events to such lifestyle adaptations.

Conclusions The herein presented phylogenomic reconstruction led to re-establish the branching position of the "*Candidatus* Hepatincolaceae", thus allowing to re-interpret their evolutionary features. Accordingly, they independently adapted from free-living ancestors to association with Ecdysozoa, with consistent physiological traits, as well as with lineage-specific peculiarities.

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IMPIEGO DI UNA COMBINAZIONE DI TRATTI MORFO-FUNZIONALI COME METODO ALTERNATIVO PER L'ANALISI DELLA STRUTTURA DELLA NEMATOFAUNA MARINA E TERRICOLA

La pressione antropica sugli ecosistemi, marini e terrestri, spesso li altera, fino a comprometterne, il corretto funzionamento. Al fine di prevenire danni insanabili agli ecosistemi, è importante identificare rapidamente le situazioni di criticità e i nematodi hanno tutti i requisiti per essere considerati degli ottimi indicatori di disturbo antropico. Una generale limitazione al loro impiego nel biomonitoraggio è dovuta alla loro complicata identificazione tassonomica, che richiede molto tempo ed esperti del settore. Pertanto, è stato recentemente proposto un metodo alternativo che combina 4 tratti morfo-funzionali (anfidio, cuticola, cavità boccale e forma della coda) per rilevare cambiamenti nella struttura di comunità dei nematodi marini (SEMPRUCCI, *et al*., 2022). L'approccio è stato testato in cinque casi studio effettuati nelle coste italiane: due porti (Voltri e Marina degli Aregai), un'area costiera influenzata da apporti fluviali (Adriatico Centrale) e due impianti di acquacultura (Olbia e Vibo Marina). I risultati dell'analisi multivariata hanno rilevato che la semplice combinazione dei tratti in codici numerici univoci rispecchiava perfettamente i cambiamenti della struttura tassonomica della nematofauna a livello di genere. Alla luce dei risultati promettenti in ambiente marino, è stato testato lo stesso approccio in ecosistemi terrestri (SEMPRUCCI, *et al*., 2024). In particolare, questo è stato effettuato utilizzando tre serie di dati che comprendono studi di varie regioni Europee (Danimarca, Spagna, Slovacchia e Svezia) e diversi tipi di ecosistemi: foreste, praterie e coltivazioni di mais. Anche in questo caso l'analisi multivariata ha messo in luce come la semplice combinazione di quattro tratti (morfologia della cavità boccale, anfidio, cuticola e forma del faringe) in un singolo codice numerico possa rispecchiare perfettamente le variazioni della struttura di comunità. Pertanto, ipotizziamo che risultati simili possano essere ottenibili anche codificando direttamente i campioni di nematodi con i tratti selezionati e prevediamo nuovi importanti progressi se questa procedura potrà essere accoppiata con l'apprendimento automatico avanzato.

JONATHAN TEMPESTI[1], DOMINGO BELCARI[2], VALERIA CROCE[3], GABRIELLA CAROTI[3], SIMONETTA MENCHELLI[2], FERRUCCIO MALTAGLIATI[1]

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3 Dipartimento di Ingegneria Civile e Industriale, Pisa, Italia

THE ZOOLOGICAL CONTRIBUTION TO THE MULTIDISCIPLINARY STUDY OF TWO SHIPWRECKS OFF TUSCANY COASTS (ITALY, WESTERN MEDITERRANEAN)

This work highlights the contribution of zoology in a multidisciplinary project combining ecological, archaeological and engineering expertises in the study of shipwrecks. The project aims at reconstructing the history and 3D morphology of shipwrecks, and their effects on local marine biodiversity. Shipwrecks originate habitats that are more heterogeneous than the surrounding environment. The effects of this heterogeneity on local biodiversity are still unclear, especially in terms of composition and dynamics of associated biological communities. Hence, our study aims at describing the zoobenthic communities associated to the shipwrecks, assessing their variability related to habitat heterogeneity.

We selected the “Melania” and “Genepesca” shipwrecks located in the Vada Shoals (Tuscany coasts, W Mediterranean) at depths of 8-14 m (Melania) and 19-33 m (Genepesca).

Three “conditions” were considered: (1) external and (2) internal parts of the shipwreck, and (3) nearby natural hard bottom. In September 2019, benthic communities were sampled by SCUBA divers, scraping 20×20 cm^2 areas. Samples were sieved with a 0.5 mm mesh and fixed in 70% ethanol. Macrofaunal organisms were identified at the lowest possible taxonomic level. nMDS and SIMPER were used to assess the among-condition differences that were successively tested by PERMANOVA.

A total of 186 and 319 species were identified for Melania and Genepesca, respectively. nMDS and SIMPER showed a good segregation of samples according to relative conditions, which were statistically significant at PERMANOVA.

The following macrozoobenthic species were rare or typical of deeper grounds: the annelids *Aurospio banyulensis* (Laubier, 1966), *Josephella marenzelleri* Caullery and Mesnil, 1896, *Metavernilia multicristata* (Philippi, 1844), *Miscellania dentata* Martin, Alós and Sardá, 1990, *Micronephthys sphaerocirrata* (Wesenberg-Lund, 1949), *Phascolion tuberculosum* (Théel, 1875), the crustaceans *Eisothistos pumilus* Wägele, 1979, *Metaphoxus simplex* (Spence Bate, 1857), *Paraphoxus oculatus* (G.O. Sars, 1870), and *Phoxocephalus aquosus* (Karaman, 1985), the cnidarians *Caryophyllia smithii* Stokes and Broderip, 1828, *Leptopsammia pruvoti* Lacaze-Duthiers 1897, the mollusc *Arca tetragona* (Poli, 1795), and the brachiopod *Argyrotheca cuneata* (Risso, 1826). In conclusion, results suggest that shipwrecks may act as “local biodiversity enhancer”; however, more in-depth investigations on other wrecks are needed to clarify this role.

giovedì 12 settembre
ore 15:00 - 17:00

Simposi 3, 4, 5, 6

RELAZIONI IN SESSIONI PARALLELE

SESSIONE PARALLELA SIMPOSIO 3

ELENA TRICARICO[1], SARA FORNI[1], BEATRICE MELONE[2,3], MATTEO ORLANDO[1], ASIA ROSSI[1], MARCO MORBIDELLI[1]

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2 FINCONS SPA –Vimercate (MB)
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LO STATO DI CONSERVAZIONE DEL GAMBERO NATIVO DI FIUME *AUSTROPOTAMOBIUS PALLIPES* COMPLEX (DECAPODA: ASTACIDAE) NEL PARCO DELLE FORESTE CASENTINESI

Il gambero nativo di fiume *Austropotamobius pallipes* complex è classificato dalla IUCN come specie minacciata ed è protetto a livello europeo, nazionale e regionale. Le sue popolazioni sono in declino in tutta Europa a causa di numerose minacce, come perdita e frammentazione dell’habitat, pesca illegale, cambiamento climatico, inquinamento delle acque e presenza di specie aliene invasive (quali il gambero rosso della Louisiana *Procambarus clarkii* e il procione *Procyon lotor*). L’obiettivo dello studio è stato quello di aggiornare la distribuzione e lo stato di *A. pallipes* complex nel Parco Nazionale e nelle Riserve Statali delle Foreste Casentinesi, confrontando la situazione attuale con quella passata e valutando la presenza e gli effetti delle potenziali minacce per questa specie. Nel 2021-2023, sono stati condotti 66 campionamenti nel versante toscano e romagnolo del Parco, in siti in parte già oggetto di un precedente monitoraggio avvenuto tra il 2012 e il 2016. I gamberi sono stati catturati a mano lungo un transetto di 100 m durante le ore notturne. Gli individui campionati sono stati sessati e misurati, ed è stata anche annotata la presenza di malattie, parassiti ed eventuali tracce di predazione da parte del procione, come impronte o resti di gamberi. Dai risultati è emersa una significativa riduzione delle popolazioni, o la loro locale scomparsa, in entrambi i versanti del Parco, particolarmente drastica in Toscana. Il diverso andamento delle popolazioni di gambero di fiume nei due versanti potrebbe essere dovuto alla presenza di un impatto antropico più rilevante nei corsi d’acqua del versante toscano, a causa di bracconaggio, captazioni, scarichi abusivi e presenza di specie aliene invasive. È necessario intraprendere appropriate misure di gestione delle minacce e di conservazione, ed una corretta educazione ambientale per arrestare il declino delle popolazioni del gambero nativo di fiume nel Parco.

TOMMASO RIGHI[1,2], ANDREA SPLENDIANI[1], TATIANA FIORAVANTI[1], FRANCESCO PALMAS[3], ANDREA SABATINI[3], DIEGO MICHELETTI[2], ANDREA GANDOLFI[2], VINCENZO CAPUTO BARUCCHI[1]

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STRUTTURA GENETICA DELLA TROTA FARIO (*S. ghigii* Pomini, 1941): NUOVE EVIDENZE DALLE POPOLAZIONI NATIVE SARDE E PENINSULARI TRAMITE APPROCCIO GENOMICO (GBS)

La storia evolutiva della trota fario nell'area mediterranea è stata profondamente influenzata dalle fasi glaciali-interglaciali del Quaternario e dagli eventi correlati di estinzione locale e ricolonizzazione. A seguito dell'isolamento prolungato, le isole mediterranee, tra cui la Sardegna, rappresentano importanti hotspot di diversità. Un recente studio filogenetico del genere *Salmo* basato sull'intero genoma (SEGHERLOO *et* al., 2021) suggeriva che le trote sarde potrebbero rappresentare una specie distinta. L'analisi, tuttavia, includeva solo pochi individui da una singola popolazione, potenzialmente sottostimando la variabilità genetica insulare. Infatti, analisi molecolari tradizionali (SPLENDIANI *et* al., 2023) hanno rivelato una forte differenziazione tra le popolazioni selvatiche native sarde, identificando anche un nuovo sotto-lignaggio mitocondriale (mtDNA Corso-Sardo) endemico di Corsica e Sardegna. L'approccio genomico di genotipizzazione tramite sequenziamento (GBS) è stato applicato per indagare la struttura genetica in 130 individui provenienti da 9 popolazioni di trota native dell'area mediterranea (5 peninsulari e 4 sarde). I campioni sono stati selezionati includendo solo popolazioni non introgresse con *S. trutta* atlantica domestica, per evitare il potenziale effetto di omogeneizzazione e rappresentare al meglio la diversità genetica originaria delle popolazioni italiane di trota fario riferibili a *Salmo ghigii*. I valori di differenziazione genetica tra singole popolazioni (Pairwise FST) risultavano elevati e significativi. La più elevata differenziazione genetica è stata osservata tra le popolazioni peninsulari e quelle sarde. I risultati delle analisi di struttura genetica (STRUCTURE, PCA, DAPC) e di delimitazione di specie tramite l'utilizzo di algoritmi di Unsupervised Machine Learning (UML) (Random Forest, RF, e t-Distributed Stochastic Neighbor Embedding, t-SNE) hanno identificato ogni popolazione come un cluster genetico distinto, confermando l'elevata differenziazione genetica tra le singole popolazioni native analizzate. Sulla base delle evidenze ottenute, le pratiche gestionali e di conservazione di questa specie dovrebbero essere realizzate considerando ogni singola popolazione come un'unità gestionale indipendente. La tutela di tale diversità è fondamentale per garantire la persistenza nei bacini idrici italiani della trota nativa, già gravemente a rischio a causa di numerosi impatti antropici e dei drastici cambiamenti nelle condizioni climatiche.

GIOELE CAPILLO[1,2], CLAUDIO D'IGLIO[1], DARIO DI FRESCO[1], NUNZIACARLA SPANO'[1,2], MARCO ALBANO[3], SERENA SAVOCA[1,2]

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3 Department of Veterinary Sciences, University of Messina, Messina, Italy

DO FAUNAL BIOINVASIONS PASS TROUGH MARINE LITTER POLLUTION? THE CASE OF A BRACKISH COASTAL LAGOON IN THE CENTRAL MEDITERRANEAN SEA

Biodiversity depletion is one of the major concerns regarding the conservation of marine ecosystems worldwide, with biological invasions representing its primary driver, especially in the Mediterranean Sea. This allowed the scientific community to enhance the attention on the monitoring of the distribution and the establishment of non-indigenous species (NIS) in the entire basin. Transitional waters (such as brackish coastal lagoons) are widely considered sensitive environments for native biodiversity conservation, and hotspots for the settlement and spread of invasive alien species, especially due to their exploitation for aquaculture. Here is reported the analysis of the epibenthic fauna associated with anthropogenic litter, aiming to monitor the bioinvasion status of the Faro Lagoon (part of the Capo Peloro Natural Reserve), that represents a natural observatory to investigate the arrival, diffusion, and successful establishment, of marine invasive NIS.

A total of 79 anthropogenic debris (from 4 different areas inside the lagoon), settled on the bottom and completely colonized by macrozoobenthic organisms, were collected during 9 samplings performed by free diving, twice a week between January and April 2024. Once collected, samples were transported to the "E. De Domenico" laboratory of the University of Messina, where sorting and identification, to the lowest taxonomic level, of the associated macrozoobenthic fauna were performed. All the identified NIS species were photographed using a Motic Panthera C2 Trinocular stereoscope, equipped with a Moticam 1080 N camera.

The taxonomic analysis of the macrozoobenthic organisms showed the presence of 34452 individuals, belonging to 64 taxa, associated with the sampled anthropogenic debris; among these, 6,77 % (1631) belonged to 7 NIS: *Dorvillea similis,* Crossland, 1924, *Eurythoe complanata*, Pallas, 1766, *Hydroides elegans*, Haswell, 1883, *Isognomon legumen*, Gmelin, 1791, *Mesanthura cf. romulea*, Poore & Lew Ton, 1986, *Paranthura japonica*, Richardson, 1909, *Pinctada radiata* Leach, 1814.

The results providing evidence of the presence of these species (some not yet reported in the area), associated with marine litter confirm the possible roles of anthropogenic debris' both as NIS introduction vectors and as exploitable benthic habitat. This is especially true in the case of *E. complanata*, *M. cf. romulea*, *P. japonica*, and *P. radiata* that, considering their abundance, seem to have established stable populations.

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HONEY BEES IMPACTS ON WILD BEES BIODIVERSITY IN A SMALL AND PROTECTED ISLAND THROUGH EXPLOITATIVE COMPETITION: THE CASE STUDY OF GIANNUTRI

The massive presence of managed honey bees (*Apis mellifera* L.) has recently emerged as serious threat to local pollinators. Indeed, the honey bees workers, due to their high density and foraging ability are prone to compete with wild pollinators for resource exploitation. The potential negative effects of this trophic competition are particularly detrimental in small and fragile ecosystems such as small Mediterranean Islands. We studied this interaction on Giannutri Island, a protected island within the Tuscan Archipelago National Park, which recently experienced the presence of beekeeping. We started this project in order to understand i) the effects of trophic competition and ii) individuate conservation actions aimed at preserving local biodiversity. To study the wild bees fitness, we monitored, through walking transects, the abundance of wild bees on the island for 4 consecutive years. We adopted a multifaceted experimental framework to measure the effect of honey bees on resources availability and on wild bees behaviour. We studied this by creating two experimental conditions: hives open (honey bees regularly foraging on the island) and hives closed (no honey bees on the island). In these experimental conditions we measured the nectar volume and concentration of the main flowering species (*Teucrium fruticans* L and *Salvia Rosmarinus* L), the number of anthers bearing pollen on *T. fruticans* , the activity and foraging behaviour of two most abundant wild bee species (*Anthophora dispar* Lepetelier and *Bombus terrestris* L). We documented a constant decline of both wild bee target species in 4 years suggesting a reduction in fitness. When honey bees are foraging (hives open) we found a reduction in nectar volume available of both species and also a reduction in anthers bearing pollen. We also documented a significative reduction in foraging time and an increase in searching time for resources of wild bees when honey bees are also foraging on the island. These result indicate the presence of exploitative competition. There is thus evidences that the decline of wild bees is likely due to the alteration of foraging behaviour caused by honey bees: smaller energy uptake and higher energy investments of wild bees. We highlight the importance of population and ethological monitoring to actively protect wild pollinators and we demonstrate that the presence of beekeeping in protected areas need to be carefully evaluated in order to not harm the local biodiversity.

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PARALEUCILLA MAGNA (PORIFERA, CALCAREA): IL CONTRIBUTO DI UNA SPUGNA ALIENA IN UN MARE DI CAMBIAMENTI

Paraleucilla magna Klautau, Monteiro & Borojevic, 2004, è una spugna calcarea aliena nel Mar Mediterraneo, invasiva nei mari di Taranto (Mar Ionio settentrionale). Nel Mar Mediterraneo, *P. magna* prospera a basse profondità in condizioni di scarso idrodinamismo, come porti, bacini semichiusi, acque calme e aperte o in impianti di maricoltura, spesso all'interno della comunità *fouling*, su substrati duri sia naturali che artificiali. Grazie alla morfologia e alla conformazione del suo sistema acquifero, *P. magna* fornisce un habitat adatto ad ospitare diverse comunità epi- e/o endobiotiche.

In questo lavoro, è stata studiata la fauna associata a questa spugna aliena per valutare il suo ruolo come ingegnere ecosistemico. A tale scopo, dieci esemplari di *P. magna* sono stati raccolti mensilmente nel Mar Grande di Taranto, per un periodo di un anno. I campionamenti sono stati eseguiti in immersione con autorespiratore e ogni esemplare di spugna è stato inserito in un sacchetto di plastica prima di essere prelevato dal substrato, al fine di prevenire la fuga della fauna vagile. In laboratorio, è stato misurato il volume di ogni esemplare e, mediante microscopio da dissezione, è stata prelevata la macrofauna (lunghezza corporea >1 mm) presente all'interno e/o sulla superficie esterna. Gli organismi raccolti sono stati separati in base al gruppo tassonomico di appartenenza, e successivamente ne sono state calcolate l'abbondanza e la frequenza relativa.

Complessivamente, sono stati raccolti 4791 individui di fauna associata, suddivisi in 6 phyla, su un volume totale di spugna di 3863 mL. La maggior parte degli individui rinvenuti appartengono al phylum Crustacea, seguito dal phylum Mollusca e Annelida, mentre meno rappresentati sono i phyla Briozoa, Chordata ed Echinodermata. Dopo i crostacei, il secondo taxon più abbondante è quello dei molluschi, probabilmente a causa del reclutamento del bivalve *Mytilus galloprovincialis*, diffusamente allevato nel Mar Grande di Taranto. Anche per la frequenza relativa, in un anno di osservazione, i gruppi tassonomici rinvenuti maggiormente sono i crostacei, i molluschi e gli anellidi (100%), seguiti dai briozoi (27%) e dai cordati ed echinodermi, rinvenuti in un solo campionamento (9%).

Lo studio della fauna associata a *P. magna* permette di raccogliere informazioni utili per descrivere i cambiamenti delle comunità bentoniche di ambienti semi-confinati e/o particolarmente antropizzati soggetti a significative fluttuazioni dei parametri ecologici. Infine, i risultati acquisiti supportano l'ipotesi che l'introduzione di determinate specie alloctone in un ambiente può incrementare la complessità e la struttura dell'habitat, fungendo da "*living hotel*", fornendo nuovi spazi per l'insediamento di altre specie.

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BATHYMETRIC DISTRIBUTION AND CO-PRESENCE IN CORALLIGENOUS COMMUNITY OF *EUNICELLA CAVOLINI* (KOCH, 1887) AND *PARAMURICEA CLAVATA* (RISSO, 1827)

Octocorals play a crucial role in marine ecosystems, contributing to increase structural complexity and biodiversity. Their presence and health can indicate the overall status of marine ecosystems, acting as bioindicators. This study aims at analysing coralligenous community, bathymetric distribution and co-presence of *Eunicella cavolini* and *Paramuricea clavata*.

Surveys were carried out in 2018 and 2021, at 30-100 m depth, in 2 areas off the Campania coast. 6 sites per area were selected, and, at each site, 3 video-transects 200 m long were carried out. Coralligenous composition and species richness were evaluated. Density and dominance of epimegabenthos were investigated. Density of *E. cavolini* and *P. clavata* colonies was calculated as number of colonies/100 m^2 and morphometry was calculated as average height. Spatial and temporal differences between colony densities and heights were assessed using the PERMANOVA test, while correlations of density and height with depths were assessed with linear regressions.

A total of 32 different species and other 10 morphological groups were detected. The highest number of species identified belonged to 3 Phyla: Bryozoa, Porifera, and Cnidaria. In 2018, 12±3 species were identified and, in 2021, 15±3 species. Density of epimegabenthic organisms is 48±19 individuals or colonies/100 m^2 in 2018, and 166±78 individuals or colonies/100 m^2 in 2021. *E. cavolini* is the dominant species for both years (61% in 2018 and 55% in 2021). *E. cavolini* in 2018 has a density of 105.9±35.3 colonies/100 m^2 and a height of 24.7±4.4 cm; in 2021 it has a density of 84.8±35.0 colonies/100 m^2 and a height of 21.2±2.8 cm. *P. clavata* in 2018 has a density of 45.4±26.2 colonies/100 m^2 and a height of 37.1±9.8 cm; in 2021 it has a density of 67.7±24.0 colonies/100 m^2 and a height of 32.9±11.5 cm.

Community resulted rich and diverse, with densities higher in 2021. Differences in spatial distribution of size and density between the species were found. *E. cavolini* is present throughout the bathymetric interval and is denser and shorter than *P. clavata*, which has the upper colonization limit at -50 m depth. The density of *E. cavolini* is positively correlated with depth and density of *P. clavata*. In fact, the co-presence of the two species positively influences the density of both. Further multidisciplinary investigations could clarify this co-presence effect and the potential factors that could determine it.

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VALUTAZIONE IN CAMPO DEI POSSIBILI EFFETTI DELL'OLIO ESSENZIALE DI *OCIMUM BASILICUM* L. SULLE COMUNITÀ DI NEMATODI A VITA LIBERA DEL SUOLO

Per far fronte ad una crescente richiesta di cibo, l’agricoltura intensiva ci ha condotti ad un sovrasfruttamento delle risorse naturali e all’alterazione del funzionamento dell’ecosistema suolo; questo principalmente a causa dell’abuso di fitofarmaci di sintesi. La Commissione Europea ha perciò adottato il programma New Green Deal, che mira a dimezzare l’uso di tali prodotti nel tentativo di ripristinare o limitare la perdita di biodiversità negli ecosistemi terrestri e acquatici. Gli oli essenziali (OE), attualmente utilizzati prevalentemente in campo farmaceutico e nella cosmesi, possono rappresentare una valida alternativa sia nella protezione di colture che di derrate alimentari da parassiti e malattie. Comunque, nonostante il crescente interesse della comunità scientifica in questo campo, ad oggi, la maggior parte degli studi sugli OE sono stati condotti *in vitro* su organismi target o al limite su organismi modello, mentre sono del tutto assenti studi sui potenziali effetti degli OE sulle comunità in campo. Per valutare i possibili effetti di uno degli OE attualmente più promettente in agricoltura, è stato allestito un esperimento direttamente in campo con un approccio sperimentale Before-After-Control-Impact e sono stati analizzati gli effetti del trattamento sulla nematofauna a vita libera. In dettaglio, semi di ceci sono stati trattati prima della semina applicando un rivestimento ad alta concentrazione dell’OE di *Ocimum basilicum* (25% v/v) e la composizione tassonomica e funzionale della comunità è stata monitorata prima e dopo la semina a distanza di 7, 14, 28 e 56 giorni. L’analisi GC-MS della composizione dell’OE ha evidenziato un chemiotipo a metil cavicolo, fenilpropanoide che costituisce oltre il 78% della composizione totale. I dati, ad oggi raccolti, hanno evidenziato che l'OE di *O. basilicum*, nonostante le alte concentrazioni applicate, non ha avuto significativi effetti sulla diversità tassonomica e funzionale della nematofauna corroborando il suo possibile utilizzo come prodotto green.

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QBS-ar VS QBS-e: A COMPARISON OF THEIR PERFORMANCE ON ARABLE LAND UNDER DIFFERENT MANAGEMENT PRACTICES

According to the European Green Deal, policies aimed at conserving biodiversity should include not only natural but also agricultural areas, which cover more than half of Europe's land surface and where farming practices are recognized as a major cause of the loss of wildlife species, especially invertebrates. Proposals for more sustainable agricultural systems have been advanced, the implementation of which also requires an assessment of efficiency in agronomic, economic and ecological terms. With regard to this last aspect, soil is a key element of the landscape estimated to host about than 60% of the planet's biodiversity, and its monitoring and safeguard should therefore be of utmost importance. Several methods are currently applied to determine the biological status of soils, based on the analysis of different soil taxa. Among these, arthropods and earthworms, part of the meso- and macrofauna, have been shown to be particularly responsive to soil disturbance in agroecosystems. In Italy, these taxa formed the basis for the development of two soil biological quality indices, namely QBS-ar(thropods) and QBS-e(arthworms), which involve the assignment of scores to the collected individuals according to their functional adaptations to soil life and thus their sensibility to soil alterations. In this study, for the first time, such indexes have been applied together on arable land managed with different techniques (strip cropping and pure stand), with the aim of comparing the outcome of the two indices. A total of 18 soil samples for arthropods and earthworms each were collected in April 2023, along with soil chemical and physical data. After identification of specimens and calculations, statistics were applied to check for trends among QBS-ar and QBS-e and the other parameters. The two indexes are not correlated in this study, although they can be explained by different environmental variables: earthworms appear to be more sensible to chemical gradients, such as those due to fertilization, whereas the distribution of microarthropods revealed to be mostly associated to crop and management type, and spatial patterns (i.e. slope). Despite a relatively small sample size and a study area influenced by multiple factors, these results offer promising information for the selection of the soil biological index appropriate to specific contexts and objectives.

SESSIONE PARALLELA SIMPOSIO 4

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NOTES ON THE USE OF *ARTEMIA SALINA* (LINNAEUS, 1758) AND CONGENERS IN SCIENTIFIC RESEARCH

Zooplankton is pivotal in the aquatic trophic webs, carrying energy and matter among different trophic levels and depths. As non-selective filter-feeders, through biomagnification phenomena, these organisms could transfer any internalized molecule to their predators, comprised of many pollutants dispersed in aquatic ecosystems. Brine shrimp, *Artemia salina* (Linnaeus, 1758), is a small crustacean living in extreme environments, such as highly saline lakes and pools, that mainly feeds on microalgae through filtration representing an important food source for many aquatic animals. Due to their small size, transparency, life cycle and simple breeding, the species of the genus *Artemia* represent a good model organism for environmental toxicology studies.

Our research activity started from the limited number of studies conducted on the effects of microplastics (MPs) on brine shrimp. Hence, we evaluated, within the first 7 days of the life cycle, the ingestion and influence of 10 µm polystyrene microspheres on the growth and feeding behavior of *A. salina*, in the presence of microalgae *Dunaliella salina* (Teodoresco, 1905). We demonstrated that the uptake of MPs in this organism is enhanced by the simultaneous presence of plastic debris and microalgae, thanks to the transparency of its body that allowed us to easily identify the ingested (blue-dyed) MPs under the microscope. The fast-growing life cycle of *A. salina* resulted essential in highlighting the developmental delay and reduction in the total body length due to MPs exposure.

Recently, within the Samothrace Project (CUP B63C22000620005), we focused on heavy metals' effects on zooplankton. To investigate the mechanism of cadmium's acute toxicity on zooplankton, we exposed *A. salina* nauplii to cadmium chloride dissolved in water. We detected no influence on the developmental stages during the first 72 hours of the life cycle, while measurements from the photographs taken under the microscope highlight differences in total length with an unexpected positive effect after 48 hours. Survival resulted in 53% on average, thanks to the possibility of counting individual specimens given by small experimental volumes.

Intensifying the research on the biological and developmental effects of various pollutants in *Artemia* species would be essential to understanding how these mechanisms could influence the aquatic trophic webs, also considering their ability to live in extreme conditions and the possible relapses in human health due to biomagnification phenomena.

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HISTOPATHOLOGICAL ABNORMALITIES IN ZEBRAFISH LIVER INDUCED BY DIMOXYSTROBIN, A SYNTHETIC STROBILURIN FUNGICIDE

In the European Union (EU), the best-selling pesticide group is fungicides, and a large share of the market is held by strobilurins, a class of synthetic fungicides with a highly rapid and efficient broad-spectrum activity (FENG et al., 2020). Dimoxystrobin (DIM), authorized in 16 EU Member States in 2020, has been included in the 3rd Watch List (WL) since it poses a significant risk to aquatic species being persistent and toxic (GOMEZ CORTES et al., 2020). In 2023, the European Commission decided not to renew the DIM authorization, but this fungicide is still commercialized in other countries. To date, there is a lack of information on the sub-lethal effects of DIM on aquatic biota, with only two reports available on fish (AHMED et al., 2023; 2024). Here, we investigated for the first time the histopathological alterations induced in zebrafish (*Danio rerio*) liver by two sublethal and environmentally relevant concentrations of DIM (6.56 and 13.13 µg/L) after a short-term exposure (96 h). The pathological effects were first evaluated through an in-depth histological examination, followed by a morphometric analysis, which allowed the quantitative evaluation of lipid droplets and glycogen granules.

After exposure to the low concentration, the liver parenchyma lost its structural arrangement due to lysed area formations. Some hepatocytes showed a highly stained cytoplasm and many vacuolizations were detected in their cytoplasm; bile ducts were also structurally modified. The severity and intensity of alterations significantly increased in the high-concentration group. Both apoptotic and necrotic hepatocytes were often visible along with large lysed areas. Macrophages were detected in vessels, sinusoids and scattered in the liver parenchyma. After exposure to both DIM concentrations, glycogen granules significantly decreased, whereas the lipid droplet amounts increased.

Our results demonstrate that both DIM doses induce conspicuous alterations in zebrafish liver. The severity of detected alterations increases with the dose, leading to a complete disarrangement of the liver structure in the high DIM exposed group. This research emphasizes the importance of in-depth morphological investigation when assessing the toxic potential of both currently used and new agrochemicals, and the urgent need for this type of study in the field of environmental toxicology.

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CLEARWING MOTHS (LEPIDOPTERA: SESIIDAE) AS EFFECTIVE MODELS FOR STUDYING THE EFFICIENCY OF MIMICRY IN PREDATOR-PREY INTTERACTIONS

Many dangerous insects manifest their toxicity by expressing conspicuous warning displays across all possible sensory channels: vision, hearing, olfaction and taste. Batesian mimicry is a survival strategy in which harmless species resemble those possessing defence mechanisms. These remarkable imitations comprise one of the most fascinating phenomena in insect evolution. Clearwing moths (Lepidoptera: Sesiidae) are perfect models to explore Batesian mimicry because they have evolved an autapomorphy among Lepidoptera making them closely resemble bees and wasps. However, predators exploit all possible sensory signalling to select and capture prey and, depending on the predator species, they can hunt both models and mimics. We verified whether clearwing moths have evolved to mimic more than just the visual features of their model hymenopterans by recording and comparing the acoustical parameters of sounds produced by sesiids in flight. Our results show acoustical resemblance in two bee-mimicking Southeast Asian clearwing moth species and two wasp-like European sesiids, indicating convergent evolution of models and mimics. Through field-based experiments, we compared the response of an avian predator, the European robin, to models and mimics as closely resembling live, potential prey as possible, presenting visual and acoustical signalling combined. We demonstrated that: 1) robins exhibit variable responses to models, being deterred only by the most harmful hornet; 2) the predator’s response to models and mimics is comparable in each studied case and only the hornet mimic evokes aversive behaviours. Our work based on clearwing moths as study models demonstrates that mimicry can involve multiple modalities exploited by predators, quantifies the efficiency of mimicry and aposematism in predator-prey interactions and contradicts the assumption that aposematism and Batesian mimicry provide generalized protection to insects, as some, less harmful species may still fall within the range of edible prey.

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GENUS *LEPIDURUS* (CRUSTACEA, NOTOSTRACA) AS A MODEL FOR STUDY THE BIOLOGICAL RHYTHMS

All living organisms have ‘‘biological clocks’’ that regulate biological functions by means of rhythms similar to the geophysical rhythms of the earth; these rhythms have an evident adaptive value to enable organisms to anticipate and, hence, to prepare for predictable changes in their environment. This occurs as interaction between the clocks and exogenous time cues, the most prominent of which is the 24-h light–dark cycle.

There is a growing realization that the degree of circadian organization differs widely depending on species' biology. If studied by improved recording techniques or under different environmental conditions, some organisms that were thought to show robust daily rhythms instead showed extended intervals of around-the-clock activity with ultradian rhythmicity, or arrhythmicity, without negative effects. Because these observations seem inconsistent with the idea of universal benefits of daily cycles, a closer look could refine our understanding of the mechanisms, functions and adaptive value of circadian clocks in general. This contribution focuses on circumstances wherein animals show prolonged intervals of activity with no circadian rhythm.

My studies have been focused on characterizing circadian organization in individuals of the genus *Lepidurus* (Notostraca, Crustacea) invertebrates representing a largely extinct lineage of arthropods (Fryer, 1988). No work on the circadian biology of this fascinating group has been published so far, and behavioural and metabolic rhythmicity of such crustaceans is of great interest from an eco-evolutionary perspective. *Lepidurus* should be an ideal model to investigate issues related to circadian rhythms because conspecifics can be found from the Equator to the Polar Circle in very different photoperiod conditions. Hence it is possible to perform comparative experiments to confront both behaviours and genetic aspects, and also to assess the heritability of circadian traits.

Lepidurus arcticus and *L. couesii* were collected respectively in Ny-Alesund - Svalbard (80°N) and in San Donaci (Br) – Italy (40°N). Locomotor activity was recorded in natural and experimental condition. The melatonin concentration was measured under natural condition.

Data on locomotor activity in *L. arcticus* and *L. couesii* do not show a clear circadian rhythmicity although a response to the photoperiod was present in some animals. Data on melatonin showed that the hormone was present in *L. arcticus* and *L. couesii,* but data did not support the presence of a daily variation of its concentration.

Future studies and integration with data on molecular clock mechanisms will contribute to the comprehension of the biological rhythms in this genus, representing a model of animals living under different photoperiod conditions.

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OLFACTION IN THE BLACK SOLDIER FLY *HERMETIA ILLUCENS*

The Black Soldier Fly (BSF) is highly valued in the insect feed industry and circular economy, significantly contributing to the 2030 Sustainable Development Goals by reducing carbon dioxide emissions and facilitating the circular management of organic waste, animal manure, and plant residues. Despite the industrial importance of BSF and the large amount of data published annually, there is a notable and surprising gap in knowledge about adult BSF biology and sexual behavior, which has likely hindered optimal mass production.

In this context, the present research investigates the olfactory capabilities of male and female BSF in response to odorants commonly associated with organic decomposition in substrates suitable for mating and egg laying, as well as volatile organic compounds (VOCs) emitted by BSF that may be relevant in courtship and mating. The study utilizes electroantennographic recordings (EAG), electron microscopy observations of the antennal sensilla, and coupled gas chromatography–electroantennography (GC-EAD) recordings to analyze active mixtures and identify active compounds in VOCs emitted by potential mates using coupled gas chromatography-mass spectrometry (GC-MS).

Our results demonstrate the olfactory capabilities of BSF antennae for the first time and present the first dataset of substances emitted by decaying organic matter detected by both male and female flies, along with active VOCs collected from potential mates. Additionally, the current EAG recordings allow comparisons with molecular data previously obtained through in silico and in vitro methods, highlighting the need for a multidisciplinary approach in studying insect chemical ecology. These findings enhance our understanding of BSF chemical ecology, which is essential for effective reproduction and could significantly optimize global breeding systems.

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DALL'ETOLOGIA ALL'ECOTOSSICOLOGIA: LE VESPE CARTONAIE COME ORGANISMI MODELLO NELLA RICERCA SCIENTIFICA

Le vespe cartonaie del genere *Polistes* hanno rappresentato per decenni degli organismi modello nella ricerca in ambito etologico e sociobiologico. Dalle prime osservazioni di Leo Pardi, che a metà del ventesimo secolo descrisse per la prima volta la presenza di gerarchie di dominazione in un invertebrato proprio nella vespa cartonaia europea *Polistes dominula* (Christ) (PARDI, 1948), fino agli studi su altruismo, comunicazione e processi di riconoscimento coloniale (GAMBOA et al. 1986; QUELLER *et al*., 2000; DANI *et al.,* 2001; TIBBETTS and DALE, 2004; CAPPA *et al*., 2020). In anni più recenti, tuttavia, le vespe cartonaie del genere *Polistes* hanno iniziato a ricevere una crescente attenzione per via del loro potenziale ruolo di agenti naturali di controllo nei confronti di svariate pesti in contesti agricoli e forestali (SOUTHON et al. 2019). La diffusione di tali organismi in ambienti antropizzati li espone tuttavia a svariati contaminanti ambientali. Pertanto, abbiamo voluto indagare gli effetti letali e subletali di biopesticidi e microplastiche sull'organismo modello *Polistes dominula*, tramite un approccio olistico focalizzato non soltanto sull'individuo, ma sull'intera colonia. I nostri risultati hanno mostrato che dosi di campo di due biopesticidi comunemente usati in agricoltura biologica, il fungo entomopatogeno *Beauveria bassiana* e l'azadiractina, principio attivo dell'olio di Neem, così come la microplastica polimetilmetacrilato (Plexiglass), causano su tali vespe numerosi effetti avversi che includono: (i) riduzione dell'ovodeposizione e dello sviluppo ovarico nelle femmine riproduttrici; (ii) rimozione selettiva di larve esposte; (iii) alterata risposta difensiva nei confronti di conspecifici estranei e predatori; (iv) alterazioni individuali nella morfologia e capacità immunitaria. In conclusione, le ampie conoscenze acquisite su questo organismo modello ci hanno permesso di traslare i protocolli messi a punto in ambito etologico e sociobiologico per un approccio applicativo di valutazione del rischio dimostrando come tale specie possa rappresentare anche un ottimo modello in ambito di studi ecotossicologici.

SESSIONE PARALLELA SIMPOSIO 5

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L'USO DELLE TELECAMERE TEMPORIZZATE NELLO STUDIO DELLA DIMENSIONE TEMPORALE DELLE COMUNITÀ MARINE

Lo studio delle comunità bentoniche e bentopelagiche marine su scala temporale giornaliera o annuale, è un argomento di grande interesse che si scontra con le notevoli difficoltà nella raccolta dei dati. Tali difficoltà diventano quasi insuperabili quando si tratta di comunità viventi nella zona mesofotica o batiale, virtualmente inaccessibili ad una osservazione diretta prolungata. Da un paio di decenni questo problema è diventato affrontabile grazie all'uso di telecamere temporizzate che sono in grado di registrare immagini per un tempo considerevole rilevando contemporaneamente una serie di parametri ambientali. In questo modo è possibile realizzare studi dinamici della biodiversità e del funzionamento di ecosistemi remoti e contemporaneamente complessi e vulnerabili.

A livello circadiano un esempio di grande interesse è stato lo studio della fauna ittica legata alle foreste mesofotiche di coralli neri che ha mostrato il ritmo giornaliero nell'utilizzo della foresta della castagnola rossa *Anthias anthias* ed il suo comportamento durante il sonno in termini di fedeltà ai siti di riposo, durata del sonno e cause dei risvegli. Lo stesso tipo di studio condotto su fondi batiali all'interno di reef di *Madrepora oculata* ha dato un importante contributo alla conoscenza della biodiversità ittica di questi ambienti senza evidenziare pattern ciclici su base circadiana, ma sottolineando l'importanza della corrente e della sedimentazione nello sfruttamento della canopy corallina. L'uso delle telecamere temporizzate diviene estremamente utile anche nello studio dei comportamenti degli invertebrati. Per esempio, un monitoraggio continuo di estese aggregazioni mesofotiche del polichete tubicolo *Bispira riccardi* ha rivelato che la contrazione della corona branchiale non è influenzata da ritmi circadiani mentre è positivamente condizionata dalla temperatura e dalla corrente, rispondendo rapidamente agli eventi meteorologici superficiali. L'attività di filtraggio e l'alta densità di questi campi di sabellidi suggeriscono un considerevole impatto sul collegamento pelagico-bentonico e sulla quantità di materia organica nei sedimenti.

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KILLER WHALES FORMATION SWIMMING: RELATIVE ENERGETIC COSTS AND GROUP GEOMETRY

One of the most frequently observed gregarious behaviours in free-ranging cetaceans is swimming in defined formations (SIMARD and GOWANS 2008; SANTOS et al. 2019; DANS et al. 2022). However, the benefits this behaviour can bring and the factors that determine the structure and arrangement in the group are still poorly studied, as they are difficult to observe in the wild. In recent years, the use of unoccupied aerial vehicles (UAV) has proven to be a high-resolution non-invasive method to study this behaviour (FIORI et al. 2017). Using this approach, we recorded drone video of travelling groups of Southern Resident killer whales (*Orcinus orca*) in the Salish Sea (WA, USA) to analyse both the energetic aspects and the spatial arrangement of a swimming formation. We tested the effect of swimming speed, relative positioning within the group (e.g., leaders, whales in the middle of the group, or followers), sex, and size on individual tailbeat and breathing frequencies as proxies of relative swimming costs. In addition, we studied how individual positioning within a formation could be influenced by social hierarchies and social ties of the whales.

Our results revealed the energetic benefits of swimming in a formation when considering multiple factors at play: intervals between surfacing events lasted longer in large trailing individuals, but the overall breathing frequency was similar in all formation members regardless of their position. Tailbeat frequency was mainly associated with size, sex, and swimming speed, but showed a decreasing trend as the number of individuals in formation increased (SPINA et al. 2024).

The analysis of whale spatial arrangement within a formation revealed a non-random positioning of individuals reflecting the matrilineal social structure of the Southern Residents population. Moreover, the observation of distance and angle relative to the nearest neighbour suggested a preferential positioning depending on the size of the individual, the social bond with the neighbour, and the number of members in the formation.

Our study suggests that in Southern Resident killer whales swimming in formation may be the result of a complex combination of factors. Energetic saving may not be the main driver of swimming in the wake of conspecifics. Given the tight social structure of these whales, both kinships and social hierarchies within the population could play a major role in determining the spacing pattern of killer whales in formation.

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YAWN CONTAGION IN ZEBRAFISH (*DANIO RERIO*): PRELIMINARY DATA FROM A MULTIDISCIPLINARY APPROACH

Yawning (Y) is a fixed action pattern widespread in vertebrates, from fish to humans. Y can be linked to the physiological state of the yawner and the social contexts in which it occurs. Despite Y apparent simplicity and automaticity, many endothermic species exhibit the ability to respond with a Y to others' Ys (yawn contagion, YC). One explanation for YC is the 'chameleon effect,' which posits that perceiving a behavior leads the observer to unconsciously imitate the gesture, aligning individuals' activities. This convergence fosters group cohesion and coordination in social animals. To understand the evolutionary roots of Y and YC, exploring these phenomena in ectothermic groups is essential. Zebrafish (*Danio rerio*), a freshwater fish, is a valuable model in behavioral research. Due to its social habits, the species is suitable for studying not only spontaneous Y but also YC, which has never been reported in ectothermic species. One of the most challenging aspects in the study of Y in fish is its unbiased detection. To address this, we collected video data on 3 males and 3 females of zebrafish and classified 136 yawns. We extracted 10 frames from each Y and simple breathing event (B). These frames were used to train a deep learning model (YOLO v8.0) to distinguish between Y and B events, achieving approximately 70% classification accuracy. A Y event involves a rapid stop in locomotion, mouth opening, rapid eye movements, fin stretching, and tail lowering. To test for the presence of YC, we used the previously classified Y and B events to create two video stimuli, each lasting four minutes. The control video (B_{video}) consisted of a sequence of empty-tank clips followed by a clip containing 10 Bs, repeated three times. The experimental video (Y_{video}) followed the same structure but included Y events instead of Bs. Both videos were presented to the same fish (N=15) in a randomized order, and the yawns performed by the fish under each condition were counted. A Generalized Linear Mixed Model analysis revealed a significant effect of condition (Y_{video} vs. B_{video}) on the number of yawns emitted, with a higher number of yawns occurring during the Y_{video} condition. These preliminary results indicate for the first time the presence of YC in an ectothermic species. Further studies harnessing new approaches and techniques will provide major advances in understanding the potential role of Y and its contagiousness in the evolution of social life.

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INDIVIDUAL PERSONALITY AFFECTS THE BEHAVIOURAL RESPONSE OF FREE-FLYING HOMING PIGEONS TO AN ARTIFICIAL PREDATOR

Many aspects of a species' ecology are influenced by individual personality. One example are those scenarios of known predator presence in which an animal needs to decide whether (or in which measure) to be exposed to this threat. In these kinds of conditions personality-mediated differences in risk assessment may affect individual response. Our aim was to assess the effect of individual personality on the behaviour of homing pigeons (Columba livia domestica) repeatedly exposed to a remotely controlled robotic predator (RobotFalcon). Pigeons were first tested to assess their level of reactivity in two personality tests (ERT: Escape Reaction Time, FID: Flight Initiation Distance). After being repeatedly released from the same site and having acquired a stereotyped homing route, experimental animals were exposed to the RobotFalcon, a drone mimicking a peregrine falcon (Falco peregrinus) in morphology and behaviour, in an area they consistently flew over during three successive homing flights (Risk Area) and then released one last time with no predator present. Homing paths were recorded using GPS loggers. Route tortuosity, flight speed and altitude were calculated for the route segments from the release site to the start of the Risk Area (Approach phase) and from the end of the Risk Area to 1.7 km from the release site (Escape phase). All birds reduced their flight altitude when the RobotFalcon was present in both phases, but no subject avoided the Risk Area either during predator exposure or in the following release. In the Approach phase, animals with lower FIDs increased their flight speeds after the first exposure to RobotFalcon and birds with higher FIDs tended to increase route tortuosity after being repeatedly exposed to the RobotFalcon. During the Escape phase, birds with lower ERTs dramatically reduced the flight speed after the first encounter with the RobotFalcon and progressively increased speed in successive flights, reaching pre-treatment levels in the last release, possibly suggesting habituation to the experimental treatment. From these results it appears that personality-dependent and personality-independent elements coexist in the anti-predator response of homing pigeons. Moreover, individual variability of the anti-predator response seems to be affected by different aspects of animal personality.

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QUALITATIVE AND QUANTITATIVE SAMPLING OF EPIGEAL SOIL MACROARTHROPODS: DIFFERENT METHODS FOR DIFFERENT OBJECTIVES

During the last 90 years, pitfall traps have been frequently used as efficient, simple, and cost-effective devices to investigate the spatiotemporal variability of the relative abundance of epigeal arthropods in a wide range of terrestrial ecosystems, at variable temporal scales (e.g., BROWN and MATTHEWS, 2016). In Italy, this method is extremely widespread (e.g., BAINI *et al.*, 2014; FATTORINI *et al.*, 2019). Pitfall sampling is considered to be well-suited to sample ground-dwelling, faster, and medium- to large sized epigeal arthropods (e.g., Araneae, Carabidae, Formicidae).

However, these advantages are undermined by several sources of bias, including a lack of standardisation hampering comparisons among studies, and misconceptions about the method's capacity to provide data to answer ecological questions (e.g., ADIS, 1979; SKVARLA *et al.*, 2014; HOHBEIN and CONWAY, 2018).

Activity levels vary at both inter- and intraspecific levels and with both habitat type and environmental conditions, following temporal fluctuation patterns different than those of density (e.g., LUFF and EYRE, 1988; TOPPING and SUNDERLAND, 1992; MELBOURNE, 1997; 1999). Capture efficiency and retention capacity are also affected by the traps' activation time (depletion and digging-in effects), disturbance, attractive or repellent properties of killing preservatives and of decaying captured animals, highly variable ethological responses at intra- and interspecific levels, and even pheromones released by captured animals, with synergistic effects (e.g., DIGWEED *et al.*, 1995; GERLACH *et al.*, 2009; ZALLER *et al.*, 2015; CSÁSZÁR *et al.*, 2018). New regulations involving prohibited chemicals (e.g. formalin solutions) can also limit comparisons with historical data. These problems arguably make pitfall traps unsuitable to estimate densities, especially when quantitative data are needed for ecological inference of different sites and assemblages, using environmental correlates of spatiotemporal variation.

We also present and discuss some field collections of epigeal soil arthropods made using pitfall traps (three different killing preservatives), and a standardised metal frame to collect soil litter (e.g., POTAPOV *et al.*, 2022).

While recommending the complementary use of other methods to integrate pitfall data for phenological or taxonomic studies, we advocate the use of quantitative sampling methods (e.g., D-Vac; photoelectrons, metal frames), whenever density estimates are needed for ecological inference.

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APPLICATION OF INNOVATIVE IMAGING TECHNIQUES TO THE STUDY OF THE PROBOSCIS OF *AEDES ALBOPICTUS* (CULICIDAE)

The Asian tiger mosquito *Aedes albopictus* (Skuse, 1895) is an invasive species which expanded worldwide during the last decades and which is competent for the transmission of many arboviruses. Among blood feeding mosquito species, males feed exclusively on nectar, while females need to acquire blood from vertebrate hosts as an essential nutrient source for egg production. The proboscis is a complex organ used to feed by mosquitoes. It includes the labrum, which is inserted in the skin, forms the alimentary canal and distally harbours sensilla potentially involved in the sensation of stimuli during blood feeding on the vertebrate host. Four pairs of sensilla were described at the tip of the labrum of the yellow fever mosquito *Aedes aegypti* (Linnaeus, 1762) (LEE, 1974): apical and subapical sensilla are involved in sensing gustatory stimuli, labral ridges receptors and campaniform sensilla are possibly related to proprioception and mechanoreception.

In the present work, we exploited innovative imaging techniques (WITHERS et al., 2021; COLLINSON et al., 2023) to characterise the morphology of the proboscis and of the labrum of *Aedes albopictus* female mosquitoes. Micro-tomography (MT) and nano-tomography (NT) were performed at the Swiss Light Source (Paul Scherr Institute, Villigen, Switzerland) and at the European Synchrotron Research Facility (Grenoble, France). Volume electron microscopy was performed in collaboration to the Advanced Light And Electron Microscopy Node Prague CZ in the Euro-Bioimaging network. Particularly, Array Tomography (AT) and Focus-Ion-Beam Scanning Electron Microscopy (FIB-SEM) were applied to study this organ. For MT, samples were collected at different developmental instars and stored and acquired in ethanol. For NT, AT, and FIB-SEM, specimens were fixed, stained with osmium tetroxide, dehydrated and included in epoxy resin with specific adaptation of sample preparation steps.

The collected datasets were segmented to perform a 3D reconstruction of the proboscis stylets in different stages of development (MT), of the tip of the labrum (NT), and of some proboscis and labrum sensilla (AT and FIB-SEM) using Slicer 3D and Dragonfly software.

This approach enabled to follow the development of adult mosquito mouthparts and to carry out a morphological characterization of mosquito proboscis, representing a basis for future functional and molecular investigations on this organ.

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AN ECOLOGIST-FRIENDLY R WORKFLOW FOR EXPEDITING SPECIES-LEVEL CLASSIFICATION OF CAMERA TRAP IMAGES

Camera trapping has become increasingly common in ecological studies, but is hindered by analyzing large datasets. Recently, artificial intelligence has emerged as a promising solution. However, applying deep learning for images processing is complex and often requires programming skills, reducing its accessibility. Some authors addressed this issue with user-friendly software, and a further progress was the transposition of deep learning to R, a statistical language frequently used by ecologists, enhancing flexibility and customization of deep learning models without advanced computer expertise. We aimed to develop a user-friendly workflow based on R scripts to streamline the entire process, from selecting to classifying camera trap images. Our workflow integrated the MegaDetector object detector for labelling images and custom training of the state-of-the-art YOLOv8 model, together with potential for offline image augmentation to manage imbalanced datasets. We tested our workflow on images collected within a project targeting medium and large mammals of Central Italy, and obtained an overall precision of 0.962, a recall of 0.945 and a mean Average Precision of 0.913 for a training set of only 1,000 pictures per species. Furthermore, the custom model achieved 91.8% of correct species-level classifications on a set of unclassified images, reaching 97.1% for those classified with > 90% confidence. YOLO, a fast and light deep learning architecture, enables application of the workflow even on resource-limited machines, and integration with image augmentation makes it useful even during early stages of data collection.

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INTEGRATING FOSSIL DATA INTO ECOLOGICAL NICHE MODELS TO FORECAST THE EFFECT OF CLIMATE CHANGE ON MAMMAL BIODIVERSITY

Ecological Niche Models (ENMs) can experience niche truncation issues when calibrated with occurrence data representing only a limited portion of the fundamental niche's environmental gradients. This research investigates if and how the integration of fossil data with modern occurrences into ENMs can mitigate niche truncation by modelling current and future distribution of 38 IUCN-listed threatened terrestrial mammals. We constructed two sets of ENMs: one using only modern data and another combining modern with fossil data (i.e., pooled ENMs). These models were projected onto current and 2080 climate change scenarios. Starting from spatially–explicit projections, we calculated the range net change (RNC) in species distribution generated from only-modern and pooled ENMs, along with the difference in RNC between values predicted from each model set (ΔRNC). Additionally, we determined the percentage increase in niche width as a consequence of incorporating fossil data (%IGFD). The relationship between these metrics was analyzed using a linear mixed model, with ΔRNC as the dependent variable and %IGFD as the independent variable. Furthermore, two Random Forest models were utilized to explore how the climates introduced by fossil data affect species outcomes under various climate change scenarios, as alternatively predicted by only–modern and pooled ENMs. The findings of this study demonstrated that fossil data consistently expand species' climatic niches, though not all the species improved their outcomes against 2080 climate change when modelled with integrated fossil data. Specifically, ENMs incorporating fossil data for species with niches that include colder and wetter climates predict more adverse future outcomes compared to those with warmer and drier climates.

SESSIONE PARALLELA SIMPOSIO 6

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URBAN BIODIVERSITY AND APPLIED ZOOLOGY: A MARRIAGE OF FORENSIC INTEREST

Implementing any urban biodiversity conservation strategy relies on effective collaboration between sectors, communities, and perspectives. Understanding the capabilities and skills of each member of a working coalition is critical to success, as well as blending these complementary elements in an inclusive way to form a collective agreement and a path forward.

One potential way to foster a sense of collective ownership and involvement in this process is to create a conceptual architecture that provides guidelines that recognize various forms of expertise and their relationships to each other. Therefore, we propose a framework that classifies urban conservation research and practice into its parts, making the discipline more manageable and less overwhelming. This framework is not just a tool, but a collaborative effort that invites anyone to be a part of.

This framework divides urban conservation into four main areas: ***Conservation in Cities***, ***Conservation of Cities***, ***Conservation for Cities***, and ***Conservation with Cities***.

Conservation in Cities aim to protect and enhance the diversity of genes, physical traits, and living communities to support healthy ecosystems. These efforts are influenced by principles of conservation biology and are adapted to urban environments.

Conservation of Cities involves considering the biological, social and built elements of urban ecosystems to manage how ecosystem processes such as water systems, nutrient flows, and interactions are influenced by social and ecological processes.

Conservation for Cities principle operationalizes the lessons from the 'in' and 'of' components to establish a model for action. Conservation for Cities provides a justice-based framework and solutions that emphasize a collective and unified approach.

Conservation with Cities approach offers a transformative path for significant change in how we conduct scientific research and practice. It not only highlights the importance of fair and equitable urban development to conserve urban biodiversity and address the global biodiversity crisis but also inspires hope for a better future.

In this case, applied zoology in urban biodiversity becomes an essential subject for interpreting evolution in a context where its components vary predictably or unpredictably, creating complex scenarios that follow lines with sometimes random directions. Regulations and laws must, therefore, be applied in contexts that do not simply follow case law. Therefore, the figure of the forensic expert in the zoological field becomes essential to support the work of jurists not so much for the development of new regulations but for their placement in the evolving context.

The concept goes beyond academic boundaries. It requires active collaboration, moving away from traditional research perspectives, and placing importance on community knowledge. It also involves fair distribution of resources and recognition, paving the way for a more inclusive and sustainable future.

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THE ARTHROPOD-BASED BIOLOGICAL SOIL QUALITY INDEX (QBS-AR): THREE-YEAR APPLICATION IN THE SENTINA RESERVE (ITALY)

Soil microarthropods are reliable soil health indicators, as they are highly sensitive to alterations in soil conditions and mechanical disturbances. However, taxonomic identification for most of the taxa is rarely performed as it requires the involvement of expert taxonomists and the use of molecular techniques. In contrast, soil microarthropod morphological traits are commonly used as indicators, as exemplified by the arthropod-based soil biological quality index (QBS-ar). The aim of the study was to apply the QBS-ar index to monitor the soil health of farms located within the Sentina Reserve (Italy), over a three-year period (2021-2023) across two seasons (spring and autumn). The objective was to assess the ability of the index to discriminate between different levels of intensity of agricultural practices applied in two conventionally managed farms (FE= high intensity, RL= low intensity).

To determine the impact of the agronomic practices (i.e., tillage depth, fertilizers and pesticides application, use of nitrogen-fixing and cover crops) on soil microarthropods, two sites (i.e., arable fields) were selected for each farm. The QBS-ar, and other indices, including density were determined. The soil microarthropod community composition was analysed using ordination analysis. Over the three-year, high biological soil quality was observed in all sites and seasons. The highest QBS-ar scores were recorded in 2023, probably due to a rainy season. Generally, RL farm showed a better performance compared to FE; QBS-ar and microarthropod density were significantly higher in RL than FE in spring (124 vs 103| 2138 vs 870 ind/1000cm^3) and autumn (132 vs 105|3626 vs 1046 ind/1000cm^3). Interestingly, microarthropod community composition differed between farms, although not significantly. The farms were located within a protected area, characterised by a mosaic of arable land, grasslands, dunes and wetlands. This high landscape complexity has possibly contributed to the maintenance of an excellent soil quality, serving as a reservoir for biodiversity. This was crucial for the recolonization of the arable land by soil fauna, following soil disturbance. Moreover, less intense and sustainable soil management, proved their effectiveness in the preservation of edaphic biodiversity and soil health. The QBS-ar index confirmed its reliability in the detection of different levels of disturbance in arable lands.

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SYMBIOTIC PERITRICHS (CILIOPHORA: OLIGOHYMENOPHOREA) OF THE OKAVANGO PANHANDLE, BOTSWANA

The Okavango Delta, situated in the north-western corner of Botswana, is one of the largest inland deltas in the world that provides an array of seasonal and permanent ecosystems. Broadly, the Okavango Delta can be divided into two main regions; the panhandle with a large meandering river bordered by seasonal floodplains, and the delta proper, that forms an alluvial fan to the south of the panhandle (MCCARTHY *et al.*, 1998). This river system also boasts with 15 families of freshwater fish, comprising 88 species in total, all indigenous, as no introduced or translocated species have been introduced (VAN AS & BASSON, 1992; RAMBERG *et al.*, 2006). This isolated indigeneity makes for an ideal parasitological survey, which the Aquatic Parasitology Research Group of the University of the Free State, South Africa has extensively investigated over two and a half decades. During this period all 88 species of fish were screened for parasites and other symbionts. Ciliate symbionts, specifically members of the Peritrichia (Sessilida and Mobilida), have been well studied in the rest of southern Africa, but to date no sessiline data has been published from the Okavango Delta with only two papers on mobilines, the first on trichodinids occurring on anabantid fishes (BASSON & VAN AS, 2002), followed by *Trichodina koloti* from anuran tadpoles (DE JAGER & BASSON, 2015). During a recent fieldtrip to the flood plains of the Okavango Panhandle fish, anuran, gastropod and planktonic crustacean hosts were examined. Preliminary results indicate that there may be two *Riboscyphidia* and three *Apiosoma* species associated with fish hosts and *Epistylis* species associated with anuran tadpoles, crustaceans and gastropod hosts. Two *Trichodina* species (*T. compacta* on the skin and *T. centrostrigeata* from the gills) and possibly two *Tripartiella* species were found associated with fish hosts.

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ANALISI DEL MICROBIOMA INTESTINALE E DEI PARASSITI GASTROINTESTINALI IN *LEPUS CORSICANUS* (DE WINTON, 1898)

La lepre italica, *Lepus corsicanus* (de Winton, 1898) è una specie endemica presente nell'Italia centro-meridionale ed in Sicilia, la cui identità tassonomica è stata solo recentemente confermata (alla fine degli anni '90) da studi su caratteri morfologici diagnostici e analisi genetiche. Questa specie è considerata dalla IUCN come vulnerabile e pertanto necessita di azioni volte alla sua conservazione.

In questo studio presentiamo un'analisi congiunta del microbioma intestinale e dei parassiti gastrointestinali in un gruppo di lepri italiche provenienti dalla Sicilia, in modo da fornire conoscenze che possano essere un utile punto di partenza per ulteriori studi riguardo a questa specie.

Il campione analizzato è composto da 25 individui, risultanti dalla stagione di caccia 2019/2020 e 2020/2021, provenienti da diverse aree della Sicilia.

Riguardo allo studio del microbioma, per la sua analisi sono stati prelevati campioni dal cieco. Le componenti microbiche e la loro abbondanza relativa sono state caratterizzate tramite *metabarcoding* sulla regione V3-V4 del gene codificante l'rRNA 16S. L'analisi dei parassiti è stata eseguita utilizzando la Tecnica della Sedimentazione e Conteggio su ogni soggetto. I parassiti rilevati (la ricerca è stata orientata esclusivamente agli elminti) sono poi stati analizzati al microscopio ottico per l'identificazione, mediante l'utilizzo delle appropriate chiavi di identificazione, e per l'attribuzione del sesso.

I phyla microbici di gran lunga più rappresentati sono risultati essere i phyla *Firmicutes* (29,4%-70,0%) e *Bacteroidetes* (1,9%-55,5%). L'analisi multivariata (PCoA) non evidenzia differenze tra i gruppi di età ed i due sessi nei campioni analizzati, ci sono invece differenze statisticamente significative nel valore dell'indice di Shannon e del numero delle componenti microbiche riguardo all'età, entrambi i valori risultano maggiori nei giovani rispetto agli adulti. Negli individui analizzati dal punto di vista parassitologico è stata individuata unicamente la specie *Trichostrongylus retortaeformis*.

I risultati ottenuti costituiscono la prima caratterizzazione del microbioma batterico intestinale in questa specie, successivi studi saranno necessari per indagare l'eventuale relazione tra comunità microbica e parassiti.

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PLAYFUL PACKS: FACIAL EXPRESSIONS AND MIMICRY IN WILD *CANIS LUPUS ITALICUS*

Play fighting, the most common form of social play in mammals, often involves a combination of motor sequences with various competitive elements. The high variability in play fighting demands advanced communicative skills in quickly adjusting signals to handle the unpredictability and rapidity of each action. To ensure successful play, species have developed context-dependant signals that typically punctuate the interactions, thereby enhancing mutual understanding between participants. Although most research on playful facial signals has focused on human and non-human primates, some evidence on the presence of Relaxed Open Mouth (ROM) are emerging for domestic dogs and captive or hand-reared wolves. Here, we provide new insights on playful facial communication in wild wolves (*Canis lupus italicus*). We used 240 videos on play gathered via cameratraps from five different areas in Tuscany (Italy), 82 of which included playful interactions. From a frame-by-frame analysis, we obtained 90 play sessions involving 64 subjects (adults=51; immature subjects=13) individually recognized. Once detected, each ROM event was described by quantifying the correspondent recruitment of muscular units by using the DogFACS (https://animalfacs.com/dogfacs_new) and the R package "NetFACS". Then, via Linear Mixed Models, we tested the possible effect of the presence of ROM on the level of competition of the play session (measured by analysing each pattern composing the session). We found that the play sessions including at least one ROM were less competitive than those without, thus suggesting that ROM has a possible role in regulating playful roughness as in several mammal species. Finally, through a Generalized Linear Mixed Model, we checked for the presence of the Rapid Facial Mimicry phenomenon (RFM). Perceiving a ROM evoked a rapid (< 1sec) replication of the same facial expression. In several mammal species, including humans, RFM has a role in sharing affective states and synchronizing motor actions thus influencing the ongoing interaction. Although we are far from understanding the role of RFM in wolves, our study represents the first step in unveiling the complexity of visual communication in dogs' wild counterparts.

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PRIMATES EXTRACT SOCIAL INFORMATION FROM VOCAL INTERACTIONS: A PLAYBACK EXPERIMENT IN WILD GELADAS (*THEROPITHECUS GELADA*)

The ability of primates to extract salient social information by simply listening to vocal exchanges between conspecifics is highly adaptive in complex social systems. More in detail, recognizing the prosocial nature of vocal interactions is a crucial yet understudied aspect of social behaviour. Geladas (*Theropithecus gelada*), with their high social complexity and rich vocal repertoire, serve as ideal models to explore the evolution of the capacity to detect vocal behaviours intended to benefit others. In a field playback experiment in the unprotected area of Debre Libanos (Ethiopia), we exposed wild adult male geladas to vocal exchanges featuring unfamiliar female victim screams paired with male affiliative calls. These calls were arranged in either prosocial (scream-affiliative call) or non-prosocial (affiliative call-scream) sequences, with varying levels of prosocial effort indicated by the type of affiliative call used, affiliative grunts (low prosocial effort) or affiliative moans (high prosocial effort). Geladas demonstrated sensitivity to the prosocial role of affiliative vocalizations by looking longer and more frequently at the loudspeaker when the acoustic sequence violated prosocial norms. They also showed sensitivity to prosocial efforts toward female victims by interrupting their feeding activity for longer periods in response to vocal exchanges with affiliative vocalizations conveying higher emotional arousal. In contrast, no discernible change was observed in self-directed behaviours across experimental conditions. Geladas thus seem not only capable of recognizing the composition and empathic nature of vocal sequences, but their responses also vary according to the perceived emotional content and prosocial effort of the vocalizations. The study suggests that the ability to process vocal exchanges as holistic third-party interactions may have existed in our common ancestors with cercopithecines. Overall, we emphasize the importance of small field experiments in studying animal cognition and in elucidating the evolutionary pathways of the primate social mind.

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CAN SEA URCHIN WASTE BE USED AS A VALUABLE SOURCE OF CALCIUM FOR LAYING HENS?

Background: In Italy, about 2.000 tons of sea urchins (mainly *Paracentrotus lividus*) are harvested every year. Gonads are the only edible part, that represent a small percentage (10-30%) of the total animal mass. Consequently, all the remaining (test, spines and soft tissues) constitutes a waste, which must be disposed off in landfills, an environmentally and economically costly practice. The sea urchin test and spines are mainly composed of calcium carbonate, rich in magnesium. In line with a Circular Economy approach, the aim of this study was to verify if sea urchin wastes can be used in laying hens feed as a valuable substitute for non-biogenic (limestone-derived) calcium carbonate. Particularly, the goal was to assess if this substitution could have effects on egg quality and animal welfare, considering that a calcium deficiency has critical impacts on these parameters. **Methods**: sea urchin wastes were collected from restaurants and food industries, oven-dried, ground, and included in laying hens feed. One hundred twenty-eight hens were reared in enriched cages, divided into two groups (control and treatment), and their welfare was assessed in three time-point during the trial, in accordance with the Welfare Quality® Protocol (Welfare Quality Network®, 2019). At the end of the cycle, the tibia breaking strength was measured. Moreover, every month, 48 eggs per group and their components were weighed, eggshell thickness, ultrastructure and yolk colour were assessed, and the egg breaking strength was measured. **Results**: eggshell weights did not differ significantly between the two groups, but the treated group showed significantly thicker eggshell, this likely affecting the shell barrier function. Despite the increased thickness, no significant differences were found in the breaking strength, as found by other authors (SWIATKIEWICZ *et al.,* 2015). As for welfare evaluation, the treated group showed fewer feather lesions in different bodyareas. Additionally, no significant differences were found between the two groups regarding tibia breaking strength. **Conclusion**: the positive results obtained in the welfare evaluation coupled to the absence of relevant differences in egg quality and in bone breaking strength, apparently suggest that sea urchin waste can be used as valuable alternative to limestone-derived calcium carbonate.

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WHEN ZOOLOGY MEETS DESIGN: THE SEA URCHIN AS A MODEL FOR BIOMIMETICS

Sea urchins are very common and ancient inhabitants of marine ecosystems. Their evolutionary success is due to a series of peculiar morpho-functional adaptations. Among these are their globous dermaskeleton, consisting of several tightly connected and morphologically specialized plates, surrounded by external appendages such as the spines and pedicellariae. All these elements are characterized by the versatile and specific use of the stereom, the 3D lattice-like meshwork composing the skeleton, as well muscles and dynamic connective tissues (MCTs). Overall, at both macro and micro scale, these structures are designed to meet specific structural and mechanical needs based on a direct and clear structure-function relationship. Thanks to the individual functional solutions, these skeletal elements can be a source of inspiration in human applied fields, including design. This transfer of knowledge from biology to applied technical sectors is called Biomimetics, a new and emerging disciplines which uses nature as an inspiring model to design new and sustainable technologies or products (PERRICONE, 2020). In this context, our research project aims to acquire morpho-functional knowledge on three skeletal elements of the sea urchin *Paracentrotus lividus* (Lamarck, 1816) i.e. the madreporite plates, the spine-tubercule attachment system, the pedicellariae, and transfer them to the development of new design objects inspired by them.

The project was based on multidisciplinary and creative approach including expertise from zoologists (UniMi) and designers (Hybrid Design lab-UniNa), in which the two disciplines constantly communicated to reciprocally direct both biology-addressed morphological analyses (light and electron microscopy) and design product development.

As results, we have developed new, unconventional and competitive design products for the international market. Thus, the madreporite plate has inspired the creation of a modern and functional fruit bowl designed slow down the ripening of fruit; the dynamic architecture of pedicellariae has inspired the design of a flexible, multifunctional lamp; finally, the spine-tubercle attachment system has inspired the development of a contemporary armchair for home training.

Overall, this project underlines the importance and productivity of a cross-talk between apparently distant disciplines as zoology and architecture, thus opening new perspectives on the applicability of zoological studies.

venerdì 13 settembre
ore 09:00 - 11:00

Simposio 2

Variabilità, Plasticità e Resilienza in Un Mondo in Rapido Cambiamento

coordinatori: Piero Giulianini, Cristina Miceli, Alessandro Massolo

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PLASTICITY IN BEHAVIOURAL RESPONSES TO PREDATOR RECOLONISATION: UNGULATES, FOXES *VULPES VULPES* AND WOLVES *CANIS LUPUS* IN A MEDITERRANEAN AREA

Behavioural plasticity is key to drive individual responses to environmental changes, with implications arising at the population-to-community level. We assessed the responses of three wild ungulates (the wild boar *Sus scrofa*, the fallow deer *Dama dama*, and the roe deer *Capreolus capreolus*) and a mesocarnivore (the red fox *Vulpes vulpes*) to the recolonisation of an apex predator (the wolf *Canis lupus*) in a Mediterranean protected area (the Maremma Regional Park, central Italy, 2016-2023). By combining camera trapping and diet analyses, we assessed (*i*) a progressive shift of temporal activity of fallow deer from crepuscular/nocturnal to diurnal patterns, initially detected only in sites with high wolf detection rates, and then widespread in the area along with the consolidation of wolf presence; (*ii*) a progressive increase of wild boar group size, not explained by variations of densities; (*iii*) a milder response for roe deer (a secondary prey to wolves, in the area), probably based on reduction of activities in high-wolf sites during brightest nights; (*iv*) a substantial temporal overlap between the red fox and the wolf throughout the study period, with an increased use of ungulate carcasses with respect to times when the wolf did not occur in the area; (*v*) a progressive increase of wolf synchronisation on wild boar, as well as a complementary role of fallow deer and wild boar in the wolf diet, and (*vi*) a dynamic pattern of wolf food habits and prey selection, switching from fallow deer to wild boar as main prey along with the increase of the diurnality of the former. Plasticity in spatiotemporal activity and/or gregariousness resulted in species-specific patterns of prey and fox responses to predators, emphasising both the dynamic nature of interspecific interactions, and the role of prey diversity in promoting community resilience to predation.

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THE SELECTION OF THERMAL REFUGIA IS THE MAIN DRIVER OF BEHAVIOURAL CHOICES IN ALPINE IBEX (*CAPRA IBEX*) RESPONDING TO GLOBAL WARMING

Behavioural adaptations are the quickest responses animals exhibit to environmental stressors. Consequently, such adaptations are expected to be prominent in reaction to rapid environmental changes, potentially offering organisms a swift mechanism to cope with variations like global warming. It is well-understood that investment in behavioural thermoregulation necessitates the allocation of time and energy at the expense of other essential activities, such as energy intake or predator avoidance. However it remains unclear how animals deal with these trade-offs. Additionally, other anthropogenic disturbances may interfere with these trade-offs, further complicating our understanding of animal responses to global changes.

To explore these topics, we utilized the Alpine ibex (*Capra ibex*) as a model species. The Alpine ibex is a heat-sensitive species and is one of the most sexually dimorphic ungulates, leading to differential overheating and predation risks between the sexes. In the Gran Paradiso National Park, we monitored the behaviour of Alpine ibex from 2010 to 2023 through direct observations and GPS collars equipped with accelerometers. This data allowed us to examine spatial resource selection, feeding strategies, and activity rhythms in response to environmental changes primarily driven by global warming, as well as the potential impacts of anthropogenic activities such as livestock presence and tourism.

Our findings indicated that the necessity to select thermal refugia compelled ibex to select suboptimal foraging areas. Ibex were unable to compensate for reduced food intake by selecting richer forage during grazing or by increasing feeding times during daylight hours. Instead, ibex increased nocturnal activity following warmer days, but this occurred at the expense of an increased predation risk. The presence of domestic animals and tourists exacerbated the use of lower-quality areas, thereby intensifying the impacts of global warming.

Our studies provide compelling evidence that Alpine ibex favours thermoregulation instead of energy intake and predation risk. The long-term implications of these behavioural responses are uncertain, but our predictive models forecast a reduction of suitable habitats by more than 50% by the end of this century. Although actions to immediately mitigate the effects of global warming are unfeasible, it is crucial to minimize other forms of disturbance, such as those caused by livestock, to alleviate the adverse consequences for ibex survival.

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ON THE WINGS THROUGH THE STREETS: A SOLITARY BEE SHOWS MORPHOLOGICAL, PHYSIOLOGICAL AND BEHAVIOURAL SHIFTS IN HEAVILY URBANISED AREAS

Urbanisation is a main driver of land-use change, leading to rising temperatures (Urban Heat Island effect) and fragmentation and reduction of green areas. Bees (Apoidea) are suffering a global decline due to anthropogenic pressures, including the increase of urban areas. While responses of bees to urbanization were highlighted at community diversity level in many investigations, analyses on how these insects may respond to this disturbance via changes in phenotype are still scarce, despite shifts in a variety of morphological, physiological and behavioural traits can be expected. Here, we present our results from studies carried out to evaluate urbanization-driven changes in the solitary, hole-nesting bee *Osmia cornuta*, using the metropolitan area of Milan as a case study site. We found a number of relevant shifts at all levels of analysis (morphology, physiology and behaviour). First, we found smaller individuals in warmer areas along the urbanisation gradient. Having a smaller body may result from accelerated development in hotter areas and may negatively impact foraging success, dispersal ability and fecundity. Second, lower wing loading (body weight/wing area ratio) was recorded at more fragmented sites, suggesting at least a better flight maneuverability in areas full of obstacles. Third, *O. cornuta* showed marginally higher ommatidia density and smaller ommatidia diameter in more fragmented sites (suggesting a better navigation in such sites), as well as marginally fewer (cold-adapted) thermoreceptors in hotter urban sites, probably because a great investment in such sensilla is not necessary under such climatic conditions. Fourth, we found that the cuticular hydrocarbon (CHC) profile significantly changes with temperature, and that bees showed hydrocarbons with a higher mean carbon chain length, and a higher number and diversity of compounds at warmer sites. Such chemical traits are expected to provide a better defense against desiccation. Fifth, the behavioural profile of *O. cornuta* expressed during intra-specific encounters was largely aggressive at all sites (likely due to nest usurpation risk), with such aggression increasing with mean site temperature (likely due to the stress caused by the Urban Heat Island effect). Finally, bees also were more likely to avoid interacting in greener, less urbanised areas. Overall, *O. cornuta* shows an important plasticity for many different phenotypic traits along the urbanisation gradient, adjusting some of these traits to cope with heavily urban environments, and perhaps reflecting adaptation processes.

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EFFECTS OF TIRE PARTICLES AND ASSOCIATED-CHEMICALS ON THE PACIFIC OYSTER *CRASSOSTREA GIGAS* PHYSIOLOGY, REPRODUCTION AND NEXT-GENERATION

The mass of tire particles in the ocean is expected to represent 93% of the aquatic plastic contamination by 2040. This might have consequences on organisms due to chemical risk following the leaching of tire-associated chemicals. In such context, it is pivotal to assess the risk posed by this stressor in marine living organisms in the context of long-term chronic exposure scenarios. In the present study, a multidisciplinary and multigenerational approach was implemented in the Pacific oyster *Crassostrea gigas*.

The effects of tire particles, tire leachates and natural particles were investigated at individual scale over a 6 weeks exposure in a flow-through system using endpoints reflecting different organization levels up to offspring performance. Secondly, the G1 offspring performance was monitored over one year up to their ability to reproduce, providing unprecedented views about the potential long-term risks from exposure to tire particles at environmentally relevant concentrations for marine organisms. No significant differences in ecophysiological parameters and haemocytes features were observed between exposed parental conditions whereas molecular analyses revealed the disruption of energy metabolism and stress response following leachates exposure. Oocytes had the highest number of differentially expressed genes; among these, many were associated with endocrine disruption and demonstrated that oocytes are mostly targeted in case of prolonged exposures of the broodstock during gametogenesis. Microbiota analysis revealed the over-representation of *Tenacibaculum* spp., a gram-negative and motile bacterial genus, which suggested the onset of dysbiosis following exposure to high concentration of both tire particles and leachates. Parental exposure had an impact on gamete quality with a 22% reduction of motile spermatozoa in the leachate conditions but had no consequences on the fertilization success. Considering the concept of energy-limited tolerance to stress, it would be of great interest to test tire risk in the context of harsher natural conditions.

Overall, while our results bring a positive note on the apparent resilience of Pacific oysters to tire particles exposure, caution should be taken when extrapolating these results to other rubber materials or to natural – harsher – conditions occurring in coastal ecosystems, bearing in mind that the first answer to plastic pollution is to reduce its production and usages whenever possible.

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ECOTOXICOLOGICAL EFFECTS OF TYRE WEAR ROAD PARTICLES: METAL ACCUMULATION AND PHYSIOLOGICAL RESPONSE IN *TENEBRIO MOLITOR*

The abrasion of tyres and brake pads in high traffic areas leads to the production of cosmopolitan contaminant dust (tyre wear road particles, TRWPs), which is a significant source of microplastics in the natural environment. These particles have been found to persist in river sediments, soil, and vegetation. In addition, TRWPs act as carriers for other pollutants, such as heavy metals and hydrocarbons, from fuel and lubricating oil consumption or from the industrial tyre process, which contributes to their dispersion and persistence in the environment. Despite their potential ecotoxicity, there is a lack of studies investigating the effects of TRWPs on soil organisms.

This study aims to provide insight into the potential effects of exposure through ingestion of TRWPs on organisms, such as insects, which provide important ecosystem services in soil trophic webs and serve as important indicators and effective models for ecotoxicological studies.

Tenebrio molitor Linnaeus, 1758 (Coleoptera, Tenebrionidae) was used as model to evaluate the effect of TRWPs and the accumulation of metals. The beetle is a primary consumer and a pest of stored grain with a well-characterised ecology and physiology and represents an appropriate model organism.

Two hypotheses were tested. The first was that trace elements contained in TRWPs could be transferred from contaminated food to primary consumers, leading to bioaccumulation. The second hypothesis was that the ingestion of TRWPs may affect the physiology and immunity of beetles. Exposure experiments were carried out on newly emerged adults, exposed to contaminated flour (enriched with 5 and 10% TRWP) and uncontaminated flour over a period of 20 days after metamorphosis.

The results of the ICP-MS analysis showed that 36 trace elements, including heavy metals (e.g. Cr, Ni, As, Cd, Pb) and rare earth elements (e.g. La, Ce, Nd and Sm), were associated with TRWP. Several elements were found to be transferred from the contaminated food into the beetle's tissues.

The exposure to TRWPs did not affect survival, but did affect several physiological parameters associated with sexual maturity of the beetles, including severe relative mass loss, increased haemocyte density and phenoloxidase activity. The effects varied depending on the age and sex of the beetles.

The study highlights the importance of investigating the potential long-term effects of chronic exposure to TRWP, as it can enter the food chain via various products and have adverse effects.

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A MULTIDISCIPLINARY APPROACH UNVEILS THE RESILIENT BEHAVIOR OF *CHAMELEA GALLINA*, A CASE STUDY

Chamelea gallina represents a precious fishing resource in the whole Mediterranean basin. In the last three decades, environmental perturbations to which it is continuously subjected and several mortality events, together with fishing effort, resulted in a strong decline of clam beds. In line with these premises, using a multidisciplinary approach, we comprehensively explored the biological status of *C. gallina* processing specimens collected from sampling sites characterized by different environmental parameters. On one side, the functional status of *C. gallina* was investigated through mRNA-seq evidencing the ability of this species to re-program gametogenesis and shell mineralization processes in relation to factors such as salinity and food availability. On the other side, a first investigation of the genetic diversity of Italian wild populations of the Adriatic and Thyrrenian Sea was performed through ddRAD-Seq highlighting a considerable genetic variability attributable to a high larval dispersal rate that might play a compensatory role against factors threatening this species.

Taken together, these results can be translated in an "opportunistic" behavior of *C. gallina*, able to exploit local fluctuations in nutrient availability. Moreover, concerning its genetic variability, we can affirm that this species has a good adaptive potential to face the environmental perturbations to which it is continuously subjected.

Currently, we are moving towards a characterization of the levels of genetic diversity in specimens coming from 10 selected sites located in the Mediterranean Sea, the Atlantic Ocean and the North Sea that will provide for the first time a holistic view of the genetic variability of *C. gallina*.

The employment of molecular techniques represents an inestimable tool useful to manage this fishery resource and to implement, where necessary, safeguard measures and restocking programs with social and economic positive impact on Italian and Mediterranean fisheries.

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LIVING IN A CONTAMINATED ENVIRONMENT: THE ROLE OF THE MIDGUT IN BLACK SOLDIER FLY LARVAE

The larvae of *Hermetia illucens*, also known as Black Soldier Fly (BSF), are efficient decomposers of waste streams thanks to their ability to grow and develop on a wide variety of decaying substrates, which can be highly contaminated by bacterial, fungal and viral pathogens. Thus, these larvae have evolved peculiar strategies that are essential for their survival in an environment extremely rich in microorganisms. Among these, the BSF larval midgut, which represent the first barrier against the entrance of non-self agents into the insect body, shows morphofunctional properties that are crucial to guarantee the saprophagous habits of this insect on such challenging environments.

Although the literature provides evidence regarding the plasticity and adaptation of BSF larvae to the presence of different microorganisms in the rearing substrate, little is known about the biological mechanisms involved in the larval resistance to pathogens. To address this aspect, BSF larvae were reared for 3, 24, and 48 hours on a substrate contaminated with *Staphylococcus aureus* or *Escherichia coli*, two of the most common bacterial pathogens associated with the organic waste, and then the presence of both pathogens was quantified in different BSF larval midgut regions -anterior, middle, and posterior-, as well as in the hindgut.

Our results demonstrate the absence of *S. aureus* in the posterior midgut and in the hindgut at each considered time point. This evidence suggests that the middle midgut environment represents an efficient barrier against the passage of this pathogen. Differently, *E. coli* was found in all the gut regions at all the time points, indicating a completely different fate of Gram-negative compared to Gram-positive bacteria. For an in-depth analysis of the biological players responsible for *S. aureus* elimination, the lumen content of the middle midgut was isolated and the role of its physiological properties (i.e., acid pH, antimicrobial peptides, and lysozyme) was tested. Our results demonstrate how the joint action of antimicrobial proteins and pH are fundamental to rapidly reduce *S. aureus* load in the gut lumen, thus allowing the growth and development of these larvae even on highly contaminated substrates.

The results herein obtained represent a starting platform to fully understand the link between the evolution of specific biological properties in these larvae and their feeding habits.

The study was supported by EMBO Short Term Fellowship to DB.

venerdì 13 settembre
ore 11:30 - 12:30

Simposio 7

Premio UTET: Didattica, Divulgazione e Social Media in Zoologia

coordinatori: Graziano Di Giuseppe, Elisabetta Palagi

WILLY GUASTI

BESTIE DEL WEB: SOCIAL E ZOOLOGIA

La comunicazione delle scienze è da tempo approdata, anche nel nostro paese, sui social. Su ogni piattaforma fioriscono anche contenuti a tema animali - con tutti i risvolti, positivi e negativi, che possono esserci. Quanto questi strumenti possono essere utili (e soprattutto, efficaci) per una corretta informazione a riguardo? Quali sono i principali lati negativi? E quali le più grandi potenzialità?

NICLA PANCIERA

GIORNALISMO SCIENTIFICO: SFIDE VECCHIE E NUOVE

Oggi innumerevoli comunicatori scientifici, dagli addetti stampa agli stessi scienziati, lavorano per promuovere una visione positiva della scienza attraverso nuovi strumenti narrativi. Nell'era della comunicazione digitale e dei social media, c'è ancora spazio per i racconti giornalistici sulle meraviglie della ricerca scientifica, che ne ritraggano in modo accurato pregi e difetti e che affrontino questioni importanti relative alla vita, alla società e all'ambiente.

venerdì 13 settembre
ore 15:00 - 16:30

Simposio Satellite

Esperienze di progettazione internazionale in zoologia per Junior and Senior Investigators

coordinatori: Cristina Giacoma, Giulio Petroni

MARCO MUSIANI[1]

[1] Dipartimento di Scienze Biologiche, Geologiche e Ambientali (BiGeA), Università di Bologna, Italy

AN ITALIAN ZOOLOGIST ABROAD: PERSONAL EXPERIENCE, MYTHS AND REALITY

Dr. Prof. Marco Musiani (Marco) leads a research group, the Musiani Lab, focused on zoological matters regarding terrestrial mammals. This presentation very briefly illustrates his projects in Canada (where he resided from 1998 to 2022, and became citizen), in Italy (2022-) and in other countries, but emphasis is given to opportunities that all zoologists have. Overall, a key message is that the major reason for not funding any proposal is failure by proponents to submit applications in the first place – it is always worth a try!

Marco holds undergrad/Master's from the Universities of Roma "La Sapienza" and of Siena. However, his Master's thesis was conducted in the field with a scholarship at the Mammal Research Institute, Polish Academy of Sciences. Then, he applied for PhD admission and scholarships in North America. He had his PhD from the University of Calgary. Finally, Marco's Postdoc was funded by Canada, but held abroad again at "La Sapienza". This talk will therefore emphasize the strategic importance of submitting applications to multiple embassies, universities and agencies, for example the Consiglio Nazionale delle Ricerche (CNR). He will also highlight the opportunity of international exchanges in general, including those not within Europe.

Marco became Assistant Professor at the University of Calgary in 2005, then Associate Prof., then Prof.. Finally he "came back home" to the University of Bologna: via the so called "Ritorno dei Cervelli". This talk will thus illustrate the opportunities offered by having an international background, ranging from the intellectual to the practical. Marco will also make the case that this "itinerary" is not unique, as other Italian zoologists have had similar experiences.

All projects have been managed in collaboration with colleagues from Canadian, American and Italian universities. However, a leadership role was often also held by Master's or PhD students, who then worked in academia, with government and with NGOs, especially in the field of environmental impact assessment.

Marco's professional activity is fundamentally academic. However, this talk will also illustrate other opportunities, for example for the FAO (Food and Agriculture Organization of the United Nations), where projects can deal with applications of zoological knowledge.

MANUELA MAURO[1], HORNSBY LUCIE BRANWEN[1], FRANCESCO LONGO, AITI VIZZINI, CLAUDIO GARGANO[1], MIRELLA VAZZANA[1], VINCENZO ARIZZA[1]

1Department of Biological, Chemical and Pharmaceutical Sciences and Technologies (STEBICEF), Palermo, Italy

THE ROLE OF ZOOLOGIST IN INTEREG PROJECTS THROUGH SELECTED EXAMPLES

Today, the issue of fishery waste is a significant environmental challenge, with large quantities of by-products often being disposed of unsustainably, contributing to marine pollution and the waste of valuable natural resources. The extraction of bioactive molecules from fishery waste represents an emerging frontier in bioeconomy and sustainability. This process aims to valorise fish by-products, transforming what is traditionally considered waste into valuable resources, such as bioactive molecules, which have potential applications across various industries, including pharmaceuticals, cosmetics, and food. This topic is particularly relevant in the context of increasing global attention towards waste reduction and the sustainable use of natural resources. Two important projects, Bythos and Bythos-Extend (Interreg Italia-Malta), coordinated by the University of Palermo, through advanced extraction and purification techniques, explored methods to effectively isolate these molecules. During the Bythos project, protocols for the extraction of collagen, chitosan, astaxanthin and hyaluronic acid were developed from fish waste. The products obtained have been used in various fields: for the production of antimicrobial biofilms useful for the improvement of the shelf life of foods or for the creation of scaffolds for cell growth. During Bythos Extend, a mobile FRAP (fish residue automated processing) unit was developed capable of integrating the innovative biotechnological supply chain and facilitating a circular economy with the use of residues from the fishing industry. FRAP modifies fish waste until stable products are obtained (e.g. fish flours and oils) for subsequent processing, and can be stored at room temperature, without the use of cold storage. The extraction protocols developed by Bythos were then applied to silage produced by the FRAP for the production of high value-added products aimed at new "takers". The international collaboration and the integration of knowledge from diverse disciplines, such as zoology, chemistry, and engineering, are crucial for developing innovative and scalable solutions. This interdisciplinary approach not only promotes sustainability but also opens new economic and commercial opportunities, positioning fishery waste as a key resource for the future.

IRENE PICCINI [1]

[1] Department of Zoology, Poznań University of Life Sciences, Poznań, Poland

MSCA INDIVIDUAL FELLOWSHIPS (AND SIMILAR GRANTS): A PERSONAL EXPERIENCE IN "POLLINATORS ET AL." PROJECT

In October 2023, I started my current truly international project POLLINATORS ET AL. at Poznan University of Life Sciences and in collaboration with 5 other Universities across Europe, spanning from Sweden to Italy. The project is co-funded by the Polish National Science Centre, the EU H2020 research and innovation program under the MSCA Grant Agreement. It aims to investigate mobility of pollinator, pollinator and vegetation communities, their interaction (e.g. pollination) and pollen transport along urban road verges across Europe. During the presentation, I will discuss my experience on applying to international calls, finding partners, consolidate networking, writing and developing an international project with specific attention to challenges and opportunities.

ANTONIO SABBATELLA[1], FRANCESCO NAPOLITANO[1], EMILIANA MINENNA[2], EDNA CARMELINO DO NASCIMENTO[3], PAOLO BONIVENTO[1, 2]

1 Istituto di Studi Europei "Alcide De Gasperi", ROMA
2 RYSA srl – via Enzo Ferrari 16, BS
3 Dance For Water ETS – via dei Ludi 14b – 01015 SUTRI, VT

MATTEI PLAN AND INSTITUTE OF EUROPEAN STUDIES "DE GASPERI" AS NEW OPPORTUNITIES FOR INTERNATIONAL EMPLOYMENT IN TRAINING AND APPLIED RESEARCH FOR YOUNG ZOOLOGIST: THE EXAMPLE IN ANGOLA AND MAURITANIA WITH STUDIES ON *HIPPOTRAGUS NIGER VARIANI* (THOMAS , 1916) FOR THE MANAGEMENT AND PROTECTION OF AN IMPORTANT BIOINDICATOR OF WATER AND ENVIRONMENTAL QUALITY

Angola is home to a diverse range of ecosystems and species, but there is a lack of documentation compared to other countries in the region. Despite challenges from colonial history and wars, there has been a growing collaboration between Angolan researchers and international scientists since peace was achieved in 2002, leading to increased biodiversity research. However, there is a need for a comprehensive review of existing knowledge due to the limited accessibility of published information.

This study will focus on the Hippotragus niger variani (Thomas, 1916), also known as Palanca negra or Giant Black Antelope. This species is important as it is a symbol of Angola and is at risk of extinction due to changes in its ecosystem. Its role as a sentinel animal allows us to monitor the complex Central African ecosystem through observation and potential repopulation efforts.

The first goal of the project is to systematically gather existing scientific results on Angola's landscapes, ecosystems, flora, and fauna to facilitate collaborative research for biodiversity conservation and territorial applications. Evaluating natural and urban biodiversity is crucial for understanding and achieving a balanced scenario, which will guide the repopulation efforts of the Palanca negra, positively impacting both natural and human-influenced ecosystems.

The initial step of the project involves establishing a taxonomic and ecological framework to understand the distribution of different subspecies across the territory and their permanent habitats.

The project aims to establish an Italian/Angolan team to study the issue and provide comprehensive training to young Angolan graduates in life sciences. The team will also assist in the training of additional staff, inform the public, and promote the project through traditional and digital channels.

ALESSANDRA BARDI[1]

1 Alessandra Bardi, freelancer and junior expert in marine biodiversity, alessandrabardi85@gmail.com

A ZOOLOGIST IN A MULTIDISCIPLINARY CONTEXT OF INTERNATIONAL COOPERATION: A PERSONAL EXPERIENCE

From a theoretical perspective, zoologist job profile and the broader field of biology-related roles offers several advantages: from extreme versatility to a rigorous scientific education. Although the potential occupations for zoologists are numerous, in practice, the range narrows significantly. When faced with the age-old question, "What will you do after graduation?", a zoology degree candidate will find it difficult to answer with certainty.

Typically, the most common paths involve an academic career or teaching, and in rare cases, the possibility of entering highly sought-after and competitive contexts, such as museums and aquariums. Public sector employment is the most frequent solution, and self-employment is traditionally uncommon among biologists. In particular, the number of self-employed professionals is even lower when considering zoologists within the broader field of biology. On one hand, zoologist job profile is almost unknown in the world of self-employment, and the applicable ATECO codes are very few. On the other hand, this same role is attracting the attention of new stakeholders due to the growing need to adequately consider nature conservation and ensure ecosystemic services.

In light of the various threats to biodiversity and climatic change that may compromise ecosystem balance, the international community is exploring potential solutions for progress and innovation that are sustainable from an environmental, economic, and social point of view, in line with the Sustainable Development Goals of the 2030 Agenda.

In this context, zoologic knowledge and skills become relevant and can be useful, or even indispensable, within multisectoral contexts aiming at counteracting threats to biodiversity, both in terms of mitigation and adaptation. A potentially suitable sector that may benefit from zoological technical expertise is international development cooperation, where a zoologist can contribute across multiple lines of intervention, from project design to monitoring and technical documentts drafting.

Despite the urgent need of zoologists technical know-how in offices working on solving global issues, these multidisciplinary contexts are traditionally dominated by other professions and zoologist inclusion may imply new challenges, such as learning a highly burocratic language, widely spread within international cooperation.

This presentation aims to describe, through a complex and still evolving journey, possible employment perspectives for zoologists.

ELISABETTA PALAGI[1]

1 Unit of Ethology, Department of Biology, University of Pisa, Pisa

BEHIND THE SCENES: THE EVALUATION STEPS FOR THE ADVANCED ERC PROJECTS

In this brief presentation, the phases, methods, and procedures for evaluating Advance ERC grants projects will be presented. Some behind-the-scenes information will be provided that may be useful for anyone wishing to apply. Additionally, some recent developments that have already been or may be introduced in upcoming calls will be illustrated.

MASCHA STROOBANT [1]

1 Dipartimento di Biologia, Università di Pisa

EU PROJECT PITFALLS: WHEN EVERYTHING GOES WRONG (NOT ONLY) ON FRIDAY THE 13TH

In this short speech, we will explore the common pitfalls that can derail a project, during the project preparation and later on, during its implementation. Firstly we will will cover essential tips for preparing EU funding applications, such as understanding the Horizon Europe Work Programme, building a strong consortium, and addressing evaluation criteria like ‘Excellence’, ‘Impact’, and ‘Quality and efficiency of the implementation’. Then, we will discuss real-life examples, analyze the causes of these failures, and provide strategies to mitigate risks and ensure project success despite the odds. By the end of this speech, you will be equipped with practical advice to navigate project challenges and secure/maintain funding successfully.

Sabato 14 settembre
ore 09:00 - 11:00

Simposio 1

Zoologia Molecolare

coordinatori: Marco Passamonti, Filippo Barbanera, Giulio Petroni

MARTIN KOLISKO[1]

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

CULTURING, SINGLE CELL SEQUENCING AND PHYLOGENOMICS: ADVANCING OUR UNDERSTANDING OF THE DIVERSITY AND EVOLUTION OF EUKARYOTES

It is not unlikely that more scientists study sparrows than all the free-living microbial eukaryotes combined. However, microbial eukaryotes (protists) are immensely important for our understanding of eukaryotic diversity and evolution. Although funding bodies are not easily convinced to fund research projects aimed at finding and characterizing novel lineages of microbial eukaryotes, such investigations usually bring new and truly fundamental insights into cell biology, evolution, and ecology. These discoveries have been facilitated recently either by establishing novel laboratory cultures or by single cell sequencing of yet uncultured organisms. Here, I will summarize recent advancements in resolving the eukaryotic tree of life and show some of the most impactful discoveries of the diversity of eukaryotes. In the second part of my talk, I will demonstrate in depth how combining phylogenomics, culturing and single cell sequencing has fundamentally improved our understanding of the evolution of specific microbial eukaryotic groups of utmost importance: Apicomplexa and Metamonada.

SIMONE DI CRESCENZO[1], CARIANI ALESSIA[2], VALENTINA CROBE[2], ALICE FERRARI[2], MARTINA SPIGA[2], RICCARDO MELIS[1], ANDREA BELLODI[1,3], ANTONELLO MULAS[1], MARIA CRISTINA FOLLESA[1], RITA CANNAS[1]

1 Department of Life and Environmental Sciences, University of Cagliari, Cagliari, Italy
2 Department of Biological, Geological and Environmental Sciences, University of Bologna, Bologna, Italy
3 Stazione Zoologica Anton Dohrn Contrada Porticatello, Messina, Italy

WE CAN'T CHANGE WHO THEY ARE: INTEGRATING PUBLIC AND NEW COI, NADH2 AND 12S SEQUENCES TO BUILD REFERENCE LIBRARIES FOR CARTILAGINOUS FISH SPECIES

The number of threatened cartilaginous fishes has grown at an alarming rate in the last decades. Accurate identification of species becomes a critical aspect to assess and plan accurate conservation and management measures for this important group.

In the past, the identification was based on morphological methods that have been progressively integrated with molecular tools. Therefore, it becomes extremely important to maximise the sensitivity of molecular approaches improving the reliability and the accuracy of the public databases.

The present work aims to a) evaluate the robustness of the public databases NCBI and BOLD for the discrimination of Elasmobranchii and Holocephali species recorded in five FAO areas and b) to produce curated reference libraries for three of the most widely used markers on cartilaginous fishes (COI, NADH2 and 12S). To reach this scope over 28000 sequences belonging to over 400 putative species were analysed, including both public and newly produced data.

The results obtained revealed the presence of errors in public repositories such as: a) mislabelling and/or misidentification and b) old nomenclature and/or data not updated. The results outlined: c) presence of possible new species not yet described and d) clades which require further analysis to solve taxonomic uncertainties.

COI and NADH2 showed a higher number of total sequences and a similar number of species recognizable in final datasets, suggesting the high potential for these two markers for the molecular taxonomic, particularly when compared to 12S. Additionally, the results highlighted how the discriminant power at the species level decreases using short vs long 12S sequences (usually used in metabarcoding/eDNA and phylogenetic analyses, respectively). In fact, using the shorter sequences the possibility to discriminate many species that were clearly divided using longer 12S sequences was often lost.

Overall, our results highlight the 12S current limits, mainly linked to its low species coverage rate. Contrarily, both COI and NADH2 proved to be useful and valid tools, showing a solid species coverage. Anyway, further work is needed to complete and improve the reference libraries. In particular, the obtained results suggest a careful scrutiny and manual corrections of publicly obtained sequences by experts prior to their use.

FAUSTO TINTI[1], ALICE FERRARI[1], VALENTINA CROBE[1], ALESSIA CARIANI[1]

1 Lab. GenoDREAM, Dip. BiGeA, Università di Bologna, Ravenna, Italia

ESSERE O NON ESSERE *RAJA* L. 1758: QUANDO E QUANTO TASSONOMIA E SISTEMATICA MOLECOLARE SONO NECESSARIE PER LA BIODIVERSITÁ DELLE RAZZE

Le razze (Elasmobranchii, Rajiformes, Rajidae) mostrano elevati livelli di conservativismo morfo-ecologico e paradossalmente una straordinaria diversità specifica con numerosi endemismi in molte faune e taxa, inclusa la fauna Atlantico-Mediterranea. Senza dubbio lo studio di questo ossimoro naturale è stato ulteriormente complicato da noi zoologi marini negli ultimi 266 anni, con sinonimi e specie non valide o descritte su un solo individuo, creando così un notevole disordine tassonomico e determinando problemi e impatti nella valutazione e gestione della biodiversità. Da circa 20 anni stiamo cercando di riordinare e ricostruire la storia naturale del genere *Raja* L. 1758 mediante un approccio integrato di tassonomia e sistematica molecolare intra- ed interspecifica. Campionamenti a mare prolungati e massivi hanno permesso 1) l'identificazione tassonomica molecolare delle specie (DNA barcoding) e ricostruzione delle relazioni filogenetiche utilizzando la variazione nucleotidica di geni mitocondriali per superare la grande incertezza dei caratteri tassonomici tradizionali a causa della variabilità intraspecifica e alla crescita e 2) l'analisi genetica del differenziamento tra le popolazioni con loci nucleari microsatelliti per superare il rallentamento dell'orologio molecolare del mtDNA degli elasmobranchi e considerare l'ampia distribuzione zoogeografica e i *life-history traits* di alcune specie. L'approccio bi-genomico ha permesso di indagare anche le strategie riproduttive e l'ibridazione interspecifica. Abbiamo così ricostruito che la biodiversità attuale di *Raja* include verosimilmente un minimo di 15 specie valide distribuite nell'Atlantico Orientale (dal Mare del Nord al Capo di Buona Speranza), in tutto il Mediterraneo e Mar Nero e nell'Indiano Sud-occidentale. La storia naturale di *Raja* è prevalentemente caratterizzata da processi di speciazione geografica a partire dal Miocene medio-inferiore, in cui stadi gerarchici a crescente biocomplessità ne rappresentano fotogrammi evolutivi, dalla strutturazione spaziale con isolamento riproduttivo di popolazioni identiche morfologicamente in specie ad ampia distribuzione (*R. miraletus*, *R. clavata*, *R. straeleni* e *R. asterias*) alla speciazione criptica con complessi di specie (*R. miraletus*, *R. parva* e *R. ocellifera*), da specie allopatriche di origine recente che possono ibridarsi in zone di contatto (*R. polystigma* e *R. montagui*) a specie molto divergenti simpatriche (*R. undulata*, *R. microocellata*).

ROBERTO ARRIGONI[1], TULLIA I TERRANEO[2], FABIO MARCHESE[2], CHAKKIATH P ANTONY[3], NICOLAS OURY[2,4], FEDERICA BARRECA[2], SILVIA VIMERCATI[2,4], GIOVANNI CHIMIENTI[5,6], SAM J PURKIS[7,8], CARLOS M DUARTE[2,4], MOHAMMAD A QURBAN[9], MATTIE RODRIGUE[10], AMEER A EWEIDA[7,11], FRANCESCA BENZONI[2,4]

1 Department of Biology and Evolution of Marine Organisms (BEOM), Genoa Marine Centre (GMC), Stazione Zoologica Anton Dohrn–National Institute of Marine Biology, Ecology and Biotechnology, Genoa, Italy
2 Red Sea Research Center, King Abdullah University of Science and Technology (KAUST), Thuwal, Saudi Arabia
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5 Department of Biosciences, Biotechnologies and Environment, University of Bari Aldo Moro, Bari, Italy
6 CoNISMa, Rome, Italy
7 Rosenstiel School of Marine and Atmospheric Sciences, University of Miami, Miami, FL, United States
8 Khaled Bin Sultan Living Oceans Foundation, Annapolis, MD, United States
9 National Center for Wildlife Development, Riyadh, Saudi Arabia
10 OceanX, New York, NY, United States
11 Marine Conservation Division, Nature Conservation Authority, NEOM, Saudi Arabia

POPULATION GENETICS OF A HABITAT-FORMING SCLERACTINIAN CORAL IN THE MESOPHOTIC AND DEEP-SEA OF THE RED SEA

Understanding the connectivity of species is fundamental to identifying population units and implementing conservation actions. During the last years, population genetic patterns of shallow (< 30 m depths) reef taxa have been increasingly investigated in the Red Sea, providing evidence of dispersal breaks and the role of environmental gradients in shaping the distribution and connectivity of shallow-water reef organisms. Nevertheless, dynamics for the mesophotic and deep-sea fauna remain largely unexplored in this basin. Here, we collected coral colonies of the habitat-forming species *Dendrophyllia* sp. at depths between 78 and 344 m across nine areas of the Saudi Arabian Red Sea, covering 1,400 km of overwater distance, from the Gulf of Aqaba to the Farasan Islands. By applying a Restriction-site Associated DNA Sequencing (RADseq) approach, we gathered genetic information on 62 individuals at 7,247 putatively neutral SNPs. Population structure analyses suggested the presence of two distinct clusters, a northern and a southern one, with individuals collected at latitudes between 20.5°N and 22.0°N showing an admixed signal with a major assignment to the southern cluster. The genetic connectivity of the scleractinian *Dendrophyllia* sp. was strongly determined by an isolation by distance pattern while, considering environmental parameters, differences in dissolved oxygen concentration, rather than in salinity and temperature, correlated with the population differentiation. Out of the 29 candidate outlier SNPs potentially under selection between the two clusters, we found loci putatively involved in energy metabolic processes and response to stress, including for example hypoxia. This study represents the first population genetic assessment of a deep-sea taxon of the Red Sea and suggests that the peculiar geological, ecological, and environmental conditions in the Farasan Banks (southern Red Sea) may influence the dispersal of the investigated coral species. Furthermore, these results provide basic knowledge for the identification of large-scale mechanisms determining the connectivity of deep-sea benthic organisms in the Red Sea to better inform monitoring and conservation strategies.

GIOBBE FORNI[1], BARBARA MANTOVANI[1], ALEXANDER S. MIKHEYEV[2],
ANDREA LUCHETTI[1]

1 Dip. Scienze Biologiche, Geologiche e Ambientali (BiGeA), University of Bologna, Bologna, Italy
2 Research School of Biology, Australian National University, Canberra, ACT, Australia

PLEIOTROPY DRIVES THE CRYPTIC PERSISTANCE OF MALE REPRODUCTION IN PARTHENOGENETIC STICK INSECTS

Our understanding of how traits evolve along the Tree of Life is advancing rapidly beyond the simplistic paradigm of novel trait emergence and irreversible trait loss. A closer look reveals that some complex adaptations of extant species can be explained as the reversal of traits that were once lost in their ancestors. Yet, theory predicts that after the loss of a trait the molecular machinery underlying its phenotypic expression should decay. To bridge this knowledge gap, we test the hypotheses that (i) the molecular ground plan of a lost trait could persist due to pleiotropic effects on other traits and (ii) that gene co-expression network architecture could constrain individual gene expression. Our testing ground has been the *Bacillus* stick insect species complex, which contains close relatives that are either bisexual or parthenogenetic. After the identification of genes expressed in male reproductive tissues in a bisexual species, we investigated their gene co-expression network structure in two parthenogenetic species. We found that gene co-expression within the male gonads was partially preserved in parthenogens. Furthermore, parthenogens did not show relaxed selection on genes upregulated in male gonads in the bisexual species. As these genes were mostly expressed in female gonads, this preservation could be driven by pleiotropic interactions and an ongoing role in female reproduction. Connectivity within the network also played a key role, with highly connected - and more pleiotropic -genes within male gonad also having a gonad-biased expression in parthenogens. Our findings provide novel insight into the mechanisms which could underlie the production of rare males in parthenogenetic lineages; more generally, they provide an example of the cryptic persistence of a lost trait molecular architecture, driven by gene pleiotropy on other traits and within their co-expression network.

MARCO BARUCCA[1], CHIARA SPINSANTE[1], FEDERICA CARDUCCI[1], ELISA CAROTTI[1], ADRIANA CANAPA[1], DAVIDE BIZZARO[1], MARIA ASSUNTA BISCOTTI[1]

1 Dipartimento di Scienze della Vita e dell'Ambiente, Università Politecnica delle Marche, Ancona, Italy

MULTIPLE RECEPTORS FOR MULTIPLE VITELLOGENIN FORMS?

Vitellogenins (Vtgs) are apolipoproteins that play a key role in constituting nutritional reserves for embryo development in oviparous and ovoviviparous species. In vertebrates, *vtg* genes are present in multiple copies but only one gene encoding vitellogenin receptor (VTGR) is indicated. The gene encoding this receptor, crucial for the uptake of vitellogenin into oocytes, is a member of the Low Density Lipoprotein Receptors (LDLRs) gene superfamily. Given the presence of multiple Vtg forms, the receptor function might also be played by other members of LDLR gene superfamily. In tetrapods, information about *vtg* and *vtgr* genes is limited to a few taxa. Therefore, in this study, *Cynops orientalis* (Amphibia, Caudata) was employed as target species to perform an extensive characterization of these genes. Interestingly, four complete vtg sequences were identified in the fire belly newt. Moreover, through a phylogenetic analysis, insights on the evolutionary history of the LDLR receptors superfamily were inferred. Secondary structure predictions and gene expression analysis allowed to suggest LRP8 as additional Vtg receptor.

CLAUDIO ALIMENTI[1], BILL PEDRINI[2], PIERANGELO LUPORINI[1], ADRIANA VALLESI[1]

1 School of Biosciences and Veterinary Medicine, University of Camerino, Camerino (MC), Italy
2 Paul Scherrer Institute, Villigen PSI, Switzerland

THE WATER-BORNE PROTEIN PHEROMONE FAMILIES OF THE CILIATE *EUPLOTES*: AN IMPROVED VIEW OF THEIR STRUCTURAL EVOLUTION

In ciliates, gene flow and breeding structure (hence, speciation) are regulated by so-called mating-type systems. Species may either include only two mutually mating compatible cell-types, or multiple numbers of cell-types which, as is the case in self-incompatibility systems of flowering plants, determine outbreeding and heterozygosity. High-multiple systems are pervasive among spirotrichous ciliates, and historically have more profitably been studied for their genetic determinants and molecular basis in *Euplotes* species. In addition to being easily isolated from every aquatic habitat and stably cultivated in laboratory, they are unique to constitutively secrete workable amounts of the protein pheromones (originally named ‘mating-type substances’) that chemically distinguish from one another the multiple co-specific mating cell-types, each being encoded by one of a series of multiple alleles at the same Mendelian locus of the germinal (micronuclear) genome.
Long lasting analyses of NMR spectroscopy and X-ray crystallography have previously resolved the folded forms of various members of the *E. nobilii*, *E. raikovi* and *E. petzi* pheromone families, and opened the way to an initial picture of the various degrees of intra- and inter-specific conservation and polymorphism of the relevant structural components. These determined molecular structures have now been used as templates to improve the predictive fidelity of the new AI model, AlphaFold 3, in reconstructing the folded forms of the pheromone primary amino acid sequences that have more recently been resolved (in our and other laboratories, via genetic and/or chemical approaches) from a number of other species branching in key positions of the *Euplotes* phylogenetic tree. The updated picture of the *Euplotes* pheromone structural evolution suggests, first, that this evolution may well be synthesized by the common tenet “the earlier, the smaller and simpler”. Second, it identifies an alpha-helix as the structural motif that is most tightly conserved (in relation to backbone, size and amino-acid residue composition) at both intra- and inter-specific level. This conservation well accounts for the central role played by this motif in the signaling pheromone/receptor interactions on the cell surface, as well as for common observations of cross-mating induction and hybridization between morphologically distinct species.

Sabato 14 settembre

ore 11:30 - 13:30

Simposi 1 e 2

RELAZIONI IN SESSIONI PARALLELE

SESSIONE PARALLELA SIMPOSIO 1

MARIA CARMEN VALOROSO[1], MONICA VAGHI[1], GAETANO AUFIERO[2], NUNZIO D'AGOSTINO[2], SILVIA CACCIA[1]

1 Dipartimento di Bioscienze, Università di Milano, Milano, Italia
2 Dipartimento di Agraria, Università degli Studi di Napoli Federico II, Portici, Napoli, Italia

CARATTERIZZAZIONE MOLECOLARE DELLE RISPOSTE DELLE LARVE DI ZANZARA *AEDES ALBOPICTUS* ALL'ENTOMOPATOGENO *BACILLUS THURINGIENSIS*

Il cambiamento climatico e la globalizzazione hanno fortemente contribuito alla diffusione di insetti vettori dalle zone tropicali di origine alle regioni caratterizzate da clima temperato. Tra questi insetti, la zanzara tigre asiatica (*Aedes albopictus*), una specie che predilige ambienti domestici e peridomestici, si è particolarmente diffusa nella zona mediterranea dove rappresenta un pericolo visto l'alto numero di arbovirus di cui la femmina adulta è potenzialmente vettore e può quindi trasmettere durante il pasto di sangue sull'uomo. In quanto determinante per la capacità vettoriale e quindi per la trasmissione dei patogeni, il sistema immunitario delle zanzare adulte è stato molto studiato, mentre la risposta immunitaria delle larve è poco nota. Tuttavia, lo studio dell'immunità delle larve è di interesse non solo per comprendere le interazioni tra le larve acquatiche e i numerosi microorganismi e parassiti presenti nel loro habitat, ma anche perché utile per sviluppare strategie che migliorino l'efficacia dei mezzi di controllo larvale basate sull'utilizzo di entomopatogeni.

Per caratterizzare dal punto di vista molecolare la risposta immunitaria delle larve, abbiamo effettuato l'analisi trascrittomica di larve esposte ad un bioinsetticida a base di *Bacillus thuringiensis* var. *israelensis* (*Bti*) a tempi e concentrazioni diverse. Tali risultati ci hanno permesso di identificare alcuni geni immunitari e di caratterizzare i pathways che sono alla base del sistema immunitario umorale e cellulare delle larve di zanzara. Studi precedenti hanno dimostrato che il gene *102* nelle larve del lepidottero *Spodoptera littoralis* ha un ruolo chiave nella risposta immunitaria al *B. thuringiensis*. A tal proposito, abbiamo individuato e caratterizzato molecolarmente il gene *Aea102* in larve di *Ae. albopictus* e abbiamo osservato, mediante esprimenti di espressione genica, il suo coinvolgimento nella risposta delle larve al trattamento con *Bti*.

La nostra ricerca offre una prima descrizione delle risposte, immunitarie e no, messe in atto dalle larve di *Ae. albopictus* esposte all'entomopatogeno *Bti.* Queste importanti informazioni sulla biologia delle larve acquatiche di zanzara saranno anche utili dal punto di vista applicativo per la definizione di strategie di controllo larvale basate sul potenziamento dell'attività dei bioinsetticidi microbici attraverso l'utilizzo di molecole immunomodulanti.

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GENETIC BASIS OF REPRODUCTIVE HOST PLANT PREFERENCES IN *CACOPSYLLA MELANONEURA* (HEMIPTERA, PSYLLIDAE).

Apple proliferation (AP) is one of the most significant diseases in apple cultivation in Europe. AP is associated with the bacterial pathogen '*Candidatus* Phytoplasma mali', which causes serious damage by altering photosynthesis, metabolic processes, and hormonal balance in the plant. Like other phytoplasmas, 'Ca. P. mali' is an obligate symbiont that colonizes both the plant's phloem and the insect vector's hemolymph. The insect vectors of 'Ca. P. mali' are the apple psyllids, *Cacopsylla picta*, and *Cacopsylla melanoneura*. The latter spends most of the year on conifers but reproduces on apple or hawthorn, and in some regions, is the sole vector for 'Ca. P. mali' diffusion in apple orchards. Laboratory experiments suggest that populations reproducing on apple are ecologically different from those that use hawthorn, supporting the idea that populations adapted to apple cannot survive or reproduce on hawthorn, and vice versa. The goal of our study is to identify the genetic basis of the different reproductive host preferences in *C. melanoneura*. For this purpose, we sequenced, assembled, and annotated the genome of *C. melanoneura* using a combination of long and short-read technologies. The genome has highly repetitive content, with nearly 30,000 annotated genes. Subsequently, we investigated genetic differences between pairs of sympatric wild populations collected from apple and hawthorn plants across Europe. Single Illumina reads from individual specimens have been aligned against the newly generated genome. With this approach, we have confirmed the presence of two genetically distinct groups of individuals showing different host preferences and identified genomic regions particularly enriched in single nucleotide polymorphisms between these two groups. Finally, these results will also be useful for monitoring the spread of 'Ca. P. mali' vectors in Europe and for shedding new light on the genetic basis of reproductive host preferences in *C. melanoneura*.

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REDISCOVERING THE *ALECTORIS* PARTRIDGES (PHASIANIDAE): ADVANCES AND PERSPECTIVES IN THE GENOMIC ERA

The genus *Alectoris* (KAUP, 1829) includes seven closely related polytypic game species exhibiting either allopatric or parapatric distribution in the Palaearctic: the red-legged partridge (*A. rufa*), the rock partridge (*A. graeca*), the chukar partridge (*A. chukar*), the rusty-necklaced partridge (*A. magna*), the Barbary partridge (*A. barbara*), the Arabian partridge (*A. melanocephala*), and the Philby's partridge (*Alectoris phylbyi*). During the 1990s, the great socio-economic relevance associated with hunting activities has spurred interest in studying the evolutionary relationships of this species complex and of some taxa in particular, primarily the red-legged partridge, which is referred to as one of the most important small game in southwestern Europe. Nevertheless, such interest soon diminished in favour of other quarry species and the genetic results insofar obtained were not further explored with genome-wide approaches. It is only recently that the application of next generation techniques has revived a lively interest in *Alectoris* partridges, opening new exciting research avenues. For instance, the generation of the first *de novo* genome (CHATTOPADHYAY et al., 2021) of *A. rufa* paved the way to a comprehensive investigation of the genome-wide diversity in this species (based on over 168,000 loci), suggesting that the human-mediated introgressive hybridisation with *A. chukar* might not been so extensive as previously invoked with traditional genetic tools (FORCINA et al., 2021). On the other hand, the first phylogenomic study based on whole genome resequencing data (17,595,257 loci) for 25 individuals and all seven species confirmed the systematic relationships formerly established with mitochondrial markers and supported the exclusion of *A. melanocephala* - as previously suggested by WATSON (1962) - from the genus *Alectoris*. Interestingly, the Sicilian rock partridge (*A. g. whitakeri*) was confirmed as the most basal within its genus. This result contradicts expectations based on the biogeographic patterns of the majority of the sedentary species occurring in Sicily, raising the question of a possible human-mediated ghost introgression with other Mediterranean *Alectoris* species in historical times. The next research milestone is the ongoing whole-genome resequencing of *Alectoris* museum specimens (1800-1980s) preceding the intensive management as a fundamental prerequisite to evaluate human-mediated genetic change in a temporal other than spatial perspective.

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EVIDENCE OF CONVERGENT EVOLUTION IN THE NUCLEAR AND MITOCHONDRIAL OXPHOS GENES ACROSS SQUAMATA DEEP LINEAGES

The monophyletic origin of Iguania (Pleurodonta + Acrodonta) is rejected using mitochondrial markers, which instead strongly support a close sister relationship between Acrodonta (particularly the Agamidae family) and Serpentes. This contrast in topologies may stem from an ancient episode of convergent evolution between the two lineages in the OXPHOS pathway. Four out of the five complexes that constitute the OXPHOS system are composed of both mitochondrial (mtOXPHOS) and nuclear (nucOXPHOS) subunits that must coevolve to ensure proper OXPHOS functioning.

We retrieved mtOXPHOS and nucOXPHOS sequences for 56 species (25 families) within the Squamata Order and compared the phylogenetic signal and evolutionary rate correlations. Furthermore, we performed an approach to detect signals of convergent evolution across the Squamata topology, applied to both datasets.

Phylogenetic analysis restricted to the subset of nuclear subunits that tightly interact with mitochondrial subunits (contact nucOXPHOS) mirrored the mitochondrial topology, strongly supporting a close sister relationship between agamid lizards and snakes. This result was consistent with the evolutionary rate correlation (ERC) analysis, which reported a positive linear correlation between branch lengths for mtOXPHOS and nucOXPHOS subunits (especially for contact nucOXPHOS). Furthermore, almost all mitochondrial subunits showed clear evidence of convergent evolution between agamids and snakes, and nearly 30% of nucOXPHOS genes followed the same pattern.

Thus, the convergent hypothesis extends beyond mitochondrial subunits (which constitute the cores of OXPHOS complexes) to genes involved in the same metabolic pathway and that closely interact with mitochondrial counterparts.

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MOLECULAR ARCHITECTURE AND GENE REARRANGEMENT IN THE MITOCHONDRIAL GENOMES OF GASTROTRICHS

Gastrotrichs are microscopic, free-living aquatic worms that thrive in meiobenthic environments. Currently, over 890 species are classified into two orders: Macrodasyida, including approximately 377 species, predominantly marine or estuarine with only four exceptions, and Chaetonotida, with 483 species, mainly freshwater, though it was suggested that about one-fourth have reinvaded marine environments during their evolution. These organisms exhibit diverse adaptations to marine and freshwater habitats and possess a fascinating array of reproductive strategies, including hermaphroditic species with varied reproductive system organizations and parthenogenetic species, some of which are also ovoviviparous. Despite their intriguing biology, the evolutionary history of gastrotrichs is primarily inferred from morphological data, with molecular information available for less than 10% of the known species. This molecular data often includes just 1-3 genes, such as 18S rDNA, 28S rDNA, mtCOI, and the complete mitochondrial genome for only two species, which presents a challenge to understanding the deep evolutionary history of the group. Mitochondrial genomes, which are typically conserved in many vertebrates and invertebrates, have shown gene rearrangements in various taxa, providing valuable evolutionary insights. Our study aims to investigate the molecular architecture of mitochondrial genomes in gastrotrichs and compare the mitochondrial gene rearrangements across different lineages to identify potential evolutionary events. Using a whole-genome amplification pipeline, we sequenced and analysed the mitochondrial genomes of 20 gastrotrich species belonging to an ample taxonomic spectrum. Our analyses reveal a clear separation between two gastrotrich orders in terms of mitochondrial genome rearrangement and the number of protein-coding genes. A working hypothesis suggests that the retention of ATP6 and ATP8 genes in parthenogenetic, mostly freshwater chaetonotidans and their potential relocation from mitochondria to the nucleus in hermaphroditic marine macrodasydans could be due to selective bioenergetic advantages. However, we cannot exclude that the loss of ATP6 and ATP8 happened independently in macrodasydan lineages during evolution. Furthermore, we will discuss and compare mitogenome size, gene arrangement, gene gain and loss among the studied gastrotrich families, which may correlate with different aspects of their physiology and evolutionary processes.

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ADVANCING TARDIGRADE BIODIVERSITY MONITORING IN LEAF LITTER: THE POTENTIAL OF eDNA METABARCODING

Describing and monitoring biodiversity over time is a challenging task that must be performed efficiently and accurately. Among habitats, leaf litter has a high faunal biodiversity, including tardigrades, yet the latter biodiversity and its influencing factors are often overlooked due to the time-consuming nature of traditional extraction methods and the need for expert taxonomists. eDNA metabarcoding offers high-throughput capabilities, potentially surpassing traditional methods in speed and accuracy, while also shedding light on population dynamics. However, its effective implementation requires primers tailored to specific research goals and robust reference libraries linking each sequence to a morphotype. This study aims to achieve two integrated goals: i. developing an efficient method to quantitatively extract tardigrades from leaf litter samples for population dynamic studies, ii. investigating tardigrade biodiversity using eDNA metabarcoding and comparing obtained data with integrative taxonomy data.
As regards the former goal, various Baermann funnel configurations were tested on beech leaf litter from the Tuscan Emilian Apennines. The most effective method involved the use of fragmented leaf litter divided among different funnels, with an efficiency rate of 95,4%.
As regards the latter goal, 17 and 9 primer pairs for COI and 18S genes respectively were identified from the literature and tested *in silico*. While a suitable COI primer pair was selected among them, a specific 18S primer pair had to be designed for Eutardigrada, the dominant tardigrade class in our latitude. From nine samples from Tuscan-Emilian Apennines, more than 3,000 tardigrades were extracted for morphological identification and reference library implementation, while parts of substrates were kept for eDNA metabarcoding extraction and primers validation. Morphological observations of extracted tardigrades revealed at least 20 morphotypes belonging to 15 different genera. DNA barcoding on 18S and COI genes is also being conducted on these morphotypes to build a more comprehensive reference library.
In conclusion, this study allows to advance the understanding of tardigrade biodiversity and population dynamics in leaf litter. By employing eDNA metabarcoding techniques and refining extraction methods, biodiversity monitoring in ecosystems can be conducted with enhanced precision and efficiency.

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TARDIGRADES BIODIVERSITY IN ITALIAN ROCK POOLS REVEALED TROUGHT METABARCODING

Background: Concerns for preserving biodiversity are widespread among the general public and the scientific community. To be conserved, biodiversity needs to be thoroughly understood and quantified. Quantification and catalogation of biodiversity is a long and complicated task, but molecular techniques (such as metabarcoding) are proving to be extremely helpful in this task. Tardigrades are a group of microinvertebrates known for their ability to survive almost complete desiccation. Tardigrades have been traditionally collected from mosses, lichens, leaf litter, ponds, and stream and marine sediments; however, many other habitats have been to date neglected. To help alleviate this situation, we surveyed tardigrade diversity in freshwater rock pools: eroded depressions that occur in a matrix of bedrock, with the aim to both describe their biodiversity and identify tardigrade taxa adapted to this specific habitat.

Methods: For this study, we sampled more than 100 rock pools from the Northern Apennines and Central Alps and used DNA metabarcoding of the markers SSU and COI to characterize the tardigrade communities that inhabit them. SSU metabarcoding was performed on the native sediment with universal Eukaryotic primers, whereas COI metabarcoding was performed on tardigrades-enriched sediment with tardigrade specific primers. Additionally, tardigrades density was manually counted.

Results: In the analysed native sediment samples, tardigrades density ranged from 0 to 1090. individuals/gr of dry sediment, whereas and the proportion of tardigrades reads over all the SSU reads ranged 0.13 % to 70.29 %. The four most abundant tardigrade genera identified were *Ramazzottius*, *Acutuncus*, *Macrobiotus* and *Milnesium*, showing two different patterns: *Ramazzottius* and *Acutuncus* were present with only one species in almost all the samples, whereas *Macrobiotus* and *Milnesium* were less common and present with different species sorted according to the sampled locations.

Conclusions: Those results suggest that: i) tardigrades are abundant member of alpine rock pool communities and their abundance can be inferred from metabarcoding data; ii) whereas some genera (*Macrobiotus* and *Milnesium*) seems to colonize rock pools opportunistically, some species of *Ramazzottius* and *Acutuncus* could be adapted and specialized to this particular habitat.

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A FULL RAFT: THE NUDIBRANCH FAUNA (MOLLUSCA, GASTROPODA) TRAVELING ON BOARD THE BRYOZOAN *AMATHIA VERTICILLATA* (DELLE CHIAJE, 1822)

The Mediterranean Sea is a hotspot of biodiversity currently threatened by global warming and increased naval traffic, two of the major factors affecting Mediterranean biodiversity and its endemic and autochthonous fauna. Considering introduction and spread of Non-Indigenous Species (NIS) are among the main threats to biodiversity globally, the early detection and monitoring of NIS are crucial to understanding the dynamics driving environmental changes. The widespread bryozoan *Amathia verticillata* (delle Chiaje, 1822), described from the Gulf of Naples, is currently considered cryptogenic. This hermaphroditic species is capable of sexual and asexual reproduction, a useful ability to rapidly colonize different areas. It lives on natural and artificial substrates and this plasticity, coupled with being a species 'bearer of other species', makes it very useful to early detecting new NIS and to investigate their dispersal thorough the Mediterranean Sea. Even if scattered studies have highlighted the link between *A. verticillata* and some nudibranchs (FURFARO et al., 2018; MIONI and FURFARO, 2022), to date a comprehensive view of the Nudibranchia associated fauna is still lacking. For this reason, the main aim of this study is to update the list of nudibranchs possibly associated to this bryozoan and investigate the geographic range of distribution of the species recorded. Surveys have been carried out in different anthropized area in southern Italy, together with broad bibliographic research. Nudibranchs were observed and morphologically identified using optical microscope and then catalogue and store in EtOH 96% for further molecular analyses. DNA barcoding technique confirmed the species identification and allowed to investigate the phylogenetic relationships with congeners and the patterns of species distribution. A total of 34 sequences were obtained by the mitochondrial COI and 16S (10 and 12 respectively), and the nuclear H3 (12) allowing to confirm nine species directly or indirectly associated to *A. verticillata.* Among them, some revealed rare or very rare with one being reported only twice for the whole Mediterranean basin and here molecularly characterized for the first time. Furthermore, *A. verticillata* confirmed to be an important primary and secondary vector of NIS even if it is noteworthy that most of the associated nudibranchs have an Atlantic/Mediterranean origin, suggesting *A. verticillata* could share the same origin.

SESSIONE PARALLELA SIMPOSIO 2

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IL DELFINO COMUNE DEL MEDITERRANEO: RICOSTRUZIONE DELLA STORIA ECOLOGICA ED EVOLUTIVA ATTRAVERSO I REPERTI OSTEOLOGICI

Il delfino comune (*Delphinus delphis*, Linnaeus, 1785) è una delle specie più enigmatiche del Mar Mediterraneo. Un tempo ampiamente diffusa, alla fine degli anni '60 ha subìto un declino significativo in gran parte del bacino. Le ragioni e i meccanismi alla base di questo declino rimangono in gran parte sconosciuti o poco compresi. Tuttavia, è stata identificata una serie di potenziali cause, tra cui le campagne di abbattimento, la morte accidentale in attrezzi da pesca, la ridotta disponibilità di prede e il degrado dell'habitat. Le stime attuali ottenute da indagini e campagne di monitoraggio suggeriscono la completa assenza o la quasi scomparsa dei delfini comuni dalle aree storicamente note per ospitare popolazioni consistenti. L'Unione Internazionale per la Conservazione della Natura ha designato la sottopopolazione di delfino comune del Mediterraneo come "Endangered".
Abbiamo ricostruito la poco conosciuta storia naturale di questa specie utilizzando reperti museali osteologici degli ultimi due secoli. L'approccio multidisciplinare, che consiste nell'analisi genetica del DNA antico, nella morfometria geometrica dei crani e nell'analisi degli isotopi stabili del collagene, ha permesso di comprendere meglio l'ecologia della popolazione storica di delfino comune del Mediterraneo. I principali risultati della ricerca includono: i) l'approccio integrato molecolare/morfometrico ha permesso di identificare con successo gli esemplari museali a livello specie-specifico e di evidenziare errori di identificazione nelle collezioni museali e nella letteratura storica, i quali rappresentano un *bias* nell'identificazione delle specie di delfini mediterranei e nella conoscenza della loro storia demografica ed ecologica; ii) le analisi genomiche preliminari hanno evidenziato la perdita della diversità genetica di *D. delphis* nel corso degli ultimi decenni; ii) i risultati dell'analisi degli isotopi stabili ($\delta^{13}C$ e $\delta^{15}N$) indicano diversi modelli ecologici e/o trofici del delfino comune mediterraneo nel corso del tempo, suggerendo un possibile spostamento della nicchia ecologica nel corso degli ultimi secoli. In conclusione, i risultati suggeriscono che il declino del delfino comune sia stato innescato da un insieme di fattori di natura antropogenica che hanno portato non solo alla competizione con l'uomo, ma anche a una competizione interspecifica con altre due specie ampiamente diffuse nel Mediterraneo: *Stenella coeruleoalba* e *Tursiops truncatus.*

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UNRAVELING THE IMPACT OF URBANIZATION ON *BOMBUS TERRESTRIS* (LINNAEUS, 1758) THROUGH A MULTI-OMICS APPROACH

Pollinators play a crucial role in maintaining ecosystem functionality and enhancing food security. However, rapid urban expansion is changing their habitat, phenology and behaviour, favouring those species more adaptable to urban environments. In this framework, we investigated the effects of urbanization on *Bombus terrestris* (Linnaeus, 1758), a widely distributed bumblebee in Italian cities, using an integrated multi-omics approach encompassing transcriptomic and metabolomic analyses. This interdisciplinary approach aims at comprehensively evaluate the impact of urban stressors on bumblebee populations and explore potential strategies of adaptation to the urban environments. We conducted a nationwide sampling campaign across four major Italian metropolitan areas: Milan, Rome, Turin, and Florence, and collected approximately 240 specimens across 26 sampling sites varying in the degree of urbanization, ranging from highly urbanized to semi-natural environments. Total RNA and metabolites were extracted from the whole body of specimens and analysed through mRNA sequencing and LC-MS analysis. The first results of our investigation, based on samples from Milan and Turin, revealed significant variation between urban and semi-natural individuals. We identified a pool of genes involved in various biological functions that were differentially expressed in urban individuals compared to their semi-natural counterparts. Additionally, we identified consistent variations in the production of stress-related and adaptive metabolites. For example, urban bumblebees exhibited higher proportions of unsaturated phospholipids, potentially representing an adaptation mechanism to improve cell membrane tolerance to the higher temperatures typical of urban landscapes. The obtained results will contribute to a deeper understanding of how urbanization affects pollinators and inform effective conservation strategies and urban planning policies. By elucidating the molecular responses of *B. terrestris* to urban stressors, our research seeks to provide valuable insights for sustainable urban development and biodiversity conservation.

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USING THERMAL PRIMING TO MITIGATE THE LETHAL EFFECTS OF MARINE HEATWAVES ON THE MANILA CLAM *RUDITAPES PHILIPPINARUM*

Bivalve aquaculture is threatened by extreme events such as marine heatwaves (MHWs). In shellfish farming the scope for contrasting MHWs is limited but heat-priming may be an effective solution. Priming, a plastic response of the phenotype triggered by non-lethal stress, might reduce the impact of a subsequent lethal stress. Here we assessed whether heat-priming Manila clams *Ruditapes philippinarum* at 30 ˚C could increase survival to a lethal MHW two weeks after priming and show long term (> one month) protective effects. Half animals were subjected to priming (Primed, P), while the remaining were kept at normal summer conditions (Naïve, N) for 7 days. After a recovery phase of 15 days, for each group half of the animals were exposed to a simulated HW (Heat wave challenged, H), while the remaining were not (Controls, C), in a 2x2 full factorial design (four groups: PH, PC, NH, NC). Mortality was recorded daily. Immediately after the HW, clam burrowing behaviour was tested, while 15 days after the end of the thermal challenge, the animal antioxidant activity, digestive gland transcriptome and microbiome were evaluated. A higher survival rate in PH clams was found after HW. At behavioural level, 64% of PH clams were able to fully hide in the sand, while only 20% of NH clams did so. At the transcriptomic level we found upregulation of HSPs expression and metabolic pathways in PH clams. Beneficial bacterial taxa were more abundant in PH clams while detrimental families were more abundant in NH clams. Signatures of putative protective changes were evident 38 days after priming in PC clams (primed, but not exposed to HW). Those changes included higher antioxidant activity and upregulation of metabolic pathways. Overall, evidence suggests long-term protective effects of priming and its potential as a mitigation strategy to alleviate the negative consequences of MHW.

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2 Museo delle Civiltà, Roma

CAMBIAMENTI CLIMATICI E VARIAZIONI NELLA DIVERSITÀ GENETICA DELLA TROTA FARIO (*SALMO TRUTTA* COMPLEX) IN ITALIA MERIDIONALE: EVIDENZE DAL DNA ANTICO (aDNA)

L'attuale biodiversità nell'emisfero boreale è stata modellata dalle oscillazioni climatiche avvenute durante il Quaternario (HEWITT, 2000). La trota fario (*Salmo trutta* complex) offre un chiaro esempio dell'impatto dei cambiamenti climatici del passato sulla storia evolutiva delle specie. Infatti, l'alternanza di fasi glaciali/interglaciali ne ha profondamente condizionato il ciclo vitale, influenzando la capacità di migrare verso il mare per scopi trofici (anadromía). Questo fenomeno è stato inferito grazie all'analisi dell'aDNA estratto dalle ossa di 35 individui di *S. trutta* rinvenuti nella “Grotta della Madonna” (Praia a Mare, CS). Tali esemplari, verosimilmente catturati dalle popolazioni umane che abitavano la grotta (DURANTE, 1978), abbracciano una sezione stratigrafica che si estende dal Dryas recente (~12.800-11.600 anni fa) all'inizio dell'Olocene (~9.000 anni fa). L'analisi è stata condotta sequenziando parzialmente la regione di controllo del DNA mitocondriale utilizzando coppie di primer appositamente disegnate. Un totale di 252 individui moderni sono stati campionati in 13 corsi d'acqua di Campania, Basilicata e Calabria allo scopo di confrontare gli aplotipi mitocondriali attuali con quelli risalenti alla transizione Pleistocene/Olocene. Dei campioni antichi, quelli risalenti all'inizio dell'Olocene mostravano un aplotipo appartenente al lignaggio mitocondriale Atlantico (AT) presente in Nordafrica e Sicilia; quelli riferibili al Dryas recente presentavano due aplotipi dei lignaggi Mediterraneo (ME) e Adriatico (AD), rispettivamente. Negli esemplari attuali sono stati osservati 12 aplotipi, dei quali 4 appartenenti al lignaggio AT nordeuropeo (di origine domestica), 2 al lignaggio Mediterraneo e 6 a quello Adriatico, mentre non è stato riscontrato l'aplotipo di origine nordafricana. L'analisi della diversità genetica dei campioni antichi ha evidenziato una netta discontinuità nella composizione aplotipica alla transizione Pleistocene/Olocene. Gli aplotipi dei lignaggi ME e AD, infatti, furono sostituiti da un aplotipo AT di origine nordafricana, verosimilmente giunto sulle coste dell'Italia meridionale grazie a individui anadromi che migrarono verso nord in un contesto di rapidi cambiamenti climatici. Il confronto tra campioni antichi e moderni ha mostrato la probabile scomparsa di questo lignaggio mitocondriale nei corsi d'acqua appenninici e l'ampia diffusione di aplotipi alloctoni (lignaggio AT nordeuropeo) di origine antropogenica.

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COMPARATIVE HEAD MORPHOLOGY IN ADULT OF TIGER BEETLES OF THE GENUS *CALOMERA* BY GEOMETRIC MORPHOMETRICS

Tiger beetles are a group within Adephagans that comprise about 2800 described species. Thanks to their diversity they have worldwide distribution except for Polar Regions and some oceanic islands (PEARSON and VOGLER, 2001; JASKUŁA et al., 2019). The taxonomic position of tiger beetles in suborder Adephaga is not fully clarified and their systematic placement within the Coleoptera remained largely controversial. The morphological features of the head of adult tiger beetles has been shown to be of taxonomic value (VOGLER and PEARSON, 1996; BEUTEL et al., 2020; DURAN and GOUGH, 2020). Tiger beetle head is well-scletorized and have well-differentiated structure with the presence of large bulging eyes that makes it wider than the pronotum. The head is one of the several characters that distinguish tiger beetles from all other groups of Adephaga, especially from the family Carabidae (PEARSON and VOGLER, 2001; ASSMANN et al., 2018). Therefore, given its significance in classification of tiger beetles, it became essential investigate the head of these beetles. In the present study we improved knowledge on the head morphology of adult of three species of tiger beetle: *Calomera fischeri fischeri* (Adams, 1817), *Calomera littoralis mandli* (Mandl, 1967) and *Calomera caucasica* (Adams, 1817), revealed through geometric morphometrics. The landmark coordinates of 90 specimens were used for the head shape analyses. Further analyses of landmark configurations were done by using MophoJ v1.07a. Statistical analysis results by mean centroid sizes revealed that the three species differed in head size and all of them were characterized by sexual dimorphism. Mean centroid size of females were significantly larger than males. We used size-corrected shape variables to assess shape differentiation and canonical variate analysis showed a clear separation among species. There are not significant differences in the head shape variations beetween sexes. Further attention with ecological characteristics testing with geometric morphometrics could give insight to understand morphological divergence of tiger beetle head. In addition, inter- and intraspecific dimorphism of different body traits between different taxa by geometric morphometrics could aid to solve many taxonomic complexities even morphological variations are limited.

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CHEMICAL AND VIBRATIONAL CUES INVOLVED IN THE HOST LOCATION OF *SCLERODERMUS CEREICOLLIS* AND *SCLERODERMUS DOMESTICUS* (HYMENOPTERA: BETHYLIDAE)

Sclerodermus cereicollis Kieffer and *Sclerodermus domesticus* Latreille (Hymenoptera: Bethylidae) are two idiobiont ectoparasitoids of xylophagous beetles, mainly from the families Ptinidae and Cerambycidae. Bethylid species are often employed in biological control programs for managing various xylophagous pests (YANG et al., 2014), but they are also known to cause sting dermatitis in humans (BREWER et al., 2020; PAMPIGLIONE and TRENTINI, 1996). To shed light on the host location of these species, the role of chemical and vibrational cues was investigated. For testing the chemical cues involved in the host location process, a Y-tube olfactometer and a still-air olfactometer were used. The behavioral responses of naïve mated females towards volatile stimuli from the host's microhabitat, i.e. from sawdust of the host's woody plant, and derived from the host, i.e. from frass and larvae, were evaluated. Additionally, the parasitoid responses to non-volatile chemicals from the host larvae were evaluated using an open arena. We categorized these chemical stimuli into three main groups: those from *Trichoferus holosericeus* and *Hylotrupes bajulus* (Coleoptera: Cerambycidae), and those from the factitious host *Corcyra cephalonica* (Lepidoptera: Pyralidae). For vibrational tests, xylophagous larvae of *H. bajulus*, were kept in wooden blocks. In the experiments, two wood blocks - one infested with a larva and one without - were placed in opposite quadrants of a circular arena, and larval vibrations were recorded using a laser vibrometer. Females of both species were found to perceive and respond to a range of volatile and non-volatile chemicals from the host environment, including seasoned wood sawdust, frass from *H. bajulus* and *T. holosericeus*, and cuticular hydrocarbons from larvae of these beetles. Preliminary observations in vibrational bioassays suggest that *S. cereicollis* adults spend more time near the wooden block infested with cerambycid larvae, supporting the hypothesis that they are attracted to the host's vibrational cues.

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IBRIDAZIONE NATURALE ED ANTROPOGENICA, E POTENZIALE ADATTATIVO NEL CARIBÙ (*RANGIFER TARANDUS)* E IN ALTRE SPECIE

In natura, l'ibridazione può rivelarsi un importante fattore evolutivo, ma è stata spesso considerata un problema se di origine antropica. Tuttavia, nuove ricerche mettono in discussione queste rigide distinzioni, e la zoologia e la biologia della conservazione hanno bisogno di linee guida innovative per la gestione delle specie ibride e delle popolazioni in via di ibridazione. Questa presentazione illustra le relazioni tra popolazioni ibridanti e non ibridanti di specie che hanno avuto un impatto notevole sulle strategie di conservazione in Europa (esempio, il lupo, *Canis lupus*) ed in Nord America (esempio, il caribù, *Rangifer tarandus*). Sono presi in considerazione in dettaglio l'uso di strumenti molecolari, morfometrici e computazionali recentemente sviluppati, usando il caribù come modello di studio.

Le preoccupazioni riguardanti l'ibridazione si sono spesso incentrate sulla perdita della "purezza" genetica e dell'adattamento alle condizioni ambientali locali. Tuttavia, in alcuni casi, l'ibridazione tra specie o popolazioni può essere facilitata da processi interamente naturali e/o può creare nuova diversità genetica, e quindi potenziale adattativo, su cui può agire la selezione. Nel Canada occidentale, i cicli glaciali hanno dettato cicli di colonizzazione-estinzione locale-ricolonizzazione delle specie terrestri. Qui documentiamo l'ibridazione di due lignaggi di caribù. Utilizzando genotipi SNP per ~43.000 loci e per ~700 caribù, abbiamo scoperto: (i) come l'ibridazione post-glaciale abbia contribuito alla diversità genetica delle popolazioni in una vasta zona ibrida, (ii) che la selezione favorisce entrambi i lignaggi.

Questo contributo fornisce un messaggio complesso agli zoologi. Le conseguenze dell'ibridazione e dell'introgressione genetica sull'adattamento sono ancora poco conosciute. Di conseguenza, strategie di conservazione efficaci per gli ibridi spesso devono ancora essere definite e implementate. In particolare, rimane controversa la gestione delle popolazioni miste e degli individui che si ibridano per cause antropiche, principalmente mediante incroci con animali domestici conspecifici. Pertanto sono richiesti: (1) ricerca scientifica di casi di studio sull'ibridazione, (2) dibattito su risultati da parte degli zoologi e di tutti gli altri gruppi interessati, e (3) lo sviluppo di procedure di monitoraggio e gestione applicabili nel mondo reale della conservazione, un mondo forse più inclusivo nei confronti degli ibridi.

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INTRA-GUILD COMPETITION AND ECOSYSTEM SERVICES OF MAMMAL SCAVENGERS IN A NEW COLONIZED WOLF LANDSCAPE

Carcass utilization by scavengers is crucial for ecosystem dynamics, influencing energy transfer, nutrient cycling, and disease regulation. Through the provision of unconsumed carcasses, the return of wolves (*Canis lupus*) to European ecosystems can trigger complex cascading effects on scavenger communities.

We investigated the scavenging dynamics of mammalian species in a prey-rich Mediterranean coastal area (San Rossore, Migliarino and Massaciuccoli Regional Park) five km apart from the Pisa city center, where wolves have recently returned. Using camera traps, we monitored the scavenging activity on fallow deer (*Dama dama*) carcasses preyed upon by wolves over a five-year period following the predator's return, and developed models to analyze the temporal patterns in the utilization of carcasses by red foxes (*Vulpes vulpes*), wild boars (*Sus scrofa*), and wolves themselves. The latter exhibited a consumption of only minor portions of prey and a negligible reuse of carcasses, while foxes and wild boars competed for access to this emerging trophic niche. We revealed a notable temporal change in scavenging activity along time, with wild boars emerging as the primary scavenger and providing a substantial removal of carcass biomass.

Our findings underscore the importance of considering scavenger dynamics in the context of apex predator recolonization and highlight the potential implications for ecosystem functioning and disease regulation. Further research is warranted to elucidate the long-term effects of scavenger interactions on community structure and ecosystem services in the face of increasing wolf populations across Europe.

Sabato 14 settembre
ore 15:00 - 16:00

Società Italiana di Protistologia

Comunicazioni in plenaria

coordinatori: Anush Kosakyan, Adriana Vallesi

EWA JOACHIMIAK[1]

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DIVERSITY AND SIMILARITY OF CILIA TIP ACROSS THE EVOLUTION

Cilia are an early invention in eukaryotic evolution, believed to be present in the Last Common Eukaryotic Ancestor. At present, cilia are assembled by organisms from nearly all modern lineages with the exception of some fungi and the majority of seed plants. During the evolution cilia underwent functional specialization giving rise to motile cilia, motile nodal cilia and immotile sensory cilia of different types. Importantly, throughout different eukaryotic lineages, the structure and function of cilia is retained. The main structural component of all types of cilia are microtubules. The presence of additional multiprotein complexes causes formation of the specialized ciliary zones such as a transition zone at the cilium base, a middle segment, containing, depending on cilia type, motor or sensory complexes, and a ciliary tip at cilium distal end.

While the components of the transition zone and middle segment were broadly studied, much less is known about the composition and function of the ciliary tip proteins. The ultrastructural analyses using electron microscopy revealed significant differences in the architecture of the distal tip in sensory and motile cilia. On the other hand, there is some similarity in the composition of ciliary tip in motile cilia assembled by various, evolutionarily distant organisms. Interestingly, few known ciliary tip proteins seem to be common for all types of cilia. In my talk I will summarize current knowledge regarding the structure, protein composition and functions of ciliary tips from different organisms.

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AN ENDOSYMBIOSIS THAT GOT STUCK? OBSERVATIONS OF GENOME EVOLUTION IN THE MIXOTROPHIC CILIATE *MESODINIUM RUBRUM*

Mesodinium rubrum is a distinctive marine microbial eukaryote associated with some of the largest red tides on Earth. *M. rubrum* captures, redistributes and harnesses the plastids, mitochondria and nucleus of the cryptophyte algae *Teleaulax amphioxeia*. We obtained draft somatic (~191 Mbp) and germline (~347 Mbp) genome assemblies for *M. rubrum* using nuclear flow sorting. Remarkably, we could not detect the defining eukaryotic genomic sequence feature — spliceosomal introns — in either genome, nor most of the necessary spliceosomal ncRNAs and proteins. The key proteins for nonsense-mediated decay of aberrantly spliced mRNAs, Upf1, Upf2 and Upf3 also appear absent. In contrast, one kind of non-spliceosomal intron has been retained in *M. rubrum*'s standard tyrosine tRNA genes, as have ribosomal RNA ITS sequences, consistent with known functional roles for both noncoding sequences in other eukaryotes. Furthermore, *M. rubrum*'s germline genome contains thousands of internally eliminated sequences (IESs): intron analogs which are spliced out of DNA during germline to somatic genome development. As far as we are aware, the only other eukaryotic genomes reported without spliceosomal introns are extremely reduced (< 10 Mb), belonging to an intracellular parasite and a vestigial endosymbiont nucleus (nucleomorph). Contrary to the popular notion that alternative splicing is selectively advantageous, observations in the *M. rubrum* lineage fit the idea that no spliceosomal intron provided an appreciable benefit like the non-spliceosomal tyrosine tRNA intron; thus all spliceosomal introns have been lost.

Sabato 14 settembre
ore 16:00 - 18:30

Simposi 1 e 2 SIP

RELAZIONI IN SESSIONI PARALLELE

SESSIONE PARALLELA SIMPOSIO 1-SIP

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INTEGRATIVE TAXONOMY REVEALS MULTIPLE INVASIONS OF THE MEDITERRANEAN SEA BY INDO-PACIFIC *DORVILLEA* (ANNELIDA: DORVILLEIDAE)

Non-indigenous annelids are characterised by a high frequency of taxonomic uncertainties if compared to other marine taxa, which hinder a precise reconstruction of their origin, introduction pathways, and climatic affinities, making predictions on their success of establishment and spread difficult and unreliable. In this study we focused on *Dorvillea similis* (Crossland, 1924), an Indo-Pacific species known in the Mediterranean Sea since at least 2005 and considered a Lessepsian immigrant. Individuals assigned to *D. similis* were sampled in several localities in Italy, Greece, Cyprus and Lebanon, as well as in some localities in the northern and central Red Sea; their characterisation followed an integrative approach, taking into account both morphological characters and two mitochondrial markers.

Molecular data showed that *D. similis* is comprised of at least seven lineages, five of which occur in the Mediterranean Sea. The two most widespread lineages found in the Mediterranean Sea corresponded to individuals sampled in the northern Red Sea and in the Hawaii Islands, respectively, directly confirming their exotic origin. Morphological data showed that live colour pattern is the most reliable character allowing for the distinction of divergent lineages; conversely, jaw apparatus features showed a limited utility, and chaetal features broadly overlapped among different lineages. These results highlight the challenges in the identification and description of *Dorvillea* species based on preserved specimens, that usually lose any trace of the live pigmentation, as well as in the comparison between historical descriptions, mainly based on live material, describing the live appearance, but lacking fine morphological details, and more recent ones, based on fixed material.

This study shows that what was thought to be a single non-indigenous species represents in fact a species complex including several lineages, likely with different geographical origin, and different introduction pathways. Preliminary data on other polychaete groups suggest that similar cases are widespread among non-indigenous marine annelids, stressing the need for further, detailed investigations on their diversity and origin.

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MOLECULAR PHYLOGENY AND SPECIES DELIMITATION REVEAL HIDDEN DIVERSITY WITHIN THE WATER BEETLE SPECIES OF THE *OCHTHEBIUS QUADRICOLLIS* COMPLEX (COLEOPTERA: HYDRAENIDAE) FROM ATLANTIC AND W- PALAEARCTIC MARINE ROCKPOOLS

Species detection and delimitation remains difficult for morphologically similar, hardly distinguishable and in some cases geographically overlapping species, as occurs in members of the Western Palaearctic water beetles of the genus *Ochthebius* Leach, 1815 inhabiting the Mediterranean and east Atlantic supratidal marine rockpools. In this study, we investigate the phylogenetic and biogeographic relationships of the water beetles *Ochthebius quadricollis* species complex (previously known also as the "*Calobius*" subgenus or lineage), using a combination of two mitochondrial markers (cytochrome c oxidase subunit I and 16S ribosomal RNA) and two nuclear fragments (28S ribosomal RNA and a portion of the rudimentary gene CAD). Species delimitation analyses were also performed by combining a distance-based method (ASAP) and two tree-based methods (GMYC and mPTP) to explore cryptic diversity, clarify taxonomy and validate species boundaries. Finally, we used a divergence time estimation to define a timeframe of diversification of distinct clades within this complex. The results of the species delimitation analyses identified thirteen independent lineages, confirm the status of five currently described and recognized species of *Calobius* and well support preliminary identification of additional eight new putative cryptic species. The identified new (or not currently formalized) species are distributed throughout most of the areas included in the overall distribution of this highly specialized group (Macaronesian areas to the Atlantic North Africa, and across the entire Mediterranean Basin). Molecular dating and biogeographic analyses suggest that this univocally monophyletic lineage likely originated in proto-Mediterranean areas (maybe following the tectonically driven Cenozoic closure of the Tethys Ocean) approximately 25 Mya, during the Oligocene/Miocene transition, whereas most of the diversification occurred between 17 and 8 Mya. Overall, our results underline the importance of molecular approaches and the assessment of genetic variation at the areal level for discovering hidden diversity and, in particular, for the taxonomic evaluation of morphologically similar species with partially overlapping ranges.

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LA DIVERSITÀ CROMATICA E MOLECOLARE IN *SCOLOPENDRA CINGULATA*, LATREILLE, 1829, RIVELA EVENTI MULTIPLI DI COLONIZZAZIONE IN SICILIA

La fauna autoctona terrestre siciliana ha colonizzato l'isola in diversi periodi e modalità. Essa deriva in buona parte da colonizzazioni attive via terra dal nord Africa (Miocene e Pliocene) e dalla penisola italiana (Pleistocene). Questo contributo analizza la variazione del gene mitocondriale COI (citocromo-c ossidasi subunità 1) e della livrea del chilopode *Scolopendra cingulata* in Sicilia e Aspromonte (Calabria), con lo scopo di indagare la variabilità della specie nell'area di studio e tracciare possibili eventi di dispersione attraverso lo stretto di Messina.

Per ciascun individuo è stata rilevata la tipologia della livrea, distinguendo un morfotipo chiaro e uno scuro, e sono stati campionati piccoli frammenti di tessuto da cui è stato estratto il DNA e amplificato un frammento di COI di 625 bp. Le sequenze sono state analizzate tramite inferenza bayesiana e i cladi maggiori sono stati utilizzati come gruppi per il confronto *ex post* fra le livree riscontrate.

Sono stati individuati tre cladi: *S/M*, include animali provenienti da Malta e dall'intero territorio siciliano, eccetto l'estremità orientale dei monti Peloritani; *Me*, include animali provenienti dai monti Peloritani orientali; *As*, include i campioni aspromontani. La distanza (*p*-distance) fra i cladi è consistente, variando da 8% (*As vs. Me*) a 11% (*S/M vs. As*; *S/M vs. Me*). Le livree giovanili si allineano con l'assetto filogenetico dei gruppi. Tutti gli individui del clade *"S/M"* posseggono un morfotipo chiaro, mentre quelli dei cladi *Me* e *As* un morfotipo scuro aposematico, con estremità anteriore e posteriore di colore rosso. Anche gli adulti del clade *S/M* hanno un morfotipo chiaro, quelli del clade *Me* un morfotipo scuro, mentre quelli del clade *As* presentano entrambi i morfotipi. Non sono state rilevate popolazioni miste, eccetto in uno dei sei siti campionati presso l'area di transizione putativa fra *S/M* e *Me*, in cui sono stati rinvenuti due giovani appartenenti ai due cladi. In questi individui sintopici si è riscontrata perfetta congruenza tra clade di appartenenza e morfotipo.

La distintività dei tre gruppi indica lunghi tempi di isolamento reciproco ed eventi multipli di dispersione, possibilmente avvenuti durante le connessioni legate alle fluttuazioni eustatiche del Mar Mediterraneo. Meritano ulteriori verifiche il flusso genico fra i cladi *S/M* e *Me*, in continuità territoriale ma solo marginalmente sintopici, così come i processi che hanno determinato la divergenza cromatica fra i gruppi.

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LA PRESENZA DI *PSEUDORCA CRASSIDENS* (ODONTOCETI, DELPHINIDAE) IN MEDITERRANEO VALUTATA TRAMITE ANALISI GENETICA DI CAMPIONI MUSEALI E MODERNI

La pseudorca (*Pseudorca crassidens*, Owen 1846) è un cetaceo odontoceto appartenente alla famiglia Delphinidae. Le pseudorche sono distribuite nelle acque tropicali e temperato calde di tutti gli oceani, con una predilezione per le acque oceaniche profonde, comportamento che ne rende difficile l'osservazione e lo studio in natura (BAIRD, 2009). A livello globale la specie è classificata come "prossima alla minaccia", ma le conoscenze che si hanno su di essa provengono principalmente dallo studio di poche popolazioni residenti dell'Oceano Pacifico mentre in altre aree, come l'Oceano Atlantico, la specie è molto rara e le informazioni limitate (BAIRD, 2018). La pseudorca è attualmente considerata "visitatore occasionale" nel Mediterraneo, anche se una revisione del suo status è stata suggerita perché si hanno evidenze della sua presenza fin da tempi storici e, di recente, si è registrato un aumento delle segnalazioni di gruppi comprendenti anche giovani e neonati (ACCOBAMS, 2021; CALOGERO *et al.*, 2021). In questo studio, al fine di chiarire l'origine e lo status di conservazione delle pseudorche che frequentano il Mediterraneo, sono state eseguite analisi genetiche su individui museali e moderni di provenienza nota. Il DNA genomico è stato estratto utilizzando protocolli specifici e la regione di controllo del DNA mitocondriale (mtDNA CR) amplificata mediante coppie di primer appositamente disegnate. Le sequenze ottenute sono state allineate e confrontate con quelle descritte finora per la specie a livello globale (MARTIEN *et al.*, 2014; PALMER *et al.*, 2023) e le relazioni evolutive tra gli aplotipi e le aree geografiche di provenienza sono state evidenziate tramite costruzione di un network aplotipico. Le analisi genetiche hanno evidenziato l'appartenenza del campione moderno (neonata spiaggiatasi in Calabria nel 2019) ad un aplotipo diffuso nell'Australia settentrionale mentre tutti i campioni museali, datati tra il 1868 e il 1989, mostrano un unico nuovo aplotipo geneticamente affine a quelli dell'Atlantico occidentale. Il nuovo aplotipo che caratterizza tutti gli individui museali di pseudorca suggerirebbe che in passato il Mediterraneo fosse abitato da una popolazione residente di questa specie, oppure che individui da una popolazione atlantica entrassero attraverso lo stretto di Gibilterra. Il ritrovamento di un aplotipo australiano nel campione moderno analizzato supporterebbe invece l'ipotesi di una recente migrazione lessepsiana.

SESSIONE PARALLELA SIMPOSIO 2-SIP

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SYMBIOSES BETWEEN PROKARYOTES AND CILIATES IN THE NATURAL ENVIRONMENT: DISTRIBUTION, PATTERNS, AND GLIMPSES INTO EVOLUTIONARY DYNAMICS

Associations between protist and bacteria are extremely common, yet largely unknown. Among them, the *Euplotes* spp.-bacteria symbioses emerged as models for interactions between prokaryotes and eukaryotes, and a great amount of data is now available on this system. A group of *Euplotes* species is dependent from essential symbionts and many different accessory symbionts can be additionally hosted by these ciliates, too. The relationship between *Euplotes* and its essential symbionts challenged the consolidated view of obligate symbioses as permanent associations: phylogenomics showed that this is an ancient symbiosis for the host, but permanent integration of the essential symbionts never occurs. Most studies on the symbionts of *Euplotes* and other ciliates concern laboratory cultures. Therefore, as for most known microbial symbioses, information on natural populations is almost completely lacking. Here we describe the first survey of bacterial symbionts in natural populations of a ciliate (*Euplotes*), using a single-cell microbiomic approach. Obtained results reveal an unexpected variability, with different individual ciliates within the same population harboring very different sets of accessory bacterial endosymbionts. In some cases, co-occurring *Euplotes* can even harbor different essential symbionts, *Polynucleobacter* and "*Candidatus* Protistobacter". This finding suggests that replacement events could be more frequent in nature than previously hypothesized. Moreover, some specific association patterns were detected between host and symbiont species (e.g. affinity between "*Ca.* Bandiella" and *E. woodruffi*) and between different accessory symbionts (e.g. mutual exclusion between "*Ca*. Cyrtobacter" and "*Ca*. Anadelfobacter"). Overall, we assess the prevalence and patterns of bacterial symbionts in natural populations of *Euplotes* and show more diversity in natural populations than is reflected by lab cultures. Finally, findings on essential symbionts' distribution open new scenarios for small-scale evolutionary dynamics of these associations.

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PREDATOR-PREY INTERACTION BETWEEN THE FRESHWATER CILIATED PROTIST *COLEPS HIRTUS* AND THE MICROTURBELLARIAN FLATWORM *STENOSTOMUM SPHAGNETORUM*

It is known that the catenulid microturbellarian *Stenostomum sphagnetorum* can defend itself against predators by extruding mucous material from its secretory glands. In this study, we investigated the nature of this secretion and evaluated the efficiency of this defensive mechanism against the predatory ciliate *Coleps hirtus*. The ciliate attacks the flatworm using a mix of toxic free fatty acids contained in its offensive organelles, called toxicysts. Our results show that the glandular secretion of the flatworm is mainly composed of mucopolysaccharides, and effectively defends *Stenostomum* from *Coleps* attacks. Specifically, *Stenostomum* treated with lysozyme, which induces the discharge of glandular secretions without harming the organisms, are more vulnerable to *Coleps* attacks than untreated specimens. Additionally, lysozyme-treated *Stenostomum* are significantly more sensitive to the toxic predator's discharge and to the five fatty acids most represented in the toxic discharge. In conclusion, the glandular secretion of *Stenostomum* defends the organism through physical and chemical mechanisms. In fact, the discharge of the mucus material separates the prey from the predator, halting the attack while the prey escapes, and in addition significantly reducing the efficiency of the predator's toxic discharge.

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UNDERSTANDING ECOLOGICAL ADAPTATION IN THE CILIATE *TETRAHYMENA PYRIFORMIS* THROUGH THE LENS OF ENERGY ALLOCATION

To survive and reproduce, living organisms need to maintain an efficient balance between energy intake and energy expenditure. When the environment changes, a previously efficient energy allocation strategy may become inefficient in the new environment, and organisms are required to adapt to the new environment by changing their morphology, physiology, and behaviour. However, how multiple organism traits interact with each other and with the characteristics of the environment to determine energy allocation is poorly understood. To address this knowledge gap, we adapted axenic populations of the ciliate *Tetrahymena pyriformis* to different environmental conditions of temperature and resource levels, and measured population growth, metabolic rate, cell size, and movement speed. On a very short time scale, movement speed and metabolic rate increased with environmental temperature in a way that could be predicted from simple physical scaling relations such as the Boltzmann-Arrhenius equation and the `viscous drag' impacting movement. However, soon after the introduction of *Tetrahymena* into a novel environment, all measured quantities were further modulated in a direction that likely provided higher biomass production in the new environment. Changes in cell size played a central role in mediating these adaptations, by simultaneously affecting multiple phenotypic traits, such as metabolic rate and the energetic costs of movement, and happening over timescales that – in a small organism like Tetrahymena – are rapid, relative to the timescales of ecological changes and seasonal environmental fluctuations.

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SYSTEMATIC REVIEW OF GENUS *LACRYMARIA* WITH MORPHOLOGY-BASED IDENTIFICATION KEY

The ciliate genera *Lacrymaria* Bory de St. Vincent, 1824 and *Phialina* Bory de St. Vincent, 1824 have a long and complex taxonomic history, which includes genus *Phialina* being merged into *Lacrymaria* by Alfred Kahl (1930) and separated again by Wilhelm Foissner (1983) on the basis of various morphological features (the discriminant currently being the presence or absence of a contractile neck). Now it might be the time to merge them again as molecular studies show them to be non-monophyletic separately but monophyletic collectively (RAJTER *et al*., 2019; ALLIEVI *et al.*, in preparation). These genera include a great number of morphologically diverse species many of which have been observed and/or described rarely or just once. This study takes the form of an extensive bibliographical research and compilation, with a fourfold aim: 1) systematically collect and re-assess all descriptions of species ever published under either generic name, and point out opportunities for lumping and splitting in future studies; 2) propose to re-assign all species of current genus *Phialina* to *Lacrymaria*; 3) summarize the taxonomic history of this genus; 4) provide an extensive morphology-based guide to the identification of all *Lacrymaria* species, as well as make available the original description of each in the original authors' own words.

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MULTIDISCIPLINARY DESCRIPTION OF A NEW SPECIES OF CILIATE, *FRONTONIA MODERATA* SP. NOV. (CILIOPHORA, OLIGOHYMENOPHOREA) FROM ITALY AND SOUTH AFRICA

Among Oligohymenophorea (Ciliophora, Alveolata) the subclass Peniculia stands as one of the most well-known groups. *Frontonia* is the largest genus of Peniculia, and its representatives are spread in any type of water bodies as well as in soil. At a first glance, *Frontonia* species exhibit an overall similar morphology, and form a well-recognizable taxon of ciliates. Despite the general morphological homogeneity, the phylogenetic analysis based on the 18S rDNA sequencing showed that *Frontonia* is a non-monophyletic group. In the present work, we provide the description of a new species *Frontonia moderata* sp. nov. newly found in Italy and South Africa, presenting its multidisciplinary description.

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TRANSCRIPTOMIC RESPONSE TO URBANIZATION IN TWO WILD BEE SPECIES, *BOMBUS PASCUORUM* (SCOPOLI, 1763) AND *OSMIA CORNUTA* (LATREILLE, 1805)

Land use change, habitat loss, and habitat fragmentation associated with urbanization significantly impact biological and functional diversity of wildlife globally. Notably, wild bees are experiencing a decline in their diversity, abundance, trophic interactions, and phenology due to the increase of impervious surfaces, and subsequent decrease of green areas extent and connectivity. Nevertheless, some of these important pollinators still find suitable habitats in highly urbanized environments. However, the possible adaptive mechanisms allowing them to survive in such environments and the effects of urbanization on their biological functions remain largely unexplored.

In this study, we investigated the transcriptomic responses to urbanization of two bee species with contrasting social behaviors: the eusocial bumblebee *Bombus pascuorum* (Scopoli, 1763) and the solitary mason bee *Osmia cornuta* (Latreille, 1805), by comparing populations living in urban areas and in semi-natural sites in the metropolitan city of Milan, Italy. Specimens were collected from areas with varying degrees of urbanization, ranging from highly urbanized to semi-natural areas. Total RNA was extracted from whole organisms and mRNA was sequenced to obtain detailed transcriptomic profiles for each specimen.

The obtained results revealed significant differences between urban and semi-natural populations for both species. While most genes were co-expressed in both environments, distinct sets of transcripts were exclusive to either urban or semi-natural treatments. Differential gene expression analyses revealed a substantial number of genes up- or down-regulated in urban specimens compared to the semi-natural ones, with more pronounced changes observed in *O. cornuta*. Enrichment analysis of differentially expressed genes revealed multiple biological functions and pathways affected by urbanization, also showing species-specific differences.

Overall, our results shed light on the effects of urbanization on the transcriptome of wild bees, revealing differences between urban and semi-natural populations and between species with different social behaviors. These results lay the ground for further, currently ongoing, analyses, including a broader sampling effort and the integration of other ‘omics’ technologies, such as genomics and metabolomics, to comprehensively characterize how wild populations respond and adapt to urban-related stressors.

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HONEY BEE PATHOGENS: WHO WINS IN THE CITY? URBANISATION AFFECTS PATHOGEN TRANSMISSION TO WILD BEES AND WASPS

A wide spectrum of pathogens often infects honey bees, and it is common to observe interspecific transmission of microorganisms to wild bees and wasps. Since these insects provide important ecosystem services but their health status is threatened by anthropogenic land-use changes, studying how pathogen load vary across land-use gradients is relevant. Here, the presence and abundance of 10 honey bee pathogens were evaluated in the bees *Anthophora plumipes* (males), *Halictus scabiosae* (females), *Osmia cornuta* (females), and the wasp *Polistes dominula* (females) across a gradient of urbanisation (described by temperature and green areas fragmentation) in the metropolitan area of Milan (Northern Italy). Overall, pathogen profile was significantly different between the four studied species. When analysing the presence and abundance of individual pathogens, some common trends emerged. The presence of *Apicystis bombi* (Apicomplexa) increased in more fragmented (urban) areas for *A. plumipes*, *O. cornuta* and *P. dominula*. However, urban areas seemed to overall reduce the presence and abundance of the other pathogens. For example, hotter (urban) areas reduced the presence of the deformed wing virus (DWV) and the microsporidia *Nosema ceranae* in *O. cornuta.* Hotter and more fragmented (urban) areas also reduced the abundance of acute bee paralysis virus (ABPV) in *A. plumipes* and DWV in *A. plumipes* and *O. cornuta*. Hence, these study shows for the first time that urbanisation influences pathogen load in the analysed bee and wasp species. The higher presence of *A. bombi* in more fragmented (urban) areas may be find a possible explanation for the higher chance of spillover from high-density bee populations in small green patches, possibly through scattered patches of flowers. On the other hand, the higher temperatures that characterise more urban areas may inactivate pathogens, reducing their presence. Overall, the inherent characteristics of cities may shape the pathogen load of wild bees and wasps, adding a new but still poorly understood layer to the impact of urbanisation on these insects.

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DIETARY PROTEIN: CARBOHYDRATE RATIO MODULATES THE IMMUNE RESPONSE IN BLACK SOLDIER FLY LARVAE

The larvae of black soldier fly (BSF), *Hermetia illucens*, are increasingly recognized as a valuable source of protein and fat for animal feed production. However, their rearing on decaying organic material exposes them to diverse microorganisms, which can potentially compromise the quality of insect-derived products. Therefore, enhancing the immune system of BSF larvae is crucial for ensuring the safety and quality of BSF-based biorefining products. This study investigates how varying the dietary protein-to-carbohydrate (P:C) ratio impacts the immune response of BSF larvae when exposed to Gram-negative and Gram-positive bacteria.

Larvae reared on diets with varying P:C ratio were challenged with a bacterial mixture of *Escherichia coli* and *Micrococcus luteus*, and their immune response was assessed by evaluating markers associated with the cellular (haemocyte number and phagocytosis) and humoral (lysozyme activity and antimicrobial peptide expression) branches of the immune system. Our findings revealed significant differences between the diets, with larvae reared on a high P:C ratio diet demonstrating superior performance. In particular, the levels of cellular markers and the antimicrobial peptide expression were significantly higher in larvae reared on the protein-rich substrate. These results indicate that the nutritional composition of the rearing substrate significantly impacts on the immune response of BSF larvae and contribute to our understanding of optimal dietary parameters for BSF rearing, aiming to balance larval growth with improved resistance to bacterial infections.

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