IB 23

4th SIB Conference on ISLAND BIOLOGY
Lipari 2 - 7 July 2023

ISBN 978-88-97603-42-9

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€ 30

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Ecological and Evolutionary Processes on Real and Habitat Islands

BOOK OF ABSTRACTS

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(2-7 July 2023, Lipari, Italy)

Edited by

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How you can cite this book:
Fattorini S. (ed.), 2023. *Island Biology 2023. Evolutionary and Ecological Processes on Real and Habitat Islands. Book of Abstracts. 4th Conference of the Society of Island Biology (2-7 July 2023, Lipari, Italy).* Associazione Nesos & Edizioni Danaus, Lipari, xxiv+121 pp.

ISBN: 978-88-97603-42-9

9 788897 603429

Associazione Nesos
Via Vittorio Emanuele, 24 – 98055 Lipari, Italy
www.nesos.org
Edizioni Danaus
Via Vincenzo Di Marco, 43 – 90143 Palermo, Italy
www.edizionidanaus.com

Island Biology 2023: Ecological and Evolutionary Processes on Real and Habitat Islands

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(2-7 July 2023, Lipari, Italy)

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The conference is organised by Associazione Nesos under the patronage of the Municipality of Lipari and with the collaboration of Parco Archeologico delle Isole Eolie and Federalberghi Isole Eolie.

CONTENTS

FOREWORD

The present volume collects the abstracts of four plenary talks, 141 contributed talks and 58 posters presented at the 4th Conference of the Society of Island Biology, entitled *Island Biology 2023: Ecological and Evolutionary Processes on Real and Habitat Islands* (2-7 July 2023, Lipari, Italy).

The four plenary talks are focused on some new perspectives in island biogeography, ecology, conservation, and evolution. By using examples from both simulations and real-world systems, Strona discusses how (and where) network thinking can improve our understanding of ecological patterns and processes in island biology. Beierkuhnlein illustrates how both physical and biological processes interplay in the evolution of endemics, leading to an Endemism-Ecosystem Area Relationship when biotic interactions such as competition are prominent and disturbances are low. Llorente-Culebras et al. illustrate how the extinction of threatened species changes functional diversity on islands. Using examples stemming from long-term datasets of fossil pollen, charcoal, and tephra records from world islands, Nogué et al. discuss how and why island biodiversity changed following human settlement.

Contributed talks (T) and posters (P) are organised into four sections, which reflect the complexity and variety of the issues addressed. All these contributions, presented by scientists from all over the world, form an exciting picture of the most vital and intriguing areas of research in island biology.

The section *Island Biogeography and Macroecology* includes 55 talks and 12 posters, which deal with the biogeographical and macroecological characteristics of isolated systems. Various contributions presented in this section investigate **island biogeographical patterns and processes from historical perspectives**, with reference to palaeogeographical and palaeoecological scenarios. Alsos et al. (T) illustrate new perspectives offered by ancient sedimentary DNA in reconstructing long-term ecosystem changes. De Groeve et al. (T) present a streamlined workflow to quantify the responses of islands to past and future sea level fluctuations. Foufopoulos et al. (T) discuss the role of island fragmentation and climate warming on the extinction of reptile populations on Mediterranean islands. Vidal-Hosteng et al. (T) show how the geo-environmental dynamics within an archipelago shape phylogenies. Santos-Rivilla et al. (P) investigate the origin of the disjunction (East Asia vs Western Europe and Macaronesia) of Woodwardioideae ferns. Schifani & Alicata (T) summarise the historical biogeography of the ants of Sicily. **Colonisation patterns and mechanisms**, and their role in driving the structure and evolution of island biotas, are the object of various works. Gíslason & Pálsson (T) illustrate trichopteran colonisation pathways for Iceland. Gómez-Zurita et al. (T) illustrate the importance of long-distance dispersal in South Pacific leaf beetles. Hébert et al. (T) explain how the source pool diversity has a strong influence on the composition of insular mammal assemblages worldwide. Nichols et al. (T) illustrate the crucial role of host dispersal and colonisation in shaping parasite assemblages on islands. Walentowitz et al. (T) reconstruct palaeoecological trajectories of island colonisation by non-native plants. Clegg et al. (T) report the hybridisation between two birds, an ancient island endemic and a recent colonist that did not compromise the integrity of the native species. Costa et al. (T) investigate the influence of colonisation origins (endemic, native non-endemic, and introduced) on the vertical stratification of spiders on Macaronesian islands, while Aguado-Lara et al. (P) present a study on the origin of the flora of sub-Antarctic archipelagos. The importance of considering **functional aspects in island biology** is stressed by a number of contributions. The functional diversity of the Canary flora is discussed by Barajas Barbosa et al. (T) and Irl & Hanz (T). García-Verdugo et al. (T) illustrate how phylogeographic information can inform functional trait analyses. Schrader et al. (T) present an equilibrium model for plant traits on islands. Petrocelli et al. (P) evaluate the performance of different imputation methods to deal with the lack of data for plant traits in island floras. Chen & Wang (T) explore the mechanisms that regulate functional and phylogenetic nestedness. Four contributions deal specifically with bird functional diversity. Heinen et al. (T) reveal how introductions led to taxonomic and functional homogenisations in plant-frugivore communities worldwide. Kalusche et al. (T) illustrate how the study of functional diversity can provide new information on the climatic drivers of assemblage-level changes in species abundances. Matthews et al. (T) present a study on the loss of avian functional diversity on islands worldwide, and Sayol et al. (T) identified the most important drivers which made some bird species more prone to extinction. In the era of big data, there is an increasing interest in assembling and using **large**

databases for biogeographical studies, and this is shown by various contributions presented in this section. By analysing data from 1,254 islands, Cardoso et al. (T) highlight how the increasing expansion of urban areas and agriculture may determine the imminent extinction of endangered birds on oceanic islands. Pasta et al. (T) present a comprehensive database on the flora of the Aeolian Islands. Santi et al. (T) present a comprehensive dataset of climatic, geographic, geo-topographic, and anthropic variables for 2,545 Mediterranean islands. Schrader et al. (T) illustrate a publicly available checklist of plant species for a global evaluation of endemicity patterns on islands worldwide. Using a global database, Steibl & Russell (T) show how the high natural disturbance regimes of atolls act as an important filtering mechanism in species assemblages on these islets. Weigelt et al. (T) illustrate how the Global Inventory of Floras and Traits can be used for island research. Pascucci et al. (P) present a database reporting the occurrence of native and invasive species on Italian small islands. The study of **radiation patterns and processes** is a classic theme of island biogeography, and it is the subject of many contributions in this section. Brée & Rigal (T) show the importance of the island geo-environmental dynamics in determining radiations patterns. Dimitriou et al. (T) focus on the importance of investigating intra-island diversification patterns. Reynolds (T) presents a study on the evolution of West Indian Boas. Si et al. (T) explore the joint effects of adaptive radiation and dispersal filtering in shaping island mammal assemblages. Fernández et al. (P) investigate the evolution patterns in a fern genus with a giant genome. Estandia et al. (T) present a study in which they identify loci highly associated with morphological variation in bird populations that are exemplifications of island rules. Roeble et al. (T) illustrate the diversification of Asteraceae on islands worldwide, while Abe et al. (P) review the evolutionary history of *Camellia* section in Japan. Lizards are known to be subject to rapid evolution on islands, and Gallozzi et al. (T) illustrate the existence of a new ancient insular clade in the Italian wall lizard *Podarcis siculus* in the Tuscan Archipelago, whereas Maselli et al (P) present a study on the speed of evolution in a melanic insular lizard population. **Methodological advancements** (both theoretical and practical) are the focus of various contributions. Wang et al. (T) propose an integrative model that combines the small-island effect and nestedness patterns. Dehayem Nanwou et al. (T) provide indications to improve sample strategies for community-level phylogenetic analyses in island biogeography. Benavides et al. (P) discuss important issues in the applications of species distribution models to island species, and Patiño et al. (P) illustrate the importance of using fine resolution climate datasets in species distribution modelling in topographically complex oceanic archipelagos. Fedele & Bertorelle (T) present a portable and cost-effective laboratory system for in-field DNA metabarcoding analysis, and Spagnuolo et al. (T) illustrate the possibilities offered by a permanent laboratory on the island of the Panarea for investigations on carbon dioxide geological storage. Finally, D'Alessandro et al. (P) present a study on the possible role of a sea snail as a bioindicator of metals in hydrothermal vents. The importance of taking into account **ecological relationships** in explaining biogeographical patterns is illustrated by: Lussu et al. (T), with a study on the influence of pollination syndromes on the species-area relationship of orchids growing on small Mediterranean islands; Petanidou (T), with an investigation on the biogeography of plant-pollinator networks on the Aegean islands; and Takahashi et al. (P), with a study on the role of deer herbivory in the evolution of dwarfism in endemic plants on a continental island in Japan. Island biology is not limited to true islands but may involve any type of isolated environment. In this section, some contributions deal with **habitat islands**. Eibes et al. (T, P) present two contributions on the flora of quartz islands in western South Africa. Itescu et al. (T) discuss if gulls in urban environments have island syndromes. Zelený & Sekerková (T) identify the extinction of rare species on smaller islands as the key mechanism behind the species-area relationship on acidophilous habitat patches. Finally, Castillo-Chora et al. (T) apply island biology principles to explain avian diversity in a mainland, isolated area (the Peninsula of Yucatan). Islands are extremely useful places to investigate macroecological patterns like changes in **biodiversity along latitudinal and elevational gradients**. Delavaux et al. (T) discuss the latitudinal diversity gradient for vascular plants on oceanic islands; Vetaas & K. Bhatta (T) use islands to test the importance of water-energy dynamics, production, and null models in explaining how plant richness varies with elevation; Craven et al. (T) investigate the effects of the number of individuals, species abundance distribution, and spatial aggregation on local diversity along elevation gradients on Pacific islands. Various contributions present overviews of the **biogeography of different archipelagos**. Two contributions deal with the biogeography of Greek islands: Lampou et al. (T) discuss the freshwater macroinvertebrates in the Aegean Archipelago, whereas Panitsa et al. (P) analyse biogeographical and diversity patterns in the flora of the

Aegean and Ionian archipelagos. Blaya et al. (T) present a study on the ants of small islands around Corsica, whereas Hobohm (T) discusses the influence of climate and land use change on the conservation of the Wadden Sea Islands. Jourdan et al. (T) present an overview of the levels of endemism and biogeographical connections of New Caledonia, the world's oldest oceanic island. Finally, the interest in **marine biogeography** is testified by three contributions dealing with marine organisms. Alves et al. (T) and Baptista et al (T) explain how the genetic structure of marine invertebrates reveals colonisation patterns and ecological differentiations in the Macaronesian region, while Sinigaglia et al. (T) describe biogeographic patterns of marine bivalves in oceanic islands of the Atlantic Ocean.

The section *Conservation on Islands* includes 35 talks and 16 posters, which discuss both theoretical and practical aspects of biological conservation on islands. One of the most important drivers of extinction risk in island ecosystems is represented by **invasive species**, and many communications deal with this issue from a variety of viewpoints. Arjona et al. (T) integrate both phylogenetic and functional approaches to explicitly assess the invasive potential of insular alien species. DeVore et al (T) discuss the impacts of an invasive ant on the seabirds and terrestrial crabs of a Polynesian atoll. Helmer et al. (T) illustrate how an extreme weather event may induce a fast-growing non-native tree to overtake the island-wide biomass of the most common group of native tree species. Holthuijzen et al. (T) investigate the diet of the introduced house mouse (*Mus musculus*) on a small, subtropical island, and the implications for mouse eradication. Jourdan et al. (T) present a comprehensive study on the presence of alien species in New Caledonia, illustrating how the invasion is facilitated by taxonomic disharmonies in the native fauna. Lapiedra (T) illustrates how predator invasions on islands alter not only the biology and population dynamics of their prey species but also the structure and stability of their ecosystems. Mairal et al. (T) explain how the interplay between multiple introductions and convergent reproductive strategies drives genetic diversity and structure in the annual bluegrass, the most invasive plant in the Sub-Antarctic. Rocamora et al. (T) present a review of recent achievements, currently planned operations, key limiting factors, and future prospects for rodent and cat eradication projects in the Western Indian Ocean. Russo et al. (T) discuss the impacts of the hala scale on native hala forests in the Hawaiian Islands. Spatz et al. (T) present a review of global trends in invasive vertebrate eradication actions and the associated conservation gains. Tsafack et al. (T) propose a novel approach to assess the biotic integrity of native forests using indices that consider the richness and abundance of endemic, native non-endemic, and introduced arthropods, whereas Oyarzabal et al. (P) present a project aimed at uncovering the patterns and drivers behind the extinction and invasiveness risk of arthropods in the Macaronesian archipelagos. Zhu et al. (T) demonstrate that the impact of plant invasion is context-dependent, and that generalist native frugivores with high dispersal potential may accelerate plant invasion in fragmented landscapes. Morente-López et al. (P) illustrate how functional relatedness between exotic species and native communities, together with species richness, play a role in invasion success in the Canary Islands. Pimentel & Elias (P) present the results of a 10-year study on the effect of removal of the invasive plant *Pittosporum undulatum* in experimental plots in the Azores. Various contributions discuss conservation issues from **landscape ecology** perspectives, with emphasis on how species use different habitats and the increasing role of remote sensing approaches. Nóbrega et al. (T) describe the landscape ecology, trophic interactions, and phylogeny of the threatened Madeira pipistrelle in Porto Santo Island. Price et al. (T) illustrate how combining individual species models makes it possible to obtain native community distribution models useful to assess habitat quality, define specific ecological restoration objectives, and identify sites that might be prone to be colonised by invasive species. A.S. Fernandes et al. (P) and A.C. Fernandes et al. (P) describe the influence of habitat types in the distribution and activity patterns of insectivorous bats of São Tomé Island. Kapralova et al. (P) present a standardised approach to detect salmonid spawning habitats. Nóbrega et al. (P) illustrate the idiosyncratic responses of birds to habitat type in Madeira. Ros-Prieto et al. (P) show that arthropod diversity and abundance have higher values in native forests than in pasture hedgerows in Pico Island (Azores). The importance of the use of remote sensing approaches is shown by Rocha et al. (T), who illustrate the power of remote-sensing technologies to investigate the spatiotemporal dynamics of insular vertebrates and their interspecific interactions. The effects of **isolation in non-island environments** are addressed in contributions dealing with the bryophyte communities in caves and outside habitats in Terceira Island (Azores) (Gabriel et al., T); the use of species distribution modelling to identify habitat islands suitable for narrow endemic climate relicts (Gristina et al., T); and the diversity patterns and conservation status of plant species associated with Greek cliffs

(Kontopanou & Panitsa, P). Two contributions present projects involving ***ex situ* interventions**. Blandino et al. (T) present *ex situ* projects (based on the application of germination and cultivation protocols) for the reinforcement of extant populations or for their reintroduction in island sites where they went extinct, whereas Lo Cascio et al. (P) illustrate a conservation project for the Aeolian wall lizard in which new-born individuals obtained during a captive breeding program will be released in nature. The importance of **long-term research projects** is illustrated by Borges (T), who presents the main results obtained during 20 years of arthropod sampling in the Azorean native forests by using sea, land, and air Malaise (SLAM) traps, and by Kreiling & Hansen (T), who offer an overview of the sampling methods and results obtained in a long-term species inventory program in Koltur (Faroe Islands). Assessing **conservation status** and **levels of protection** of populations, species, habitats, and ecosystems is of paramount importance, as exemplified by the variety of cases illustrated by several studies presented in this section. Órfão et al. (P) illustrate a conservation study on the European eel (the only native freshwater fish) in Madeira. Valli et al. (P) evaluate the conservation biology of three threatened *Limonium* species endemic to the Ionian Islands. Wiemers et al. (T) present the results of a study to assess the conservation status of Madeira's threatened endemic butterflies. Russo et al. (T) examine the conservation status of bat populations in European islands and (P) the conservation efforts to protect bats on the island of Pantelleria. In two contributions, de Lima (T, P) illustrate how increasing knowledge may change the assessment of conservation priorities (red-listing and reserve networks) in the São Tomé and Príncipe islands. Kunttu (T) presents the red-list assessment of coastal habitat types in Finland (including the Finnish archipelago). Testolin et al. (T) present an overview of the proportion of land enjoining some form of protection in the Mediterranean islands, which appears very far from European Union targets. Unfortunately, this reflects a more general failure to meet targets proposed to reduce biodiversity loss, but new opportunities are emerging, like those offered by the global implementation of biodiversity markets, as illustrated by Field (T). The identification of species traits and environmental factors that increase species **vulnerability** is of paramount importance for understanding extinction processes and assessing conservation priorities. This is illustrated by a study on the correlation between extinction vulnerability and species traits in amphibians on oceanic land-bridge islands (Chen & Wang, T) and a study on the factors influencing the population dynamics of an island threatened endemic plant on La Palma (Canary Islands) (Matthies & Kienberg, T). The importance of considering the complexity of **interspecific interactions** in biological conservation is clearly exemplified by two studies presented at this conference. Taylor et al. (T) illustrate a study on the influence of mycorrhizal fungi on orchid distributions in the Canary Islands which underscores the importance of mycorrhizal availability for specialist orchids and emphasises the urgent need to integrate plant-fungi interactions into conservation programs. However, documenting interspecific interactions (like those between plants and pollinators) through direct observations can be time-consuming and expensive, particularly on remote islands. As a practical tool to survey plant-pollinator interactions, Serra et al. (T) illustrate a novel approach based on automatic cameras and deep learning algorithms. Island biotas experienced the highest **extinction** rates, with dramatic consequences for biodiversity conservation. Lomolino et al. (T) review the impacts of humanity on the evolution, diversity, distinctiveness, and extinction of insular vertebrates. Michielsen et al. (T) measured how long it would take to restore Madagascar's mammalian biodiversity, leading to the conclusion that an extinction wave with a deep evolutionary impact is imminent in Madagascar unless immediate conservation actions are taken. Finally, three contributions in this section focus on the sustainability of marine areas. Gomez et al. (T) describe the unsustainability of artisanal fishery inside a UNESCO Marine Protected Area in Coiba National Park (Panama). Using São Tomé and Príncipe as a case study, Nuno et al. (T) illustrate an approach where marine spatial planning was employed as an operational framework for a marine protected areas-establishment initiative for sustainable small-scale fisheries. Nuno et al. (P) also present a project to gain behavioural insights on the non-compliance among fishers and deterrence effects in marine protected areas of the British Indian Ocean Territory.

The section *Humans and Islands* collects six talks and three posters dealing with the multiple relationships between people and island ecosystems. Many island ecosystems have been profoundly shaped by the **influence of human presence through time,** and hence reconstructing the past human presence and the cultural drivers of ecological changes in island ecosystems is crucial to understand their current biotas. Brown et al. (T) reconstruct the chronology, functions, and palaeobiology of agricultural terraces in Mediterranean islands. de Nascimento et al. (T) reconstruct past vegetation, fire regimes, the presence of introduced herbivores, and other local environmental conditions for arid sites on the Canary Islands, showing the occurrence of woodlands in nearby areas that are no longer present. Schouten & Borregaard (P) present a detailed reconstruction of the land-cover, degradation, and invasion histories of Mauritius and Reunion. Because of the many constraints imposed by insularity, past human societies developed peculiar adaptations to the limited insular environments. Speciale et al. (T) present an analysis of plant and animal remains from two central Mediterranean small islands that illustrate the adaptations in the human communities that occupied them. Lakes are frequently considered habitat islands threatened by the human presence in the surrounding matrix. Hammoud et al. (T) present a study on the communities of trematode parasites in crater lakes in western Uganda along a gradient of anthropogenic disturbance, suggesting that agricultural land conversion could lead to increased parasite transmission, thereby impacting aquatic and terrestrial ecosystem health. Because of anthropogenic causes, islands are experiencing a disproportionate loss of species, which stresses a need for **effective management** for preserving both **biological and cultural diversity**. Burt et al. (T) present the results of a survey of practitioners working in island ecosystem management across many countries to identify the barriers influencing the effectiveness of island ecosystem management. Since promoting awareness is crucial for biological conservation, it is important to adopt strategies that improve respect for, and understanding of, biodiversity in young people. A study conducted by Gabriel et al. (P) in the Azores illustrates how increasing the exposure of students to nature through field trips and leisure activities might be a valuable approach to fostering a greater appreciation of the ecological, environmental, physiological, and evolutionary significance of bryophytes. An important aspect of the management of island ecosystems is monitoring the human presence in protected areas. Reynolds (P) illustrates how daily satellite imagery can be used for this purpose. There is an increasing need for preserving not only the biological diversity of islands, but also the traditional knowledge of their human inhabitants, and this is clearly shown by a study on the linguistic diversity of bird names in Eastern Polynesia (Thibault et al., T) presented in this section.

The section *Island Ecology* presents 25 talks and 16 posters dealing with a variety of ecological patterns and processes that characterise isolated systems. Island ecosystems are extremely vulnerable to **disturbance**, and the increasing diffusion of alien species is one of the most widespread forms of disturbance. In the context of disturbance ecology, Jentsch (T) et al. examine plant species diversity patterns on roadsides and in native vegetation along an elevation gradient on La Palma (Canary Islands). Using an ecological network approach to compare islands with different degrees of invasion impacts, Quitián et al. (T) illustrate how invasive species have affected the original island pollinator community of the Ogasawara Islands (Japan). Free-ranging cats often represent the top predators in island ecosystems, yet little is known about their trophic ecology, population status, and ecological drivers in these contexts. Soto et al. (T) demonstrate that free-ranging cats are abundant in a protected area of Madeira, posing an important threat to the native vertebrates of this island. Soto et al. also (P) illustrate how ferrets pose a significant threat to the conservation of Madeira's native fauna and highlight the need for evidence-based management of invasive mammals. By investigating the functional niche of locally interacting native and non-native bird species on oceanic islands, Jørgensen et al. (P) suggest that both competition and environmental filtering play a role in non-native establishment, and stress the importance of trait selection in the analysis of functional diversity. Eruptions are one of the most important forms of ecological disturbance on volcanic islands. Medina et al. (T) investigate the effects of ash accumulation on the seed bank of the Canary pine forest on La Palma (Canary Islands), whereas Guerrero-Campos et al. (P) found that the Canary pine has great resistance to high temperatures and direct effects of pyroclasts, and it is able to recover from the chlorosis caused by volcanic gases. Fire is a prominent type of disturbance worldwide, with potentially dramatic effects on island ecosystems. Nouioua et al. (T) present a study on the effects of fire on the bats of Madeira. Guarino et al. (P) use remotely sensed data to describe the intensity and the extent of a large fire event that occurred on a small volcanic island in the Mediterranean. Nakas et al. (P) describe the self-restoration of pollination services in a post-fire community on a Greek island. Several contributions address the connection between **behaviours** and isolation. In this context, Bours & Liedvogel (T) explore the genomic machinery that modulates the migratory behaviour in the Eurasian blackcap, whose insular populations tend to forgo migration and adapt to a resident lifestyle. Ducatez & DeVore (T) discuss the impacts of invasive rats on the survival, abundance, morphology, and behaviour of ghost crabs on a South Pacific atoll. Hervías-Parejo et al. (T) present a study showing that island lizards and birds have different fruit choices, with lizards selecting fruits according to their morphological traits, while birds consume more nutritious fruits. Zeng et al. (T) illustrate how defaunation due to habitat loss and isolation influences the functional diversity of personality traits in small mammals. **Species interactions** are investigated in various contributions. Thanks to their well-defined borders and simplified communities, islands offer intriguing opportunities to apply network analyses. Building a quantitative multilayer network including plants, animals, and fungi on a small island of the Balearics, Traveset (T) et al. investigate the multifunctionality of species within ecological communities. Using hummingbirds and their flowers as a model system, Dalsgaard (T) shows that trait evolution, resource specialisation, and species vulnerability to the extinction of interaction partners depend on mainland versus island settings, as well as on the environmental conditions within islands. Silva et al. present a contribution (P) on plant-pollinator interactions in Madeira, focusing on the relationships involving two invasive and one critically endangered plant species. Nogales et al. (T) describe the ecological collapse of mutualistic interactions that occurred in a high oceanic mountain environment because of historical human intervention. Arifin (P) presents a study on the interaction dynamics among cascade frogs in Sumatra, suggesting the possibility of interspecific competition. van der Geer & Lyras (T) illustrate the morphological divergence among eight congeneric endemic species of deer co-occurring during the Pleistocene on the island of Crete, where they evolved under conditions of ecological release from terrestrial predators and limited interspecific competition. Zhang et al. (P) explore how habitat fragmentation alters network specialisation across different interaction types and the effects of connections across multiple trophic levels on network specialisation. Romero et al. (P) illustrate the potential of long-distance seed dispersal by pigeons and the functional loss in island ecosystems due to pigeon population decline. Wang et al. (P) demonstrate that higher trophic levels, and species with poorer dispersal traits, are more susceptible to habitat loss on island fragments, stressing the need to consider the trophic interactions and the dispersal limitations of the species in order to conserve continuous habitats. Silva & Aguín-Pombo (T) investigate the taxonomic status of the Madeiran population of bumblebees (the most important pollinators of wild plants and crops on this island), which show peculiar clusters of colours of uncertain origin (hybridisation with an introduced species or habitat effect?). Terrestrial ecosystems are regarded as carbon sinks mainly because of the presence of forests, but in insular ecosystems other vegetation types may play an important role in **carbon stock** as well. Rocafull et al. (T) illustrate the role of native shrub species for carbon stock on islands dominated by shrublands, whereas Sierra Cornejo et al. (T) investigate the magnitude and vulnerability of soil organic carbon stocks in shrublands of the island of Tenerife (Canary Islands). Some contributions presented in this section discuss issues central to **environmental conservation**. Donoso et al. (P) present a project aimed at investigating the effects of climate change on seed dispersal in entire island communities, whereas Gil-Ramos et al. (T) illustrate the consequences of sea level rise due to climate change for snakes. Two contributions deal with the edge effects. Fragmentation processes reduce habitat size, increase isolation, and expose the remaining fragments to higher edge effects. Edge effects typically exacerbate the negative consequences of habitat loss on biodiversity, but Ren et al. (T) show that forest edges increase pollinator network robustness to extinction with the declining area, whereas Tsafack et al. (P) demonstrate that edge effects constrain endemic, but not introduced arthropod species in a pristine forest on the island of Terceira (Azores). Senterre (T) discusses the importance of using ecosystem distribution maps to improve the network of protected areas on the Seychelles. Rita et al. (P) illustrate temporal changes in plant records in a protected area that comprises nine islets subject to repeated sampling. Various contributions focus on the identification of the major **drivers of ecological patterns**. Using haemosporidian infections in birds in human-induced fragmented habitats at both individual and species levels, Wu et al. (T) demonstrate the importance of considering ecological hierarchy when studying disease risk. Yan et al. (T) explore the influence of island size and remoteness, in combination with land use intensity and pinewood nematode invasion, on plant and soil fauna diversity. Constantinou et al. (P) investigate the main abiotic factors that influence plant and beetle communities of habitats with *Quercus alnifolia* (an oak species endemic to Cyprus). Zhang & Yu (T) investigate the multi-scale and multi-dimensional plant diversity in forest plots in Thousand Island Lake (China). Zhao et al. (T) illustrate how land-use change interacts with island biogeography to alter bird community assembly. Hansen & Kreiling (T) discuss the influence of environmental variables in the diversity of water beetle and water boatman communities in Faroese ponds. Bergamaschi et al. (P) illustrate how elevational patterns in ground-dwelling arthropod diversity in the Madrean Sky Island Region (USA) can be explained by environmental filtering. Fattorini et al. (P) apply principles and methods of island biogeography to detect which factors influence bird richness in urban green spaces, finding that size is more important than isolation.

The section *Evolution of Islands and Their Biotas* includes 21 talks and 12 posters, covering many facets of evolutionary processes on islands. Islands are ideal laboratories to study the role of geographical isolation and selection in the process of speciation, and various contributions are dedicated to the study of **diversification processes** at population and species levels on islands. Taiti & Campos-Filho (P) investigate the diversity of isopods in the Mascarene Islands, showing the presence of several new species and the need for further investigation in poorly sampled islands. Campos-Filho et al. (T) use an integrative taxonomy approach to investigate the diversification of an isopod lineage in Cyprus, disclosing unexpected biogeographical patterns. By combining genome-wide DNA analyses with conventional plant taxonomic surveys, Suyama et al. (P) discover unknown cryptic plant lineages and genetically unique local populations in New Caledonia. Vangestel & Hendrickx (T) present a study on the progressive parallel adaptive radiation of caterpillar-hunter beetles in the Galápagos. Arifin et al. (T) present a phylogenetic analysis of the Asian ranid frogs belonging to the genus *Huia*. A series of contributions presented in this section investigates diversification processes in the Canary Islands. Curto et al. (T) illustrate the evolution of species syngameons in the genus *Micromeria* (Lamiaceae), while Spilani et al. (T) illustrate colonisation, diversification, and speciation patterns in a butterfly genus in the same archipelago. Bellvert et al. (T) illustrate the results of a study aimed at describing the diversification of red devil spiders with reference to the role of trophic specialisation, whereas Recuerda & Milá (T) present a study on the common chaffinch which suggests a strong role for polygenic selection in driving local adaptations. Island biotas are frequently characterised by peculiar **adaptations**. Not only insular species may differ from their continental counterparts in morphology, ecology, physiology, and behaviour (island syndromes), but they can show important phenomena of local adaptations between islands of the same archipelago or even between different environments within the same island. Cerca (P) reviews the literature for insular adaptive radiations, uncovering about 150 hypothetical adaptive radiations on islands. Whittaker et al. review the recent literature on island evolutionary syndromes in both animals (T), with a focus on the link between these syndromes and vulnerability to anthropogenic change, and plants (P), with a focus on plant and plant-animal interaction syndromes. Gavriilidi et al. (P) compare multiple aspects of animal personality and cognition in mainland and island populations of the Aegean wall lizard. Mizusawa (T) reviews the hypothesis that long-distance dispersal to oceanic islands selects for uniparental reproduction, showing that both self-compatibility and selection for outcrossing can coexist on islands. Murakami et al. (P) investigate the process of stepping stone island colonisation and the associated loss of seed dispersal ability in a *Hydrangea* endemic to the Japanese islands, whereas Watanabe (P) reviews the occurrence patterns of heterostyly this archipelago. Freitas et al. (T) illustrate song differences among locally adapted populations of the common chaffinch on the island of La Palma (Canary Islands). Cambria & Blandino (T) illustrate the influence of environmental variables on the evolution of morphological traits in species of the genus *Solenopsis* living on Mediterranean islands. Islands tend to show phenomena of **rapid evolution** and speciation. Harmon (T), however, explains that this idea is potentially confounded by the ubiquitous scaling of evolutionary rates, and stresses the importance of considering island age in evaluating evolutionary rates on islands. Jiménez-Ortega et al. (P) investigate the diversification dynamics in Caribbean rain frogs, showing an early rapid diversification that gradually decreases towards the present. An obvious factor that may promote rapid evolution on islands is the small size of populations that inhabit them. However, the small size of island populations can make them particularly prone to accumulate deleterious mutations because of the strong effects of drift. In this context, Gabrielli et al. (T) show how the populations of the Aeolian wall lizard from two very small islands are characterised by an accumulation of deleterious mutations, whereas Van Linden et al. (P) present a project in which the Italian wall lizard will be used as a model system to investigate how and why island populations survive, adapt, and thrive despite their low genetic diversity. A better understanding of species' ability to face the challenges imposed by selection on small islands may have important implications in biological conservation, and this is exemplified by studies on the evolutionary plasticity of a lizard (Fulgione et al., T; Buglione et al., P). Highly different phenotypes can arise even from very small genetic differences. Kapralova & de la Cámara (T) use the Arctic charr in Thingvallavatn (Iceland) as a model system to study the transition to piscivory, showing that two very different morphs, a small planktivorous and a large piscivorous, belong to the same genetic group, with differences in isolated regions of the genome. With a study on the Cabo

Verdean endemic sparrow, Cerca et al. (T) found that the age of genomic variants predates the calculated colonisation of the archipelago, which suggests that phylogenetic approaches may be biased by ephemeral population dynamics. Various presentations deal with the **evolution of island biotas**, including the proposal of new general models. Fernández-Palacios et al. (T) apply, for the first time, the taxon cycle paradigm to plants, showing the presence of four distinct stages for the Canary flora. Using snails from different archipelagos, Parent & Kraemer (T) propose a model that describes how functional diversity on islands changes through time. Platania & Gómez-Zurita (T) investigate the relationship between macroevolutionary processes and microendemic ranges in two genera of New Caledonian leaf beetles. With a study on the flora in the Ryukyu Islands, Suyama et al. (T) illustrate how genome-wide DNA analysis targeting multiple species may be an effective method for clarifying the formation and actual state of biotas in island ecosystems. Valente et al. (T) use empirical case studies from angiosperms, arthropods, and vertebrates from islands worldwide to discuss how phylogenetic data, palaeogeographical reconstructions, trait evolution, and biotic interactions can be incorporated into dynamic models of island biogeography which may be even surprisingly simple. Finally, Froyd et al. (P) use sedimentary ancient DNA from wetlands in the coastal lowlands of northern Mauritius as proxy records for the reconstruction of the palaeoecology of the offshore islands.

Collectively, the many contributions presented at this conference represent a unique opportunity for promoting discussion, comparing experiences, and developing new ideas in the kaleidoscopic world of island biology.

As editor of the Book of Abstracts, I had the privilege not only of reading in advance all the abstracts submitted to the conference but also of interacting with the other members of the International Scientific Committee during the evaluation process. I would like to express my gratitude to them for their invaluable assistance.

I thank all authors for submitting the results of their research to this conference, whose exceptional interest arises from the value of their work.

Simone Fattorini

University of L'Aquila, L'Aquila, Italy

☙ Plenary Talks ❧

Invited Speakers

(From: L. Figuier, Vita e costumi degli animali: rettili, pesci e animali articolati. Fratelli Treves, Milano, 1881)

Speciation happens in company, not in isolation!

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Islands are known for their high degree of endemism, contributing far above average in relation to their small total area to global biodiversity. The Canary Islands are well studied for their flora. However, the provision of a new checklist that is based on new records, species descriptions, and accepted taxa reveals clear endemism patterns not only for islands but also for ecosystems. The age, area, elevation, and topographic heterogeneity of islands have a strong influence on endemism. However, endemism is not evenly distributed across life forms and functional groups. They differ in their proportional contribution to multi-island endemic, single island endemic, native, and non-native plant species. There is a very high proportion of endemic plant species among shrubs and chamaephytes. Surprisingly, the proportion of non-native plants is highest for trees, that are mostly found in cultural landscapes and settlements. Since Charles Darwin pointed at it, the tendency towards island woodiness is under debate. Currently, several mechanisms are discussed, but hitherto volcanic impacts were not highlighted, although volcanism is an intrinsic process on all oceanic islands. The recent eruption of the Tajogaite Volcano on the island of La Palma gave the opportunity to study surprising selective effects of volcanic gases and tephra deposition. However, evolution and speciation are unlikely to be driven by abiotic mechanisms or by spatial isolation alone. Plants evolve within the matrix of ecosystems, where diverse biotic interactions take place, among plants, but also with other components of ecosystems such as pollinators or herbivores. In consequence, endemism (be it multi-island or single-island) should be related to ecosystems that differ substantially in terms of vegetations structure, light regime, and resource availability. Differences between ecosystems in these site conditions are likely to translate into life cycles and population turnover, and speciation. Here, I will present a new data set that links the distributional patterns of all Canary Island plant species to ecosystems and their current area on islands, respectively. Ecosystems that are dominated by long-lived trees and a closed canopy resulting in light limitation are characterized by a large proportion of multi-island endemics, but less single-island endemics. The latter are more abundant in open woodlands, and rocks. The area of ecosystems, however, translates clearly into the diversity of endemic plants in general for all (open and closed) natural and semi-natural ecosystems with woody vegetation (forest types and shrublands). In continuation of the Species-Area Relationship, I suggest that there is also an Endemism-Ecosystem Area Relationship, if biotic interactions such as competition are prominent and disturbances are low.

How might the extinction of threatened species change functional diversity on islands?

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Although islands occupy only a very small portion of Earth's surface, they are biodiversity hotspots, being home to a high diversity of endemic species that have evolved unique traits that distinguish them from their mainland relatives. However, a large proportion of island species are threatened and, indeed, most of the known extinctions of the last centuries have occurred on islands. It is therefore important to identify and preserve the most vulnerable species, considering their functional features and the role they might play in the ecosystems stability and functioning. Here I present a study in which we evaluated the consequences of species loss on islands functional space and identified the characteristics of the islands most vulnerable to this loss. To address this objective, we compiled information of mammal species occurrence from the literature for 318 islands worldwide. We quantified for each island the functional richness and functional redundancy that would potentially be lost if the species categorized by IUCN as threatened disappeared, evaluating also how much of such potential loss deviates from a random pattern. Finally, we modelled which island characteristics (e.g., area, elevation, climate, human footprint, distance to mainland, or percentage of protected surface) could influence the functional vulnerability of mammal island communities. Preliminary results indicate that in most islands, the potential loss of threatened species leads to lower functional diversity (and higher redundancy) than expected if extinctions were random and independent of species threat category. Also, islands with smaller areas and higher species richness will have less functionally diverse and more redundant communities, in case threatened species are lost. These results can help to understand the ecological consequences of species extinction, and also pinpoint where more conservation efforts should be made.

Trajectories of biodiversity change on islands

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Preparing and managing for ecosystem change is one of the major challenges that island societies are currently facing. Palaeoecological research has already demonstrated to add valuable information on patterns and trends to further understand the impacts of e.g., people, volcanic eruptions, and sea-level change on island's biodiversity. Using examples stemming from long-term datasets of fossil pollen, charcoal, and tephra records from sedimentary sequences from world islands we will discuss how and why island biodiversity changed significantly during the years following human settlement and other drivers of change. For example, we will show evidences of an increase in rates of turnover and the role of people on the introduction and spread of non-native taxa. Finally, these examples highlight the importance of integrating standardised palaeoecological datasets with modern ecological observations to understand island ecosystems more fully.

Network thinking in island biogeography

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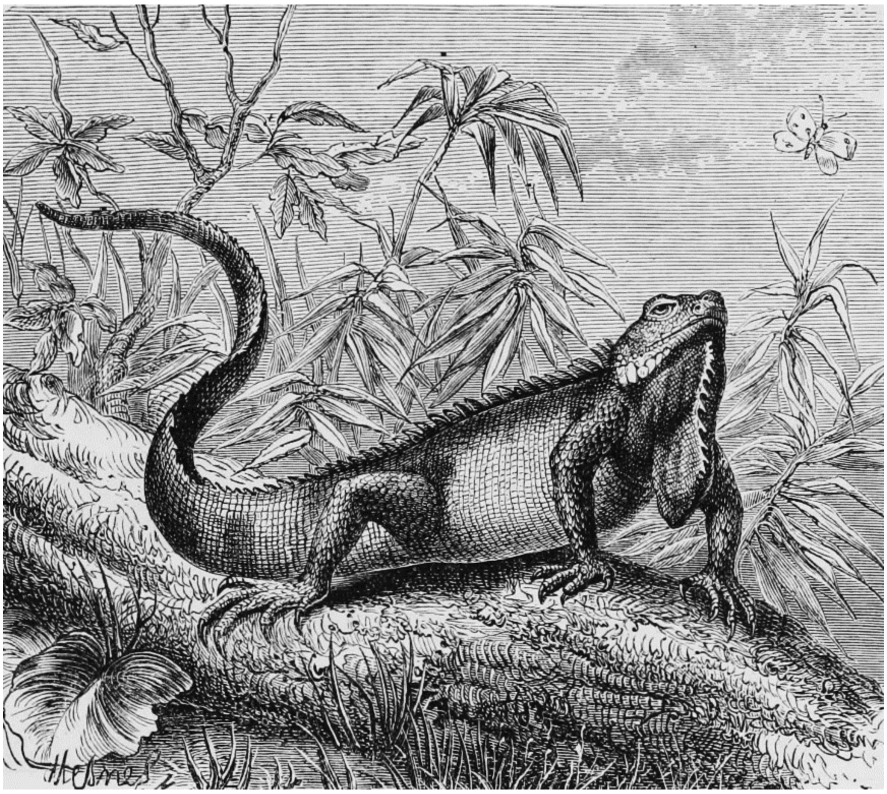
Network analysis offers a convenient and powerful framework to model real world systems. In ecology, networks have become extremely popular to investigate how biotic interactions are organized and how they can shape and affect communities. There, network analysis offers quantitative tools (often developed in different fields, mainly physics and mathematics) permitting to tackle the natural, overarching complexity that emerges when pairwise species interactions are combined into higher levels of organization. Understanding how ecological networks arise and how they respond to change is fundamental not only to describe current biodiversity patterns, but also to predict how natural systems will respond to the ongoing and future global change. This is particularly relevant in isolated/fragmented habitats, where colonization and extinction dynamics might both modulate and be controlled by the underlying "meta-networks" mapping the potential interspecific ecological interactions in the regional species pool. To complicate things further, how the meta-network translates into local networks/communities depends on yet another network. In fact, archipelagos—as well as non-island isolates—can be viewed as spatial networks where links represent, for instance, the likelihood of species dispersal between any two nodes/islands based on their distance (or on more sophisticated criteria, such as connectivity measures derived from sea current models). In principle, the structural properties of such networks could provide better predictors of diversity patterns than those stemming from the classical, simplified spatial assumptions of the Equilibrium Theory of Island Biogeography (e.g., distance from mainland). Still, the information obtained from this approach depends on the actual placement of the islands, more specifically on the extent to which it departs from a purely random (or perfectly regular) spatial arrangement. In this talk, I will attempt to bridge these two intertwined topics, trying to advance our understanding of how the structure of the island-connectivity network affects not only the diversity of the isolated communities, but also the structure of the ecological networks these underlie. More in general, by using examples from both simulations and real-world systems, I will discuss how (and where) network thinking can improve our understanding of ecological patterns and processes in island biology.

☙ Island Biogeography and Macroecology ❧

Contributed Talks



(From: L. Figuier, Vita e costumi degli animali: Molluschi e zoofiti. Fratelli Treves, Milano, 1882)

Contribution of ancient sedimentary DNA to understand island biology

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Ancient sedimentary DNA (sedaDNA) has revolutionized our understanding of long-term ecosystem changes especially for arctic and alpine regions. Due to general higher taxonomic resolution than pollen, and more consistent detection than macrofossils, it may greatly advance our understanding of biodiversity dynamics. We have analysed Late Glacial and Holocene lake sediment record from several distant islands (Spitsbergen, Bear Island, Iceland) and near shore (N Norway) in the arctic and boreal region for plant DNA. When we compare these to mainland sites with similar ecosystems, we see a steeper initial accumulation of species and fewer late immigrants especially in Iceland, most likely related to differences in dispersal vector. Further, in the ongoing ERC project TIME-LINES, we explore the possibilities to expand sedaDNA to temperate and tropical islands. A limiting factor is the availability of DNA reference library. The DNA marker that gives the highest taxonomic resolution in sedaDNA studies, the P6loop region of the chloroplast trnL (UAA) intron, is not a standard barcode and therefore not routinely sequenced for DNA reference libraries. However, with increasing large scale genome skim efforts, this is changing. Further, DNA preservation it is generally thought to be poorer in warmer regions, but we have obtained good quality DNA from several sites in the Mediterranean region such as Sicily and Crete for over 1000 year old soil-sediment samples, suggesting that even in warm environments DNA preservation may be sufficient. Thus, sedaDNA may have great potential for increasing knowledge on island biology from sub-tropical as well as temperate and arctic biomes.

Population genetics within two Grapsidae species (Crustacea: Brachyura) indicates long distance dispersal in the NE Atlantic and between Macaronesian Islands and the Mediterranean

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The genetic structure of marine species tends to reflect marine currents and wind patterns. This may hold in some cases, but there is increasing evidence of exceptions in the marine realm, as past demographic events, sea level fluctuations, duration of larval phase, ecological niche requisites and biogeographical barriers can also influence gene-flow patterns. To test if there is a trend affecting population structure of planktotrophic marine species in the NE Atlantic Ocean and Mediterranean Sea, a de novo set of microsatellites markers was developed for two Grapsidae species with planktotrophic larval development – *Grapsus adscensionis* (Osbeck, 1765) and *Pachygrapsus marmoratus* (Fabricius, 1787) – based on microsatellite genotyping by amplicon sequencing (SSR-GBAS). Sampling was performed at the Azores, Porto (mainland Portugal), Cabo Verde and Barcelona (mainland Spain). A total of 11 and 15 microsatellites loci were genotyped with Illumina MiSeq for *Grapsus adscensionis* and *Pachygrapsus marmoratus*, respectively. The absence of genetic differentiation inferred with microsatellite data within the studied distribution range of the species contributes to the conclusion that these species form panmictic populations throughout the NE Atlantic and Mediterranean Sea. In this case, the factor that seems to play a major role in the genetic structure of the populations is the duration of the pelagic life stage of their larvae. This work contributes to a new perspective of long-distance exchanges across the Macaronesia, with evidence that planktotrophic crustacean larvae are able to cross large distances and important biogeographical barriers in the marine realm, obscuring signatures of isolated populations across the different archipelagos.

Interspecific gene flow and ecological differentiation drive the evolution of the bryozoan genus *Reteporella* in the Azores Archipelago

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The processes shaping the population dynamics of benthic marine invertebrates with non-planktotrophic larvae are still poorly understood but now profit from the application of integrative taxonomic approaches. Among those taxa, bryozoans are particularly understudied and many of their ecological, biological, and evolutionary traits remain unknown. Following a recent review of the diversity comprised by the genus *Reteporella* Busk, 1884 in the central North Atlantic Azores Archipelago, the found patterns indicated that this bryozoan's genus constitutes an interesting proxy to explore genetic structure and population dynamics of marine invertebrates in oceanic islands. Therefore, a population genetic study was conducted on five *Reteporella* species from the Azores, aimed at clarifying the factors affecting connectivity amongst these sessile marine animals in these remote islands. The chosen markers were the mitochondrial COI and microsatellites genotyped by amplicon-sequencing (SSR-GBAS), a method that has been shown to be highly effective in discriminating genetic structure in non-model organisms. Discordant patterns were inferred amongst the microsatellite and mitochondrial datasets. Signatures of interspecific hybridization, with a directional gradient of shared clusters within the Azores, were detected in the SSR-GBAS dataset. This is attributed to semipermeable species boundaries that allow for local exchange of neutral nuclear loci between sympatric congeneric *Reteporella* species, whereas the phylogenetic identity of each species is retained by the maternally inherited mitochondria. A divergent lineage of *Reteporella atlantica* (Busk, 1884), restricted to the shallow waters of the easternmost Santa Maria Island, was also detected in this study. The finding of a lineage potentially under ecologically-driven incipient speciation poses new questions regarding the role of bathymetry as a promoter of differentiation in the marine realm. The occurrence of hybridization, introgression events, and ecologically-driven differentiation in bryozoans has important evolutionary and biogeographical consequences, which should be more widely considered in marine invertebrates.

Assembly of functional diversity in an oceanic island flora

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Oceanic island floras are well-known for their morphological peculiarities and exhibit striking examples of trait evolution. These morphological shifts are commonly attributed to insularity and are thought to be shaped by the biogeographical processes and evolutionary histories of oceanic islands. However, the mechanisms through which biogeography and evolution have shaped the distribution and diversity of plant functional traits remain unclear. Here, we describe the functional trait space of the native flora of an oceanic island (Tenerife, Canary Islands, Spain) using extensive field and laboratory measurements, and relate it to global trade-offs in ecological strategies. We find that the island trait space exhibits a remarkable functional richness but that most plants are concentrated around a functional hotspot dominated by shrubs with a conservative life-history strategy. By dividing the island flora into species groups associated with distinct biogeographical distributions and diversification histories, our results also suggest that colonisation via long-distance dispersal and the interplay between inter-island dispersal and archipelago-level speciation processes drive functional divergence and trait space expansion. Contrary to our expectations, speciation via cladogenesis has led to functional convergence, and therefore only contributes marginally to functional diversity by densely packing trait space around shrubs. By combining biogeography, ecology, and evolution our approach opens new avenues for trait-based insights into how dispersal, speciation, and persistence shape the assembly of entire native island floras.

Long-term dynamics of ant communities on small Mediterranean islands

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MacArthur & Wilson (1967)'s dynamic equilibrium theory states that immigration rate is equal to extinctions, resulting in a steady species richness and a turnover in the composition of isolated communities over time. However, studies have shown that small islands can stand an anomalous feature of the linear species-area relationship. Discussions on the Small Island Effect (SIE) has increased questioning over the island biogeography paradigm and highlighted the need to assess datasets with various temporal and spatial scales. The aim of this study is to assess ant community dynamics on small Corsican islands over 37 years. Ants, considered as ecosystem engineers, are good biological models as they are ubiquitous on islands and relatively easy to sample. Moreover, no study, that we know of, has investigated community dynamics of these organisms over such a long time. Ants were surveyed during spring 2023 on 45 small islands around the main island of Corsica. Islands range between 0.01-ha and 22-ha and are prospected randomly using hand-collecting method similarly to samplings done 37 years ago. Effects of time and island spatial characteristics on community structure and specific and functional composition are assessed. Previous studies that spanned on less than 20 years have shown that turnover was low and that habitat diversity and surface was the best predictor for species richness. As social insects, ants have many ecological characteristics, such as their sedentarity and their long-lived, and sometimes multiple, queens, explaining that they experience relatively low turnovers. Thus, we expect that species turnover will still be low even if the study period is twice as long, and that some ants on smaller and more isolated islands will be more prone to extinctions. Results will be further described and analyzed after collection.

Macroecological patterns of oceanic island evolutionary radiations

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Evolutionary radiations are major contributors to the biodiversity of oceanic archipelagos. Their study began more than 150 years ago with the description of the iconic Darwin's finches, and has greatly improved our knowledge of the ecological and evolutionary processes taking place in island systems. However, very few studies have investigated the factors influencing the geographic patterns of species richness that emerge from island radiations. Yet, seeking environmental and geographical factors that influence these patterns could prove crucial for our understanding of the diversification dynamics taking place in oceanic archipelagos. In this study, we build on long-standing macroecological hypotheses to seek island features that affect the species richness of oceanic island radiations. Specifically, we ask the following questions: (1) Do patterns of species richness resulting from evolutionary radiations scale with key biogeographic factors? (2) Are species richness patterns of evolutionary radiations in the same archipelago predicted by the same set of biogeographic factors, or is the importance of these factors more related to the intrinsic features of the radiations, such as the number of species, age, or taxonomic affiliation? To achieve our goal, we identified more than 90 radiations distributed across four iconic oceanic archipelagos (Hawaii, Canary Islands, Galápagos, and Fiji) and retrieved island characteristics, including area, geological age, environmental heterogeneity, and island isolation. We combined linear regressions, multivariate analyses, and mixed models to identify the best set of factors explaining diversity patterns of radiating clades and determine whether the relative importance of these factors depended on archipelago identity and/or radiation characteristics. Overall, our results revealed the role of the archipelago in driving geographic patterns of species richness for oceanic island radiations, with radiations of the same archipelago being governed by the same factors. This study highlights the predominant role of the geo-environmental dynamics of the archipelago in channeling diversification patterns.

Do human impacts explain the proportion of threatened bird species on islands?

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Marine islands are often referred to as nature's laboratories due to their unique geography and rich biodiversity. However, the isolation and narrow distribution of their fauna make islands species' highly susceptible to recent human impacts. While conservation efforts are necessary, there is little research that explains why some islands host proportionally more threatened species than others. Therefore, identifying regions with high proportions of threatened species is crucial to plan conservation actions that will provide the most benefit to biodiversity. The higher proportion of threatened species on islands may result from the interaction of environmental factors that promote species diversity, the occurrence of extinction-prone species, and human threats. Although we have a good understanding of the processes that promote species diversity on islands, few studies have assessed the impact of human activities on island biotas. To address this, we analyzed bird data from 1254 islands and found that the probability of a given bird species being threatened on islands can be mostly explained by the spatial factors, including area, isolation, and climate. We also found that the human appropriation of primary production (HANNP) and the proportion of land impacted by urbanization are the human impacts that most influence the proportion of threatened species on islands. Our results suggest that the expansion of urban areas and agriculture, especially on oceanic islands, must be carefully observed to prevent the imminent extinction of endangered species in these ecosystems.

An island biogeography approach explains the high avian diversity of a peninsular system

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Island biogeography theory explains the species richness in oceanic islands by the interplay of colonization from the mainland, local extinction, and speciation. However, several non-oceanic systems can be treated like isolated systems, for example lakes, mountains or peninsulas, and their richness may also be explained by the same main processes. Here we consider the avian community on the Peninsula of Yucatan (PY). The PY is located in eastern Mexico, Belize and the northern part of Guatemala. This region is characterized by its exceptional richness of species of several groups, particularly avian species. The emergence of the PY occurred in several stages, during the Pliocene (5.5 MYA) and the Pleistocene (1.8 MYA). Currently, the main ecosystems in this region are a tropical rain forest in the south and the tropical seasonally dry forest in the north, which allows the coexistence, in some parts, of several species with different climate tolerances and life traits. The avian diversity of the PY is around 500 species, which represents around the 5% of the worldwide avian richness. In this study we used calibrated phylogenies of 60 of the ~100 passerine species with distribution in the PY to infer the rates of colonization, extinction and speciation from these phylogenetic data. In this presentation we will show how this informs us about the relative importance of these processes for the assembly of the passerine community. Furthermore, we discuss whether there are other factors affecting these rates, such as the ecosystem preference of the species (wet or dry forest) or their origin in South America or North America.

Do functional and phylogenetic nestedness follow the same mechanisms as taxonomic nestedness?

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Nested subset patterns have been raised to explain the distribution of species on islands and habitat fragments for over 60 years. However, previous studies on nestedness focused mainly on species richness and composition, ad overlooked the roles of species traits and phylogeny in generating and explaining the nestedness. To address this gap, we sampled amphibians on 37 land-bridge islands in the Zhoushan Archipelago to explore nestedness as well as the underlying causal processes through three facets of diversity, i.e., taxonomic, functional and phylogenetic diversity. The taxonomic nestedness was measured by organizing the species incidence matrix to achieve a maximum value, while the functional and phylogenetic nestedness were quantified by incorporating how similar species were in terms of their ecological traits and phylogeny. We considered six island characteristics and seven species traits as predictors of nestedness. We found that amphibians were significantly nested in these three facets of diversity. When relating different predictors to nestedness, we found that island area, habitat diversity and species traits were highly correlated with taxonomic nestedness. Moreover, island area and habitat diversity significantly influenced functional and phylogenetic nestedness patterns. Therefore, the results support the selective extinction and habitat nestedness hypotheses. Interestingly, although we did not observe significant influences of isolation on taxonomic nestedness, functional and phylogenetic diversities were significantly higher than expected when matrices were ordered by increasing distance to mainland. This result suggests that there are more functionally and phylogenetically diverse species on less-isolated islands, reflecting a selective colonization process overlooked by the traditional analysis of taxonomic nestedness. Our results show largely congruent nested patterns and underlying processes across three facets of diversity, and distance-related functional and phylogenetic nestedness for amphibian assemblages. Hence, we highlight that a framework which simultaneously considers taxonomic, functional and phylogenetic nestedness contributes to a complementary understanding of nestedness processes.

The dynamics of recent hybridisation in island white-eyes

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Hybridisation between animal species was once considered atypical in nature. We now know it occurs widely, and can result in a variety of evolutionary outcomes from adaptive introgression to the collapse of two species. Here we use whole genome sequencing to characterise hybridisation between two bird species, an ancient island endemic white-eye, *Zosterops tenuirostris* on Norfolk Island, and a recent colonist (1904 CE), *Z. lateralis*, two species separated by approximately two million years divergence time. Based on specimen collections soon after colonisation by *Z. lateralis*, it was suggested that hybridisation occurred only briefly, then ceased. We show that hybridisation has left a signature of heterogeneous introgression across the genome, with high levels of introgression seen in a neo-sex chromosome. Demographic modelling reveals that hybridisation has been ongoing throughout the 20th century, but not to the extent that species integrity has been compromised. However hybridisation is a dynamic process, and changes to relative population sizes may impact mate choice opportunities, which could have future consequences for the near-threatened island endemic.

Vertical stratification of spiders in Macaronesian forests

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Insular biotas are extremely vulnerable to the expansion of introduced species, as many native species currently occur exclusively in the remnants of native habitats. Spiders are among Macaronesia's most diverse and yet threatened groups of arthropods. Found in most habitat types, they occupy the vertical gradient from ground to canopy level of native forests. As introduced species arrive mostly using shipping containers and similar means, they should mostly occupy the lower levels in the gradient. To test our hypothesis, spiders were sampled from epigean to arboreal micro-habitats (2 to 4 m high) on 45 sites across five islands of three Macaronesian archipelagos (Azores, Madeira and Canary Islands). The vertical stratification of spiders with different colonization origins (endemic, native non-endemic and introduced) was described by two indicators (average and standard deviation of verticality distribution), obtained for each captured species at Macaronesian and archipelago levels. No differences were found between the average verticality of introduced and either endemic or native non-endemic species, except in Madeira Island, where introduced species were on average lower in the gradient than native non-endemics. Native non-endemics tended to be arboreal dwellers, but occupied a significantly larger vertical range than introduced species. Although the patterns are not clear across all archipelagoes, our expectations were partly confirmed. This has implications for the conservation of native and endemic species, as ground dwellers might be more prone to competition from invasive species, adding pressure to the usual pattern of smaller ranges by endemic and endangered species. The approach taken here can be used in multiple other studies that aim to describe the differences in species abundance along a habitat or microhabitat gradient using standardized protocols.

A streamlined workflow for reconstructing changes in island configuration in response to sea level dynamics

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Islands and archipelagos are highly dynamic. Over time, their configuration, size, and connectivity change as a result of climatic and geological dynamics. Examples include glacial-interglacial sea level fluctuations, uplift and subduction of tectonic plates, and volcanism and erosion. Earlier studies have shown that these dynamics can have profound implications in shaping modern biodiversity patterns. The General Dynamic Model and the Glacial Sensitive Model have been proposed to reflect on the ecological changes that might result from these dynamics. While theories have been developed, a standardized and reproducible workflow capturing these dynamics is lagging behind. So far, progress is limited by the availability of accurate reconstructions of past sea level and geological changes. Here we present a streamlined workflow to quantify the responses of islands and archipelagos to past and future sea level fluctuations, while correcting for crustal deformations and gravitational forces resulting from ice sheet loading, as well as including geological conditions resulting from uplift and subduction. To promote reproducibility and interoperability, we have implemented the entire workflow in TABS, an R package for reconstructing the Altitudinal Shifts in terrestrial and marine Biomes over Time. The package has a built-in standard set-up that can be easily applied to reconstruct configurations for any island across the globe. However, the package also offers the possibility to customize the set-up, for example by providing a local bathymetric model or incorporating local uplift or subduction rates. While the package was initially developed to model changes in island and archipelago configurations in response to sea level fluctuations, we are currently implementing changes to incorporate altitudinal shifts in other terrestrial and marine biomes, such as shelf seas, corals, and mountain ecosystems. While TABS can be used for reconstructing past dynamics, it can also be applied to model island responses to future sea level rise.

Optimal sample strategy for community-level phylogenetic analyses in island biogeography

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Phylogenetic trees based on molecular data of island species and their mainland relatives are increasingly being used to infer processes that have generated biodiversity on islands. However, for diverse island communities that are composed of multiple lineages (some of which can be large radiations, others single species), complete data collection and DNA sequencing covering all island species and their close relatives (outgroups) is often difficult to achieve. We used simulations to find the best sampling strategy to minimize bias in the estimation of parameters using the island biogeography model DAISIE (Dynamic Assembly of Island through Immigration, Speciation, and Extinction) when there is a constraint on the number of species that can be sampled. DAISIE is a likelihood-based approach to quantify the rates of colonization, speciation, and extinction that have generated an island community, given their colonization and branching times extracted from phylogenetic data. We considered three different sampling strategies: i) the species selected for sampling are randomly chosen from the entire focal community, without a particular interest in the diversity of any of the lineages; ii) more effort is put into sampling island lineages that are species-rich or iii) species-poor. Within each lineage, we also considered five ways of removing (i.e. choosing not to sample) species: randomly, entirely, youngest, oldest, and outgroup species. Our analysis shows that parameter estimates are least biased when the species missing from the phylogeny are from the least diversified lineages (species-poor on the island). Sampling one or two outgroup species per lineage is also very important for the precision of parameter estimation. Thus, if data collection is limited by time or budget, our study suggests prioritizing sampling species from the most diversified lineages, preferably including the early-diverging species.

Mutualism limitation, habitat heterogeneity, and isolation weaken the latitudinal diversity gradient among island floras

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The latitudinal diversity gradient (LDG) in plant species dominates global patterns of diversity, but the factors underlying the LDG remain elusive. Here, we use a unique global dataset to show that vascular plants on oceanic islands exhibit a weakened LDG and explore potential mechanisms to explain why. In particular, we explore how classic abiotic island biogeographical variables and biotic interactions explain the lack of species on islands relative to mainland communities at a given latitude (island species deficit). We further quantify the contributions of three different mutualist plant types to the island species deficit: (1) mutualists with pollinators, (2) mutualists with mycorrhizal fungi, and (3) mutualists with nitrogen-fixing bacteria. Our results show that traditional abiotic drivers – namely area and isolation – influence the species deficit, but that biotic interactions are also instrumental. In particular, an increased proportion of mainland plants that engage in a biotic mutualism was correlated to an increase in the island species deficit. Moreover, plants that are biotically pollinated or associate with dispersal limited arbuscular mycorrhizal fungi were the dominant contributors to the species deficit near the equator, with decreasing contributions with increasing absolute latitude. These patterns suggest that biotic filters combine with classic island biogeographical factors to reduce the LDG on oceanic islands, and provide empirical evidence that mutualisms, habitat heterogeneity, and dispersal are key to the maintenance of high tropical plant diversity. These results have important implications for island conservation, ecological theory, and our understanding of global diversity.

A comparative multi-taxon study on intra-island diversification patterns on Cyprus

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Despite the quite large literature on among-islands evolutionary divergence patterns that have led to important insights relevant to both biogeography and evolutionary processes, the study of within-island diversification dynamics has received little attention. Such dynamics are expected to be more apparent on isolated oceanic islands, especially those hosting a relatively wide range of habitats. Cyprus is such an oceanic island, in the sense that it was never connected to any mainland, that hosts many habitat types and has a respectable size. During most of its ca. 20 My of subaerial existence had the form of two major paleoislands that were eventually connected to form the modern island in the mid- to upper Pleistocene. These paleoislands roughly correspond to the two main mountain ranges seen today, namely Troodos Mt. at the central-western part of the island, and Pentadaktylos Mt. at the north-northeastern part. We studied patterns of divergence among populations distributed throughout the island of four lizard species and four isopod groups comprising potential 'superspecies' and/or other congeneric species. In order to reveal phylogenetic relationships and possible geographic structure of populations, we applied genetic and genomic analyses, combining classical Sanger sequencing of mtDNA and nuDNA gene markers, and ddRAD sequencing. The results were quite surprising, since we found far more extensive clade divergence than what is seen in morphological characters, leading to identification of new species for science, the documentation of a rare event of island-to-mainland dispersal, plus the recovery of the paleoislands' signal in the genetic structure of populations. The patterns found were quite compatible among different taxa, a fact increasing the robustness of results. This first multi-taxon approach to intra-island evolutionary diversification, underlines the importance of diversity studies at a local scale on islands which may significantly increase our knowledge on actual levels of insular biodiversity.

Habitat island biogeography of natural edaphic islands

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The term habitat island refers to various island systems that are potentially isolated by a contrasting surrounding. To predict biodiversity patterns on these habitat islands, island biogeographic parameters which were developed on true islands are commonly used, e.g., island area and geographic isolation. However, besides these important parameters, other factors arise in habitat island archipelagos that can have a major impact on biodiversity but are less frequently considered. Therefore, we selected quartz islands in western South Africa as an edaphic island model system to test the effect of different biogeographic and landscape ecological parameters on the diversity of the local, unique flora. We investigated the effects of different island-biogeographical (island area and isolation, habitat diversity), landscape ecological (matrix contrast, edge effects) and edaphic factors (soil abiotic parameters) on the taxonomic diversity, habitat specificity as well as on endemism of the local, very unique flora. Results revealed scale-dependent effects of the different parameters: edge effects across the boundaries between the edaphic islands and the matrix were driven by small-scale changes in the soil abiotic variables; island area and habitat diversity best-predicted species richness and the number of habitat-specialized plants, while classical measures of spatial isolation proved to be weak predictors in all models. The matrix contrast index we developed specifically for the island system increased the explained variance of some models but was a weak predictor on its own. We conclude that edaphic islands like the studied quartz islands represent a kind of intermediate island system between true oceanic islands and fragmented habitats. As a result, studies of such island systems would therefore benefit from a separate habitat island biogeography that critically discusses the use of classical metrics and also incorporates new factors developed specifically for habitat islands.

The genomics of the 'island rule' in an island-colonising bird

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Repeated patterns of evolution are commonly observed across populations of island-dwelling birds; including changes in morphology, reduced dispersal capacity, and a slowed pace of life. This set of repeated evolutionary changes is known as the 'island syndrome'. However, whether convergent phenotypes arise from standing genetic variation and potentially have the same genetic basis, or whether different de novo mutations are responsible, remains largely unexplored. Silvereyes, of the white-eye bird family Zosteropidae, show several features of the island syndrome, including an increase in body size. The species is a prolific natural coloniser of southwest Pacific islands: its island populations vary in age from very recent (<200 years) to intermediate (4000 years) to very ancient (>100 thousand years). To explore how the island syndrome unfolds at the genomic level, we have sequenced 400 silvereye whole genomes from 31 different populations. We identify loci highly associated with morphological variation (body size and bill size). We find de novo mutations associated with body size in Vanuatu. Other associated loci are common across all populations, suggesting that standing genetic variation also underlies rapid changes in morphology following island colonisation.

A standardised portable DNA metabarcoding system for biodiversity monitoring on remote islands

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There is mounting evidence that we are now heading towards the 6th mass extinction event since life arose on planet Earth. Scientists have been warning of the potential consequences that species loss can have on ecosystem stability and the livelihood of billions of people that depend on it. Urgent measures are thus needed to turn the tide on the current biodiversity crisis. However, effective policies require knowing which drivers are contributing to species extinctions and understanding how natural communities are responding to both global and local threats. Rapid and accurate species identification is an essential aspect of ecological research and monitoring. While conspicuous species can be identified easily, others require laborious and complex taxonomic work, which undermines the feasibility of urgent monitoring programmes. As a response, we have seen an upsurge in the use of DNA metabarcoding for the study of highly diverse animal communities. Traditionally, however, this has relied on expensive laboratory equipment, the distribution of which seldom matches areas of high biodiversity. We have been developing a portable and cost-effective laboratory system for in-field DNA metabarcoding analysis – via Oxford Nanopore Technology plc MinION sequencing – to monitor terrestrial arthropod community shifts in response to increasing anthropogenic pressures on the remote islands of the Aeolian archipelago (Southern-Italy). Additionally, the system will be applied to investigate competitive trophic interactions between the critically endangered Aeolian wall lizard (*Podarcis raffonei*) endemic to the archipelago and the invasive Italian wall lizard (*Podarcis siculus*). Validation was conducted using samples provided by collaboration with the Natural History Museum of Ferrara. The approach reduces times and costs of sequencing while also opening to the opportunity of establishing an on-site investigation approach that could be scaled up to study the biota of other remote and biodiverse areas of the world.

Island fragmentation and global warming drive early extinctions in Mediterranean island reptiles

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A warming climate in conjunction with habitat fragmentation and loss, are expected to be the primary drivers of species extinction in the future. Nevertheless scientists have only a very poor understanding of how these combined processes affect species survival. Here we assess how reptile population extinctions on Mediterranean islands have been influenced since the Last Glacial Maximum (LGM) by the interactive effects of island area, timing of fragmentation, changing climate, and changing topography. By using cutting-edge geophysical models of sea-level rise we produce island-fragmentation cladograms which depict the sequence and timing by which 81 present-day islands plus 40 paleo-islands, located in the Aegean and Ionian seas, progressively became separated from paleo-landmasses. These cladograms are then used to reconstruct the progressive sequence of local reptile population extinctions that occurred on these islands going back to the LGM. We characterize a set of landscape and climate parameters for each present-day and paleo-island that we relate to local extinctions. Extending existing conservation theory this work demonstrates that population extinctions rise linearly with increased duration of isolation and also how they correlate negatively with (paleo-) island area. In addition, number of extinctions is positively associated with higher summer temperatures implicating heat stress, as well as with higher island topographic roughness, a measure of diminished resource availability. Extinctions are positively associated with higher pre-fragmentation island precipitation, an indication that reptile population persistence may be impacted by steeper declines in pre- versus post-fragmentation vegetation lushness. These conclusions point forward towards understanding, predicting, and eventually preventing future species extinctions due to climatic change.

The intriguing biogeographic pattern of the Italian wall lizard *Podarcis siculus* (Squamata: Lacertidae) in the Tuscan Archipelago reveals the existence of a new ancient insular clade

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The Tuscan Archipelago is one of the most ancient and ecologically heterogeneous island systems in the Mediterranean. The biodiversity of these islands was strongly shaped by the Pliocene and Pleistocene sea regressions and transgression, resulting in different waves of colonization and isolation of species coming from the mainland. The Italian wall lizard, *Podarcis siculus*, is present on the following islands of the Tuscan Archipelago: Elba, Giglio, Giannutri, Capraia, Montecristo and Cerboli. The species in the area displays a relatively high morphological variability that in the past led to the description of several subspecies. In this study, both the genetic and morphological diversity of *P. siculus* of the Tuscan Archipelago were investigated. Specifically, the meristic characters and the dorsal pattern were analyzed, while the genetic relationships among these populations were explored with mtDNA and microsatellite nuclear markers to reconstruct the colonization history of the Archipelago. Our results converge in the identification of at least two different waves of colonization in the Archipelago: Elba, and the populations of Cerboli and Montecristo probably originate from historical introductions from mainland Tuscany, while those of Giglio and Capraia are surviving populations of an ancient lineage which colonized the Tuscan Archipelago during the Pliocene and which shares a common ancestry with the *P. siculus* populations of south-eastern Italy. Giannutri perhaps represents an interesting case of hybridization between the populations from mainland Tuscany and the Giglio-Capraia clade. Based on the high phenotypic and molecular distinctiveness of this ancient clade, these populations should be treated as distinct units deserving conservation and management efforts as well as further investigation to assess their taxonomic status.

Trait variation in islands at shallow evolutionary levels: phylogeography meets functional biogeography

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Islands have traditionally been described as 'natural laboratories' for our understanding of organic evolution, and recent advances in genetics and trait-based ecology are providing key insights into the processes shaping island biodiversity as a whole. However, most of the on-going research is focused on macroecological and macroevolutionary patterns, which leaves a knowledge gap at lower evolutionary scales. Using several Macaronesian island lineages as an example (e.g., *Periploca*, *Olea*, *Chrysojasminum*), we will discuss in this talk how phylogeographic information (i.e., species-level genetic information) can inform functional trait analyses. We will also identify some current limitations and potential ways to increase our understanding of incipient evolutionary processes using the combination of both approaches. We will conclude that both phenotypic and genetic data are needed to investigate biodiversity patterns as a whole and can help us find repeatable (across-species) patterns in space and time. We argue that this type of information will be increasingly solicited for the implementation of holistic conservation actions in these islands, and other, threatened habitats.

Relationship of Trichoptera species in Iceland with other North-Atlantic islands and the mainland of Europe

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Analysis of geographic variation in the COI mtDNA barcode marker in ten of the Trichoptera species from Iceland indicates distinct histories where different species show indication of varying time since colonization of the island and separate evolution restricted to Iceland. One of the three Holarctic species, the parthenogenic *Apatania zonella*, appears to have originate near the Bearing Strait and dispersed from there west to Scandinavia and diverged into a separate lineage within Iceland, where another route was east N-America to Greenland and the populations met more recently in Iceland. The other two, *Limnephilus fenestratus* and *L. picturatus* do not show a clear split between the Nearctic and Palearctic, but the former has been poorly sampled. Three of the palearctic species *L. affinis*, *L. griseus*, *L. sparsus* present unique lineages within Iceland, suggesting an early colonization after the Ice-age; the poorly sampled *L. elegans* shows also a divergence pattern restricted to Iceland. Variation within the three other species reflect a recent origin. *Potamophylax cingulatus* originates in Central Europe and its variation reflects a migration route west to France and then north the coast to Britain and finally to Iceland in the 20th century. Similarly, *L. decipiens* and *Microptsectra sequax*, a very recent colonizer (21st century), fall genetically in with other European species, both in Scandinavia and central Europe. No information on the DNA is available for the Icelandic *Agrypnia picta* and *Grammotaulius nigropunctatus*. Five of the ten species show unique mtDNA lineages within Iceland suggesting an early colonization. The close similarity of the mtDNA sequences within the other species suggest a more recent origin and that the postglacial colonization is still ongoing, which is supported by the known colonization of two out of 12 species in Iceland during the last 70 years.

Historical biogeography of a hyper-diverse endemic lineage of South Pacific leaf beetles

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The South Pacific region, a wide area formerly occupied by the lost continent of Zealandia, with islands of different sizes, origins and environments, and characterized by highly endemic biotas, attracts many biogeographic studies. Each group of organisms experienced different processes in the region over time, and each evolutionary pathway is unique, although some patterns are recurrent and need to be studied in a case-by-case basis. Eumolpinae leaf beetles are a highly diverse group widely distributed in the region, with an uncertain relationship with the surrounding faunas. In this system, up to 140 species of Eumolpinae in the tribe Eumolpini have been identified, with 120 species endemic to New Caledonia. We use the first dated phylogeny of South Pacific Eumolpinae based on five mtDNA and single-copy nuclear genes to infer their historical biogeography using standard event-based inferences. With only two exceptions, the Eumolpinae of the region are monophyletic, dated between the end of the Cretaceous and the early Paleogene, and their sister group remains unknown based on the information available, including potential relatives worldwide. A drop in substitution rate in the stem branch of this clade required the implementation of multi-gamma site models for reliable age estimation, inferred in the Eocene-Oligocene transition, and also with interesting potential implications for the founding events of this lineage, perhaps massive extinction of the original stock. The inferred history was dominated by New Caledonia as the source area for most lineages within the region with repeated long-distance dispersal events to other islands through the Oligocene and Miocene, the only possible exception being the colonization of Norfolk Island from New Zealand in the Pliocene. New Caledonia is identified as both a hub, but also a pump of Eumolpinae biodiversity for the entire South Pacific, a relatively uncommon pattern in this region, where Australia or New Zealand tend to occupy this central role in the biogeography of most organisms.

Source pool diversity and proximity shape the compositional uniqueness of insular mammal assemblages worldwide

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Islands have been the test bed of several theories in community ecology, biogeography, and evolutionary biology. Progress within these disciplines has given a more comprehensive and mechanistic understanding of the processes governing variation in species richness among islands. However, it remains unclear whether these same processes also explain variation in species and phylogenetic composition among islands. Integrating theory from ecology and biogeography, we infer the roles of dispersal, selection, and stochasticity on the composition of insular assemblages within archipelagos. We further assess the influence of source pool diversity and connectivity on the compositional uniqueness of insular assemblages. We compiled data on species composition of nonvolant mammals on ~200 islands in nine archipelagos distributed worldwide from the literature. We used variation partitioning to quantify the relative influence of the environment (selection) and geographic distance (dispersal) relative to a null model (stochasticity, randomness) on taxonomic and phylogenetic compositional turnover within archipelagos. We then used a linear mixed model to gain further insight into the underlying mechanisms shaping variation in assemblage composition among islands at a global scale. Specifically, we assessed the influence of source pool diversity, isolation from the source pool, and island characteristics on compositional uniqueness. Our results suggest that within-archipelago variation in the composition of insular mammal assemblages is associated with stochastic or unmeasured processes rather than abiotic selection or dispersal limitation. The diversity and proximity of the source pool, as well as some island characteristics, explained variation in phylogenetic, but not taxonomic, compositional uniqueness globally. Globally, isolated islands associated with phylogenetically diverse source pools exhibit high phylogenetic uniqueness whereas well-connected islands associated with phylogenetically clustered source pools show the opposite trend. Phylogenetically unique assemblages also tend to occur on islands with a small elevational span and low annual temperature variation. Taken together, our results suggest that source pool diversity, along with the potential for colonization from those pools, has a strong influence on the composition of insular mammal assemblages worldwide.

Introductions outweigh extinctions in shifting seed dispersal potential across 111 island plant–frugivore communities worldwide

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First paper of the Frugivory on Islands Globally (FIG) consortium of 30 island biologists. Oceanic islands are hotspots of both anthropogenic extinctions and introductions of non-native species, leading to marked functional shifts in island communities. Functional shifts threaten to disrupt key species interactions, such as animal-mediated seed dispersal, with potential long-term impacts on the integrity of island plant communities and vegetation structure. Though some recent studies of individual taxa and islands have confirmed such shifts, it remains unknown whether animal community trait shifts actually translate to ecologically relevant mismatches with native plant species, and whether these mismatches are globally uniform in intensity and effect. Here, we document extensive functional remodelling of 111 island frugivore communities within 19 archipelagos worldwide, based on seed dispersal-specific traits from all native, extinct and introduced vertebrate frugivores (birds, mammals and reptiles), and relate them to seed traits of the native plant communities. There is an overall pattern of taxonomic and functional substitution, mainly of large-gaped flying seed dispersers, by mostly terrestrial mammalian omnivores, which has caused a mismatch between frugivore gape sizes (e.g. bill width) and seed sizes. This shift in seed dispersal potential would be underestimated in single-taxon studies. However, the general pattern is modulated by substantial spatial variation and idiosyncratic functional shifts for individual island systems. Together with variation in plant seed size distributions this means that the realized functional mismatch varies substantially among island systems. A story of similar functional homogenization across the world's archipelagos is thus oversimplified.

Climate and land use change on Wadden Sea Islands

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Barrier islands of the Wadden Sea in The Netherlands, Germany and Denmark are like a chain located parallel to the coastline. The effects of climate change over the past decades on the distribution of island ecosystems and species compositions are difficult to detect, with the exception of slow shifts of the range of individual species to the North most likely caused by global warming. The frequency of storm surges did not increase significantly in the South of the North Sea, and the hypothesis of the drowning landscape in the course of sea level rise cannot explain the growth of the islands during the last decades and centuries. On the other hand, changes in the living world can largely be explained by historical and current environmental conditions under the influence of land use change. This raises the question of the balance between coastal defence measures against climate change, rising sea level and severe weather, and the management of land use and nature conservation, i.e. the need to fasten salt marshes and dunes in areas with a positive sediment balance or not, but also to allow grazing in selected salt marsh and dune areas. The artificial reduction of natural dynamics on these islands is one of the greatest concerns for the existence of rare and threatened species and communities. The use of pesticides and fertilizers in agriculture, but also dredging activities in the lower reaches of rivers have a significant impact on the environmental conditions in the Wadden Sea region, even if these activities are carried out far from the Sea. Furthermore, a significant reduction of anthropogenic turbidity in shallow waters of the North Sea remains an important goal of nature protection.

Functional island biogeography of the flora of the Canary Islands

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Island biogeography has traditionally focused on species diversity and endemism in describing drivers of diversity on islands. However, species have been usually treated as functionally equivalent in island biogeography, although island biota have evolved a remarkable array of unique functional traits and life forms. Using the flora of the Canary Islands – an enigmatic archipelago with about equal shares of endemic, non-endemic native and non-native plant species – as a model system, this talk will address i) the functional trait space of different biogeographic groups, ii) how climate drives the distribution of individual functional traits and plant life forms, and iii) the impact of climate change on the distribution of functional traits in the native flora. Trait space of endemic and non-endemic native species overlapped considerably, while alien species added novel trait combinations, expanding the overall functional space of the Canary Islands. Climate-driven patterns in the distribution of plant life forms emerge. Interestingly, species expressing insular woodiness are less strongly affected by climate change than non-woody, herbaceous species. As climate is a major driver of functional diversity and individual functional traits, climate change will alter the distribution of different functional traits on the Canary Islands. We show that using functional island biogeography as a tool, expands our understanding of the fundamental processes governing diversity on islands, and likely also beyond.

Island biology in cities: Testing the Island Syndrome Hypothesis in gull populations

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The island syndrome predicts that insular populations have different life-history traits compared to mainland populations due to differences in ecological conditions. In recent years, the urban environment has been suggested as a potential analog to islands, as both exhibit high levels of isolation and distinct ecological conditions. This study investigated whether the island syndrome applies to gulls in urban environments, using a global dataset of breeding data for six species that we assembled from the literature. We compared mainland versus island and urban versus rural populations, examining four life-history traits and testing how two types of isolation affect patterns of these traits. Surprisingly, we found that only the number of fledglings per nest differed between mainland and insular populations, with mainland populations having higher reproductive success. Comparing urban and rural populations, we observed a similar pattern, with higher reproductive success in urban populations at the fledgling stage. Isolation had a weak effect on the patterns, at best. Our results suggest that gulls do not follow the predictions of the island syndrome, and that urban populations are more mainland-like in terms of reproductive success. We propose that factors like predation pressure, resource availability and particularly access to anthropogenic food sources may have driven the observed patterns of reproductive success in gulls. Overall, our study contributes to the understanding of urban biodiversity and indicates the potential of studying urban areas in an island biology framework approach. This can provide valuable insights into the complex dynamics of wildlife in urban environments and the challenges of conserving biodiversity in an increasingly urbanized world.

The fauna of the oldest oceanic island

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New Caledonia is the world's oldest oceanic island and fascinates naturalists for the rates of endemicity of its fauna and flora. In spite of this old knowledge for many different groups, only now we have a complete dataset that allowed us to examine this statement for all faunal components. Our study was first designed to complete the dataset of the New Caledonia fauna in TAXREF, the French Taxonomic Repository. Besides, we assembled data on the distribution of the species in a database named FATERCAL (Faune Terrestre de la Nouvelle-Calédonie). Our dataset shows that the New Caledonia fauna is composed of 7484 native species, 3158 genera, and 746 families. Endemism is indeed very high at both the species (5707 species, 76.3%) and genus (533, 16.8 %) level. Two families, Rhynochetidae Carus, 1868 and Troglosironidae Shear, 1993 are endemic. Accumulation curves indicate different tendencies for non-endemic and endemic species. For all orders, the number of non-endemics described is stabilized. Conversely, more than the half of the endemic species were described in the last three or four decades, suggesting that an important fraction of the endemic fauna is yet to be discovered. Concerning the geographical distribution, the distribution in the archipelago is quite uneven, because the area and the diversity of habitats is disproportionately higher in the Mainland (16,372 km^2) when compared to the Loyalty Islands (1,981 km^2). Although only 860 species occur in the Loyalty Islands, they contribute with 183 endemic species. The analysis of the distribution of non-endemic species in the other countries where they occur, showed that they can be also found in all continents, but the number of shared species is strongly correlated with the geographical distance of the centroid of the country to New Caledonia.

The functional diversity of birds on the East Frisian Islands across space and time in the context of climate change

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The population trends of birds in the Wadden Sea - one of the most important stopovers for more than 20 million birds along the East Atlantic Flyway - have been the subject of ornithological research for decades. The populations of breeding birds and of resting birds (waterbirds and waders) are, among other factors, the basis for determining the status of the Wadden Sea National Parks and the World Heritage Site. Although trait-based Functional Diversity (FD) can provide a stronger link between ecological functions of species and the environmental factors influencing an ecosystem, mainly organism- and abundance-based studies have so far reported spatial differences and temporal changes of bird populations in the Wadden Sea. Thus, trait-based analyses can now be used to assess impacts within the ecosystem and provide valuable information for nature conservation. In our study, we use abundance data of breeding and resting birds of the East Frisian Islands from 1996 to 2021 and link them to a matrix of species-specific functional traits to derive different aspects of FD. Using Null Models based on the observed changing structure of species abundance, we calculate the potential range of FD measures to estimate the impact of environmental changes such as climate change on FD. Our results show that FD varies between breeding and resting birds and between islands over time. We found that abundance-based diversity measures such as the Shannon index are increasing through time, which affects FD. Measured values are in the lower range of potential FD and are significantly linked to trends in the climate variables (air temperature, precipitation and wind speed). For example, increasing air temperature influences an increase in Functional Dispersion. Given the observed links between the strong differences in temporal dynamics of FD across the East Frisian Islands and their different degrees of environmental change, we conclude that investigations of FD can provide new information on the climatic drivers of assemblage-level changes in species abundances.

Biogeographical regions of freshwater macroinvertebrates in the Aegean Archipelago (Greece)

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Biogeographical regions are geospatial units characterized by unique species distribution. Islands are ideal study systems for the delineation of biogeographical regions because they contribute to the understanding of key ecological and evolutionary processes (e.g., immigration, extinction, turnover, speciation) and biodiversity patterns. Despite the amount of biogeographical work carried out in Greek Islands, no information is found about biogeographical regions for many freshwater groups. To fill this gap, we delineated the biogeographical regions for Trichoptera in the Aegean Archipelago and explored their relation with environmental and geological drivers. We obtained species distribution data of 166 Trichoptera in 21 islands and applied Hierarchical Clustering Analysis (HCA) and Non-Metric Multidimensional Scaling (NMDS) ordination to dissimilarity matrices between all pairs of islands. We also used Generalized Linear Models (GLMs) and deviance partitioning to investigate the role of environmental and geological drivers in the biogeographical regions' definition. Results revealed 6 biogeographical regions: Thrace, Northeastern Aegean, Crete - Southeastern Aegean, Central Aegean, Northern Sporades and Western Aegean. Regions' borders are generally attributed to the well-known palaeogeography of the area. These regions are similar to those obtained from other terrestrial (e.g. plants) and freshwater (e.g. fishes) organisms. For example, the islands Thasos and Samothraki grouped together for Trichoptera, fishes and plants. On the other hand, Crete and Karpathos are grouped together for freshwater organisms (both Trichoptera and fishes) but not for any terrestrial taxon (e.g. plants, land snails). The outcome of this study contributes to the understanding of freshwater biodiversity in island ecosystems, as a first step to promote the conservation of their fragile freshwater ecosystems.

Biogeography of orchids and their pollination syndromes in small Mediterranean islands

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Orchids represent a significant proportion of biodiversity, and show a wide variety of sophisticated pollination syndromes. Islands cover a small proportion of earth surface but are crucial for understanding eco-evolutionary processes and, despite the amount of research on orchid pollination, few studies focused on orchids' geographic distribution on islands. By using island species-area relationships, we investigated the orchids' biogeography across islands of the Central West Mediterranean Basin, focusing on pollination syndromes as a proxy to establish permanent populations, we ask: i) how pollination syndromes differ between continental and oceanic islands; ii) how the c and z parameters of ISARs differ across pollination strategies; iii) which are the most influential factors in shaping orchids' distribution on islands. Orchid flora were obtained for 112 islands of Central Western Mediterranean Basin. The Arrhenius power function ($S = cA^z$) was used to fit ISARs and estimate c and z values for pollination strategies and island types. We used GLM to examine the relation between species and pollination syndromes with area and isolation as well as elevation, island origin, taxa richness of the source area and habitat diversity. Our results shows that ISARs differ between continental and oceanic islands depending on isolation. z-values were found to be higher for more specialized pollination strategies while the c-value increases from autogamic to allogamic strategies, supporting the role of these two parameters in understanding distributional patterns. Distance from the mainland is a negatively related to all strategies except when deception is decoupled; island area is a positive predictor only for allogamic, deceptive and food deceptive strategies, while habitat diversity is a positive predictor for allogamic, rewarding and deceptive strategies. In order to better understand insular biogeography, we propose that trait-based research defines ISARs as being complimentary to a conventional taxonomy approach.

Threatened and extinct island birds of the world: implications for species loss on functional diversity

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While we have some knowledge of the number of bird species that humans have driven extinct over the last 125,000 years, we have far less understanding of the functional diversity (FD) that has been lost and how this has affected the ecosystem services birds provide. To answer this question, we compiled a global database of functional traits of all known extinct bird species, mirroring a recent trait database for all extant bird species. We used these databases to undertake a comprehensive evaluation of the avian functional diversity that has been lost through anthropogenic extinctions, and what may be lost in future through the loss of currently threatened species, both on islands (which have suffered the majority of known extinctions) and more broadly. Coupled to this, we assessed how these extinctions have affected our understanding of "natural" island biogeography and ecology. We find that the amount of avian FD that has been lost through extinction far exceeds that expected based on the number of extinctions, which will likely have had substantial impacts on ecosystem functioning, particularly on certain islands. The loss of currently threatened species will result in even larger losses in FD. Extinctions have changed the form of many biogeographical and macroecological patterns, and have thus potentially shaped our understanding of the natural world.

Investigating parasite dynamics during a sequential island colonisation using Whole Genome Sequence data

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Island colonisation exposes organisms to vastly different biotas, resulting in novel interactions that can impact broadscale ecological and evolutionary processes. Host-parasite interactions are liable to change during island colonisation. While successive colonisations have been shown to reduce genetic and phenotypic diversity in free-living animal populations, the effects of successive colonisation on the diversity of endogenous parasites carried by hosts have received less attention. In this study, we investigate changes in the parasite community during the historically documented sequential island colonisations by the silvereye (*Zosterops lateralis*), a passerine bird, in the southwest Pacific. Leveraging Whole Genome Sequence data, we demonstrate that parasite diversity decreases along the colonisation continuum and examine whether these endogenous parasite communities conform to island biogeography principles. Our findings underscore the crucial role of host dispersal and colonisation in shaping parasite assemblages and have implications for the conservation of insular communities.

***Tentamen Florae Aeolicae*: updated checklist and biogeographical analysis of the vascular flora of the Aeolian Archipelago (Sicily, Italy)**

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The first comprehensive checklist of the vascular plants ever reported to occur in the Aeolian Archipelago (Southern Tyrrhenian Sea, Italy) is presented, along with descriptive statistics related to their life forms, distribution ranges, statuses (native, casual, naturalized, invasive), Ellenberg-type Ecological Indicator Values, dispersal strategies, and preferred habitats. Field surveys, carried out during the last 30 years, yielded a significant update of the floristic knowledge of the seven major islands, currently hosting 934 vascular plant taxa. More in detail, 94 taxa new to the whole archipelago were found; the efforts to fill the floristic knowledge gaps were particularly effective in the least explored islands, i.e., Filicudi (115 new records), Alicudi (105) and Panarea (81), as well as in the largest, topographically most complex and anthropized ones, namely Lipari (105 new taxa) and Salina (101). The number of new records for the volcanically active islands, which are also the floristically poorest and best investigated islands, is lower, with 40 new records for Vulcano and just 11 for Stromboli. The taxa whose presence was not confirmed since more than 50 years and probably disappeared from the entire archipelago (70) were also listed, as well as the doubtfully recorded ones (42), whose occurrence was not confirmed by herbarium specimens. The archipelago counts 8 endemic taxa, i.e., *Anthemis aeolica*, *Bituminaria basaltica*, *Centaurea aeolica* subsp. *aeolica*, *Cytisus aeolicus*, *Ephedra strongylensis*, *Erysimum brulloi*, *Genista tyrrhena* subsp. *tyrrhena* and *Silene hicesiae*. Special attention was given to alien taxa. The high percentage (approx. 17%) of exotic plants confirms the vulnerability of Mediterranean islands to biotic invasions and underlines the urgent need of adopting appropriate management measures. To raise scientific and public awareness about the threats posed by the introduction of alien plants, we compiled an additional checklist of 276 taxa commonly cultivated in the Aeolian Archipelago for ornamental or utilitarian purposes, some of which could potentially exacerbate the ongoing invasion processes.

The Aegean Archipelago: a cradle for flowers and bees

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Despite its low profile, the Aegean Archipelago constitutes a highly complex world. This complexity involves high species diversity vis-à-vis limited time span for the activity of these species due to harsh conditions (e.g. low earth fertility, water scarcity, high temperatures, seasonality). All the above result in a complex interaction network in which generalists prevail in structuring it, with the copious specialists struggling to be accommodated within the structure. This is exactly the case of the Aegean bees accounting ca. 850 species, which makes ca. 70% of the bee fauna of Greece and almost 40% of the bee fauna of Europe. Based on data collected systematically during the last two decades in >250 sites located in 25 Aegean islands and a few mainland areas, this talk will discuss the following issues regarding the bee fauna of the Aegean Archipelago: (i) diversity of bees and their interactions with flowering plants; (ii) diversity of cleptoparasitic bees; (iii) biogeography of bees co-considering functional aspects of the plant–pollinator system and focusing on the drivers shaping the bee diversity in the Aegean. The methodological approach of the research applies classical observation and molecular ecology, as well as novel holistic tools (e.g. ecological network analysis), covering ecological, biogeographical, and conservation/restoration aspects.

Contingency, determinism, and stochasticity in the evolution of West Indian Boas

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The West Indian Boas are a remarkable radiation of the entirely insular genus *Chilabothrus*. They occupy habitats ranging from xeric scrub to montane rainforest and have maximum adult body sizes spanning a range from<1 m to nearly 4 m. As recently as 2013, only nine species were recognized, though substantial work in the last few years has increased the number of known species by 36%. This includes the recognition of cryptic species such as the Virgin Islands Boa, the re-discovery of the Crooked-Acklins Boa, and the dramatic discoveries of the Silver Boa and the Vineboa. The last decade has also seen a substantial amount of progress in our understanding of the biology West Indian Boas. Two morphotypes have been recognized based on ecological, morphometric, and meristic analyses: large-bodied generalists and small-bodied specialists. Both large and small species are distributed across the West Indies, though no single island has more than one large species, and small species frequently co-occur with large species (with the exception of the Bahamas banks). Further, this determinism in body size and ecological evolution has been arrived at via different evolutionary pathways, notably, via accelerated rates of head shape (trophic morphology) evolution as small-bodied species evolved from larger ancestors. I will discuss 2 decades of work with this group, as well as our current understanding of the ecology and evolution of this insular radiation of boas, including the application of multivariate morphological analysis, statistical historical biogeography, molecular phylogenomics, and phylogenetic comparative methods.

Daisies in isolation: Diversity and island biogeography of the largest plant family

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The hyperdiverse daisy family (Asteraceae) contains an estimated 33,000 species worldwide and forms an iconic component of many insular floras, including spectacular radiations, such as the silverswords in Hawai´i and the woody *Sonchus* alliance across Macaronesia. A question that has long intrigued biologists is why this family is so successful on islands. To answer this, a comprehensive global picture of Asteraceae diversity on islands is needed because past research has mostly focused on specific archipelagos or single insular lineages. Here, we compile a curated global checklist of Asteraceae native and endemic to islands and combine it with environmental island characteristics to explore global biogeographic and taxonomic patterns. Main macroecological drivers influencing species richness and endemism patterns on both continental and oceanic islands were explored with mixed effects models. Additionally, we reviewed the literature on island radiations within Asteraceae to synthesize our understanding of the magnitude and scope of island radiations within the family. We find that there are approximately 5,500 Asteraceae species native to islands, nearly 2,000 of which are endemic. Despite these impressive numbers, Asteraceae do not represent the most diverse plant family across all island types (i.e. continental and oceanic) and have a lower proportion of insular species than other large angiosperm families. However, Asteraceae form the most diverse plant family on oceanic islands for natives and second for endemic species, suggesting an exceptional ability to diversify particularly in environments with high ecological opportunity. Native Asteraceae have a truly global distribution across the world's islands and the main insular hotspots for diversity are Madagascar, the Greater Antilles, and the Canary Islands. In agreement with island biogeography theory, native diversity increases with area and decreases with isolation, and endemic diversity increases with both area and isolation. With its global perspective, our analysis brings us closer to understanding the reasons for the remarkable macroevolutionary success of this plant family.

A comprehensive dataset of Mediterranean islands to promote the advancement of island biogeography and conservation biology research

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Islands have long been recognized as natural laboratories for ecological research, providing unique opportunities to study the processes of speciation, adaptation, and extinction. Island biogeography theory, pioneered by MacArthur and Wilson, has facilitated the understanding of species distribution and diversity patterns on islands, providing valuable insights for conservation biology. The Mediterranean biogeographic region, characterized by its rich biodiversity and high degree of endemism, faces numerous conservation challenges due to anthropogenic pressures and climate change. To promote the advancement of research in island biogeography and conservation biology in the Mediterranean region, we present a comprehensive dataset of 2545 islands with areas of at least 1 ha. Building upon existing global coastlines and islands shapefiles, we extracted all Mediterranean island polygons, manually verified and corrected errors, and digitized missing islands. We retrieved each island's name and compiled a set of climatic, geographic, geo-topographic, and anthropic variables. Climatic variables include CHELSA bioclimatic data (mean annual air temperature, temperature seasonality, annual range of air temperature, annual precipitation amount, precipitation seasonality, and their respective means and standard deviations). Geographic and geo-topographic variables encompass island area, perimeter, isolation metrics, elevation (mean, max, and std), ruggedness, topographic position index, Last Glacial Maximum configuration, and geology (siliceous vs. calcareous, oceanic vs. continental). Anthropic variables comprise the number and percentage of different land cover types (e.g., crops and built-up) and their evenness. This dataset aims to facilitate research in island biogeography by providing a basis for understanding the factors affecting species distribution and community dynamics on Mediterranean islands. Ultimately, we aim to provide a resource that will contribute to a better knowledge of the outstanding ecosystems of the Mediterranean Basin, streamlining conservation initiatives and defining effective management plans for their vulnerable species.

Unravelling extinction selectivity using a global dataset on species traits of anthropogenically extinct birds

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Understanding how extinction has occurred in the recent past is crucial to identify the main drivers of this process and design effective conservation practices to minimize global biodiversity loss. Variations in species extinction risk may signify extinction selectivity. Paradoxically, because the inherently most vulnerable species are already extinct, analyses relying solely on extant species can identify traits making species vulnerable to extinction but cannot assess if the identified traits are the most important ones. Here we built a trait database for all known anthropogenic bird extinctions (from the last 125,000 years until present) to explore this potential 'extinction filter bias'. The database comprises 600 species, 80% of which are island endemics, and includes geographic, ecological, and morphological traits. As a first test of the extinction filter, we focused on a cosmopolitan clade (the Columbiformes) including the most famous bird extinctions such as the dodo. We identified the most important drivers making some species more prone to extinction: foraging on the ground, island endemism, and reduced flight capacity. In addition, we show that excluding extinct species identified different extinction drivers from those when you consider extinct species only. Our results highlight the importance of including data from anthropogenically extinct species in order to reveal the complex combination of factors leading to species declines. By doing so, we will be able to identify some traits as more important drivers of extinction risk than previously acknowledged. This information should refine the design of specific management practices for each group and effectively minimize biodiversity loss.

The Sicilian biogeography explored from ants' perspective: a crossroad, an island, an archipelago

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Ants are a large and diverse insect family that has colonized almost all terrestrial habitats across the planet. Dispersal of these eusocial insects mostly relies on queens, which are capable of long-range flights in most species. The Mediterranean basin is a key diversity hotspot for ants, and its faunal assemblages are deeply affected by a very complex climatic and geographic history. Sicily is the largest and most species-rich among Mediterranean islands, hosting about 140 species. Its biogeographic history, as well as the variety of habitats it hosts are key factors shaping its actual diversity. We offer for the first time an overview of the biogeography of the island from the perspective of these insects, based on significant recent advances in the faunistic, taxonomic, and phylogenetic exploration of its fauna. Sicily is a crossroad between Africa and Europe, and between the Western and Eastern Mediterranean sectors: it was colonized through the Strait of Messina by a combination of south-western European, Balkan, Boreo-Alpine, and Apennine faunas, and through the Sicilian Channel by the Maghrebian fauna. The Sicilian Channel has represented the most significant barrier: the isolation of populations colonizing Sicily from the Maghreb frequently promoted allopatric speciation into island endemic species. The actual distribution patterns within the island appear to be strongly influenced by Sicily's paleogeographic history as an archipelago of multiple islets, with three sectors (northeast, northwest, south-east) still characterized by significant faunistic differences, and multiple narrow-endemic species. This extraordinary diversity still requires significant taxonomic efforts to be understood, while genomic data and distribution models may shed light on the complex history that led to its formation. In the wake of severe habitat alterations, climate change, and increasing alien species invasions, biogeography may be key for the biological conservation of island ant faunas across the Mediterranean.

Life in isolation: One-fifth of all vascular plant species are endemic to islands

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Islands are renowned as evolutionary laboratories supporting high numbers of species found nowhere else on Earth. Despite the enormous contribution of islands to global biodiversity and the imminent threat of extinction of many island species, there has been no attempt to comprehensively assess the entire diversity of vascular plants on the islands. Here, we present the first integrated assessment of all known vascular plant species native and endemic on islands worldwide. Our publicly available checklists are sourced from The Global Inventory of Floras of Traits including 2,919 checklists, floras, and reports and covering 958 mainland regions and 1,961 islands, and 303,965 vascular plant species in total. We find that 93,984 species are native to islands of which 63,271 are island endemics representing c. 21% of global plant diversity. Of these, 44,398 species (70%) are restricted to single islands. The number of single-island endemics increases with increasing island area and isolation as well as towards the equator. A comparison with the IUCN red list for plants shows that 65% of island endemics are listed as endangered compared to 49% of all species worldwide. 55% of the globally extinct plants were endemic to islands. Our findings fill an important knowledge gap in global plant diversity, highlight the enormous richness of island life, and also point out great conservation concerns for the world's endemic island plants.

Towards an equilibrium theory of island biogeography for traits

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The Equilibrium Theory of Island Biogeography (ETIB) posits that species richness on islands is governed by a dynamic equilibrium of immigration and extinction. ETIB is an example of neutral ecology. It makes predictions about numbers of species, but not about their identity or functional traits. However, ecologists are interested in understanding the role of functional traits in the assembly of island biotas. Here we build on the principle that island communities are at an equilibrium of immigration and extinction and ask how these processes affect functional traits over time. We assembled a novel island-trait dataset from an archipelago in Western Australia and linked seed mass, plant height and leaf area of 156 species to their occurrences on 15 islands surveyed four times within four decades. Using community trait means we tested whether trait distributions remained at equilibrium over time and identified factors affecting trait equilibria on islands. We found strong evidence that ETIB can be extended to functional traits. Community trait means remained at equilibrium on islands similar to species richness irrespective of species turnover. Environmental characteristics had no strong effect in explaining trait turnover. Species most susceptible to turnover were on average smaller and had lower seed mass than persisting species. Integrating traits to island biogeography can greatly advance our understanding of immigration and extinction dynamics on islands.

Adaptive radiation and dispersal filtering jointly shape mammal assemblages on oceanic islands

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Understanding how ecological and evolutionary processes structure island assemblages is a fundamental challenge in island biogeography. Island assemblages frequently represent unique functional and phylogenetic communities, yet species' ecological roles are largely ignored in classic island biogeography studies. Here, we examined the relative role of eco-evolutionary processes in structuring island mammal assemblages, using a global dataset of all extant and extinct species native to an oceanic island from the Holocene. We find island mammal assemblages are phylogenetically clustered relative to null expectations, with clustering increasing with island area and isolation. Functional clustering is also commonly observed, but is weaker, not ubiquitous, and generally independent from island area or isolation. These findings suggest the joint effects of adaptive radiation and dispersal filtering in shaping island mammal assemblages under pre-anthropogenic conditions, notably through adaptive radiation of a few clades (e.g., bats, with generally high dispersal abilities). Our study further provides a new conceptual framework of island community structure, and demonstrates that considering the functional and phylogenetic axes of diversity can better reveal the eco-evolutionary processes of island community assembly.

Marine bivalves in oceanic islands: investigating biogeographic patterns in the Atlantic Ocean

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In the marine realm, dispersal ability is amongst the major factors shaping species distribution. Most marine invertebrates disperse passively mostly by winds and surface-water currents. The dispersal and distribution of marine species is also impacted by glacio-eustatic sea-level oscillations, such as those triggered by Pleistocene glacial–interglacial cycles. The well-preserved marine fossiliferous deposits from Macaronesia provide remarkable information on Pleistocene geographical range expansions. Within this rich fossil record, molluscs species, particularly bivalves, are by far the best represented. Phylogenetic relationships within this taxon have been studied for decades and represent a proxy for large-scale macro-evolutionary studies. To better understand the ecological and biogeographic processes that have been shaping marine ecosystems in the NE Atlantic over geological time, we compiled a checklist of both recent and late Pleistocene shallow-water marine bivalves from the Azores Archipelago. Additionally, Atlantic and Mediterranean shallow-water bivalves were added together with information on their distribution and various functional traits. The checklist was compiled from the analysis of bibliographical sources, institutional biological collections from the Azores and continental Europe, and online databases. Environmental factors (i.e., worldwide geographical distribution, depth range, maximum length, and type of substrate) were analysed and compared to species functional traits (i.e., size, maximum length, active/passive locomotion, life habitat; and biogeographical diversity patterns) throughout the Atlantic Ocean. A detailed biogeographical and functional diversity analysis was then performed to determine any relation between species distribution and species functional traits. This work is crucial to clarify the evolution of marine invertebrates in remote oceanic islands, their reaction to glacial-interglacial cycles and what may become the future range expansion routes, considering a warmer present. A list of one-thousand-six-hundred-thirty-nine bivalve species was compiled, and it was discovered that several functional traits have a correlation with the geographical distribution of these species. The implications of such findings are discussed and contextualized in current and future climate scenarios.

Panarea ECCSEL NatLab-Italy: A unique natural laboratory for research on climate change and CO_2 geological storage

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The island of Panarea is a natural laboratory characterized by numerous and diverse submerged hydrothermal emissions of CO_2 and other gases and hot waters of volcanic origin, including a recently described site with more than 200 chimneys. This provides the unique opportunity to study gas migration in different geological settings, assess the impact of CO_2 increase on marine ecosystems and improve CO_2 monitoring techniques. Due to the unique characteristics of the Panarea Volcanic System, the Italian Ministry of University and Research (MIUR) funded the establishment of a permanent laboratory on the island, the Panarea ECCSEL NatLab-Italy, which has been providing logistical and scientific support to researchers using the site since June 27, 2015. This laboratory, managed by OGS (National Institute of Oceanography and Applied Geophysics), is one of the Italian components of ECCSEL, the "European Carbon Dioxide Capture and Storage Laboratory Infrastructure", a European initiative aiming to create a network of top-quality research laboratories devoted to developing CO_2 capture and storage (CCS) techniques and combating global climate change, enabling low to zero CO_2 emissions from industry and power generation. It is equipped with scientific instrumentations for high-level integrated multidisciplinary studies in physical, chemical, biological, and geological sciences. From the beginning of 2020, thanks to the PON IPANEMA infrastructure project, the laboratory is being implemented with new and highly technological instrumentations for laboratory analysis, sample collections and in situ experiments. Moreover, three types of highly innovative instruments, extremely versatile and functional for multidisciplinary research, are also available for integrated and high-tech monitoring of gas emissions: an AUV (Autonomous Underwater Vehicle) for water and sediment characterization; a ROV (Remotely Operated Vehicle) for background inspection and analysis, including sampling; a UAV (Unmanned Aerial Vehicle), or drone, for the characterization of the coastal area and of surface gas emissions.

Biodiversity structure and patterns on atoll islands

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Atolls form a vast mosaic of islands, stretching across the tropical to sub-tropical oceans. Because of their small land areas, simple habitat structures, young age, and high natural disturbance regimes, atolls are a unique type of island ecosystem and, in many ways, different to the high volcanic or granitic islands of the Indo-Pacific. The terrestrial biotas of atolls are generally depauperate and dominated by widespread generalist species, with low rates of endemism. The species assemblage on atolls is considered to be predominantly controlled by environmental factors, but we are still lacking a deep and global understanding of the structure and patterns in atoll biota. In this talk, we present a novel global database on atoll terrestrial biodiversity, covering 126 atolls (or ca. 40% of all atolls in the world), comprising all major terrestrial species guilds on atolls (vascular plants, land snails, insects, spiders, land crabs, reptiles, birds, native mammals), and spanning the entire geographic range from the Western Indian Ocean, Pacific, to the Caribbean atolls. We present first insights on atoll biodiversity patterns and demonstrate how the high natural disturbance regimes of atolls act as an important filtering mechanism in species assemblages on these small islets. We further showcase how this dataset can support decision-making in atoll conservation and restoration management, e.g. in endangered species re-introduction or trans-location programs. Overall, this dataset contributes to improving our understanding of atoll ecology and biodiversity, thereby supporting the growing interest in atoll conservation and restoration from a novel macro-ecological perspective.

Islands as test sites for biodiversity theory related to water-energy dynamics, production, and null models

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Geographic variation in species richness along elevational and latitudinal gradients may be controlled by energy, water and productivity, but spatial factors such as hard boundaries may also be important. This study uses large mountainous oceanic islands to test established plant diversity models such as production expressed as Actual Evapotranspiration (AET) or Net Primary Production (NPP) based remote sensing (MODIS), the null model Mid Domain Effect (MDE), and the Water Energy Dynamics (WED). The outcome will have clear implications for the validity of the theoretical species richness models. We compiled entire floras with elevation specific occurrence information for seven mountainous oceanic islands around the world. For each of the seven islands, the plant richness was estimated by interpolation for each 100m elevation bands. We compared the null model Mid Domain effect, Actual Evapotranspiration, Net Primary Production (MODIS), and Water Energy Dynamics employing Generalized Linear Models, and use Akaike Information Criteria and deviance explained to find which model has the best explanatory power of the variation in plant richness. We found a remarkably consistent pattern where precipitation had negative relationship with species richness, except on Hawaii. Water Energy Dynamics was apparently a good model, but this was because the potential evapotranspiration term was very significant, whereas prediction based on precipitation was rejected. Precipitation is underestimated at high elevation due to occult precipitation, but its effect on species richness is impeded because of low energy. Potential Evapotranspiration gave far better prediction than the energy productivity model based on Actual Evapotranspiration or Net Primary Production. The spatial null model MDE failed to offer a good explanation to species richness on the mountainous island compared to Net Primary Production and Potential Evapotranspiration.

How do the geo-environmental dynamics of an archipelago shape phylogenies?

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Recent theoretical studies show that the impact of geodynamical changes on biodiversity can be extracted from the signatures they leave on the shape of species phylogenies. Such geodynamical changes are particularly important for insular ecological communities. While geo-environmental dynamics within an archipelago are expected to influence insular species phylogeny, it remains unclear how the combination of fragmentation and connectivity variations influences phylogenies in a dynamic context. Here, we investigate to what extent phylogenetic patterns are influenced by the complex geological history of a volcanic oceanic archipelago, where islands successively emerge, vary in size and in connectivity, until submergence. We simulated, with a neutral individual-based model, these geo-environmental dynamics and eco-evolutionary processes at the individual scale and study the emerging speciation, migration and extinction rates. We show that lineage accumulation and tree imbalance are sensitive to an archipelago's geo-environmental dynamics and that the effect of these dynamics on phylogenies is directly influenced by the ratio of inter-island gene flow to continental gene flow. This ratio is determined by the geographical structure of the archipelago and its isolation from the mainland. In an archipelago emerging far from the mainland or with close inter-island distance, i.e. dominated by inter-island connectivity, we predict strong evolutionary radiations that occur in a small number of clades and describe a highly unbalanced phylogeny. By contrast, for an archipelago that is described by high mainland connectivity or by a large inter-island distance, we predict balanced phylogenies showing few evolutionary radiations limited by a strong turnover of continental colonizing species. In summary, with this model we are able to predict phylogenetic topology based on the effect of the geodynamical history of an archipelago on the distribution of lineage accumulation over time and between clades.

Palaeoecological trajectories of non-native vegetation on islands globally

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Human-mediated changes in island vegetation are caused among others by the introduction and spread of non-native plants. While current invasion statuses are well-known and insular biodiversity is continuously being monitored, a perspective on non-native plant species' abundance and the speed and magnitude of introductions predating historical documentation is largely missing. By matching fossil pollen data with status information of plants (i.e., non-native, native), we quantify the changes caused by non-native plants on 29 islands globally during the last 5000 cal. years BP. This approach allows to go beyond written records and censuses of insular non-native vegetation. In general, non-native plants started to increase massively during the last 1000 years, without any signs of slowing down. Trajectories differ between single islands and are linked to idiosyncratic settlement histories. We show that palynological data can be used to obtain a historic perspective on the development of non-native vegetation and novel ecosystems on islands.

The integration of the small-island effect and nestedness pattern

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The small-island effect (SIE) and nestedness are two important patterns in the fields of island biogeography and community ecology. However, to date, no study has tried to integrate the SIE and nestedness pattern. Therefore, the aim of this study was to integrate these two biogeographical patterns by proposing a new integrative hypothesis. The integrative hypothesis posits that the degree of nestedness of the large island matrix will be larger than that of the small island matrix split by the threshold of the SIE. We tested the integrative hypothesis by compiling 219 global datasets with both the presence-absence matrices and the variables of area and species richness. We also collected six island characteristics influencing the SIE and nestedness patterns, that is island type, taxonomic group, area range, the number of islands, species range, and matrix fill. We applied breakpoint regressions to detect SIEs and used the metric NODF (Nestedness metric based on Overlap and Decreasing Fill) to quantify nestedness. We then employed logistic regressions and an information-theoretic approach to determine which combination of island characteristics was important in determining whether the integrative hypothesis was supported. Among the 92 datasets in which SIEs were unambiguously detected, nestedness analyses showed that in 64 cases (69.6%) the values of NODFc (nestedness among sites) for the large island matrices were larger than those of the small island matrices, supporting the integrative hypothesis. Matrix fill and area range were substantially important in determining whether the integrative hypothesis was supported. By contrast, island type, taxonomic group, the number of islands, and species range received considerably less support. Our study was the first to integrate the SIE and nestedness pattern. Overall, we found prevalent support for our integrative hypothesis. The integration of the SIE and nestedness provides new and interesting insights into these two biogeographical patterns.

Using the Global Inventory of Floras and Traits (GIFT) for island research

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Answering some of the most pressing research questions related to island biodiversity requires knowledge of the plant species found on islands and their functional characteristics. Much of this information has accumulated over centuries of botanical exploration and is contained in regional Floras and checklists, which offer curated information on the species composition, species' biogeographic status and functional traits. Here, we line out how the Global Inventory of Floras and Traits (GIFT; https://gift.uni-goettingen.de), a repository of information from regional Floras and checklists, can be used for island research. GIFT integrates plant distributions, functional traits, phylogenetic information, and region-level geographic, environmental, and socio-economic data. Version 3.0 of GIFT holds species lists for 3,485 regions with full global coverage, including ~ 367,854 taxonomically standardized plant species names and ~ 4 million species-by-region occurrences. 2,251 of these regions are islands or archipelagos, for which GIFT offers additional information like, geological origin and age, geographical isolation, area, past and present climate, Last Glacial Maximum geography, and the archipelago each island belongs to. GIFT also includes species-level information for 109 functional traits and more than 5.7 million trait-by-species combinations. Data from GIFT is openly available via the GIFT R-package (https://CRAN.R-project.org/package=GIFT). As exemplified by several studies, GIFT allows for assessing the taxonomic, functional, and phylogenetic composition of island floras from regional to global scale, for assessing endemism or introduced alien species on islands and for testing hypotheses related to past and present geographic and environmental drivers or anthropogenic influences. GIFT opens up new avenues to address questions related to, for example, how dispersal filtering and in-situ diversification lead to functional traits differing among island and mainland assemblages and more.

Extinction of rare species on smaller islands is the key mechanism behind the species-area relationship on acidophilous habitat patches: an empirical study from the Czech Republic

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Three mechanisms are hypothesized to cause species-area relationship on island-type habitats: passive sampling, disproportionate response (also called "area per se"), and effect of habitat heterogeneity. We aimed to identify which of these mechanisms is responsible for the species-area relationship in patches of dry acidophilous grasslands that are scattered across the agricultural landscape of Czechia and host a number of rare and threatened vascular plant species. In each of the 44 grassland patches (100-8600 m^2), we sampled vascular plants and their cover in four randomly located 0.5 × 0.5 m plots, 3-5 m from each other. Also, we recorded all plant species in the whole patch. We used the analytical framework proposed by Chase et al. (2019, Frontiers of Biogeography) to disentangle the effect of the three alternative mechanisms. The framework uses data on multiple scales (alpha: species within each plot; gamma: species in a set of plots within the same island; beta: calculated from alpha and gamma; and island: all species in the habitat patch) and also two diversity metrics (richness, and Simpson's diversity index, focusing on dominant species). Only habitat specialists of acidophilous grasslands were used in further analysis. We found that both alpha and gamma diversity increased with the area of the patch, indicating that in addition to passive sampling, the disproportionate response ("area per se") also plays a role in the species-area relationship. Since only the species richness, but not Simpson's diversity, changed with the island area, we suggest that these disproportionate effects are related to the extinction of rare plant species in smaller patches. Beta diversity, on the contrary, didn't change with patch size, indicating that habitat heterogeneity is unimportant in this study system. We demonstrate that empirical data from habitat patches can provide insights into mechanisms behind the assembly of their plant communities.

☙ Island Biogeography and Macroecology ❧

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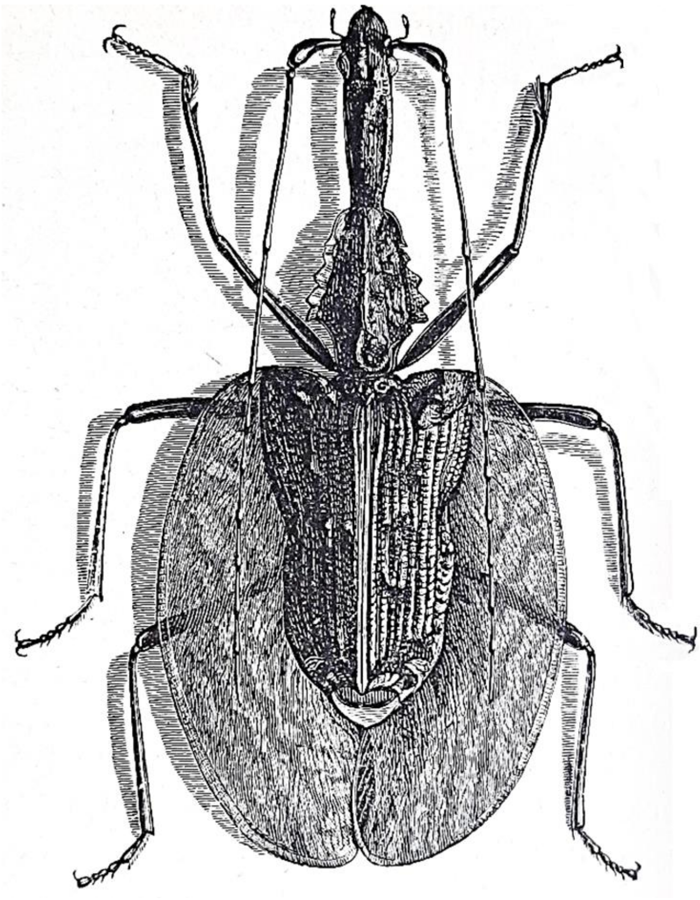

(From: L. Figuier, Vita e costumi degli animali: Gl'insetti. Fratelli Treves, Milano, 1907)

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Evolutionary history of *Camellia* section in Japan

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The genus *Camellia*, which belongs to Theaceae, is primarily distributed in East and Southeast Asia, with C. japonica and C. rusticana in sect. Camellia present on the Japanese islands. In this study, we investigated the demographic history of C. japonica, which has a wide distribution throughout the Japanese archipelago, the Korean peninsula, Taiwan and the coastal regions of China. By analyzing SNPs obtained through MIG-seq, we discovered that *C. japonica* displayed a genetic structure with three clusters: southern and northern C. *japonica*, and *C. rusticana*. Further analysis using RAxML phylogeny showed that *C. chekiangoleosa*, a related species in China, was the ancestral species, and *C. rusticana* and *C. japonica* were more closely related. DIYABC analysis estimated that *C. japonica* and *C. rusticana* diverged from their common ancestor approximately 10 million years ago, reflecting the geological history of the Japanese archipelago's formation when it separated from the mainland. We also examined the intraspecific genetic structure of *C. japonica* using ADMIXTURE analysis, which revealed that the populations were mainly divided into four groups: northern and southern populations in the Japanese archipelago, Chinese and Korean populations, and Okinawa and Taiwanese populations. Demographic analysis of these four populations indicated that the northern Japanese populations were the first to differentiate from the southern Japanese populations, followed by the Okinawa and Taiwanese populations. Subsequently, the Chinese and Korean populations returned to the mainland Asia continent from the southern Japanese populations. These results were consistent with those obtained using Ecological Niche Modeling in Maxent. Our study provides insight into the evolutionary history of these species and valuable information for their conservation and management, which may inform future conservation efforts and aid in prioritizing populations for management.

Biogeographic patterns of one of the world's most remote island floras: the sub-Antarctic archipelagos

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Sub-Antarctic archipelagos represent some of the most remote and pristine insular habitats in the world. The large distances separating these islands makes them one of the most interesting places to study terrestrial biogeography and the processes that shaped it, such as long-distance dispersal. We selected four vascular plant species that are widespread across the sub-Antarctic region and Austral continental regions, and three species that are endemic to an extremely remote sub-Antarctic province. First, we generated and compiled the available nuclear and plastid DNA sequencing data for each of these species. We then used Bayesian inference to infer phylogenetic relationships, divergence times, migration rates per species, as well as dispersal rates between islands and carrying capacities per island/archipelago; the latter were estimated by integration of the DNA sequences and the associated geographic coordinates for the voucher specimens, using the Bayesian Island Biogeographic model (BIB). We found that connectivity was higher between the sub-Antarctic islands and the nearest continental regions than with other islands, which probably facilitated the establishment of vascular plant species in these remote regions. For the most widespread species, we found that continental land masses would have acted as the source area of dispersal to the sub-Antarctic islands over millions of years (from the Miocene to the present day), probably via extreme long-distance dispersal events, likely driven by eastward-moving wind and water currents. Overall, our results reveal sub-Antarctic islands as unique biodiversity refugia over long evolutionary timescales. This, together with their latitudinal position, isolated in the farthest south of Earth, highlights the need for establishing priority conservation plans for these habitats, especially in the face of rapid climate change.

Species distribution models and island biogeography: challenges and prospects

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Species distribution models (SDMs) are the primary tools used to model and predict changes to species' ranges, and are often used to provide a quantitative baseline for conservation measures. However, most SDM methods have been mainly designed and optimised for use with species with large amounts of occurrence data and covering broad continental ranges. Islands differ from most continental systems in numerous ways, including by often having substantial topographic variation in a small area, and being surrounded by a non-permeable matrix for many organisms. As consequence, islands usually harbour species with low abundance and highly specific habitat requirements. Thus, modelling island species distributions comes with several challenges: 1) Collection of a sufficient sample of species occurrences, 2) dealing with the methodological constraints imposed by small datasets, and 3) the selection of relevant environmental predictors matching the fine-scale habitat relationships occurring on islands. By assessing published literature on SDMs in the context of islands and the global occurrence database GBIF, we identified how data deficiencies and the unique characteristics of island environments and biota may impact SDM applications. Results confirmed that island SDM implementations are frequently affected by small occurrence datasets, increasing uncertainty in predictions, particularly due to the 1) frequent use of modelling methods sensitive to small sample sizes and/or unbalanced datasets, and 2) use of large numbers of predictors relative to the number of occurrence points, resulting in overfitted models. In addition, a suboptimal selection of predictors, in terms of explanatory power and analytical scale, was identified in many island SDM studies. We propose an SDM framework for island species that promotes an *a priori* informed choice of the study grain/ predictor type, taking into consideration the spatial and ecological characteristics of island environments. Finally, we show that GBIF has the potential to close knowledge gaps in certain underrepresented island environments.

The sea snail *Phorcus turbinatus* (Von Born, 1778) as bioindicator of metals in hydrothermal vents: preliminary results

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Phorcus turbinatus is a long-lived intertidal snail of the genus *Phorcus* which, due to its wide distribution in the Mediterranean and Atlantic oceans, its year-round presence, and its ease of sampling, is studied by numerous branches of science, from paleontology to ecology. Due to its ability to accumulate relatively high concentrations of metals from water and sediments, it is also considered a good bioindicator of metal pollution. Hydrothermal vents are a source of numerous trace metals in the sea, many of which are essential micronutrients for most marine organisms. The metal composition of fluids rising from sediments depends on the geographical area and depth of the vents. In addition, exceptional degassing events, such as that occurred in the area surrounding Panarea in November 2002, can determine a huge release of trace metals (Na, K, Mg, Ca, Cl and Br), and significant input of toxic metals (Hg, Cd, Pb and As) that can last for several months causing changes in the surrounding marine ecosystems. The aim of this study is to assess the potential role of *P. turbinatus* as bioindicator of metals of hydrothermal origin. Samples were collected from different locations around the Aeolian Archipelago and Gulf of Patti, including hydrothermal and control areas. After sampling, the snails were taken to ECCSEL-ERIC NatLab Italy in Panarea and immediately stored at -20 degrees. Prior to analysis, opercula were removed, digested overnight in H_2O_2 and then rinsed with ultrapure water. The opercula were then analysed using a scanning electron microscope with energy dispersive X-ray spectroscopy (SEM-EDS). The metals that showed the highest weight percentages in opercula were Br, N, and Fe. Among all, Fe seems to be the most capable of distinguishing the hydrothermal areas from the others. Lower weight percentages were also recorded for Mg, K, and Cl.

Functional and biogeographic traits of edaphic island plants

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Edaphic islands commonly host high amounts of habitat-specialized or endemic plant species. In the case of quartz islands in South Africa, many of these edaphic island species furthermore are dwarf succulent shrubs with unusual growth forms. In this study, we ask if and how functional and biogeographic traits of these plant species correspond to the distinct soil abiotic and spatial characteristics of the edaphic island habitats in comparison to the surrounding matrix habitats. We measured various quantitative traits for 195 of the most common, perennial plant species of a quartz island archipelago in the Knersvlakte nature reserve and further supplemented these with biogeographic traits from the literature. We found that habitats on the quartz islands have higher salinity and lower soil pH values and show higher proportion of leaf-succulent species of smaller growth forms with further differences in dispersal characteristics. Thus, like other special soils, quartz islands harbor unique plant species with special traits. We discuss, how the soil environmental conditions (salinity, acidity, aridity) and selected island parameters (area, habitat diversity) might contribute to this distinct trait pattern and how the comparison of different edaphic island types might profit from a functional approach.

Giant fern genomes show complex evolution patterns: A case study in the genus *Tmesipteris* (Psilotaceae)

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Giant genomes are rare across the plant kingdom and their study has focused almost exclusively on angiosperms and gymnosperms. The scarce genetic data that are available for ferns, however, indicate differences in their genome organization and a lower dynamism compared to other plant groups. *Tmesipteris* is a small genus of mainly epiphytic ferns belonging to the *Psilotales*, that occur in Oceania and several Pacific Islands. Untangling the evolutionary history of this group will be key to better understand how giant genomes evolved. Using the Psilotales288 enrichment panel for targeted capture sequencing (of 288 single-copy nuclear orthologs), together with publicly available transcriptome, we are building a nuclear dataset to infer phylogenetic relationships. So far, only two species with giant genomes have been reported in the genus, *T. tannensis* (1C = 73.19 Gbp) and *T. obliqua* (1C = 147.29 Gbp), which have been further investigated using low-coverage genome skimming sequence and analyzed using the RepeatExplorer2 pipeline to identify and quantify the repetitive DNA fraction of these genomes. Both species share a similar genomic composition, with high repeat diversity compared to taxa with small (1C < 10 Gbp) genomes. We also find that, in general, characterized repetitive elements have relatively high heterogeneity scores, indicating ancient diverging evolutionary trajectories. Our results suggest that a whole genome multiplication event, accumulation of repetitive elements, and recent activation of those repeats have all played a role in shaping these genomes. It will be informative to compare these data in the future with data from other species across the genus, to determine if the structures observed here are an emergent common property of massive genomic inflation in the genus or derived from lineage specific processes, given the close phylogenetic proximity of the two species analyzed so far.

A review of the biogeographical and plant diversity patterns in the Aegean and Ionian archipelagos (Greece)

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The continental archipelagos of the Aegean and the Ionian at the eastern Mediterranean region have been examined in several biogeographical studies during the last two decades. Their intricate paleogeographical history has paved the ground to examine different aspects of diversity patterns in complex continental island systems. Both archipelagos display similar geological and climatic regimes, as a result of their almost identical latitudinal range and a common history of recent partition from the adjacent mainland areas. The Aegean archipelago, however, is much larger and has experienced a long and heterogeneous paleogeographical evolution compared to the relatively homogeneous and recent paleogeographical history of the Ionian Islands. Due to their spatial configuration, the two archipelagos exhibit corresponding plant diversity patterns, driven by the same abiotic factors (e.g., climate, geodiversity, human population density), yet they are quite dissimilar regarding the proportion of plant endemism and their biogeographical compartmentalization. Here, we review the spatial, geo-historical and environmental factors determining the taxonomic and phylogenetic diversity and structure of the Aegean and Ionian Island plant communities and assess the impact of climate change on the biodiversity patterns and conservation of the island endemic plants. Island area is the most powerful single explanatory predictor of all diversity metrics in both archipelagos, followed by elevation, human impact, and geological substrata, while distance from the mainland is also one of the drivers for the Ionian endemic plant diversity. Historical processes seem to have driven diversification and island endemic species richness in the Aegean, while they had a limited effect on the island endemic species richness in the Ionian Islands. The assessment of extinction risk status, for both IUCN Criteria A and B, of endemic plant taxa showed that it is very high for many of the regional and local endemics on both archipelagos.

ISiBioD, Italian Small Islands Biodiversity Database

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The vulnerability of small island ecosystems emphasizes the negative impact of Invasive Alien Species (IAS) as they can rapidly develop stable populations and compete with local species. Because of its unique biogeographical patterns, the Mediterranean Basin has one of the greatest levels of biological variety. Knowledge on Italian insular biogeography is often fragmented. To fill this gap, we aim to create the first database of the occurrence of native and invasive species of the Italian small islands for woody vascular plants firstly and then for selected vertebrate taxa. Here, we report the results for 61 Italian small islands, including the checklists of native and alien species obtained and assembled using all the existing published data. We expect to design a multi taxon relational database, written in SQL (Structured Query Language), of the native and invasive species called ISiBioD (Italian Small Island Biodiversity Database). By its harmonized structure, the heterogeneity of taxonomic groups and spatial scales it covers, the DIBIM database will provides opportunities for research focusing on biodiversity assessment and monitoring.

Beyond the concept of oceanic islands as climatic refugia: A high resolution climate dataset for the Canary Islands, CanaryClim

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Understanding how grain size affects our ability to characterize species responses to ongoing climate change is of crucial importance in the context of an increasing awareness for the substantial difference that exists between macroclimates and the actual microclimate experienced by a given species. Climate change impacts on biodiversity are expected to peak in mountain areas and montane oceanic islands, wherein the differences between macro and microclimates are precisely the largest. Here, we generated fine-scale climatic data for the Canary Islands, a mountainous oceanic archipelago and a hotspot of endemism, and compared predictions of climate change impacts on species distributions using the newly generated data at 100 m resolution *versus* available data at 1 km resolution. In particular, we compared the accuracy and spatial predictions of ensemble of small models for 14 Macaronesian endemic bryophyte species using these two climate models: CHELSA (~1 km) and the newly generated CanaryClim (100 m). We also generated future climate data from five individual model intercomparison projects for three warming shared socio-economic pathways. Based on species distribution models generated from CanaryClim and CHELSA, we found that models exhibited a similar accuracy, but CanaryClim-based models predicted buffered warming trends in mid-elevation ridges. Although both climate datasets predicted similar, high future range loss, these were lower for a number of species with CanaryClim. Predicted mean range gains were substantially higher with CanaryClim than with CHELSA. Overall, predicted species extinctions were higher with CHELSA than with CanaryClim. Our results highlight the important role that fine resolution climate datasets can play in predicting the potential distribution of both microrefugia and new suitable range under warming climate across topographically complex oceanic archipelagos.

Addressing the effectiveness of trait imputation methods for island floras

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Island researchers are increasingly incorporating functional traits into island research, and a trait-based perspective has been shown important to determine how colonization and evolution took place on islands. Despite their importance, the lack of trait data on islands represents a significant challenge. Further, removing species with missing trait data is not ideal, as this may bias the analyses. To address the issue of missing trait data, several methods for trait imputation have been developed, particularly based on allometric and phylogenetic relationships. Nonetheless, the effectiveness of these techniques might be reduced for native island species, which are prime examples of evolutionary trait shifts in response to insularity and consequently often exhibit distinct trait combinations compared to mainland ancestors, so-called island syndromes. In this study, we aim to improve our understanding of functional traits in islands. Particularly, we evaluated five widely used trait imputation methods: k-nearest neighbors, multivariate imputation by chained equations (mice), missForest, Phylopars, and Bayesian Hierarchical Probabilistic Matrix Factorization (BHPMF). We selected species lists and functional traits (plant height, leaf width and length, seed and fruit sizes) from the GIFT database (gift.uni-goettingen.de), for seven subtropical archipelagos of volcanic origin, and evaluated the performance of each method for each functional trait and for different species subsets: island endemics, island native non-endemics and mainland species. Our findings will enhance our ability to study functional traits in island ecosystems and help to understand which plant traits respond most strongly to insularity and enhance our ability to study functional traits on islands.

Exploring the extreme intracontinental Palearctic disjunction of Woodwardioideae ferns: a perspective from the Western Palearctic

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The Paleotropical floristic element of the Western Palearctic has been greatly diminished due to geological and climatic fluctuations during the Cenozoic. Among the representatives of this element stand out ferns, particularly the subfamily Woodwardioideae. This subfamily shows a great disjunction on both sides of the Palearctic, with *Woodwardia unigemmata* Makino (Nakai) in East Asia and *Woodwardia radicans* (L.) Sm. (Blechnaceae) surviving in climate refugees in Western Europe and the Macaronesian archipelagos. This distribution makes Woodwardioideae an ideal candidate for testing the evolution of the Paleotropical Geoflora in the Palearctic. To investigate the origin of this disjunction, we reconstructed the phylogenetic relationships and divergence times of the subfamily Woodwardioideae using four plastid DNA regions. Additionally, we sampled *W. radicans* throughout its distribution range and performed phylogenomic analyses based on genotyping by sequencing (GBS). Our results show a divergence between *W. radicans* and *W. unigemmata* in the Pliocene, 3.7 (1.35-7.18) Mya. Subsequently, in the western part of the distribution, *W. radicans* took refuge in Macaronesian archipelagos, from where it appears to have recolonized the continental enclaves in the last 0.8 Mya. The study provides new insights into the evolutionary history of Woodwardioid ferns, challenging the traditional view that certain Paleotropical elements are relicts from the Miocene. Furthermore, our findings highlight the pivotal role played by archipelagos as biodiversity refuges at the extremes of disjunct ranges, and as sources of diversity for recolonization of continents. This holds significant implications for conservation endeavors, particularly for populations of island species threatened by climate change and habitat loss.

Evolution of endemic dwarf plants on a continental island under intense deer herbivory

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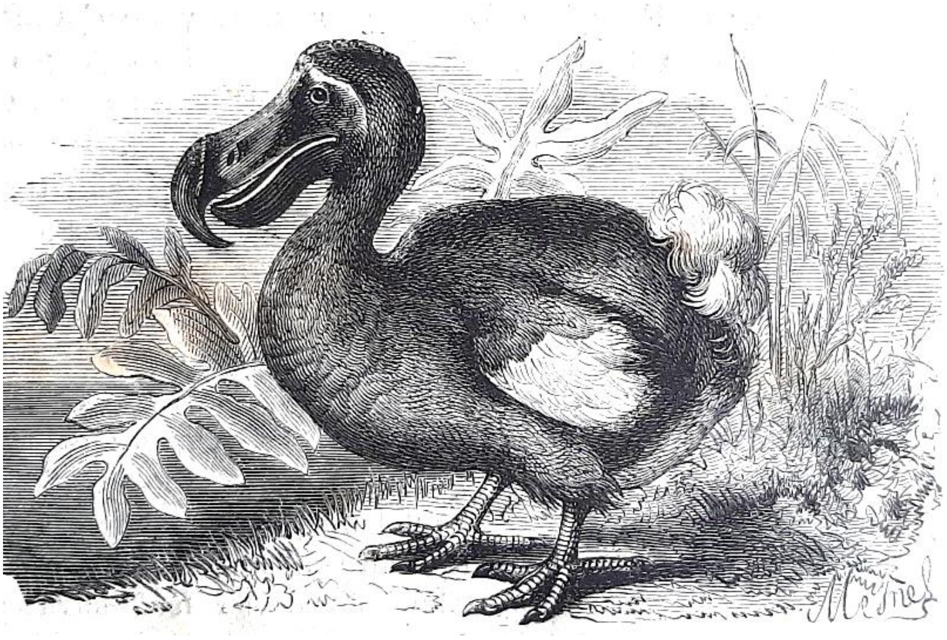
Plant dwarfism, a remarkable reduction in plant sizes, is a widespread phenomenon observed around the world. Various drivers including strong wind, poor nutrients, low temperatures, and grazing pressure of herbivores can lead to the evolution of dwarf form. One of the hotspots of dwarf plants is in the alpine area of Yakushima Island, a small continental island (approximately 500 km^2) in the Japanese Archipelago. At the alpine zone of this island, more than 80 herbaceous species are remarkably miniaturised in terms of plant heights and leaf lengths (less than 50 mm) compared with normal types distributed in main islands. These endemic dwarf plants have long intrigued many botanists, but their ecological drivers of miniaturization have not been fully understood. Since a deer species has inhabited the island for over 12,000 years, we hypothesized that historical deer grazing may have triggered the evolution of dwarf plants. To test this hypothesis, we conducted a multi-species comparison using 40 taxa-pairs including both miniaturised and non-miniaturised taxa on the island and their related taxa in the main islands. We measured the plant size of 1,945 individuals and assessed whether climatic factors, nutrient availability, deer preference, and migration timing could account for the variation in plant size. Our results showed that deer preference most significantly affected the variation in plant size among the factors studied. Genetic analyses showed that most of the dwarf taxa diverged from their counterpart populations during the last glacial period, when the island was connected to main islands by a land bridge. Overall, our study highlights that dwarf plants could have isolated to the island during the glacial period and subsequent historical deer grazing could have influenced to shaping the endemic dwarf plant flora. This finding could enhance our understanding of the relationship between plant evolution and its drivers.

Conservation on Islands

Contributed Talks



(From: L. Figuier, Vita e costumi degli animali: Gli uccelli. Fratelli Treves, Milano, 1881)

Towards a mechanistic understanding of plant invasion on islands: the case of the Compositae family in the Canary Islands

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Invasive species are recognized as one of the most important threats to biodiversity. Oceanic islands harbor a fragile and unique native biota that make them especially vulnerable to biological invasions, among other human-induced disturbances. However, the mechanisms behind the invasive success remain uncertain. Charles Darwin proposed two competing hypotheses to predict the species invasive potential, known as the Darwin's Naturalization Conundrum (DNC). First, the "pre-adaptation hypothesis" proposes that species closely related to the native community will have a higher probability of invasion because they have similar life-history traits that make them pre-adapted to establish and thrive under the same local environmental conditions. Alternatively, the "naturalization hypothesis" predicts that species distantly related to native species can exploit empty niches and avoid competitive exclusion, having a higher invasive potential. These two opposite hypotheses, which rely on environmental and biotic filtering, respectively, can decisively contribute to determine invasive success. In practice, the study of the DNC can be addressed by assessing two different dimensions of relatedness between species: phylogenetic and functional distance. Herein we present the preliminary results of a long-term project that aims to test the DNC in the Compositae family across the oceanic archipelago of the Canary Islands. From a super-phylogeny that includes all the genera and most of the species present in the archipelago, we estimated the phylogenetic relatedness between alien, non-endemic native and endemic species. In addition, functional traits were measured from all the species collected in the field and subsequently functional distances were calculated between the three functional groupings. Integrating both phylogenetic and functional approaches, it allows us to explicitly assess the invasive potential of insular alien species under the framework of the DNC.

Plant conservation in the Aeolian Islands: bringing species back from the brink of extinction

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The Aeolian Islands harbor high plant diversity, counting about 750 native taxa, of which eight are endemic to the archipelago. The recent age of the islands and their continuous volcanic activity impacted on the number of endemic taxa and contributed to the fragmentation of their populations. These taxa are particularly precious for their biogeographical value but are at high risk of extinction due to their reduced distribution and human activities' impact. The Seed Bank of the University of Catania is involved in two international projects for the conservation of four threatened Aeolian plants. The Interreg Italia-Malta SiMaSeed PLUS deals with the reinforcement of *Anthemis aeolica* Lojac., reduced to a single population on the islet of Lisca Bianca, close to Panarea. The LIFE project SEEDFORCE focuses on the conservation of 29 Annex II species of the 92/43 EU Directive "Habitat" with unfavorable conservation status. Of these, three species grow in Aeolian islands: *Cytisus aeolicus* Guss. and *Silene hicesiae* Brullo & Signor., endemic to the archipelago, and *Eokochia saxicola* (Guss.) Freitag & G.Kadereit, endemic to the South Tyrrhenian Sea. Both projects aim at using the seeds for ex-situ conservation and to produce plants for the reinforcement of extant populations or for their reintroduction in sites where they went extinct. Seed germination and plant establishment are key stages of plant life but few data are available on the four target species. Therefore, germination and cultivation protocols are being developed, genetic analysis of the donor populations will inform on the best provenance of the seeds to be used, and the trophic relationships (pollinators) are being investigated. To ensure that the conditions in the intervention sites are suitable for the maintenance of viable populations threats are analyzed and mitigated. Finally, ex-ante and ex-post monitoring will produce data on the reinforcements' success and on the demography of these species.

Long-term monitoring of the Azorean native forest arthropods: what we have learned so far

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A long-term study monitoring arthropods (Arthropoda) is being conducted since 2012 in the forests of Azorean Islands. Named "SLAM - Long Term Ecological Study of the Impacts of Climate Change in the natural forest of Azores", this project aims to understand the impact of biodiversity erosion drivers in the distribution, abundance and diversity of Azorean native arthropods. We targeted taxa for species identification belonging to Arachnida (excluding Acari), Chilopoda, Diplopoda, Hexapoda (excluding Collembola, Lepidoptera, Diptera and Hymenoptera (but including only Formicidae)). Specimens were sampled over seven Azorean Islands during the 2012-2022 period. Arthropods were sampled using passive SLAM traps (Sea, Land and Air Malaise trap). Main results so far include the following patterns: i) temporal beta-diversity was much greater for non-native species than for native species; ii) the exotic species are accumulating trough time not showing an asymptote; iii) when testing for the native species decline, we observed no decline in overall arthropod diversity, but a clear increase in the diversity of exotic arthropods and some evidence of a tendency for decreasing abundance for some endemic species. Greater turnover of non-native species is due to source-sink processes and the close proximity of anthropogenic habitats. The high rate of stochastic turnover of non-native species indicates that attempts to simply reduce the populations of non-native species in situ within native habitats may not be successful.

Correlates of extinction vulnerability and biogeographical variation in amphibians on oceanic land-bridge islands

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Identification of key factors that make certain species more vulnerable to fragmentation is vital for elucidating processes underlying extinction and targeting conservation priorities. However, past evidence was primarily from trait-based responses of species in newly formed patches, providing few inferences on the delayed species responses mediated through landscape features. To bridge the gap, we surveyed amphibians on 37 islands in the Zhoushan Archipelago, China, and on the adjacent mainland. We considered the proportion of islands occupied as a measure of species' vulnerability to long-term isolation and related it to nine species' traits to achieve the best correlates. We also explored biogeographical variation in amphibians by relating four biogeographical variables to the probability of occurrence of each species on islands through logistic regression analyses. Model selection identified that species with lower natural abundance, smaller clutches, and the combination of larger eggs and smaller clutches have a lower occupancy frequency on islands. Moreover, these three variables were also substantially important in the model-averaged analysis. The probabilities of occurrence of five species showed positive correlations with island area, and that of *Hyla chinensis* was negatively related to distance to the mainland. Area was not an important predictor for another five species, which only inhabited larger islands. By contrast, two species were widely distributed on islands, showing no correlations with any biogeographical variables. Our study stressed that amphibians were non-equally vulnerable to long-term fragmentation. Moreover, area-related extinction predominantly limited species distribution, especially for those with low natural density or 'slow' life-history strategies. We highlight that, to achieve effective conservation, management efforts should not only focus on species with extinction-prone traits but also the landscape features which threaten the persistence of populations. Particularly, conserving large islands is more beneficial for supporting populations than multiple isolated islets.

Protecting what we know: Conservation priorities in the endemic-rich islands of São Tomé and Príncipe (Central Africa)

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Prioritization is a key step towards effective conservation, which is often severely constrained by missing information. Widely recognized as a global biodiversity hotspot due to its high number of endemic species, the small developing island nation of São Tomé and Príncipe has greatly improved terrestrial conservation prioritization despite data remaining scarce. Recent species-based efforts to define conservation priorities include attempts to red list plants and invertebrates. However, even the species list of the much better-known vertebrates is far from complete, having increased from 45 to 61 endemic species since 1994. Nineteen of these are threatened but their categorization is unstable even for birds, the most studied taxa in the islands. Just over the last decade, categories of threat have changed or been proposed to change for ten (36%) of the endemic bird species, most of which due solely to improved knowledge. National site-based conservation efforts include the creation of protected areas in 2006, covering roughly the best-preserved third of the endemic-rich native forest on each island. Nonetheless, their boundaries are problematic because they were defined based on close to no data on the distribution of species and ecosystems. Recent progress has used the High Conservation Value framework to highlight 21 important zones that had been missed out, and that are now being integrated in the network of protected areas. São Tomé and Príncipe highlights how conservation priorities change with improved information, alerting for the need to assess uncertainty linked to missing data. Taxonomy, distributions, populations, phylogenies, ecological functions, and abiotic and biotic interactions are all now much better known but having increasingly more and more complex information creates new challenges to integrate information and guide conservation. Numerous recent funding also show how setting priorities was a vital first step to help refine conservation actions.

A yellow crazy ant eradication program clarifies ant impacts on the seabirds and terrestrial crabs of a Polynesian atoll

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Invasive species pose a major threat to biodiversity, especially on islands, where the identification and eradication of problematic invaders represents an important management tool. Yellow crazy ants (*Anoplolepis gracilipes*) are an invasive ant species that spray formic acid to subdue their prey. Seabirds and terrestrial crabs, two key faunal groups on atoll ecosystems, may both be affected by this invader. Here we sought to determine the extent to which ants influence these groups by relating yellow crazy ant presence and abundance to the density of ground-nesting seabirds and terrestrial crabs. We established 70 plots ($r=5m^2$) across fully invaded, partially invaded, and uninvaded (control) islets on Tetiaroa atoll (French Polynesia). Within each plot we quantified ant, crab, and seabird abundances before and after the initiation of an ant eradication program where we reduced ant abundances by deploying hydrogel crystals saturated with sugar water and insecticide. Despite low ant abundances during the pre-eradication monitoring period, we found that foraging ant abundance was negatively associated with the density of both ground-nesting seabirds (predominantly brown noddies, *Anous stolidus*) and the dominant terrestrial crab species (strawberry hermit crabs, *Coenobita perlatus*). Noddy chicks within invaded habitats were more likely to exhibit physical deformities and spent more stamping/preening than chicks in uninvaded habitats. However, monitoring data at 360 noddy nests demonstrates that egg-hatching success was unaffected by ant presence, potentially because the hermit crabs that avoid invaded areas were also important egg predators. Post-eradication monitoring demonstrated a rapid decrease in ant abundance 10-days post-baiting, and showed that non-target impacts of the baiting itself on crab communities were minimal, with visible mortality confined to two of the most terrestrial species present. Eradication programs provide both conservation benefits and a unique experimental context for investigating the effects of invaders on native fauna.

Biodiversity markets: a huge opportunity for island conservation

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Islands host a large part of global biodiversity, and this disproportionality is particularly pronounced in Europe. Much island biodiversity is threatened. While protected areas play a part in conserving island biodiversity, their implementation is often biased towards particular ecosystems (particularly those in areas of relatively low land-use value), and the protection they offer is variable. Global targets for reducing biodiversity loss have consistently been missed, as have most regional targets. Our approach to conservation to date is therefore insufficient, in the face of the extinction crisis. A new opportunity to conserve at scale is offered by the emerging biodiversity markets, which open up the potential for an order of magnitude increase in funding for conservation, mainly through private investment. Global implementation of biodiversity markets builds on lessons learned from carbon markets, but biodiversity is much more complex than carbon. I discuss current developments and opportunities for island conservation.

Comparative study of bryophyte communities in caves and outside habitats in Terceira Island, Azores

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Caves are among the richest and most interesting extreme environments for bryophytes in the Azores, however, their response to environmental and landscape matrix of these habitats has not been studied comparatively. In this study we compared the known bryophyte flora of 11 caves in Terceira Island (Azores) to the bryophyte species growing on rocks just outside their entrances. We characterized the two communities considering the diversity and number of species, their life strategies and life forms, and their environmental preferences of light, water, and soil reaction. Both studies showed acceptable completeness values of approximately 70%. This study documented a total of 101 bryophyte species, comprising one hornwort, 37 liverworts, and 63 mosses. Among them, 41 species were observed exclusively inside the caves, 39 species outside the caves, and only 21 species were found in both habitats. As expected, environmental factors such as light and moisture played a crucial role in shaping these bryophyte assemblages. As hypothesized, bryophytes with K-strategy (with longer life spans) and more complex life forms (e.g., fans, dendroids, pendants) are favoured inside caves, whereas species with more compact life forms (e.g., cushions, mats) were found in conditions of full sunlight and intermediate moisture. Species of conservation concern are more likely to occur inside caves, whereas more common species may also be found in the surrounding areas. Our initial findings suggest that there is significant potential in comparing the bryophyte species found inside and outside caves to study their taxonomic and functional diversity, as well as their ability to adapt. This approach may also reinforce the evidence for the importance of protecting caves as a refuge for threatened species.

Unsustainable artisanal fishery inside UNESCO Marine Protected Area, Red Snappers in Coiba National Park (Panamá)

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Coiba National Park (CNP), a UNESCO world heritage site in the Tropical Eastern Pacific off Panama's coast and a marine biodiversity hotspot was established in July 2004 and the enforcement of its management plan started in 2009. The primary users of the park were artisanal fishermen. This study compares the sustainability of fisheries inside the Marine Protected Area (MPA) before and ten years after the management plan. Fishing landings per trip, species, and group size were quantified at the main landing port, determining the main target species and size. A total of 148 fishing trips were recorded in 2019 from 13 vessels, 8 of them authorized to fish inside the MPA, and five on its souring areas. The Pacific red snapper (*Lutjanus peru*) was the targeted fish species, 91.5% of its landings in 2006 (pre regulations), and 80% of its landings in 2019 (ten years after enforcement) were juvenile individuals. Although fishing pressure has been significantly reduced inside the MPA, the fisheries are still unsustainable since the activity is targeted towards red snapper juveniles, a long-lived and ecologically important predator. Current regulations allow exporting juvenile red snappers from a marine protected area and UNESCO site to serve customers in the global north looking to eat a plate-size red snapper.

Species distribution modelling to identify habitat islands suitable for narrow endemic climate relicts

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Ptilostemon greuteri (Asteraceae) is one of the most fascinating narrow endemic plant species of the Mediterranean Basin. This woody broad-leaved thistle only survives in two microrefugia, distant approximately two kilometres from one another in the North-Western Sicily (Italy). Its habitat consists of NNE-facing calcareous cliffs and ledges as well as the bottom of narrow, steep and shady gorges, benefitting from the humidity rising from the sea that creates a kind of habitat islands surrounded by a contrasting climatic matrix. For this reason, *P. greuteri* can be considered a climate relict that persists in enclaves of benign environmental conditions within a nowadays inhospitable regional macroclimate. In order to discover previously undetected populations, and to select the most suitable translocation sites, we performed species distribution modelling using high resolution Digital Terrain Model (DTM) and other DTM-derived micro-topographic variables such as insolation, hillshade, aspect and Topographic Position Index (TPI). The species distribution model identified very few localities offering suitable conditions for the target species, and field validation of the model through field vegetation surveys confirms its reliability. Unfortunately, we did not discover any new population of *P. greuteri*. The first translocation activities resulted in a successful introduction of the species in a new site. Our results suggest that species distribution modelling can be a useful method to identify suitable habitat islands for translocation activities.

A nonnative tree species reclaims its prominence after extreme weather

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Uncertainties about controls on tree mortality make forest responses to land-use and climate change difficult to predict. In a 19-year study across Puerto Rico and the U.S. Virgin Islands, we found that as forests recovered from a hurricane in 1998 and earlier deforestation, young and small trees of nonnative species died at twice the rate of natives. But after Hurricane Maria struck Puerto Rico, the island-wide biomass of a fast-growing nonnative species, *Spathodea campanulata* (the African Tulip Tree), might again be overtaking that of the most common group of native tree species, which is non nitrogen-fixing broadleaf evergreen species. We tracked biomass of tree functional groups in tropical forest inventories across Puerto Rico and the U.S. Virgin Islands. Then, with random forests, we ranked 86 potential predictors of small tree survival (young or mature stems 2.5-12.6 cm diameter at breast height). Forests span dry to cloud forests, range in age, geology and past land use and experienced severe drought and storms. When excluding species as a predictor, top predictors are tree crown ratio and height, two to three species traits and stand to regional factors reflecting local disturbance and the system state (widespread recovery, drought, hurricanes). Native species, and species with denser wood, taller maximum height, or medium typical height survive longer, but short trees and species survive hurricanes better. Trees survive longer in older stands and with less disturbed canopies, harsher geoclimates (dry, edaphically dry: e.g., serpentine substrates, and highest-elevation cloud forest), or in intervals removed from hurricanes. Results call into question whether more frequent hurricanes might perpetuate this light-wooded species commonness. At the same time, drought may favor other types of species. Climate change influences on forest composition and ecosystem services may depend on the frequency and severity of extreme events.

An invasive appetite: combining molecular and stable isotope analyses to reveal the diet of introduced house mice (*Mus musculus*) on a small, subtropical island

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House mice (*Mus musculus*) are a major conservation threat on islands, where they adversely affect native species' distributions, densities, and persistence. On Sand Island of Kuaihelani, mice recently began to depredate nesting adult mōlī (Laysan Albatross – *Phoebastria immutabilis*). Efforts are underway to eradicate mice from Sand Island, but knowledge of mouse diet is needed to predict ecosystem response and recovery following mouse removal. We used next-generation sequencing to identify what mice eat on Sand Island, followed by stable isotope analysis to estimate the proportions contributed by taxa to mouse diet. We collected paired fecal and hair samples from 318 mice between April 2018 to May 2019; mice were trapped approximately every eight weeks among four distinct habitat types to provide insight into temporal and spatial variation. Sand Island's mice mainly consume arthropods, with nearly equal (but substantially smaller) contributions of C3 plants, C4 plants, and mōlī. Although seabird tissue is a small portion of mouse diet, mice consume many detrital-feeding arthropods in and around seabird carcasses, such as isopods, flesh flies, ants, and cockroaches. Additionally, most arthropods and plants eaten by mice are non-native. Mouse diet composition differs among habitat types but changes minimally throughout the year, indicating that mice are not limited by food source availability or accessibility. Eradication of house mice may benefit seabirds on Sand Island, but it is unclear how arthropod and plant communities may respond and change. Non-native and invasive arthropods and plants previously consumed (and possibly suppressed) by mice may be released post-eradication, which could prevent recovery of native taxa. Comprehensive knowledge of target species' diet is a critical component of eradication planning. Dietary information should be used both to identify and monitor which taxa may respond most strongly to invasive species removal and to assess if proactive, pre-eradication management activities are warranted.

Biotic disharmony favors invasiveness in New Caledonia

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New Caledonia is archipelago in the South Pacific, a hotspot of biodiversity marked by the extremely high levels of endemism, and by a long and unique history of introductions of alien species. Our study was designed to verify and complete the dataset on Invasive Alien Species (IAS) in TAXREF, the French Taxonomic Repository, based on exhaustive search in scientific and gray literature, and expert knowledge. Besides, we assembled data on the year of the first record in the archipelago in a database named FATERCAL (Faune Terrestre de la Nouvelle-Calédonie). Based on it we (1) evaluated the richness and diversity of the alien fauna, (2) characterized the dynamics of introduction, and (3) modeled the relative role of native fauna as a filter or as a facilitator for the introduction of alien species. The alien fauna of New Caledonia comprises 1315 species, with 22 recognized as invasive. They belong 9 phyla, 362 families and 976 genera. Arthropoda, with 78% of the species (mostly represented by Insecta = 87%) is the most diverse. Mean number of first records/year doubled after the 1940s (4.27 before; 9.4/year after). Among several factors examined (e.g., human population, years, nickel extracted and mean and maximum air temperature), human population best predicts these increases, showing a tendency of no saturation. In a business as usual scenario, the number of new records per year is expected to be as high as 13.5±2.5 by 2050. The relation with native fauna was studied with a Zero-inflated Poisson regression. The coefficient for native species is negative (native species is exp(-0.03371) = 0.9668519), meaning that as the number of native species goes up, the number of introduced species goes down, showing that IAS tend to have higher richness in families with low local diversity, and linking invasiveness with taxonomic disharmonies of the native fauna.

Capturing the biological diversity of the island of Koltur, Faroe Islands – a baseline for long-term monitoring

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Koltur is a small (2.5 km^2) island located in the central part of the Faroe Islands, an archipelago of 18 islands in the North Atlantic. Apart from two permanent inhabitants and currently 160 sheep grazing on Koltur, there is little human influence. Due to the absence of invasive species like mice, rats, and the New Zealand flatworm, Koltur supports supposedly intact native communities. Despite its small size, a variety of habitats occur on the island, e.g., steep mountain slopes, bird cliffs, grassland, streams, rocky shore, and a sand beach. Large parts of the island are in the process of being established as a Nature Reserve. An extensive project started in summer 2021 with the goal to inventory all species of plants, birds, and invertebrates on the island, which is to provide a baseline for long-term monitoring of the Koltur Nature Reserve. In this talk, an overview is given over the different sampling methods employed and the progress of the species inventory. Currently, 314 species of plants and animals have been recorded since the start of the project, the majority of which are insects. About 60 new species records for the island belong to the orders Coleoptera (beetles) and Diptera (flies and midges) alone. Some of them are not only new records for Koltur but for the Faroes. In addition, Koltur is an important breeding site for European storm-petrels (*Hydrobates pelagicus*) and other ground-nesting birds. Their populations are being studied using for example nest cameras.

The red-list assessment of coastal habitat types in Finland

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Assessments of the red-list status of species and habitat types are the most important indicators used to monitor the state of biodiversity, and their results are continuously alarming. The assessment of threatened habitat types in Finland was conducted using the standard of the IUCN's Red List of Ecosystems. The primary assessment criteria were change in habitat type quantity, change in abiotic and biotic quality, and rarity. The current trends for habitat types in terms of their state were also assessed. The assessment covered all terrestrial and aquatic habitat types in Finland (in total 388 types). Baltic Sea coast, including the Finnish archipelago, is one of eight main habitat groups. A total of 45 Baltic Sea coastal habitat types were assessed. Of these, 58% were assessed as threatened (VU, EN or CR), 15% as near-threatened and 27% least concern. The Baltic Sea coastal habitat type groups are (the number of threatened types/the total number of types): Gravel, shingle and boulder shores (0/2), Sand beaches and dunes (8/8), Meadows (1/3), Reedbeds (0/3), Drift lines with organic material (2/3), Coastal scrubs and forests (11/19), Rock pools (0/1), and Coastal habitat complexes (4/6). The group of coastal sand beaches and dunes is the most threatened. The reasons for becoming threatened and the threat factors vary between the habitat types. The main reasons were: 1) Overgrowth caused by the eutrophication, 2) Construction and mechanical wear, 3) Forestry, 4) Clearing natural vegetation for agriculture, 5) Invasive alien species, and 6) Climate change. In order to preserve threatened habitat types, there is an urgent need to expand the conservation network and carry out ecological restoration especially in open habitat types.

Rapid phenotypic shifts and community alterations caused by predator invasions on islands in the Anthropocene

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Invasive top predators wreak havoc on island ecosystems worldwide. The impact of these invasions is particularly strong when predators decimate predator-naïve mesopredators, which often play key roles for ecosystem functioning. This talk will present empirical evidence of the ecological and evolutionary processes by which novel predators alter not only the biology and population dynamics of their prey species but also the structure and stability of the ecosystems they live in. More specifically, we will focus on two major questions in invasion biology: (1) how does phenotypic variation of both mesopredators and top predators rapidly (co)evolve as a response to new selection regimes, and (2) how do these changes cascade to alter ecosystem functioning? The talk will draw on results from two different study systems, both using lizards as the study species, one in the Caribbean and one in the Mediterranean. In a field experiment manipulating predation by using small Caribbean islands as experimental replicates, we showed that natural selection rapidly alters the behavior and morphology of lizards under new predation pressures, and these behavioral shifts cascade to dramatically alter resource flow dynamics from marine to terrestrial ecosystems. In the Mediterranean, an iconic keystone species of wall lizard is being decimated by rapidly spreading invasive whiptail snakes. By combining field and lab experiments with cutting-edge molecular tools we are deciphering the evolutionary dynamics of both native mesopredators and invasive top predators and we will present evidence that the arrival of this new top predator has altered species composition in this delicate Mediterranean ecosystem. Provided that invasive predators are a major driver of species extinction worldwide, our integrative approach to understand the consequences of these invasions, from genes to ecosystems, transcends our study system and can significantly contribute to the conservation of island ecosystems worldwide.

Evolution, extinction and the paradox of anthropogenic enrichment

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One salient result of the defining feature of islands – their geographic isolation – is their distinct ecological simplicity, characterized by the absence or paucity of the diverse assemblages of competitors and predators that tend to dominate mainland ecosystems. The resultant reversals in selective pressures on islands lacking these ecological dominants create both the evolutionary marvels as well as the perils of island life. Here we focus on the natural patterns and the impacts of humanity on evolution, diversity, distinctiveness and extinction of insular vertebrates – in particular, non-volant terrestrial mammals and giant, flightless birds. Our focus includes patterns in body size evolution, resultant susceptibility to range collapse and extinctions, and a pervasive phenomenon for insular biotas, in general – what we refer to as the paradox of anthropogenic enrichment.

The interplay between multiple introductions and convergent reproductive strategies drives genetic diversity and structure in the most invasive plant in the Sub-Antarctic

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Biological invasions in remote areas that experience low human activity provide unique opportunities to elucidate processes responsible for invasion success. Here we study the most widespread invasive plant species across the isolated islands of the Southern Ocean: the annual bluegrass, *Poa annua*. To analyse geographic variation in genome size, genetic diversity, and reproductive strategies, we sampled all major sub-Antarctic archipelagos in this region and generated genotype data for 470 individual plants representing 31 populations. We found low population genetic structure and lack of isolation by distance among the sub-Antarctic archipelagos, but high population structure within each archipelago. We also identified high levels of genetic diversity, low clonality and low selfing rates in annual bluegrass populations (contrary to rates typical of continental populations). A comparison of parallel annual bluegrass invasions on human-occupied Marion Island and unoccupied Prince Edward Island revealed that annual bluegrass populations show higher genetic diversity at human landing sites on both islands. Moreover, extensive admixture and high levels of genetic diversity is evident for Marion Island populations, while Prince Edward Island populations show no apparent admixture and low genetic diversity. Our findings suggest multiple independent introductions of annual bluegrass into the sub-Antarctic, which promoted the establishment of genetically diverse populations. Despite multiple independent introductions, populations of annual bluegrass adopted convergent reproductive strategies (outcrossing) independently in each major archipelago. Subsequently, humans influenced the post-introduction dynamics of invasive alien populations, facilitating high levels of genetic variation and admixture. These demographic dynamics have probably benefited annual bluegrass invasions in the Southern Ocean by increasing genetic diversity and the species' ability to cope with novel environmental conditions.

The demography of the threatened plant *Echium pininana*, an endemic of the island of La Palma

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Species endemic to islands are often particularly endangered. Analysing the factors influencing their population dynamics can be a powerful tool guiding conservation measures for them. We studied the population biology of the giant monocarpic rosette plant *Echium pininana* in the laurel forest of the island of La Palma, Canary Islands. The pooled asymptotic population growth rate λ of six populations was 0.988 and did not differ significantly from equilibrium. However, there was considerable turnover of plants. Mortality was high for small plants, but also considerable for medium and large plants. Mean age at reproduction was 3.5 years and thus lower than for other large monocarpic rosette plants. Life table response analyses showed that the demography of *E. pininana* depended strongly on the light environment. The asymptotic population growth rate was higher in bright plots with a leaf area index (LAI) ≤ 2 than in darker plots with an LAI > 2 ($\lambda = 1.11$ vs. $\lambda = 0.73$). This was mainly due to higher recruitment and the stronger growth and higher survival of small plants. In contrast, survival and growth of large plants was higher in darker than in bright environments. In all populations of *E. pininana* single size classes were dominant and the proportion of small plants was negatively - and the proportion of large plants positively - correlated with vascular plant cover. This indicates that *E. pininana* grows mostly in even-aged cohorts that age in parallel to the course of succession in their habitats and reproduce in synchrony. *E. pininana* is not immediately threatened with extinction, but the number of extant populations is small and they are likely to be short-lived. To conserve the species frequent disturbances that occur at larger than yearly intervals are necessary.

How long would it take to recover the diversity lost due to humans on Madagascar?

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Since humans colonized the island of Madagascar, many of its unique mammal species have gone extinct. Currently, the majority of the island's extant mammal fauna is threatened with extinction. However, the severity of recent and potential extinctions in a global evolutionary context long remained unquantified. In this talk, we present a recent study in which we estimated how long it would take for Madagascar to regain its lost and threatened mammal diversity. We compiled a phylogenetic dataset for the complete non-marine mammalian biota of Madagascar and estimated the islands' natural rates of extinction, colonization, and speciation. We measured how long it would take to restore Madagascar's mammalian biodiversity under these rates, the "evolutionary return time" (ERT). We found that return from current to pre-human diversity would take 1.6 million years (Myr) for bats, and 2.9 Myr for non-volant mammals. However, if species currently classified as threatened go extinct, the ERT rises to 2.9 Myr for bats and 23 Myr for non-volant mammals. In this talk we will present these results and discuss them in a global context, comparing with examples from other islands (New Zealand, Caribbean), and evaluating the pros and cons of the use of the ERT metric. Overall, our results suggest that an extinction wave with deep evolutionary impact is imminent on Madagascar unless immediate conservation actions are taken.

Landscape ecology, trophic interactions and phylogeny of the threatened Madeiran Pipistrelle in Porto Santo Island, Macaronesia

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Around 60% of all bat species occur in islands, and nearly one in four is an insular endemic. Bats are often the only native terrestrial mammals in oceanic islands and despite increasing anthropogenic pressures, little is known about the distribution, natural history, and population status of most insular bat populations. The sub-tropical archipelago of Madeira is composed by the volcanic islands of Madeira, Porto Santo and the Desertas, and is home to the Macaronesian endemic *Pipistrellus maderensis*, to an endemic subspecies *Nyctalus leisleri verrucosus* and to *Plecotus austriacus*. *Pipistrellus maderensis* is known to both Madeira and Porto Santo, whereas the other two species have only been recorded in the former. Yet, no bats have been recorded in Porto Santo for over 15 years, raising fears that bats are probably extinct in the island. In July 2021, we conducted an island-wide acoustic survey using AudioMoth passive acoustic recorders, leading to the detection of *Pipistrellus maderensis* in 28 out of the 46 sampling sites (60%). The species' activity was strongly associated with artificial water sources, and genetic samples from six captured individuals revealed that the populations of *Pipistrellus maderensis* in Porto Santo and Madeira have a close phylogenetic affinity. Furthermore, using DNA metabarcoding, we found that the species feeds on a wide variety of insects, including several economically important pest species and disease vectors. These findings emphasise the need to target more conservation and research efforts towards extant island bat populations, and the potential ecosystem services they provide.

Establishing Marine Protected Areas: a reflection on practical challenges and opportunities for social-ecological integration

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Integrative social-ecological approaches are crucial for addressing sustainability challenges in coastal and marine systems. Several approaches have been proposed to achieve better integrated management, such as Marine Spatial Planning (MSP). The designation of Marine Protected Areas (MPAs) and MSP often take place in parallel to each other. Given the potential synergies between these processes, there is a need to address barriers to the uptake of MSP approaches for integrative conservation mechanisms. Using São Tomé and Príncipe (STP) as case study – an extremely biodiverse archipelago – we illustrate an approach where MSP was employed as an operational framework for an MPA-establishment initiative aimed at marine conservation and sustainable small-scale fisheries. Here we report the process and related consultations from its planning stage until the official designation of the first MPAs in the country, with a focus on lessons learnt and recommendations. The MSP process aimed to prioritise community engagement in MPA design, involving all local stakeholders including fishers and fish traders, local and national government, civil society organisations and private sector. Key project consultations were based on biological and social information overlaid using the tool Marxan with Zones with best available scientific knowledge. This reflection on project steps, enabling conditions and barriers hopes to contribute towards a realistic description of MSP implementation on the ground, drawing relevant lessons for conservation practitioners. Given national commitments to Blue Growth and high dependence on fisheries, with implications for biodiversity, food security and human wellbeing, developing effectively integrative MSP approaches is crucial for resilience in the light of current patterns of change.

Creating reference native communities for conservation efforts by modeling dominant plant species across Hawaiʻi

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Understanding past, present and future spatial distributions of Hawaiian plant species is key to management. However many species not only extend across a wide range of physical environments, but also vary widely in terms of local abundance (cover). We have complied an extensive database of over 3,000 vegetation plots across Hawaii to develop spatially explicit models of cover for key native and invasive species. We statistically relate vegetation cover values to biophysical variables including temperature, precipitation, cloud frequency, and substrate age, resulting in projections of potential cover that represent estimates of cover for dominant native species across Hawaiʻi. One key result of these models is a spatially explicit quantification of the influence of cloud moisture (fog) on native plant distributions. This observed effect is independent of rainfall, and may be essential in modeling other climate-dependent species. By combining individual species models, we have also successfully modeled native community distribution that serve as a baseline to 1) assess habitat quality, 2) define specific ecological restoration objectives, and 3) identify potential for key invasive species to threaten a site (even where they are presently not found). Future work will project abundances under climate change conditions to anticipate shifting baselines of native dominance and invasive threats.

Rodent and cat eradications in the Western Indian Ocean: lessons learnt and perspectives

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Islands free of exotic predators are essential for the conservation of native biodiversity, particularly for endemic plants and animals, marine wildlife (seabirds, turtles) and surrounding coral reef ecosystems. Steps to rehabilitate island ecosystems and speed-up their recovery include the eradication of invasive predators and competitors, vegetation management and conservation translocation of native wildlife. We used data from the Database of Island Invasive Species Eradications to ascertain the number and success of rat and cat eradications in the Western Indian Ocean, and we compiled from bibliography, experts and practitioners some main lessons learned and perspectives. 54 successful rodent and cat eradications (65.9% of 82 attempts) have been recorded. This includes 23 successful outcomes for Black rats (64% of 36), 5 for Brown rats (80% of 6), 10 for House mouse (56% of 18) and 16 for Feral cats (73% of 22). Rat eradication operations are particularly complex and challenging in tropical islands. The remoteness of some islands is also a difficulty. Seychelles, French territories (TAAF/Iles Eparses/Mayotte) and Mauritius represent the large majority of recorded attempts. Main lessons learned include the key importance at pre-eradication stage of species/ecosystem knowledge and feasibility studies, expert consultation, thorough but flexible planning and strong partnerships. Elimination of hotspots of rat infestation (green waste, old coconut piles, etc.) is key for eradication success. During eradication stage, exemplary waste management, a long presence of palatable bait on the ground, and keeping sufficient bait available appear also essential. Biosecurity to prevent reinvasions, and early detection and rapid reaction capacity to deal with incursions are key during post-eradication. Very significant benefits have been observed for species and ecosystems, as well as economic ones through ecotourism development. Recent achievements, currently planned operations, key limiting factors and future prospects are presented for each territory. A call is made to develop regional cooperation.

Harvesting the power of remote-sensing technologies to investigate the spatiotemporal dynamics of insular vertebrates and their interspecific interactions

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Remote-sensing based technologies such as camera traps and acoustic recorders are increasingly used in ecology and conservation. They have an enormous potential to provide critical information on the state of, and pressures on, biological diversity and ecosystem services, at multiple spatial and temporal scales. Using examples from Macaronesia and the Gulf of Guinean oceanic islands we will showcase how low-cost acoustic detectors and camera traps can be used to investigate multiple dimensions of the spatiotemporal dynamics of native and non-native island vertebrates and their interactions. For instance, we will report on how we have used AudioMoth detectors to investigate how bats on Madeira Island are affected by human-induced land-use change and orography. We obtained >63,000 bat passes across 216 sites and found species-specific and scale-dependent responses to land-use cover. The activity of *Pipistrellus maderensis*, the most common species, was positively associated with landscape-scale shrubland, cropland and Laurisilva (primary forest) cover, whereas the activity of the rarer *Nyctalus leisleri verrucosus* and *Plecotus austriacus* were negatively influenced by Laurisilva and cropland cover, respectively. Furthermore, altitude had a negative effect on the activity of *Nyctalus leisleri verrucosus* and *Plecotus austriacus* but did not seem to influence the activity of *Pipistrellus maderensis*. On a similar survey, but using camera traps instead of acoustic detectors, we found that *Crocidura fingui*, an IUCN Data Deficient shrew endemic to Príncipe Island (Western Central Africa) seems to have an island-wide distribution, inhabiting both primary forest and humanised habitats. Camera trap data revealed that the species is largely nocturnal and exhibits a considerable spatiotemporal overlap with introduced mammals such as civets, cats and rats. The combination of low-cost acoustic detectors and camera traps offers great potential for island-wide vertebrate surveys in small- to medium-sized islands and can provide much needed data for the evidence-based management of island biodiversity.

Bats of European islands are in troubled waters: setting conservation priorities

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Insular systems' colonization is influenced by various factors, with species mobility being one of the most important. Flying vertebrates such as bats are more likely to reach islands than other groups of mammals, and this has important implications for the species that inhabit these islands. Europe has several endemic bat species of significant conservation value inhabiting its islands, but insular bats often face extinction risks and are understudied. Mediterranean islands that are closer to the mainland and connected through stepping-stone insular systems are easier to reach than oceanic islands like those found in Macaronesia. The distance to the mainland can affect gene flow and speciation, leading to the evolution of endemic species like *Pipistrellus maderensis* and *Nyctalus azoreum* in oceanic systems. Even relatively narrow sea stretches like the Gibraltar Strait can prevent gene flow in bats, which may explain the occurrence of endemic species like *Plecotus sardus* on Sardinia. Some European islands, such as Pantelleria and Malta, are home to populations of North African bats, such as *Plecotus gaisleri* and *Myotis punicus* (the latter also found on Sicily and Sardinia). The small population sizes typical of island environments make these bats especially vulnerable, and several populations are now critically endangered, including *P. sardus* and the Cyprus population of *Rousettus aegyptiacus*. Insular bat populations in Europe face a range of threats, including human persecution, land use change, wildfires, and pesticide spread. These threats are often compounded by the limited research attention paid to insular bats, which can result in population declines going unnoticed. It is crucial to increase research and management efforts for European insular bat populations given their high conservation value and the critical ecosystem services they provide. Unlike on the mainland, these services are less likely to be compensated through metapopulation dynamics and species turnover.

Evaluating the impacts of the hala scale, *Thysanococcus pandani* Stickney on native hala forest, regeneration in the Hawaiian Islands

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In Hawaii, the hala scale, *Thysanococcus pandani* Stickney, was first detected in Hana, Maui in 1995. Its primary host plant is the hala tree, *Pandanus tectorius*, a native tree which form coastal forests throughout the Hawaiian Islands and play an important role in preventing erosion. Hala is frequently planted as a landscape tree and are very significant to native Hawaiian weaving traditions. Hala seeds floated over from Australia approximately 1 million years ago. After an accidental introduction on Maui, the hala scale has been found on Molokai, Oahu, Lanai, and Hawaii Island. The hala scale is currently widespread on Maui and Molokai. The insect is a sedentary feeder on the leaves and fruit of the tree and heavy infestations result in discoloration, early crown drop, and tree death. Available literature indicates that heavy infestations prevent seedling regrowth, suggesting that the hala forests on Maui and Molokai may not regenerate, leaving a critical gap that impacts coastal ecosystems and the continuation of cultural practices. To evaluate if this is the case, we are conducting a statewide plant demographic study of coastal hala forests. By June 2023 we will aim to establish a minimum of 24 plots over 8 sites on Molokai and Maui, with a similar amount of sites on Kauai and Hawaii Island. We are currently documenting population structure and hala scale intensity, along with biotic and abiotic factors that may also affect regeneration, including elevation, canopy openness, and understory invasive species cover. Our results will shed light on differences in hala regeneration on islands that do not have the hala scale (Hawaii Island and Kauai) and those that do (Maui and Molokai) and provide a baseline conservation assessment of this species. Our preliminary results indicate that there is some regeneration of hala scale forests on Maui.

Benefits of using automatic cameras to survey plant-pollinator interactions on a remote Mediterranean Island

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Pollination services are essential for maintaining healthy ecosystems, but pollinating insect populations are declining globally. Collecting data on plant-pollinator interactions through direct observations can contribute to biodiversity conservation, but it can be time-consuming and expensive, particularly on remote islands. Therefore, it is necessary to employ new techniques that enhance the efficiency of field sampling. In this study, we used automatic cameras (based on Raspberry Pi computers) and developed deep learning algorithms to detect pollinators in the videos. We tested this novel approach on Cabrera Island (Balearic Islands) throughout a flowering season. Our main objective was to compare the plant-pollinator interactions captured by automatic cameras with those documented through direct observations using ecological networks. In about 35h of recording, the cameras filmed 1114 interactions, while in 50h of direct observations, we recorded 1534 interactions. Our deep learning algorithms achieved an accuracy rate of 89% in automatically detecting pollinators, significantly reducing the time spent processing the images manually. Moreover, the cameras recorded less common interactions and foraging behaviours that we did not detect in the direct observations. In summary, using automatic cameras and deep learning algorithms to detect pollinators in videos is a promising approach to survey plant-pollinator interactions. Its main advantages include its efficiency in data collection, ability to capture rare interactions and potential for use in remote areas. However, potential limitations exist, such as the expertise to prepare this specific equipment. This technique can be important in biodiversity conservation and informing management practices for pollinator-dependent ecosystems.

The global contribution of invasive vertebrate eradication as a key island restoration tool

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Islands are global hotspots for biodiversity and extinction, representing ~ 5% of Earth's land area alongside 40% of globally threatened vertebrates and 61% of global extinctions since the 1500s. Invasive species are the primary driver of native biodiversity loss on islands, though eradication of invasive species from islands has been effective at halting or reversing these trends. A global compendium of this conservation tool is essential for scaling best-practices and enabling innovations to maximize biodiversity outcomes. Here, we synthesize over 100 years of invasive vertebrate eradications from islands, comprising 1550 eradication attempts on 998 islands, with an 88% success rate. We show a significant growth in eradication activity since the 1980s, primarily driven by rodent eradications. The annual number of eradications on islands peaked in the mid-2000s, but the annual area treated continues to rise dramatically. This trend reflects increases in removal efficacy and project complexity, generating increased conservation gains. Our synthesis demonstrates the collective contribution of national interventions towards global biodiversity outcomes. Further investment in invasive vertebrate eradications from islands will expand biodiversity conservation while strengthening biodiversity resilience to climate change and creating co-benefits for human societies.

Unravelling the influence of mycorrhizal fungi on orchid distributions: implications for island conservation

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Biotic interactions, specifically interactions among plants and their respective pollinators, seed dispersers, and mycorrhizal fungi, are crucial to the maintenance of biodiversity and ecosystem functioning. Despite this, conservation efforts on islands often overlook the critical role of biotic interactions, possibly leading to ineffective conservation prioritisation strategies. This is especially relevant for obligatory mycorrhizal plants, such as orchids, whose survival and distribution are tied to the presence of specific fungal partners (orchid mycorrhizal fungi OMF), and which are especially poorly understood in island contexts. Specifically, the extent of OMF influence on orchid distributions on islands remain unclear. Here, we sampled 430 individuals of native and endemic orchid species occurring across the Canary Islands to assess variation in OMF specialisation among different species and islands of varying age. In addition, we took soil samples at sites with and without orchids to tease apart the biotic and abiotic factors influencing orchid distributions on islands. Our findings highlight significant variations in the composition and specificity of fungal communities associated with orchids. Widespread, generalist orchids were associated with the highest diversity of OMF partners, while endemic species were associated with a narrower range of generalist fungi that were absent from sites without orchids. We conclude that free-living mycorrhizal communities do not restrain the distribution of widespread and generalist orchid species, but might limit the abundance of species with specialized interactions. This underscores the importance of mycorrhizal availability for specialist orchids and emphasizes the urgent need to integrate plant-fungi interactions into conservation programs.

Islands and protected areas in the Mediterranean towards the 2030 Biodiversity Targets

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The European Biodiversity Strategy for 2030 and the Kunming-Montreal Global Biodiversity Framework state that at least 30% of terrestrial, inland water, coastal and marine areas (with emphasis on those of particular importance for the preservation of ecosystem functions and services), should be effectively preserved by 2030 through the institution and sound management of protected areas. The EU strategy includes the additional and ambitious goal of having one third of the protected area under a regime of strict protection. Islands are known to be particularly vulnerable to biotic invasions, species extinctions, habitat degradation, and loss of ecosystem functionality. Therefore, protecting significant fractions of island areas, and possibly entire islands, is of paramount importance to guarantee the persistence of their peculiar biodiversity and ecological interactions. Here, we analysed the protection level (following IUCN classification criteria) for 2233 Mediterranean islands larger than 10.000 m^2 (84% of which - corresponding to 99% of the total island area - are part of the EU), by overlapping a new open geodatabase of island boundaries with the World Database of Protected Areas. We found that the percentage of protected land in the Mediterranean islands is relatively low (<15%) and most of the protected area is classified as the lowest conservation categories, namely IV (5.8%), V (4.4%) and VI (3.3%). The strictest conservation categories (Ia, Ib and II) cumulatively cover only 1.61% of the total land of the Mediterranean islands, indicating a substantial gap from the 10% EU target. Only 84 islands are almost completely protected (>90% of island area) under a strict conservation status, 35 of which are located in Italy, 15 in France, 13 in Spain, 13 in Greece, 3 in Lebanon, 2 in Malta and 1 in Algeria and Morocco. While these results are based on a dataset with known biases (the actual situation might be less severe), we highlight the need for a comprehensive conservation planning of Mediterranean islands to allow the long-term persistence of fundamental ecological and biogeographical processes, as well as to enhance the rewilding potential of these ecosystems.

A novel approach to assessing the ecological condition of Azores archipelago's native forests: Arthropod-based biotic integrity indices

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Island ecosystems are experiencing a significant decline in biodiversity worldwide, with forest biodiversity being particularly affected by several biodiversity erosion drivers. This alarming situation highlights the urgent need for conservationists to develop more accurate and efficient tools to assess the quality of sites. To address this issue, our study focuses on the development of two biological integrity indices (IBI) that utilize arthropod communities as indicators to measure the quality of forest sites. In accordance with studies that showed stratification of species diversity, we developed an IBI for canopy stratum (IBI-canopy) and an IBI for the forest understory (IBI-SLAM). We calibrated both indices on seven parameters for comparison purpose with a previous epigean IBI. Percentages of endemic, native non-endemic and introduced species richness and abundance were included in both indices. Percentages of Diplopoda species richness and abundance were included in IBI-canopy and percentages of Saprophagous species richness and abundance were included in IBI-SLAM. As expected, species richness and abundance of endemic species were negatively related to disturbance and selected for both IBI. Surprisingly, species richness and abundance of native non-endemic species were positively related to disturbance. The study highlights the limitations of single measurements in detecting all types of pressure sources, and proposes a multi-measurement system to provide a more comprehensive understanding of the overall system conditions. Our efficient and accessible indices confirmed low preservation status in Flores Island compared to Terceira and Pico, consistent with prior empirical studies. Our methodology has successfully been developed and tailored to the unique arthropod communities found in the Azores forests. While it may not be suitable for random forest sites, it can serve as a valuable source of inspiration for the development of arthropod-based IBIs in other islands of the world for which standardized endemic and exotic species richness and abundance could be obtained. The study also showed that arthropod assemblages mimicked forest biodiversity stratification and this is reflected in differences expressed by the IBIs.

Conserving Madeira's threatened endemic butterflies

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Madeira is a hotspot of threatened endemic butterflies in Europe. According to the most recent European Red List of Butterflies, two species, the Madeiran Speckled Wood (*Pararge xiphia*) and the Madeiran Brimstone (*Gonepteryx maderensis*), are listed as endangered, and one, the Madeiran Large White (*Pieris wollastoni*) even as Critically Endangered (Possibly Extinct). In the course of a LIFE4BEST-funded project, intensive surveys across the whole island were carried out in 2021 and 2022 with the help of volunteers to investigate the current state of the population of those three species and their threats. In the course of 648 counts along 534 km of survey routes, more than 10,000 butterflies of 14 species were recorded, among them 2176 specimens of the target species. The Madeiran Speckled Wood, which is one of the most ancient endemic butterflies of the Macaronesian Islands, turned out to remain one of the most common species, despite its decline after the introduction of the Speckled Wood (*Pararge aegeria*) in the 1960s. However, its main strongholds are confined to undisturbed laurel forests in the centre of the island, whereas the invasive congener predominates in coastal areas. In contrast, the Madeiran Brimstone has become a low density species, and only a few major breeding sites remain near steep cliffs within the laurel forest, which harbour its larval foodplant, *Rhamnus glandulosa*. No sign was seen of the Madeiran Large White, which is now presumed extinct and thus becomes the first globally extinct European butterfly. The talk discusses the reasons for the declines and possible steps to improve the conservation status of Madeira's endemic butterflies. Further monitoring is facilitated by newly set up transect routes, a recording app and training resources in multiple languages, which enable the involvement of citizen scientists, both from the local population and tourist visitors to the island.

Generalist and topologically central avian frugivores promote plant invasion unequally across land-bridge islands

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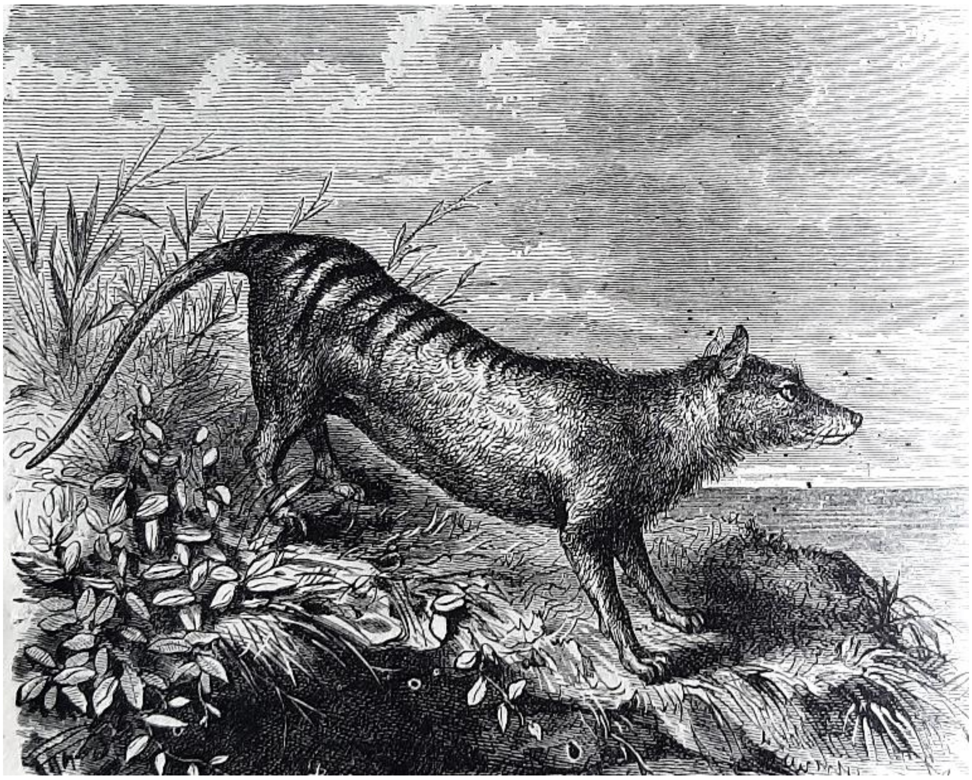
Seed-dispersal by frugivorous birds facilitates plant invasions, but it is poorly known how invasive plants integrate into native communities in fragmented landscapes. We surveyed plant-frugivore interactions, including an invasive plant (*Phytolacca americana*), on 22 artificial land-bridge islands (fragmented forests) in the Thousand Island Lake, China. Focusing on frugivory interactions that may lead to seed-dispersal, we built ecological networks of studied islands both at local island (community) and at landscape (metacommunity) levels. On islands with *P. americana*, we found *P. americana* impacted local avian frugivory networks more on islands with species-poor plant communities and on isolated islands. Moreover, as *P. americana* interacted mainly with local core birds (generalists), this indicates reduced seed-dispersal of native plants on invaded islands. At the landscape level, *P. americana* had established strong interactions with generalist birds that largely maintain seed-dispersal functions across islands, as revealed by their topologically central roles both in the regional plant-bird trophic network and in the spatial metanetwork. This indicates that generalist frugivorous birds may have facilitated the dispersal of *P. americana* across islands, making *P. americana* well integrated into the plant-frugivore mutualistic metacommunity. Taken together, our study demonstrates that the impact of plant invasion is context-dependent and that generalist native frugivores with high dispersal potential may accelerate plant invasion in fragmented landscapes. These findings highlight that it is important to take the functional roles of animal mutualists and habitat fragmentation into account when managing plant invasions and their impact on native communities.

☙ Conservation on Islands ❧

Posters



(From: L. Figuier, Vita e costumi degli animali: I mammiferi. Fratelli Treves, Milano, 1880)

Gut microbiota of insular lizard and its adaptive changes

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Animals living on small islands are more drastically exposed to unexpected environmental changes than their mainland relatives, such as food or water starvation, catastrophes, and rapid temperature shifts. Facing such higher mortality risk, they can manifest phenotypes adapted to insular conditions. For example, gut microbiota is known to be involved in many vital processes for the host, including metabolism, behaviour and immune system, changing in response to the selective pressures. Here, we explored the contribution of microbiota of a host insular population of the Italian wall lizard (*Podarcis siculus*) to the adaptation to rapid and sudden changing environmental conditions. We characterised the gut microbial community of mainland and insular lizards by 16S rRNA V3 region gene amplification and sequencing starting from faecal pellets, assessing the response under experimentally suppling of unexpected food items (exotic larvae). Our observations showed a significant difference in microbiota community of insular population compared to mainland one, depended mainly on change in relative abundance of the shared genera. When lizards were exposed to experimental diet regime only the insular population showed significant reshaping of bacterial composition of microbiota in a short time, as well as an increase in body mass. Our results could be an evidence that the higher plasticity of the gut microbial community of island lizards can be part of the adaptive strategy to efficiently respond in a short time to unexpected and unpredictable environmental changes. This would be also in agreement with the hypothesis of insular adaptation driven by regulative mechanisms rather than constitute genome mutations. Understanding the mechanisms underlying the adaptation of these island populations can contribute to their conservation and management of their biota.

Expanding the Network of Protected Areas with limited data: High Conservation Value Areas in São Tomé Island

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Important elements of biodiversity are often left out of the network of protected areas. This was the case of the Obô Natural Park in the endemic-rich island of São Tomé (São Tomé and Príncipe, central Africa), whose boundaries were defined in 2006, based on very limited information. The concept of High Conservation Value (HCV) is now being used to expand the network of protected areas on the island, while information on biodiversity is still scarce. Following a preliminary assessment in 2019, based mostly on existing biodiversity data and targeted field surveys, 21 HCV areas were identified. These were subsequently redefined and validated through public debates involving multiple stakeholders, from local inhabitants to companies, governmental and non-governmental institutions. These areas have threatened and endemic species (criterium 1), contribute to landscape cohesion (2), hold rare or vulnerable ecosystems (3), or are important for providing supporting and regulating (4), livelihood (5), and cultural ecosystem services (5). They are about to be recognized as special reserves, which will widen the network of protected areas in São Tomé. A system of priorities and management models is also being developed, ranging from strict reserves for areas that hold remarkable biodiversity, such as well-preserved native forests, to zones of community-based natural resource management, when most values are linked to ecosystem services. The HCV framework was extremely useful to identify complementary areas for protection because its simplicity allows using knowledge on biodiversity that is still incomplete, while facilitating the integration of other societal values and the communication to wider audiences. Based on this island model, we argue for the benefits of the HCV framework to conciliate improved natural resource management with the expansion of the network of protected areas, in the context of scant information on biodiversity, which is often the case in high biodiversity developing regions.

Local and landscape-scale predictors of aerial insectivorous bats in the endemic-rich island of São Tomé, West Africa

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Habitat change is the main driver of biodiversity loss worldwide, whose impacts are even more dramatic across tropical oceanic islands characterized by high levels of endemism. The Island of São Tomé, located in the Gulf of Guinea, has experienced significant agriculture-driven deforestation, yet little is known about how different humanized land use types influence the islands' native vertebrate assemblages. To address this knowledge gap, we conducted acoustic surveys of insectivorous bat assemblages across 144 sites throughout the islands' main habitat types: old-growth forest, regrowth forest, shaded cocoa plantations, small-scale agriculture, oil palm plantations, and urban areas. Based on 26,229 bat passes recorded from six taxa, we found that species richness was relatively consistent across most habitats (regrowth forest: 2.94 ± 1.30; shade plantation: 3.59 ± 1.05; agriculture: 3.83 ± 0.89; oil palm plantations: 3.40 ± 0.99; urban areas: 3.15 ± 0.69), except for old-growth forest (1.31 ± 0.48). However, certain bat species, such as *Hipposideros ruber* and *Macronycteris thomensis*, were almost exclusively found in forested areas, highlighting the critical role these habitats play in preserving the diversity of bat species on the island. Additionally, abundance was generally higher in anthropogenic habitats, likely due to higher prey availability. Our study provides valuable insights into the effects of land-use changes on the insectivorous bats of this tropical, endemic-rich island. Despite similar species richness across different habitats, certain bat species are dependent on old-growth forest, emphasizing the importance of protecting the island's native vegetation cover. Furthermore, our findings suggest that some anthropogenic habitats can sustain substantial levels of bat diversity and, considering the high levels of bat activity in agricultural areas, suggest that São Tomean bats might be acting as potential natural suppressors of agricultural pests.

The early bat catches the fly: activity patterns of insectivorous bats in the oceanic islands of São Tomé and Príncipe

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Human-induced habitat disturbances have a significant impact on biodiversity, often heavily impacting species richness, abundance and assemblage composition. Yet, behavioural responses to habitat change, such as alterations in activity patterns and partitioning along the temporal niche axis — which may represent a more sensitive indicator of species' responses to habitat conversion — remain poorly investigated, especially for data deficient insular species. Here, we evaluate the effects of the most common humanized habitats on the within-night activity patterns of insectivorous bats in the tropical oceanic islands of São Tomé and Príncipe (West Africa). Using Audiomoth acoustic recorders we sampled six insectivorous bat species (*Chaerephon* sp., *Chaerephon pumilus*, *Hipposideros ruber*, *Macronycteris thomensis*, *Miniopterus newtoni*, *Pseudoromicia* sp.) across old-growth and shaded forests, palm-oil plantations, as well as agricultural and urban areas. Over 288 sampling nights on São Tomé (124 sites) and 49 sampling nights on Príncipe Island (49 sites), we recorded >59,000 bat passes (36,497 in São Tomé and 23,563 in Príncipe). The activity of *Miniopterus newtoni*, *Pseudoromicia* sp., and *Chaerephon* sp. was highly habitat-specific, and most bat species exhibited a bimodal activity. Additionally, *Chaerephon* sp. displayed substantial differences in activity patterns between the same habitat types of both islands. Temporal overlap between species varied across habitat types, and we observed high diurnal activity in *Hipposideros ruber* on São Tomé Island but not on Príncipe. Our study contributes to a more comprehensive understanding of the effects of land use change on insular insectivorous bats and we provide much-needed information about the natural history of the poorly known bats of the Gulf of Guinea Oceanic Islands.

Remote sensing of salmonid spawning sites in freshwater ecosystems: The potential of low-cost UAV data

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Breeding habitats are vital to species survival but monitoring them can be difficult due to partial or complete inaccessibility, the need for large-scale monitoring, and the risk of disturbing species during the vulnerable breeding period. Although salmonids are especially vulnerable during their embryonic development, monitoring of their spawning grounds is rare and often relies on manual counting of the redds. This method, however, is prone to sampling errors resulting in over- or underestimations of redd counts. Salmonid spawning grounds in shallow water areas can be distinguished by their visible reflection which makes the use of standard unmanned aerial vehicles (UAV) a viable option for their mapping. Here, we aimed to develop a standardised approach to detect salmonid spawning habitat that is easy and low-cost. We used a semi-automated approach by applying supervised classification techniques to UAV derived RGB imagery in two lakes. The resulting images were processed using an image processing and analysis software. For both lakes six endmember classes were obtained with high accuracies. Most importantly, producers and users accuracy for classifying spawning redds was > 90% after applying post-classification improvements for both study areas. The approach we are proposing here is not an improvement of the redd count method, but an entirely new approach for monitoring spawning habitats which will address some of the major shortcomings of the redd count method, e.g. collecting and analysing large amounts of data cost and time efficiently, limiting observer bias, and allowing for precise quantification over different temporal and spatial scales.

Cliffs as habitat islands: Functional traits, diversity patterns of chasmophytic plant species of Greece and need for conservation objectives

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Cliffs act as natural refuges for many endemic and rare plants, specialized to their extreme ecological conditions. Plant communities colonizing such habitats show great diversity extremely rich in endemic taxa that are under the pressing current and future environmental change. For this research, a dataset has been used, including all available information concerning plant taxa growing on cliffs and slopes with high inclination, exclusively or not, to the different phytogeographical regions of Greece, and their functional traits. The high proportion (>65%) of obligate endemic chasmophytes in Greece indicates a clear correlation of chasmophytic ecology and endemism. For this reason, the areas identified as biodiversity hotspots for cliffs overlap with the threatened biodiversity hotspots in Greece. Obligate chasmophytes are strongly related to elevational gradients and most of them are range-restricted endemics. High chasmophytic taxonomic and functional diversity results to a floristic composition varied along different environmental gradients. Most of the plant taxa on cliffs are perennials, hemicryptophytes and chamaephytes, caespitose, rather late-flowering, with white or light-colored flowers, etc., indicating particular trait–process relationships essential at the scales of ecosystem and landscape. Endemic obligate chasmophytes restricted to high elevations will be severely threatened by climate warming in combination with decreasing precipitation that will give the chance to more widespread taxa to colonise higher elevational gradients and their habitats and press their vulnerable populations. The recent assessment of extinction risk status of the Greek endemic chasmophytic plant taxa for both IUCN Criteria A and B showed that more that 45% will become Critically Endangered, 31% Endangered and 17% Vulnerable in the near future. Understanding narrow endemic obligate chasmophytes' distribution, habitat requirements and functional traits, that are also ecosystem services indicators, will drive to the determination of effective monitoring and conservation objectives.

A conservation project for the Aeolian wall lizard *Podarcis raffonei*

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Podarcis raffonei is an endemic lizard of the Aeolian Islands that currently occurs with three small micro-insular populations (on Strombolicchio, Scoglio Faraglione and La Canna) and a relict population in a small area of Vulcano, one of the main islands of the archipelago. The species is classified as "Critically Endangered" by the recent IUCN Red List, but paradoxically is not included in the annex of Directive 43/92 and, despite the urgency of conservation measures, an action plan has not yet been defined. In 2022 the association Nesos launched the project STAL (Save The Aeolian Lizard), financially supported by the foundations MAVA, FPA2, Blue Marine and by the NGOs PIM and SMILO. The project will last three years and include a captive breeding phase with small nucleus of individuals from the two larger micro-insular populations (Strombolicchio and Scoglio Faraglione), after verifying the feasibility of the samples through an assessment of their demographic status. Since 2023, the new-born individuals obtained during the captive breeding program will be released on three islets near Lipari and Vulcano which have been selected on the basis of i) absence of competitors (e.g. the Italian wall lizard *Podarcis siculus*) or predators, ii) occurrence of suitable characteristics to support small populations of the species. The status and demoecology of the new populations will be constantly monitored in the next years. The aim of this project is to increase the number of sites occupied by the Aeolian wall lizard within its original range and to minimize the risk of stochastic events that may lead to its extinction. At the same time, many dissemination activities have been planned, especially at the local level, to spread the biogeographical significance and conservation importance of this threatened species.

INVASION project: Towards an integrative approach for the study of plant invasions on the Canary Islands

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One of the main threats to the conservation of biodiversity is human-mediated plant introductions. When alien species invade new territories, they can significantly modify the structure of native communities and ecosystem functioning. The study of alien-specific traits and their relationship with native communities is thought to inform us about the mechanisms that operate during the stages of naturalization and invasion. In this context, the Darwin Naturalization Conundrum (DNC) provides opposing hypotheses about the potential of alien species to invade natural communities. On the one hand, the "naturalization hypothesis" posits that alien species far related to native species should be more likely to invade due to niche partition or niche emptiness (biotic filtering). On the other hand, the "pre-adaptation hypothesis" proposes that close relativeness of alien species with native communities may facilitate establishment due to potential adaptations to similar environmental conditions (environmental filtering). In the present work, we focus on three of the main ecosystems (laurel forest, pine forest, and dry *Euphorbia* scrub) of the Canary Islands across Tenerife and Gran Canaria islands to study invasive processes under the framework of the DNC. Our main objective is to deepen our knowledge of the mechanisms of invasion in oceanic islands. We integrate ecological, functional, and phylogenetic approaches to explicitly test the DNC hypotheses posited by Darwin. Our preliminary results highlight that functional relatedness between exotic species and native communities, together with species richness, plays a role in establishment and invasion success.

Idiosyncratic responses of insular birds to habitat type in a subtropical oceanic island

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Islands contain about 20% of the world's biodiversity. Yet, our knowledge about the ecology and natural history of most insular biodiversity is still scarce. The aim of this study was to investigate how native and non-native habitats influence bird diversity and abundance in Madeira Island, Portugal. Between August and October 2021, bird assemblages were sampled in different habitats using 5-minute counts in the Ecological Park of Funchal. We recorded ca. 2000 individuals of 17 species, including several endemic species and subspecies. More species were recorded in native than in non-native habitat. Yet, several species and subspecies endemic to Madeira (e.g., the Madeira firecrest *Regulus madeirensis*) were more common in non-native than in native habitats. Our study is one of the first devoted to the spatial ecology of Madeira's non-marine birds. More studies are needed to understand the ecology and conservation status of birds and other terrestrial vertebrates in Macaronesia.

Human dimensions of the blue horizon: behavioural insights for compliance and deterrence

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Illegal fishing threatens fish populations and marine habitats, affecting the livelihoods and food security of coastal communities worldwide. It also undermines conservation and management in large Marine Protected Areas (MPA), such as the British Indian Ocean Territory (BIOT) MPA. The territory comprises the seven atolls of the Chagos Archipelago with over 1,000 individual islands. Despite its designation as a non-fishing MPA, the abundant fish and shark populations of BIOT attract Illegal, Unreported and Unregulated (IUU) fishing from surrounding countries. To manage this, it is key to understand the social context of non-compliance. Yet, we rarely use insights on social aspects of IUU to inform and test approaches in policy and conservation practices. To address IUU worldwide, we need to understand human behaviour, drivers and deterrence, as well as facilitating coordination among key stakeholders across countries. In our three-year project, we will gain behavioural insights on the fishers' non-compliance and deterrence effects. We will consider key priorities and opportunities for tackling IUU worldwide. We will also identify barriers hindering the implementation of evidence-based enforcement. By bringing together a diverse team and building an extensive regional network of researchers, policymakers, government bodies, fisheries managers, and fisher communities, we will identify actions to reduce the level of illegal fishing in the BIOT and other protected jurisdiction in the Indian Ocean. This project will provide critical insights into how to enhance the robustness of MPA management decisions, particularly when illegal behaviour is involved, with implications for MPAs worldwide.

Freshwater fish conservation in insular ecosystems: the Critically Endangered European eel in Madeira, Macaronesia

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Despite conservation efforts, the stocks of European eel (*Anguilla anguilla*) continue to dwindle. The species' spatiotemporal dynamics are not well-understood across its range, and this knowledge gap is particularly acute in Macaronesia, where the eels are the only native freshwater fish. To address this gap, we conducted a study characterizing European eel populations on Madeira Island. We gathered historical records from biodiversity databases, natural history museums, and literature, and conducted electrofishing in 10 streams across the island. Our findings confirmed the existence of eel observations in Madeira since 1825 and showed that eels are still widely distributed on the island, often co-occurring with non-native rainbow trout (*Oncorhynchus mykiss*). Furthermore, we found that eels are primarily located in the lower catchments of streams, likely due to human-imposed restrictions on upstream dispersal. This study provides critical baseline information for the conservation of this Critically Endangered species and sheds light on the poorly understood ecology of freshwater insular Macaronesian habitats.

Summarizing traits to predict extinction and invasiveness of Northern Macaronesian arthropods: The MACRISK Project

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Arthropod conservation, especially of pollinating insects, has been subject of debate for the past 15 years. Despite the awareness of their social and economic relevance, arthropod conservation is still disregarded as an urgent topic. Particularly in oceanic islands, the lack of major vertebrates turns arthropods into the main protagonists of ecosystem services such as predation, herbivory, pollination, and decomposition. Along with their endemic uniqueness, island arthropods are also under a multitude of anthropogenic impacts that affect them directly through habitat degradations. Thus, the MACRISK project aims to uncover the patterns and drivers behind the extinction and invasiveness risk of arthropods in Macaronesian archipelagoes. In this way, we are compiling and standardizing the distribution, abundance and functional traits of endemic, native non-endemic and exotic arthropods species on the Azores and Madeira. So far, we compiled data for 447 species, comprised by 192 endemic, 94 native non-endemic, 126 exotic and 35 with unknown colonization status. From those, we have compiled the abundance of 335 species that were sampled for the past 20 years using three different standardized protocols: SLAM (Sea, Land and Air Malaise) traps, pitfall traps and beating transects. Moreover, we are compiling six functional traits that are related to the species ecosystems services and that can be compared between different arthropods groups, to predict the changes in abundance through time. These traits were the species mean body size, dispersal ability, feeding trophic, number and which habitats they are present and forest vertical stratum. To date, our findings have not demonstrated a statistically significant relationship between body size and endemic species. In our upcoming analyses, we plan to examine the relationship between the remaining functional traits and other species statuses. Additionally, we aim to construct models that incorporate the effects of both abundance and traits on the risks of arthropod extinction and invasiveness.

Invasion and experimental control of *Pittosporum undulatum* Vent. in the Azores: insights from a ten-year study in Terceira Island

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In 2010, a study was conducted in Malha Grande on Terceira Island in the Azores to measure the spread of the invasive plant species *Pittosporum undulatum*. A total of 19 transepts were installed; after defining the different density levels of the invasive species (low, medium, high and woodland), 16 experimental plots of 100 m^2 (10 × 10 m) were also installed: four for each density level, two being cut (where *P. undulatum* was removed) and two controls. To compare the current degree of invasion of *P. undulatum* with the degree of invasion observed in 2010, the 19 transects were resampled in 2020. To evaluate, a decade later, the effects of the removal of *P. undulatum* in the experimental plots, the 16 experimental plots were also resampled in 2020. After 10 years, in the transects, the number of individuals, biomass and height of *P. undulatum* clearly increased. Nevertheless, in the experimental cut plots, the percent coverage of this species remained significantly lower compared to the control plots. On the contrary, *Rubus ulmifolius* cover increased significantly in almost all cut plots. On the (uncut) control plots, *P. undulatum* showed an overall tendency to increase its abundance, especially in the low-density plots. In the woodland control plots, the abundance of the dominant native endemic species (*Juniperus brevifolia* and *Erica azorica*) decreased significantly. The number of seedlings and saplings of *R. ulmifolius* was significantly higher in the high density and woodland cut plots. The control of *P. undulatum* was still effective after 10 years but its removal favored the advance of other invasive species, especially *R. ulmifolius*, but also *Persicaria capitata*. Unlike we expected, the recovery of native species was not clear, possibly, at least in part, due to the increase of those invasive species. These results give essential information for the success of future ecological restoration actions.

Biodiversity loss in the Azores: A study on arthropod diversity and abundance in native forests and pasture hedgerows

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Biodiversity provides a wide range of crucial services to humanity, yet we are currently facing a profound crisis. The primary drivers of this crisis include habitat destruction and fragmentation caused by human colonization, conventional agriculture and livestock practices, as well as other factors such as climate change, pollution, and the introduction of non-native species. In the Azores, most of the natural vegetation has been transformed or degraded by human action, with the greatest impact on the native forests. We investigated patterns of diversity by comparing the species richness and abundance of arthropods within the native forest and in the pasture hedgerows of Pico Island (Azores, Portugal). For this purpose, we selected transects of the Azorean endemic shrub *Erica azorica* and tree *Laurus azorica*. Arthropods were sampled in the canopies of the selected plants in a nested design with 10 samples within four replicates of each plant in each habitat (160 samples). Our primary hypothesis was that we would observe greater arthropod richness and abundance in trees located within native forests compared to hedgerows, specifically with regards to endemism, predators, and species with special protection status. Our results confirm our hypothesis, as we identified a higher number of species and individuals in samples taken within native forests compared to hedgerows. Furthermore, we found that mean richness and abundance were higher in *E. azorica* samples than in *L. azorica* samples, both in hedgerows and native forest. In addition, *Laurus azorica* hedgerows accumulated the highest proportion of exotics. Regarding the trophic role, we found a higher proportion of predators within the native forest, and a higher concentration of herbivores in *E. azorica* within the native forest. In conclusion, this study highlights the critical importance of native forests in supporting arthropod diversity, especially with regards to endemism, predators, and species with special protection status.

Overcoming conservation challenges: Protecting bats on Pantelleria Island, the southern edge of Europe

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The Island of Pantelleria, located in Southern Italy, is situated at the biogeographic crossroads between two continents, lying 35 nautical miles away from the African coasts and 60 nautical miles from the coasts of Sicily. Due to this unique geographical location, the biological communities on the island are characterized by disharmony and a high level of endemicity that is typical of insular systems. As volant mammals, bats play a crucial role in colonizing islands and are an important part of Pantelleria's ecosystems. The island is home to at least six bat species, including the biogeographically African *Plecotus gaisleri* and *Myotis punicus*, which are only sporadically present in Europe, typically on southern islands such as Malta, Gozo, Sicily, and Sardinia. Another species of great conservation interest, *Rhinolophus mehelyi*, also occurs on the island. Despite the biogeographic and conservation value of bats on Pantelleria, little research has been done on their distribution and habitat use. Bats are exposed to mounting pressures, including disturbance to roosts and wildfires. However, with the financial support generously provided by the Pantelleria National Park, an ongoing project on bat ecology on the island aims to identify the most important roosts and foraging habitats used by bats. The first findings of this research have been presented here, and the main goal is to develop appropriate conservation plans to ensure a brighter future for these mammals and the ecosystem services they provide. It is essential to understand the ecological importance of bats and their role in maintaining a healthy ecosystem, as well as the threats they face from habitat loss, human disturbance, and climate change. The conservation efforts to protect these fascinating mammals will not only benefit the island's biodiversity but also have positive effects on bat conservation at a European scale and the island's human population.

Conservation biology of three threatened *Limonium* species endemic to the Ionian Islands (Greece)

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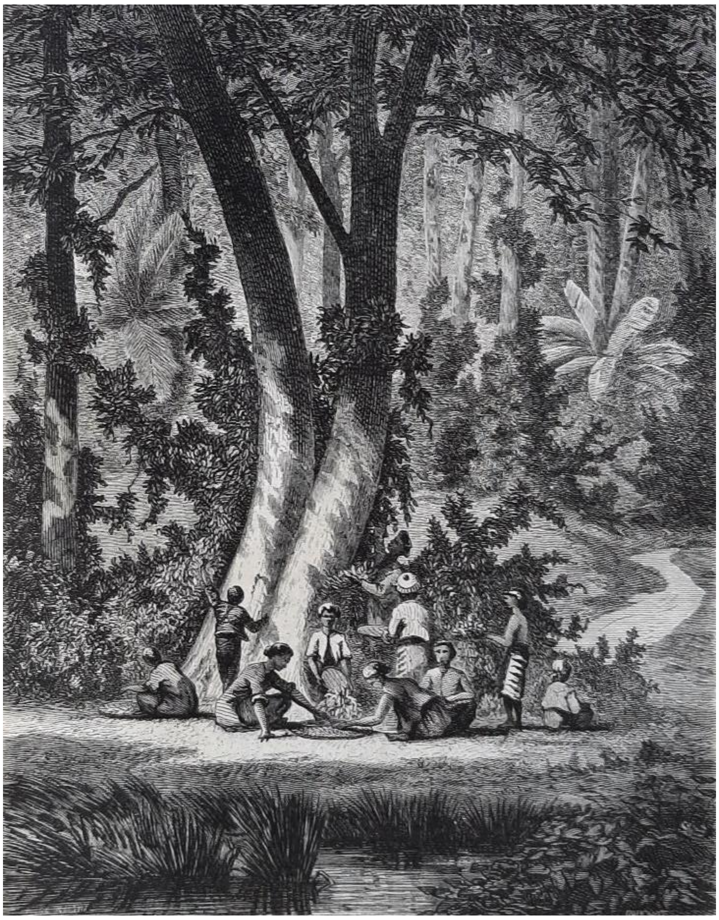
Limonium is the richest genus in endemic species in Greece and the Ionian Islands host 14 *Limonium* species, nine (64.3 %) of which are endemic to this island group. The extremely narrow distribution range of the endemic *Limonium* species in the Ionian Islands combined with the high vulnerability of their specialized littoral habitats indicate the urgent need of effective conservation measures. In this study, we assess the current conservation status and estimate the future risk of extinction of three *Limonium* species endemic to Zakynthos Island (*L. korakonisicum*, *L. phitosianum*, *L. zacynthium*), using 5-year monitoring data and compiling information on their geographical distribution, population dynamics, reproductive biology and genetic diversity. Population size exhibited increased annual fluctuation, a common characteristic among halophytes. Fecundity and Relative Reproductive Success were constantly high during the monitoring period. Five microsatellite loci for six populations of *L. phitosianum* and *L. zacynthium* were analyzed and genotyped, identifying 28 alleles in total. Three of them were polymorphic, while the other two were monomorphic. Two microsatellite loci revealed unique alleles (Ln39, Ln68), which are species and population specific and can be used as diagnostics at the population and species level. According to IUCN criteria, *L. korakonisicum* was assessed as Critically Endangered (CR), *L. phitosianum* as Vulnerable (VU) and *L. zacynthium* as Endangered (EN). According to population viability analyses results, *L. zacynthium* exhibited the highest extinction risk over the next 50 years (67.8%). The investigation of certain aspects of the species' biology resulted to important data which are necessary to identify critical aspects for the survival of the species and to propose conservation measures.

☙ Humans and Islands ❧

Contributed Talks



(From: L. Figuier, Storia delle piante. Fratelli Treves, Milano, 1882)

Mediterranean islands and agricultural terraces: chronology, geoarchaeology and sedaDNA

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Agricultural terraces are ubiquitous in the Mediterranean and particularly on Mediterranean islands. The TerrACE Project (ERC Funded) has been using new methods in order to understand the chronology, functions and palaeobiology of terraces on several islands including Sicily (at Castronovo), East Crete and Tinos (Cyclades). Indeed, some smaller islands such as Tinos and Antikythera are well-known for being almost entirely terraced. The terraces investigate span much of the mid-late Holocene from the Minoan period to the post-medieval. We have applied portable luminescence (pOSL/pIRSL), luminescence dating (OSL) and ^{14}C to date the terraces, a combination of pXRF and thin section micromorphology to unravel soil history, and phytoliths and sedimentary ancient DNA (sedaDNA) to determine past crops and vegetation. Although these methods have met with variable success on different sites, between them they have allowed chronology, history and crop use to be determined on most sites. The Sicilian site was first constructed in the 11th century AD and been subject to reconstruction in the post-medieval period. SedaDNA and phytoliths reveal a wide variety of fully Mediterranean crops including figs, olives and Arabian peas. The high prevalence of terraces on Mediterranean islands partly reflects the typical steep island topographies but also a need or advantage to self-sufficiency during various periods in the past. It also fed into periods of rapid population growth and underpinned the unsustainably high population densities seen in the post-medieval period. As such, terraces are an essential part of the history of these and many other islands worldwide.

A global assessment of the barriers influencing the effectiveness of island ecosystem management

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Island ecosystems are disproportionally impacted by biodiversity loss and as such their effective management is critical to global conservation efforts. Practitioners world-wide work to manage island sites and species to conserve them, but various day-to-day barriers compromise these efforts, reducing management effectiveness and preventing local and potentially even national biodiversity targets from being met. Identifying the most important barriers that currently impede effective island conservation could streamline investment to focus on cost-efficient interventions that better reflect realities on the ground and the need to address barriers under substantial time and budget constraints. A survey of 360 practitioners working in island ecosystem management across 77 countries was conducted. The three most common barriers perceived by practitioners to prevent them from achieving more effective management are: low staff capacity; difficulties turning data into useful information for management (including lack of capacity and time to analyse data); and lack of a research and management strategy. Practitioners' perceptions of national-level management effectiveness were mostly associated with their perception of governance issues, the presence/absence of research and management strategies and their experience of collaboration outcomes. Practitioners' experience of staffing and monitoring programme issues was important in shaping their perception of management effectiveness within the organisation(s) they worked with. Despite the indisputable need for transformative change to address the underlying causes of many of these barriers, more immediate and direct investment in strengthening the people and systems that are at the frontline of preventing biodiversity loss on islands is needed to bridge these barriers and achieve more effective management of island ecosystems.

Long-term ecology of past arid environments

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Island ecosystems are shaped by the influence of natural and cultural drivers that operate through time. Understanding long-term ecosystem dynamics (beyond centuries) requires the application of palaeoecological methods based on indicators that demand specific sites and conditions for their preservation. Many island ecosystems have “silent sites” which lack these suitable settings limiting the possibility of studying their dynamics with a long-term perspective. Arid environments occurring on dry or climatically heterogeneous islands, such as the Canaries, are a good example of “silent sites”. Lowlands and summits are (semi)arid (100-500 mm/year) areas, that host diverse communities with high endemicity and have been historically subject to human activities. Through a combined analysis of multiple indicators (i.e., fossil pollen, biogenic silica, fungal spores, charcoal and palaeoenvironmental DNA) we try to overcome such limitations and provide a robust reconstruction of these environments through time. We present environmental reconstructions including past vegetation, fire regimes, presence of introduced herbivores, and other local environmental conditions for arid sites on the Canary Islands spanning the last 3500 years. Results show past dynamics of endemic and native shrub dominated communities that resemble well-preserved contemporary scrubland areas. However, the oldest records indicate the occurrence of woodlands on nearby areas that are no longer present, probably deforested in prehistoric time (at least 2000 years ago) and maintained through the historic period (the last 500 years). Understanding the response of arid environments to human-driven disturbance is valuable to inform managers on the resilience and potential trends of such communities in the context of current and future global change.

Trematode parasite communities vary with agricultural land-use intensity in an archipelago-like system of Ugandan crater lakes

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Human-mediated environmental changes are important drivers of biodiversity loss, but their effects differ among taxonomic and functional groups. Although parasites are ubiquitous and extremely diverse, the influence of anthropogenic changes on their diversity remains poorly assessed. Like islands, crater lakes offer unique opportunities to study the ecological impact of anthropogenic environmental changes as they are similarly discrete, ecologically simple, and naturally replicated systems. Here, we study the communities of trematode parasites within populations of the intermediate snail host *Bulinus tropicus* in 34 crater lakes in western Uganda along a gradient of anthropogenic disturbance. This study system represents an ideal natural laboratory as each lake is environmentally well-characterized while jointly, they cover important variations in anthropogenic modification. Using generalised linear models and redundancy analysis, we investigate how environmental variables affect the abundance of *B. tropicus*, the abundance of the trematodes infecting them, and the diversity and composition of the trematode communities. We observe that *B. tropicus* is mostly absent from lakes located in national parks and its abundance in other lakes increases weakly with primary productivity. Trematode abundance correlates mainly with the abundance of snail hosts. Trematode diversity strongly increases with lake productivity, probably because productive lakes can sustain bigger fish populations, thereby attracting migratory and native birds acting as final host for trematodes. Because primary productivity depends both on nutrient loading from surrounding land and upcycling of nutrients stored in the lower water column to the photic layer, a combination of land use intensity and lake depth ultimately controls trematode diversity. Trematode community composition is weakly influenced by land use in the lake basins, potentially reflecting the influence of anthropogenic habitat disturbance on the presence of specific final vertebrate hosts. Our results suggest that agricultural land conversion could lead to increased parasite transmission, thereby impacting aquatic and terrestrial ecosystem health.

Humans, animals and plants on small islands: case studies from prehistoric Pantelleria and Ustica

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Archaeobotany (i.e. the analysis of plant remains from the archaeological contexts) and zooarchaeology (i.e. the analysis of faunal osteological remains) are primary methods to analyze and interpret the exploitation of botanical resources, the subsistence strategies and more in general the adaptation of past human societies to the limited insular environments. The arrival of humans on small islands has historically caused perturbations to the pre-human ecosystems. But human communities have developed specific uses of bioresources according to the features of their environments (such as wood exploitation wood cover, components of volcanic soils, biomass – weed and grass – for herding, etc.), in order to maintain a balanced economy, sometimes successfully and other times leading to the over-exploitation of the resources and, in some extreme cases, to the abandonment of the islands. Here we present the analysis of plant (wood charcoals and seeds) macroremains and animal remains from the islands of Ustica (Palermo, northern Sicily) and Pantelleria (Trapani, Sicilian channel); the site of Piano dei Cardoni (Middle/Late Neolithic, half of the 5th millennium BCE) on the former is a funerary complex; the site of Mursia (Early and Middle Bronze Age, first half of the 2nd millennium BCE) on the latter is a multi-phase fortified village. Preliminary results give insights into the selection of crop species, wood exploitation and herding strategies. Despite being different in chronology, size and ecology, the two islands show insular adaptations in the human communities that occupied them.

Bird name atlas of Eastern Polynesia

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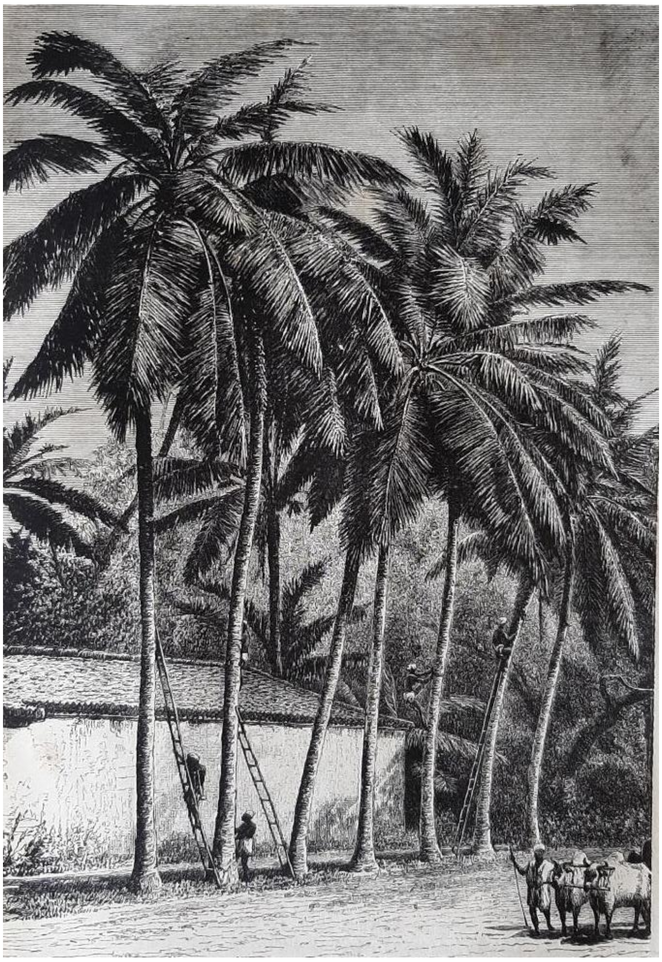
Birds have always played an important role in Polynesian societies. Present in many traditional stories and songs as well as used as resources for food or feathers, their popularity makes them today's ambassadors for the preservation of natural habitats and species. Our Bird Name Atlas unites ornithological, traditional and linguistic knowledge in compiling an exhaustive list of vernacular bird names for Eastern Polynesia, including comparisons of names from islands within the sphere of influence of Polynesian languages (islands home to Polynesian Outlier communities in the Western Pacific, Central and Western Polynesia, Hawaii, New Zealand, and Rapa Nui). Names were collected from 18th and 21st century's publications by navigators, missionaries, government officials, ethnographers, and biologists. The list was then completed by numerous interviews conducted during fieldworks in Eastern Polynesia since the 1970's. For each main group of birds - treated at family, genus, or species level - names are listed by islands and archipelagos, regrouped by linguistic similarity and, for the most diverse ones, organized by proto-name affiliations. For native species, interestingly, the linguistic diversity of bird names does not always reflect the biological diversity of the taxon: speciose groups can be named very similarly across archipelagos (for instance fruit doves), whereas a single species, like the white tern, shows a large variety of Polynesian names across the Pacific. These differences might reflect some of the birds' life traits, resident (fruit doves) or marine (tern), but the loss of traditional knowledge has led to a confusion between similar species (for instance migratory waders or petrels and shearwaters) or led to the use of the same name for several species, native and introduced ("vini"). Thus, the Atlas demonstrates the vitality of the relationships between Polynesian people and birds, but also reveals the necessity of preserving traditional knowledge associated to the natural world.

Humans and Islands

Posters



(From: L. Figuier, Storia delle piante. Fratelli Treves, Milano, 1882)

Exploring Azorean students' perspectives and knowledge of bryophytes: Implications for nature education and conservation

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The Azores, an archipelago in the Atlantic Ocean, are known for their diverse and vibrant ecosystems. Bryophytes, including mosses, liverworts, and hornworts, are important components of Azorean terrestrial ecosystems. In 2018, a study was conducted to assess the knowledge and perspectives of bryophytes among Azorean students. The research involved 250 students of varying ages attending basic or secondary education. The students completed a written questionnaire that included projective questions, such as drawing, free association, and writing a short story, to assess their understanding and perceptions of bryophytes. Literal and closed-ended questions were also included to gather information about the students' ability to identify mosses, name and recognize photosynthetic organisms, compare mosses with liverworts, and investigate their primary sources of information and preferred species. A measure of self-reported nature exposure (Nature Exposure Scale, NES) was utilized as a characterizing variable. The study found that more than half of the students across all education levels held common misconceptions about bryophytes. However, as schooling increased, their understanding of bryophyte biology improved. Nature exposure did not significantly impact the students' knowledge of bryophyte biology. However, students with higher nature exposure scores on NES reported a greater liking for bryophytes, as well as all other species tested, compared to those with lower nature exposure. Despite this, bryophytes were ranked as the second least preferred photosynthetic organism among the students, with brown algae being the least preferred. The most preferred sources of knowledge were found to be family, teachers, and outings and direct experiences. The results suggest that increasing students' nature exposure through field trips and leisure activities could be a valuable approach to fostering a greater appreciation and understanding of the ecological, environmental, physiological, and evolutionary significance of bryophytes in Azorean ecosystems. This could ultimately lead to more effective nature conservation efforts in the region.

Daily satellite imagery reveals high visitation rates of the remote Conception Island National Park, Bahamas

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Conception Island National Park is a remote insular park in the central Bahamas. It is administered by the Bahamas National Trust, an NGO tasked with managing the National Park system of the Commonwealth of the Bahamas. Conception Island is known as a "paper park" as it has no monitoring system, no warden, and no way of tracking visitation or visitor activity. We used daily satellite imagery from the company Planet® to characterize boat traffic visitation to Conception Island nearly every day going back to 2016. We obtained a total of 3,003 observation days, with 1,200 vessels observed in the park during this time period. This provides the first analysis of visitation to Conception Island and will be extremely useful as management plans are formalized. Peak visitation to the island occurs in the spring when migrating songbirds arrive and when white-tailed tropicbirds are using the island for mating. We also found that visitation remains constant most of the year but drops sharply during the hurricane season. We hope this data collection method can be used in combination with knowledge of the island's wildlife to aid park personnel in choosing when and how to allow access to the island.

Reconstructing the Anthropocene history of the Mascarenes

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This poster session will present our detailed reconstruction of the land-cover, degradation and invasion histories of Mauritius and Reunion, comparing their similarities and differences. Mauritius and Reunion were early casualties of the colonial wave of Anthropocene impacts on islands. Both saw high levels of extinctions - giant tortoises, parrots, bats and flightless birds such as the Dodo were wiped out through human consumption, predation by invasive species and large scale habitat destruction. The human population growth of the 20th century led to many near extinctions, saved at the last minute by intensive captive breeding programs. Now, the remaining native habitat is increasingly threatened by the spread of invasive plants despite their protected status. This history was recorded in various degrees of detail in maps, journals, forestry records, and early vegetation surveys. We compiled these sources, and from them extracted land-cover data to produce a temporal sequence. Intermediate time slices were estimated by using a land-cover change model. From this model we estimate 400 years of continuous spatial history. Such a high resolution, quantified history is a platform for more detailed enquiries into the causes and patterns of population changes and extinctions, and their relationship to anthropogenic drivers.

☙ Island Ecology ❧

Contributed Talks

(From: L. Figuier, Storia delle piante. Fratelli Treves, Milano, 1882)

Exploring the genomics of island residency in a migratory bird

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Bird migration is a fascinating seasonal behaviour with a demonstrated heritable component, and while immensely study over the past two centuries we have barely scratched the surface of understanding the genomics behind this behaviour. Here, we use the iconic Eurasian blackcap (*Sylvia atricapilla*) which exhibits the full range of migratory behaviour across its distribution range. This variation can be partitioned into three key traits: direction, distance and propensity. By focusing on the propensity to migrate; whether a bird migrates or not, we aim to shed light on the genomic machinery that modulates this complex behaviour. Within the blackcap system, we have to operate around a confounding factor which is the fact that the range of the blackcap encompasses not only breeding ranges across continental Europe and North Africa but also several islands and archipelagos. Interestingly, the blackcap populations on islands tend to forgo migration and adapted to a resident lifestyle instead. As the island environment brings its own set of characteristics and unique selective pressures, it is important to assess the differences between an island resident and a continental resident. To do this we need to study this within the context of geographical relatedness, i.e. how the different island populations relate to each other and the continental populations, as well as the species' evolutionary history. We analysed whole genome resequencing data of ~180 individuals across their distribution range, including the following island systems: Macaronesia, Mallorca and Crete). We performed population genomics on the variant data, encompassing SNPs and TE insertion polymorphisms (TIPs). We found a clear population separation based on the islands and resident phenotype, with distinct genomic regions selected for within certain island populations, and for both residential phenotypes.

Unveiling drivers of shifts in local tree diversity patterns across elevation gradients in Pacific archipelagos

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Biogeographical factors such as island area, age, and isolation are thought to drive large- and small-scale diversity patterns in island plant communities. However, the mechanisms underlying these shifts in diversity remain unclear, as they may emerge because of changes in the number of individuals, species evenness, or spatial aggregation. Here, we explore shifts in key components of community structure in island forests across the Pacific that underpin variations in local diversity along elevational gradients. Using a unique database of more than 5,000 forest plots distributed across the three emblematic archipelagos of the Pacific, Hawaii, New Caledonia, and New Zealand, we tested for the effects of the number of individuals, evenness (i.e., the species abundance distribution, SAD), and spatial aggregation across elevation gradients. Our results suggest that shifts in local diversity are primarily mediated via species abundance distributions, which is consistent with the idea that more energy at lower elevations relaxes competitive exclusion. Moreover, the strength of the SAD effects increases with island age, thereby unveiling the dominant mechanism through which large-scale, biogeographical drivers percolate down to local scale diversity patterns.

Hummingbirds and their flowers on islands

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Theory predicts that biogeographical regions where species have co-occurred for longer should contain species with more specialized associations and greater trait matching. At the other extreme, pollinators on oceanic islands are predicted to have generalized feeding behaviours, probably because it is advantageous to be a generalist to colonize and establish on islands. Moreover, as oceanic islands have an impoverished insect pollinator fauna, evolutionary processes may drive island pollinators, especially vertebrates, to evolve novel and generalized feeding niches. However, within islands, the most specialized and vulnerable species are predicted to be found mainly in mountains, whereas species in lowlands should be generalized and less vulnerable. We evaluated these predictions for hummingbirds and their nectar-food plants on Antillean islands. Bill and corolla length and the degree of resource specialization were similar across mainland regions, but the Caribbean islands had shorter flowers and hummingbirds with more generalized interaction niches. Moreover, the rates of hummingbird trait divergence were higher among ancestral mainland forms before the colonization of the Antilles. In correspondence with the limited hummingbird trait evolution that occurred within the Antilles, local abiotic and biotic conditions – not species traits – correlate with hummingbird resource specialisation and the vulnerability of hummingbirds to extinctions of their floral resources. Specifically, hummingbirds were more specialised and vulnerable in conditions with high topographical complexity, high rainfall, low temperatures, and high floral resource richness, which characterize the Antillean Mountains. These findings show that trait evolution, resource specialization and species vulnerability to extinctions of interaction partners are highly context dependent, depending both on mainland versus island setting as well as environmental conditions within islands.

Impacts of invasive rats on the survival, abundance, morphology, and behavior of ghost crabs on a South Pacific atoll

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On intact coral atolls, omnivorous intertidal crabs play key roles in predation, scavenging, and soil aeration. Unfortunately, many atolls have been invaded by rodents, with potentially severe impacts on intertidal crab populations. Accordingly, some studies that have considered potential rat impacts report differences in the number of crabs counted along transects on rat invaded vs. rat free islets. Such apparent differences in abundance may, however, also reflect changes in behavior in response to rat presence. Investigations of the impact of rats on crab survival, densities and behavior are needed to acquire a more mechanistic understanding of the impact of rats on crabs. We took advantage of a rat eradication program on a Polynesian atoll (Tetiaroa) to investigate the impact of rats and rat removal on horned ghost crabs (*Ocypode ceratophthalmus*). Tetiaroa offers a unique experimental setting with 12 islets, including three never colonized by rats and others where rats were eradicated in 2018 (one islet), 2020 (two islets), or 2022 (six islets). We quantified predation risk (using tethered crabs), population density, morphology, and activity periods on rat-infested and rat-free islets, and documented changes in predation risk following the 2022 eradication. Predation risk was three times higher on rat-infested as compared to rat-free islets, and significantly decreased post-eradication on islets that had been infested with rats. Crab activity, as measured with trail cameras every 15min by the number of crabs active within a 10m2 area, was also affected by rat presence. Finally, capture-mark-recapture approaches at nine sites across the atoll showed that crabs were significantly larger and more abundant on rat-free as compared to rat-invaded islands. Our results clarify the impacts of rats as invasive predators of ghost crabs, and suggest that rat eradication will have long term effects on the functioning of the intertidal ecosystems.

Potential effects of sea level rise on island snakes in the New World

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Sea level rise (SLR), one of the consequences of climate change, is a growing concern due to its negative effects on terrestrial environments and their biodiversity. Islands are particularly susceptible to SLR impacts due to their limited terrestrial area and susceptibility to habitat loss. This study aimed to estimate the loss of area and land cover types in islands under two SLR scenarios (based on IPCC scenarios): 1 and 2 m. To assess the impacts of SLR on terrestrial organisms, we used snakes as a study model. We focused on 337 islands distributed throughout the Americas that are inhabited by snakes. To estimate area loss, spatial analysis was conducted using digital elevation models and land cover data. All areas below the future sea level, according to elevation models, were considered drowned and therefore lost. The analysis was automated using QGIS software and Python language. Our results indicate that the Caribbean region would be the most affected, with approximately 75% of its area impacted by SLR. Considering the land cover categories, crops are expected to be the most affected areas, with approximately 84% of the area impacted. Regarding the snakes, about 75% of their distribution area in the islands can be affected. These results can be useful to guide conservation and mitigation efforts to the most affected areas, aiming to minimize the impact of SLR on islands of America. In conclusion, this study provides valuable insights into the vulnerability of islands to SLR. The findings highlight the importance of conducting further research to better understand the impacts of climate change on terrestrial ecosystems.

Small islands, small ponds, small communities – water beetles and water boatmen in the Faroe Islands

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The Faroe Islands in the North Atlantic consist of several small islands, and numerous freshwater ponds can be found on most of them. These ponds are inhabited by species-poor aquatic communities. Faroese ponds are simple systems which lend themselves well to studying diversity of water insects and their interactions with the environment, which ultimately contributes to our understanding of patterns of biodiversity. Water beetles of the families Dytiscidae and Haliplidae (Coleoptera) as well as water boatmen (Heteroptera: Corixidae) are well-studied groups in Northern Europe. In the Faroe Islands, their diversity is much lower than in the British Isles and Fennoscandia. Here, we first describe the communities of water beetles and water boatmen in Faroese ponds and, secondly, assess whether community compositions are driven by habitat characteristics or dispersal abilities of species. To this end, we sampled 57 ponds on the islands Streymoy and Eysturoy. Environmental variables such as pond size, temperature, pH, and depth were measured, and distance to nearest neighboring pond was calculated as a measure of isolation. We found six small species of Dytiscidae and Haliplidae (Coleoptera) and two species of Corixidae (Heteroptera). There was a higher species diversity in shallower ponds, and community composition differed according to pond size. There were species-specific relations between abundance and shoreline length, e.g., *Haliplus fulvus* and *H. palustris* being restricted to larger ponds. Lastly, water beetle and water boatmen communities in Faroese ponds are discussed in the light of island biogeography and species distributions in the North Atlantic islands.

Divergence in fruit trait preferences between birds and lizards on islands

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Interactions between fleshy-fruited plants and dispersers have resulted in groups of fruit traits that allow plant species to attract different dispersers, which ultimately may affect seed fate and plant reproduction. Foraging preferences of dispersers according to their manipulative skills or digestive abilities may lead to differential use of fruit traits. Thus, studies that integrate trait distribution patterns along multiple morphological, chemical, phenotypic, phenological, and ecological traits are necessary to achieve a more complete understanding of the drivers of plant-frugivore interactions. While birds and mammals are essential frugivores in continental ecosystems, birds and lizards are the most important in many tropical and subtropical oceanic archipelagos. Therefore, pressures exerted by lizards on islands are likely to select traits different from that preferred by mainland dispersers. Here, we examined whether fleshy-fruited species can be divided into groups based on multiple fruit traits and the preferences of the two main frugivore guilds (i.e. birds and lizards). We found that lizards and birds have different fruit choices; lizards select fruits based on their morphological traits, while birds consumed more nutritious fruits. The poorer nutritional quality of fruits selected by lizards could be explained by the more primitive sensory system of ectothermic animals. Our findings suggest that chemical traits, selected by the different guilds of frugivores based on their nutritional requirements, chemosensory system, and abilities to process macronutrients and/or metabolize toxic compounds, could reliably predict the frugivore guild on oceanic islands.

Oceanic islands contributing to the Mountain Invasion Research Network (MIREN) - Distribution of endemic, native and alien species along an elevation gradient in La Palma, Canary Islands

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Oceanic islands are observed to experience increasing rates of colonization by invasive plants and rapid spread. Here, we examine plant species diversity patterns (species richness of endemic, native and alien species) on roadsides and in native vegetation along an elevation gradient from sea-level up to 2300 m a.s.l. in La Palma (Canary Islands, Spain), at multiple spatial scales. Species richness and specific leaf area (SLA) was assessed along T-transects of 150 m × 2 m, along two major roads each placed over the whole elevation gradient. Each transect was composed of three sections of five plots each: Section 1 was located on the road edges, Section 2 at intermediate distance, and Section 3 far from the road edge, the latter representing the "native community" less affected by road-specific disturbance. The effect of elevation (climate filtering) and distance from roadsides (anthropogenic disturbance) was evaluated for endemic, native and alien species. We assume that the variation in alien species richness and composition is best explained by differences in roadside versus native habitat, while patterns in endemic and native species richness and composition are mainly determined by elevation. As specific leaf area (SLA) is commonly higher in invasive plant species than in native species, we expect higher community weighted mean SLA values along low-to-mid elevation roadside habitats than in mid-to high-elevation native habitats. Our results, however, show not significantly more alien species near roadsides than in offroad communities on La Palma. Contrary to expectations, community weighted SLA at roadsides was lower than offroad. Generally, alien and native species SLA was both highest at mid-elevations. Further studies across several oceanic islands and archipelagos are needed to better understand mechanisms of plant invasion facilitated by mechanical disturbance, yet limited by climatic constraints at high and low elevation.

Effect of ash accumulation from the Tajogaite volcano on the seed bank of the Canary pine forest (La Palma, Canary Islands)

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Ash deposition is one of the most important sudden alterations caused by volcanic eruptions on ecosystems. The eruption of the Tajogaite volcano on La Palma (September 19 - December 13, 2021) expelled more than 200 Mm^3 of pyroclastic material, mainly being deposited on the Canary pine forest. The ash accumulation on the ground decreased with distance, varying from 2.5 m to 1 cm from 150 m to 7 km from the crater, respectively. The effect of ash deposition on the seed bank and its subsequent germination success or failure has been previously studied by ash removal from the soil. However, here we present the first experimental study on the impact of ash layer thickness on activation and suppression of the seed bank. Seven thickness categories were taken as a function of distance away from the crater: 0 (control), 1, 5, 10, 45, 75 and 150 cm. Seeds were selected from the four most characteristic pine forest species representing different seed sizes, structures and growth strategies: *Pinus canariensis*, *Chamaecytisus proliferus*, *Cistus symphytifolius* and *Lotus campylocladus*. One hundred seeds of each species were used per treatment. After 5 months of exposure under ash, germination was only detected at control (germination rate of *P. canariensis* = 61%, *C. proliferus* = 4%, *L. campylocladus* = 7%, *C. symphytifolius* = 1%), 1 cm (51%, 2%, 3%, 1%) and 5 cm (*P. canariensis* = 5%, *C. proliferus* = 4%) treatments. Thus, the massive ash fall during this eruption has meant a complete reset of the seed bank in the areas located within a radius of approximately 3000 m from the crater (still buried under 5 cm thick ash layer). We therefore suspect that the current volcanic eruption will induce a change in the Canary pine forest plant community composition in those affected areas.

The ecological collapse of mutualistic interactions in a high oceanic mountain environment (El Teide, Canary Islands)

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We present ecological data about the significant environmental changes, due to historical human intervention, in the high mountain of El Teide (National Park). The aborigines, 2500 years ago, brought abundant livestock to the highlands of Tenerife and took advantage of the wood of the Canary cedars that presumably constituted an open woodland. In addition, they started fires to open the way for livestock but this conifer does not resist fire. Furthermore, European human populations also continue with the exploitation of the timber of the cedars after the conquest during the 15th century onwards. These destructive anthropic practices led to the regression of this woodland, whose cedars left confined to the escarpments of Cañadas del Teide. The disappearance of this ancient woodland, was also possibly affected by the volcanic eruptions on El Teide, triggered the spatial development of native leguminous species. These profound environmental changes probably caused the rarefaction or virtual extinction of the cohort of frugivores present in the area. Thus, birds as essential in the dispersal systems of plants in the Canaries, such as the blackbird *Turdus merula* or the robin *Erithacus rubecula*, must have practically disappeared and even today they are still scarce, although present. For this reason, other fleshy-fruited species that depended on them for their dispersal were also presumably affected since they were present all year round as residents and possibly breeding birds. These plants: *Sorbus aria*, *Rosa dumalis* ssp. *teydensis*, *Bencomia exstipulata*, *Ephedra foeminea* or *Rhamnus integrifolia* are threatened to varying degrees. For this reason, to recover the native fruit-eating guilds that participated in the aforementioned seed dispersal systems, and the urgent regeneration of the ancient cedar forest in Cañadas del Teide is highly recommended.

Effects of large-scale forest fires on insular bats

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During the last decade, wildfires have affected numerous species, many of which are already impacted by multiple anthropogenic threats. Vegetation is severely affected by fires, which affects vertebrate communities, including bats. However, detailed knowledge about the effects of fires on the activity of island bats is scarce, which hampers conservation and management in fire-prone ecosystems. Madeira Island is home to three insectivorous bat species: *Nyctalus leisleri verrucosus*, *Pipistrellus maderensis* (IUCN Vulnerable) and *Plecotus austriacus*, each representing one of the three foraging guilds of insectivorous bats. In 2016, the year in which Madeira was affected by several large-scale fires, bats were surveyed throughout the island using low-cost autonomous recorders. To investigate how the 2016 fires impacted the islands' bats, in 2021 (five years post-fire), we resurveyed 33 burned and 25 unburned sites. We found that in 2016, bat activity was consistently lower on burned sites than unburned sites, whereas in 2021, the activity of all species increased on sites that had been burned five years earlier, indicating species- and guild-specific responses to post-fire vegetation. Open space foraging bats exhibited a greater increase in activity in burned areas than narrow space foragers. Furthermore, our results indicate that forests and woodlands play an important role in the activity and social behavior of bats. This study provides valuable insights into the spatio-temporal effects of wildfires on island bat populations, with implications for conservation strategies. Considering that ca. 60% of all bat species occur on islands, and ca. 25% are insular endemics, more fire-related studies are needed in anticipation of an increased frequency and intensity of fires under future climate conditions.

Effects of plant and animal introduction of species on the pollination interaction networks of the Ogasawara Islands, Japan

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Introduction of invasive species can cause strong imbalances in ecosystem functioning, especially in sensitive oceanic islands with high endemism because the inhabitants and the interactions between them have evolved in isolation. The Ogasawara Islands of Japan is an oceanic archipelago of World Heritage status (~1,000km South of Tokyo), which in recent decades has faced increasing disturbance from invasive species including the Green anole (*Anolis carolinensis*) and the European honey bee (*Apis mellifera*). These invasive species can have strong direct and indirect effects through predation and competition on the native island pollination system which, among other pollinator groups, it originally comprised nine native bee species. In this study, we use an ecological network approach to compare islands with different degrees of impact from invasion. We present results on how these invasive species have affected the original island pollinator community and how this has influenced pollination interaction networks in different islands.

Forest edges increase pollinator network robustness to extinction with declining area

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Edge effects often exacerbate the negative effects of habitat loss on biodiversity. In forested ecosystems, however, many pollinators actually prefer open sunny conditions created by edge disturbances. We tested the hypothesis that forest edges have a positive buffering effect on plant-pollinator interaction networks in the face of declining forest area. In a fragmented land-bridge island system, we recorded ~20,000 plant-pollinator interactions on 41 islands over 3 years. We show that plant richness and floral resources decline with decreasing forest area at both interior and edge sites, but edges maintain 10-fold higher pollinator abundance and richness regardless of area loss. Edge networks contain highly specialized species, with higher nestedness and lower modularity than interior networks, maintaining high robustness to extinction following area loss, while forest interior networks collapse. Anthropogenic forest edges benefit community diversity and network robustness to extinction in the absence of natural gap-phase dynamics in small degraded forest remnants.

Preliminary quantification of the carbon stock of lowland and midland scrublands of Tenerife, Canary Islands

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The consideration of terrestrial ecosystems as carbon sinks is usually linked to forests and arboreal species. However, insular mature ecosystems dominated by native shrub species could be acting as sinks and contributing to the carbon stock on islands. In the Canary Islands, scrublands occupy around 25% of the archipelago land area. Here we present preliminary data about the total amount of carbon stored in the aboveground vegetation of mature coastal scrubland, and the lowland and midland secondary scrubs of the island of Tenerife. Five plant communities were characterized by measuring, in 40 plots of 400 m^2, the plant cover and the amount of aboveground biomass per unit area, to calculate the carbon stored in each community. We measured all the individuals of scrub and tree species in the plot, including height, two diameters, and basal steam diameters when possible. For the most frequent and abundant scrub species of Tenerife (native, endemic, and invasive), we built preliminary allometric equations using their volumetric data to estimate the biomass of individuals. The average carbon stored in each community was calculated and extrapolated to the total area occupied in Tenerife. Although the carbon accumulated in scrubs is lower than in forests, the importance of their contribution lies in their wide distribution. Information provided by this work is intended to guide management measures to maximize the compensation of the carbon footprint of the Canaries. Additionally, allometric equations will provide a non-destructive method to calculate biomass content in shrubs in the future. The need for protection and conservation of the Canarian ecosystems with the aim of preserving the natural heritage is more than accepted. However, the ecosystem service of carbon sequestration done by native species, not only trees but also shrubs, could be another reason for the conservation and restoration of natural and degraded areas.

Red listing of the ecosystems of the Seychelles granitic islands

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The Seychelles granitic islands represent an archipelago of about 40 islands that form together the smallest oceanic fragments of Gondwana. Their natural history is therefore fascinating, having evolved as remote oceanic islands with a relatively unchanged topography over tens of millions of years, and cyclical fragmentation due to sea-level variations prompted by glaciations. Although the Seychelles is a leader in terms of its coverage by protected areas (48% of the country's land area), the most inhabited islands have a much lower coverage of protected areas: 20% for Mahé and 8.6% for Praslin. It is therefore critical to improve the network of protected areas on these two islands, and we suggest that using only species distribution data is insufficient as it does not provide enough details to fine-tune the exact delineation on the lower slopes. To develop a checklist of the ecosystems of these islands, we have compiled information from the literature and we have collected new field observation data over the last fifteen years. In 2021, we developed in detail our approach to conceptualizing and naming ecosystem-types. Then we discussed the typology (or systematics) of our ecosystem-types in relation to the recently published IUCN function-based typology. We produced ecosystem distribution maps using Sentinel-2 imagery with an Object-Based Image Analysis, done in an Earth Engine script. Finally, we evaluated the risk of collapse for the most important ecosystem-types using the criteria A and B of the Red List of Ecosystem. We found 69 types of terrestrial, freshwater and subterranean ecosystems, distributed among 23 Ecosystem Functional Groups (level 3 of the new IUCN typology). Among those, we found 6 endangered (EN) and 10 critically endangered (CR) ecosystem types. Their distribution has provided keystone data that have allowed the initiation of discussions with stakeholders and landowners for the nomination of new protected areas.

The vulnerability of soil carbon stocks as particulate and mineral-associated organic carbon in shrubland ecosystems of Tenerife

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Soils represent the highest terrestrial organic carbon pool globally, storing three times more carbon than the vegetation. However, this carbon pool is vulnerable, as warming due to climate change enhances CO_2 fluxes from the soil to the atmosphere. In this context, it is relevant not only to quantify soil organic carbon (SOC) but to determine its vulnerability by assessing in which form is stored: as mineral-associated organic matter (MAOM) (more persistent due to its organo-mineral associations), or particulate organic matter (POM) (more vulnerable). This information is especially important for shrub ecosystems with semi-arid climate, where drier and warmer conditions are expected, affecting the vast carbon pool in the soils. In the case of the Canary Islands, this kind of ecosystems occupy large extensions, having a key role in their carbon storage capacity. To determine the magnitude and vulnerability of SOC stocks in shrublands of the island of Tenerife, we sampled five shrub ecosystems representing three shrubland types (coastal, secondary, and summit). We used cores down to 30 cm depth, divided in two samples (0-10 and 10-30 cm) and estimated SOC, MAOM and POM per area and in the entire surface of each ecosystem type. We assessed differences between ecosystems, depths and determine the drivers of soil organic carbon stocks by relating them to the plant community, soil type, temperature, precipitation, elevation and (macro)orientation. The obtained results are highly valuable to understand ecosystem functioning, as well as for the climate change mitigation plans of the Canary Islands, as they contribute with data about the existing carbon pools, and thus to the development of strategies to maintain or increase these important carbon stocks.

What is the taxonomic status of the most important pollinator on Madeira Island?

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Bombus terrestris is the most important pollinator of wild plants and crops on Madeira Island. It is a supergeneralist pollinator that exploits any floral resource available in any of the island's seasons and habitats. Despite its importance to the island's ecosystems, the taxonomic status of the Madeiran *Bombus* remains controversial. The Madeiran populations have been regarded as a valid species*, Bombus madeirensis*, as an endemic subspecies, *Bombus terrestris maderensis*, or as a native (but non endemic) subspecies, *Bombus t. lusitanicus* which is also present in southwestern France, the Iberian Peninsula, and the Balearic Islands. Microsatellites and DNA genetic studies suggest that the populations of Madeira differ from the mainland populations of *Bombus terrestris*. In this study, the taxonomic status of Madeiran populations has been attributed based on the colour pattern. However, *Bombus terrestris*, like other *Bombus* spp. show an exceptional diversity of colour patterns, which has led to inaccurate descriptions. So far, no quantitative and systematic study of colour variations in Madeiran populations has been carried out. Here we analyse 10 characters including body colour patterns and the length and shape of the labrum and mandible in more than 130 specimens. The results show that, although there is a large intraspecific variation in colouration, no specimens match the description of *Bombus t. lusitanicus*. The most common colouration pattern (40%) corresponds to that of *Bombus t. terrestris*, while the remaining specimens do not fit into any subspecies group. These morphological similarities do not support that the Madeiran populations belong to the subspecies *lusitanicus*. It remains to be determined whether these clusters of colour patterns are associated with the type of habitat or may be partly the result of hybridisation with commercially traded populations of *B. terrestris*.

Cute invaders: uncovering the trophic relationships and abundance of free-roaming cats on Madeira Island, Macaronesia

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Free-ranging cats (*Felis catus*) pose a significant threat to biodiversity. However, little is known about their trophic ecology, population status, and ecological drivers in insular ecosystems, where they often represent the top predator. This study used DNA metabarcoding to assess the diet of free-ranging cats and camera traps to investigate their abundance and activity in a peri-urban protected area on the subtropical Madeira Island in Portugal. Cats were found to consume a wide range of native and non-native vertebrates, including multiple endemic taxa. Based on 582 trapping-nights we estimated a density of 1.4 cats per km^2 and landscape-scale analysis showed that cat activity was positively influenced by the proportion of rocky areas in the landscape and the distance to human resource subsidies. However, no significant driver was found for cat abundance. Our results suggest that cats are highly abundant throughout the protected area and that their core home ranges are associated with rocky terrain away from the most humanized sections of the park. Furthermore, our diet data indicates that free-ranging cats do not rely heavily on anthropogenic food sources and may rely mostly on wild prey to fulfil their dietary needs. Cat abundance and activity were particularly high in the vicinity of the only known breeding colony of Manx shearwater on the island. Taken together, these findings indicate that free-ranging cats pose a significant threat to the native vertebrate fauna of Madeira Island and that their management, especially during the breeding season of nesting seabirds, should be considered.

Islands as ideal systems to assess the multifunctionality of species within ecological communities

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Detecting ecological interactions in an ecosystem and understanding their complexity is one of the big challenges in the natural sciences. As relatively simple systems with well-defined borders, islands have a great potential to advance our comprehension of nature complexity. Network theory provides hope to reach that goal. Specifically, the development of a multilayer network approach provides a promising framework to analyse multiple layers of complexity, simultaneously quantifying the intensity of intra- and inter-layer links between different types of biotic interactions. Such analytical perspective is instrumental to identifying keystone species and assessing ecosystem robustness, especially in the face of the current disturbances that islands are facing due to global change. In an unprecedented sampling effort encompassing a total of c. 700 species of plants, animals, and fungi, with over 1500 interactions across six ecological functions gathered in a small island (c. 10 ha) of the Balearic archipelago (Western Mediterranean Sea), we built a quantitative multilayer network, with a phytocentric perspective, in order to assess (1) the species' contribution to multiple functions, (2) whether the number of participating species is evenly distributed across functions, and (3) to determine if species multifunctionality is driven by neutral processes. Our common species in the six layers (ecological functions) were plants, and we studied their interactions with: (1) pollinators, (2) herbivores, (3) seed dispersers, (4) pathogenic fungi, (5) saprotrophic fungi, and (6) symbiotic fungi. We found a strong heterogeneous pattern for plant species participation, indicating that they influence community assembly in a non-random way, but such heterogeneity was unrelated to their abundance and vegetation cover in the community. We anticipate this approach will allow exploring potential common patterns across different types of island communities and ecosystems, and findings should be highly useful to both conservationists and theoreticians.

One size does not fit them all: cladogenesis in an insular megaherbivore

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Insular examples of cladogenesis in large mammals resulting in more than five species are rare. The Pleistocene Crete in the Mediterranean Sea provides such a case. Here, eight species of an endemic genus of deer (*Candiacervus*) were the dominant herbivores, all descendent from a single ancestral species. The most striking feature of these eight species is their body mass divergence. The disparity in mass in this endemic deer lineage ranges from 27.8 kg for the smallest species (*C. ropalophorus*) up to 245.4 kg in the heaviest species (*C. major*). The largest species is thus approximately eight times heavier than the smallest species. This range accounts for nearly one quarter of the total range of living and fossil Cervidae. Another remarkable feature is an unusually large variety in antler shape and size, likely accelerated by increased intra-specific male-male competition. This remarkable degree of morphological divergence, which is unique among Cervidae, apparently evolved under ecological release from terrestrial predators and with limited interspecific competition.

Infection for different reasons: ecological correlates of avian haemosporidians differ at host individual- and species-level on land-bridge islands

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Animal diseases developed from natural ecosystems usually involve host-parasite interactions embedded in hierarchical scales. However, few studies have tried to dissect different factors that are responsible for infections across the levels of ecological organization. Here, by leveraging bird communities and haemospordians in the Thousand Island Lake (TIL), China, we examined parasite infection risk in human-induced fragmented habitats at both individual and species levels. We sampled birds through mist nets and used molecular-based methods to detect parasites and to identify the sex of each bird individual. We compared haemosporidian infections between islands and mainland areas to investigate the effects of insularity on parasitism while accounting for bird phylogeny, and morphological and functional traits. Overall, we screened more than 1,000 bird individuals and identified 156 lineages of avian haemosporidians in the TIL region (60% are new records). We found reduced infection probability for individuals on islands than on the mainland overall, but this pattern was not evident when analyses were conducted separately for different parasite genus. In addition, the infection of each parasite genus was associated with different avian traits such as morphology, sex, flocking tendency, and migration status and showed distinct seasonal dynamics. At the species level, we found that the prevalence of each bird species is mainly affected by their pace-of-life: species living a relatively slower pace-of-life are more likely to be infected than fast-lived ones. Overall, our study contributes to the accumulation of avian haemosporidians data for land-bridge islands in East Asia and reveals the importance of considering ecological hierarchy when studying disease risk.

Island area and remoteness shape plant and soil fauna diversity through land use change in Zhoushan Archipelago

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Biodiversity is changing dramatically due to human-driven land use change, but our knowledge of how such driver influences plant and soil fauna diversity on island ecosystems remains limited. We built a structural equation model to explore direct effects of island size and remoteness, and indirect effects of these factors via land use intensity and pinewood nematode invasion, on the α diversity of plants and soil fauna across 37 continental shelf islands in the largest land-bridge archipelago in eastern China. We also conducted a regression analysis to examine how soil fauna β diversity between woodland and degraded grassland vary with island size and remoteness. We found that increasing island area directly promoted plant diversity. Land use intensity increased with island area which also promoted plant diversity, and loss of pine forest by the pinewood nematode invasion increased with island remoteness which reduced plant diversity. Island remoteness only indirectly reduced plant diversity through increasing pine forest loss. With increase in island area, individual density of soil fauna in litter layer of woodland and soil layer of grassland increased. With increase in island remoteness, individual density in soil layer and α diversity of soil fauna in the litter layer of grassland significantly decreased. Soil fauna β diversity between woodland and grassland did not significantly change with island area and remoteness. However, in the soil layer, the nestedness components decreased but the turnover components increased with increase in island area; in the litter layer, the nestedness components increased but the turnover components decreased with increase in island remoteness. Our findings highlight that island biogeography theory has relevance to understanding human impacts in the Anthropocene.

Cascading effects of defaunation on personality diversity in small mammals in subtropical reservoir islands

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Defaunation due to habitat loss and isolation has posed a major threat to functional diversity in island systems. Consistent intraspecific behavioural variations (or animal personality) are crucial behavioural traits that affect the fitness of individuals. Thus, the changes in personality diversity can have eco-evolutionary consequences on the persistence of populations on islands. However, we still know little about changes in functional diversity of personality traits due to the loss of large and medium mammals on islands. To bridge this gap, we investigated the changes in personality diversity of small mammals on subtropical fragmented islands of a large reservoir in China. We used the camera traps and live traps to assess the degrees of defaunation and abundance of small mammals, respectively. The open-field test was carried on to evaluate personality traits of small mammals. We used functional diversity (richness, evenness and divergence) to estimate personality diversity in populations. Structural equation models were finally conducted to estimate the direct and indirect effects of area, isolation and defaunation on the diversity of personality. The best model demonstrated that the island area indirectly increased functional evenness and divergence of personality traits via defaunation. However, the effects of island area and defaunation on the functional richness of personality traits were not detected. In addition, the island area increased rodent abundance directly or decreased rodent abundance via defaunation indirectly, while isolation had no significant effects on personality diversity. Our results indicate that the island area would have cascading effects on personality diversity due to defaunation. Preservation of large and medium mammals is crucial to maintain behavioural diversity. We also appeal for more studies on behavioural diversity and its potential eco-evolutionary consequences in island systems.

Multi-scale and multi-dimensional plant diversity in Thousand Island Lake

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Thousand Island Lake (TIL) is a large hydroelectric reservoir that was formed by the construction of the Xin'anjiang Reservoir Dam in 1959. Forests were clear-cut on the islands, and the major vegetation type is now secondary successional forest dominated by Masson pine *(Pinus massoniana*). We established forest dynamics plots on 29 islands (with a range of area and isolation) in TIL during 2009-2010 and control plots on the adjacent mainland. All trees with a diameter at breast height (DBH)≥1 cm were tagged, measured, identified, and mapped in the subplots. Functional traits and soil properties were also measured. We found that: (1) Environmental filtering underpins the island species-area relationship. (2) SLOSS-based inferences of fragmentation effects are contingent on variation in the maximum area of patches included in analyses and the slope of SARs in fragmentated landscapes. (3) High beta diversity among small islands is due to environmental heterogeneity rather than ecological drift. (4) The species diversity at the scale of plot, island and landscape is not independent, but shows an interdependent and interactive Hierarchical Patch Dynamics Paradigm. (5) Larger islands have more late-successional species of woody plants than smaller islands after 50 years of secondary succession. (6) There were significant cross-scale interaction effects of patch and landscape variables on local-scale edge effects. Altered spatial arrangement of habitat in the surrounding landscape (i.e. declining habitat amount and increasing patch density), as well as decreasing area at the patch level, exacerbated edge effects on traits distributions. (7) There were striking differences in species composition between island and mainland plots, which were mainly affected by environmental filtering and spatial variables, respectively. Functional traits exhibited significant interaction effects between isolation (island versus mainland) and underlying environmental gradients in soil fertility and stress tolerance. (8) β diversity and its turnover and nestedness components of different mycorrhizal trees showed significant divergence between island and mainland plots. AM trees are more sensitive to soil nutrients (i.e. nitrate nitrogen content), while EcM trees are more sensitive to soil physical properties (i.e. soil depth). (9) Functional diversity showed a nonlinear threshold relationship with island area. (10) Environmental filtering and competitive exclusion simultaneously drove the functional and phylogenetic clustered pattern on islands.

Land-use change interacts with island biogeography to alter bird community assembly

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Anthropogenic activities have reshaped biodiversity on islands worldwide. However, it remains unclear how island attributes and land-use change interactively shape multiple facets of island biodiversity (taxonomic, functional, and phylogenetic diversity) through community assembly processes. To answer this question, we undertook bird surveys in forest, farmland, and mixed habitats on 34 oceanic land-bridge islands in the largest archipelago of China. We find that bird species richness increases with island area and decreases with isolation regardless of land-use type, but forest habitats have lower species richness than farmland and mixed habitats. After incorporating data on avian morphological traits and phylogeny, we show that island bird assemblages are generally clustered (species share similar traits or evolutionary histories). The degree of bird community clustering from mixed habitat did not vary with island attributes. Contrary to our expectation, we find forest bird assemblages are more clustered than those in farmland, especially on large and close islands. These contrasting results indicated that land-use change interacts with island biogeography to alter community assembly of birds on inhabited islands. Our results provide evidence that the characteristics of human-modified habitats drive community assembly of island birds and further suggest that agricultural landscapes outside of forest habitats on large and close islands have essential roles in protecting countryside island biodiversity .

☙ Island Ecology ❧

Posters

(From: L. Figuier, Storia delle piante. Fratelli Treves, Milano, 1882)

Preliminary observation on the interaction dynamics of three genera of Cascade Frogs (Amphibia: Ranidae) on Sumatra island, Indonesia

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The formation of the Bukit Barisan Mountain range that stretches along Sumatra's longitudinal axis had profoundly shaped the topology of the island. As consequence, various types of forest ecosystems are available across elevational gradient, providing plentiful habitats and microhabitats for each Sumatran species, including cascade frogs. *Odorrana*, *Wijayarana*, and *Sumaterana* are the three genera of ranid frogs that are commonly observed to inhabit torrential stream habitats in Sumatra. However, the interaction among those species had never been recorded to date. During fieldwork between 2014–2015, we conducted Visual Encounter Surveys in several torrential streams in Sumatra and recorded several ecological parameters (e.g., distance from water and microhabitat) for each encountered individual of the three frogs' genera. Standard statistical analysis was performed to investigate interaction dynamics among the three genera. Our findings indicate the possibility of interspecific competition between *Odorrana-Wijayarana*, *Odorrana-Sumaterana* and *Sumaterana-Wijayarana*. Further studies are required to confirm our hypothesis. Additionally, this study shows that in biodiversity hotspot areas like Sumatra, ecological study is as important as study on species discovery.

Elevational patterns of arthropod species richness in a sky island: the role of environmental filtering processes in an isolated system

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Mountain regions represent ideal systems to understand which mechanisms regulate species richness as steep environmental changes occur from lower to higher elevations within a small area. Also, the study of biodiversity of mountain regions is of paramount importance in biological conservation, since mountains are typically important centers of diversification and endemism, with many of the world's biodiversity hotspots located on mountain regions. One of these biodiversity hotspots is the Madrean Sky Island Archipelago. This archipelago includes about 65 mountains located in the Cordillera Gap between North America's Rocky Mountains and Sierra Madre Occidental. These mountains represent an archipelago of islands of high elevation areas in a "sea" of dryland, and are therefore referred to as Sky Islands. In this study, we explored patterns of species diversity of ground-dwelling arthropods collected through pitfall traps on the Santa Catalina Mountains in the Madrean Sky Island Region. Variations in species richness along an elevation gradient of about 1500 m were investigated for ants, spiders, beetles, orthopterans, and myriapods. When these groups are considered separately, species richness showed somewhat variable patterns. Ants, spiders, and orthopterans, showed a monotonic decrease with elevation (even after correcting for the extent of available area), whereas beetles and myriapods exhibited different patterns, which reflect differences in their biogeographical history and niche conservatism. When all arthropods were combined, the overall species richness declined with elevation, which suggests an environmental filtering exerted by climatic conditions on common species pools in an isolated area. Our study highlights the importance of considering the taxonomic resolution and biology of the group examined before exploring mechanisms behind diversity patterns and planning conservation priorities. On the Santa Catalina Mountains, future biodiversity surveys may focus on ants, spiders, and orthopterans as they reflect the overall diversity of arthropods on these mountains. Future directions should also involve the study of other aspects of ground dwelling arthropod communities of the Santa Catalina Mountains, such as variations in beta diversity and nestedness patterns along the elevational gradient.

Comparison of plant and coleopteran diversity in plant communities with *Quercus alnifolia* in Cyprus

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Cyprus is the easternmost island of the Mediterranean Sea, being isolated ('oceanic') throughout its existence and experiencing very dry climatic conditions that are expected to become even harsher due to climate change. Hence, the study of its habitats and communities is of great importance for our understanding of climate change effects. *Quercus alnifolia* is an endemic oak of Cyprus that grows in elevations ranging from 600-1,525 m a.s.l. Its communities can be found throughout the island's central mountain range (Troodos Mt.) and it can be found either in mixed stands with other arborescent species or in pure stands. Six plant communities including trees or stands of *Q. alnifolia* were studied, namely a *Pinus nigra* subsp. *pallasiana* stand, a mixed stand of *P. nigra* with *P. brutia*, a *Cedrus brevifolia* stand, a *P. brutia* stand, a mixed stand of *C. brevifolia* with *P. brutia*, and a *Quercus alnifolia* stand. The plant communities are situated within two protected sites of the NATURA network. An inventory of the plant communities was compiled using the Braun-Blanquet approach, in spring and autumn. Within these plant communities, beetles were collected using pitfall traps, focusing primarily on Carabidae and Tenebrionidae. Beetle sampling was performed in spring, summer, and autumn. Abiotic parameters, such as soil humidity, air temperature, air humidity, plant litter-layer depth and mass, were also recorded. The plant communities sampled were found to comprise more than 50 plant taxa (belonging to 26 different families), more than 30 Coleoptera families, and more than 30 species of Carabidae and Tenebrionidae. The most important abiotic factors shaping plant and beetle diversity were identified. This study will provide the baseline against which to evaluate future changes of these communities in the framework of climate change effects on semi-arid insular biota.

Understanding resilience of seed dispersal in insular systems to climate change

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Global biodiversity loss is disproportionately rapid on islands, which despite being hotspots of biodiversity, comprise ~ 80% of world's species extinctions. The vulnerability of insular ecosystems to global change has been historically mainly related to the introduction of invasive species. Yet, we still lack a quantitative understanding of how other major threats such as climate change will jeopardise, not only species, but pivotal ecosystem functions derived from trophic interactions such as animal-mediated seed dispersal. To date, the scarce data and methodological limitations have entailed a lack of studies on the effect of climate change on seed dispersal in entire island communities. Here, we will present the main goals of ECORISC, a project that implies a major step ahead previous work with its integration of a new global dataset on ~65 insular seed-dispersal networks, alongside methodological approaches from the fields of interaction networks, ecological niche modelling and future climate change projections. The combination of empirical knowledge on the structure and vulnerability of current insular communities with future climate, species extinctions and interaction rewiring simulations will provide an integrated understanding of the resilience of seed dispersal in insular systems to climate change. The main outcome of ECORISC (i.e., the quantification of structural and functional consequences derived from climate-driven biodiversity loss) will provide essential knowledge needed to preserve and restore insular ecosystems and biodiversity in a changing world.

Island biogeography of urban birds: size of green spaces is more important than isolation

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Urban green spaces are frequently considered as islands of nature in a sea of concrete. Under this assumption, it has been repeatedly proposed to apply the principles and methods of island biogeography to urban parks. Urban birds largely depend on green spaces for foraging and breeding. Investigating the role of geographical characteristics of green spaces in shaping bird communities can be therefore of paramount importance to enhance their conservation in urban areas. With a population of about three million inhabitants and a surface of about 1300 km^2, Rome is one of the largest cities in the Mediterranean biodiversity hotspot. Because of its millenary history, urban Rome hosts a complex mosaic of natural, seminatural and artificial environments exploited by more than 90 bird species. In this research, we investigated the influence of structural parameters of green spaces on avian diversity in urban Rome from the perspective of island biogeography. Using multimodel selection procedures, we found that the area of the green spaces was the most important factor influencing avian species richness, and the relationship was adequately modelled by a power function. By contrast, the role of shape, position along the urban-rural gradient (distance to the city centre), shape (deviation from a circular form) and distance from potential sources of species (distance from the nearest largest green space) was negligible. Avian beta-diversity between green spaces (measured both as total beta-diversity and pure turnover) was not correlated (Mantel tests) with geographical distances. Avian communities were highly nested. These results suggest that bird communities of green spaces in urban Rome are random samples of the total urban fauna. This is consistent with the high dispersal capabilities of most bird species and the small distances between green spaces. Improving connections between green patches seems to be not a priority for bird conservation in a highly urbanized landscape, while preserving large spaces is essential to have rich communities.

Remote sensing reveals fire-driven facilitation of a C4 rhizomatous alien grass on a small Mediterranean volcanic island

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Volcanic islands are special ecosystems for studying biogeographical and evolutionary processes. Occasional disturbance events, such as eruptions, tsunami or big fires, can represent major drivers of such processes leading to biotic sterilisation or major changes in island biotas. In this study, through remotely sensed data, we investigated the intensity and the extent of a large fire event that occurred on the small volcanic island of Stromboli (Aeolian archipelago, Italy) on 25-26 May 2022, to assess the short-term effect of fire damages on local plant communities. For this purpose, two different spectrally sensitive indices, i.e. the differential Normalised Burned Index (dNBR) and the Normalised Difference Vegetation Index (NDVI), were used. The dNBR was also used to quantify the extent of early-stage vegetation recovery, dominated by *Saccharum biflorum* Forssk. (Poaceae), a rhizomatous C4 perennial grass of paleotropical origin. The burned area was estimated to have an extension of around 337.83 ha, corresponding to 27.7% of the island surface and to 49.8% of Stromboli's vegetated area. On the one hand, this event considerably damaged the native plant communities, hosting many species of high biogeographic interest. On the other hand, *Saccharum biflorum* clearly benefited from arson. In fact, it showed a very high vegetative performance after burning, being able to exert unchallenged dominance in the early stages of the post-fire succession, reaching within a few months stem density values that are only slightly lower than those of the unburned stands. Our results confirm the complex and probably synergic impact of different human disturbances (recurrent fires, introduction of invasive alien plants) on the structure and the functioning of natural ecosystems on small volcanic islands.

One year of monitoring in the most affected habitat by the Tajogaite volcano: The Canary Island pine forest (La Palma)

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The Canary pine (*Pinus canariensis*) is an endemic species to the Canary Islands that form the largest forest ecosystem in the archipelago. This pine shows some characteristics that make it unique, such as a thick bark, serotinous cones and a high capacity for resprouting. Although some studies have associated these particularities with its resistance to wildfires, others have linked its resilience to vulcanological processes that have regularly occurred in the Canary Islands. However, during the recent eruption of the Tajogaite volcano on La Palma (19 September - 13 December 2021), wildfires were not originated by any of the volcanic activities (e.g., lava flows or pyroclastic/lapilli emission). Our work consisted of monthly monitoring (January - December 2022) of the vegetation status. A total of 19 plots of 30 m^2 were established over 7 km south of the crater (the area most affected by the eruption). On these plots, vegetation was characterised by a species inventory, where abundance, cover, phenology and percentage of eruption-related damage were measured. In the case of *P. canariensis*, all individuals were tagged, measuring DBH, canopy cover, and the size of apical and axial shoots. Preliminary results showed that woody plants were the only surviving species. In addition, leguminous species (*Chamaecytisus proliferus*, *Adenocarpus foliolosus*, *Bituminaria bituminosa* and *Lotus campylocladus*) were the most abundant. The Canary pine showed great resistance to the high temperatures and direct effects of pyroclasts fallen nearby the crater. Furthermore, they recovered from the chlorosis caused by the emitted volcanic gases and damage caused by ashfall and volcanic bombs. Finally, within a 250 m radius around the crater, more than 95% of the pine trees died six months after the end of the eruption.

Flap or fail: Exploring the role of native functional richness in establishment success of non-native birds on oceanic islands

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Biological invasion is considered one of the main drivers of global biodiversity decline. Non-native species has the potential to cause significant decline in native community abundance and contribute to extinction. Island ecosystems seem particularly vulnerable to impacts of non-native species and are overrepresented in the proportion of highly threatened species and species extinctions. While ecological theories based on Biotic Resistance predicts resistance to invaders through competitive exclusion, empirical evidence has yielded inconclusive results. Recent years have seen a surge of studies exploiting the increasing data availability to calculate different measures of functional diversity using species traits, however many questions remain on how to best utilise these methods. Here, functional richness was separately calculated for traits related to resource acquisition (foraging and dietary preference) and morphology in order to allow for detection of potentially divergent mechanisms responsible for community composition. Through construction of a global database of island bird communities, we investigated the functional niche of locally interacting native and non-native bird species on oceanic islands using functional richness. By creation of a set of null models, patterns in functional richness were compared to that of communities assembled through random processes. We found that successfully established non-native species contribute less functional richness than expected by the associated increase in species richness. We additionally found evidence of overdispersion for resource acquisition and underdispersion for morphological traits, and that establishment success was correlated to low dietary diversity and high morphological diversity respectively. This suggest that both competition and environmental filtering play a role in non-native establishment and emphasises the importance of trait selection in analyses of functional diversity, since pooling traits could "drown out" divergent patterns. Due to the well-established impacts of non-native species on global biodiversity, knowledge of the processes leading from introduction to impact is needed to prioritise future conservation efforts.

Islands in fire: self-restoration of pollination services in Mediterranean post-fire communities

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Fire is an important disturbance in the Mediterranean, considered to be an integral characteristic of the region, as it is in all regions endowed with a Mediterranean climate. As a result of climate change, there is an increasing inflammability imposed on the Basin's Mediterranean systems, which appears to be threatening particularly the areas lying at the Basin's driest parts, among them, the islands. There is another reason that Mediterranean islands, especially the small- even medium-sized ones, are vulnerable to fire: they are space-limited, thus the replenishment of the burnt areas through diffusion or migration by new species populations replacing those wiped out by fire is largely challenged. This is especially true for wild bees and other important pollinator groups with short flying ranges. This work will present the results of a systematic study carried out on Chios Island, Greece, during the first three years after a wildfire (viz. 2013-2015). We focused on the two most important pollinator guilds (viz. wild bees and hoverflies) and explored a range of insect and host-plant species post-fire metrics, such as diversity (richness, abundance) and community structure (diversity indices), as well as important insect functional traits. To be noted, ca. 70% of the bee diversity of Greece is hosted in the Aegean archipelago. The entire set of conclusions stemming out from these results constitutes a valuable basis for a sustainable management of the vulnerable island systems targeting to pollinator conservation.
Acknowledgment: The research work was supported by the Hellenic Foundation for Research and Innovation (H.F.R.I.) under the "First Call for H.F.R.I. Research Projects to support Faculty members and Researchers and the procurement of high-cost research equipment grant" (Project Number: HFRI-FM17-1139).

Flora of the islets in the western part of Ibiza (Balearic Islands) and its changes over time

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The main data of the flora of the islets of the Natural Reserves of Es Vedrà, Vedranell i els illots de Ponent of Ibiza (Balearic Islands, Spain) are presented. This protected area comprises nine islets ranging in size from 104 to 1.5 ha, and an additional five smaller islets. These islets have been surveyed four times since the late 1990s (in 1998, 2001, 2010, and 2022), with a similar sampling effort each time, making it possible to compare the plant checklists over time. In total, 291 taxa have been identified. Approximately 31% of the taxa are found on only one islet, around 50% are found on only two islets, and just 2.3% of species have been found on more than eight islets. Hence, despite their close proximity, these islets are characterized by their floristic heterogeneity, which reflects the diversity of substrates, reliefs, and histories of each one. The islet of Es Vedrà was the richest islet, with 178 species and with higher number of endemic species, while the islet of Conillera, despite being the largest islet, has a smaller number of species and endemism. About 60% of the species are therophytes, a proportion significantly higher than the flora of Ibiza (44%). However, hydrophytes, geophytes, and hemicryptophytes are underrepresented. New species have been found on all the islets during each exploration. Compared to the first visit, the catalogues have increased by 8–60% depending on each islet. At the same time, other species that were previously observed have not been found among different years of sampling, these absences have ranged from 14 to 37% of the species. These differences among samplings may be due to natural turnover, but insufficient sampling cannot be discarded. The fact that these islets are part of a protected area is essential to guaranteeing their conservation.

Trophic ecology and ecological role of pigeons as seed dispersers-predators

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Pigeons are widely distributed throughout the world, including island habitats. These relatively large-bodied birds can greatly influence the functioning of oceanic island ecosystems, where large mammals and birds are scarce or absent, through the consumption of fruits/seeds. Dietary guilds of pigeons are mainly categorized into “Frugivore” and “Granivore”, both of which can act as dispersers and predators of seeds. However, the importance of pigeons in promoting biodiversity and ecosystem health has not yet been estimated on a global scale. In this study, we conducted a comprehensive review of the trophic ecology and ecological role of pigeons. From 294 scientific publications, we extracted 861 fruits-pigeon interactions on continents and 1,103 on islands. Proportions of fleshy fruits and dry fruits interactions were significant different between islands and continents ($p< 0.01$). Fleshy fruit interactions were more frequent on islands (75%) than on continents (50%), while seed dispersal represented the main plant-bird interaction (92% on island and continents) compared to seed predation. On islands, the contribution of seed dispersal and predation were different among pigeon genera: *Ducula* and *Ptilinopus* were completely seed dispersers whereas *Columba* and *Patagioenas* are both a seed disperser and a seed predator. However, we should take care of the publication bias that could underestimate the seed predation interaction due to the difficulty in the quantification of predated seeds by pigeons. The reviewed studies indicated the potential of long-distance seed dispersal by pigeons, and functional loss in island ecosystems by the population decline of pigeons, which will facilitate their conservation efforts.

Insect flower visitors of two invasive and one critically endangered plant species of Macaronesia

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For conservation purposes, three important plants in Macaronesia are *Oxalis pes-caprae* and *Tropaeolum majus*, two of the 100 most invasive species, and *Geranium maderense*, a critically endangered endemic and one of the 100 most threatened species. Introduced plants have well-documented negative impacts on island ecosystems. However, little is known about the role of pollinators in the reproductive success of invasive plants. We analyzed the insect-plant networks of these three species, and whether introduced plants and visitors interact more with each other than expected by chance. Sampling on Madeira Island was performed in Garachico (*O. pes-caprae*, *T. majus*) and São Roque (*G. maderense*), at 500 m altitude. All visitors were collected with a net on sunny days with some cloud cover between 12:00 and 14:00 in May 2020. Invasive plant species were sampled in 25 m2 plots. Only one individual of *G. maderense* with many flowers was studied. Of the 20 insect visitors, species of six, four, and three families were found on *G. maderense*, *T. majus*, and *O. pes-caprae*, respectively. The most common insects were *Apis mellifera*, *Bombus terrestris*, *Andrena wollastoni*, and *Stomorhina lunata*. *A. mellifera* and Bombus spp. visited also more flowers per individual. *Geranium maderense* and *T. majus* were visited by the same number of native species (n=13). However, *G. maderense* supported more diversity and was visited by significantly more individuals (n=147) than *O. pes-caprae* (n=75) and *T. majus* (n=76). The number of species interactions in *G. maderense* was 0.74, followed by *T. majus* (0.68) and *O. pes-caprae* (0.42). The number of native visitors in *G. maderense* was also higher (79.6%) than in *T. majus* (64.5%) and *O. pes-capreae* (46.7%). The existence of invader complexes was not supported as the native species of visitors have 71% more interactions than introduced species. These results highlight the importance of native insect-plant networks.

Widespread population of invasive *Mustela furo* (Carnivora: Mustelidae) on the Island of Madeira, Macaronesia

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Invasive species pose a serious threat to biodiversity worldwide, particularly in delicate island ecosystems where invasive mammalian predators can have devastating effects. Ferrets (*Mustela furo*), a domesticated mustelid derived from the wild polecat (*Mustela putorius*), have historically been used for hunting and are increasingly kept as pets. Escaped or released individuals have formed self-sustaining populations in several countries, including Australia, Canada, Italy, New Zealand, and the USA, as well as several oceanic islands such as the Macaronesian archipelagos of Azores and the Canary Islands, where they are a significant threat to native wildlife, particularly ground-nesting birds. In this study, we present evidence of a widespread population of feral ferrets on Madeira Island and discuss their impact on the island's native fauna. We analyzed 37 records, including photographic evidence from a 582-trapping night camera study, and confirmed the presence of ferrets in a variety of habitats. Ferrets were detected in both natural and humanized areas and were photographed consuming non-native mammals and the endemic and IUCN Endangered Zino's Petrel *Pterodroma madeira*. These findings suggest that ferrets pose a significant threat to the conservation of Madeira's native fauna and highlight the need for evidence-based management of invasive mammals.

Edge effects constrain endemic but not introduced arthropod species in a pristine forest on Terceira (Azores, Portugal)

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Pristine Azorean forests have been deeply fragmented since human colonization. Fragmentation increases the length of edges and it therefore promotes edge habitats. Studying the impact of edge habitat on species assemblages is crucial to highlight the importance of forest connectivity and guide management strategies. This study explores the impact of forest edges on arthropod assemblages, and particularly investigates the differences of arthropod communities between three habitats, along a distance gradient from the forest edge near a pasture matrix to the core forest. We also compare patterns of arthropod communities with different biogeographic status (endemic, native non-endemic, and introduced species), given the island context. We sampled in a pristine forest on Terceira Island bordered by semi-natural pastures, using flight interception traps (SLAM). Overall, endemic species dominated arthropod abundances whereas species richness and diversity were similar between the three biogeographic categories. We found evidence of a strong edge effect on arthropod assemblages, adjusted both by biogeographic categories and seasonality. Indigenous (endemic and native non-endemic) species abundances were higher in the forest interior than at the edges or intermediate habitats, suggesting that indigenous arthropod assemblages were sensitive to the distance from the edge, a distance extended over 100 m to the core forest, whereas introduced species abundances were not impacted. Species diversity and richness did not differ between the three habitats either, regardless of the biogeographic categories. The composition of arthropods between the three habitats differed significantly when we considered all species or endemic species only, but not with native non-endemic or introduced species. However, the difference got obscured when seasonality was included in the analyses, suggesting that even though edges impact species composition, this impact varies seasonally and endemic species are particularly affected in early summer. Our results indicate that forest edges impact arthropods assemblages but endemic species are more likely to be constrained by the increase of edges than introduced species. Since most of these endemic species are of conservation concern, we urge to avoid forest management strategies that increase fragmentation and call for action to increase the size of protected natural parks.

Higher trophic levels, and species with poorer dispersal traits, are more susceptible to habitat loss on island fragments

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In the face of ongoing habitat loss and fragmentation caused by human activities, it remains a central and controversial question how biodiversity loss manifests. The 'passive sampling' hypothesis and the 'ecosystem decay' hypothesis have both been proposed as mechanisms to explain the loss of biodiversity. Only considering the passive sampling and ignoring the demography of species can seriously underestimate the effects of habitat loss on biodiversity loss. The demography of species can be altered by habitat loss, and biological processes within smaller islands differ from those on larger islands, since smaller islands hold smaller populations and higher extinction risk (and lower recolonization rates after species loss). Demography is predicted to vary with trophic levels and the dispersal ability of the species. However, empirical evidence on how these species' characteristics interact with the effects of habitat loss on biodiversity loss has been inconclusive. In this study, we considered 28 islands in a subtropical land-bridge archipelago and investigated the diversity of plants, herbivorous insects, and carnivorous insects, and the community-weighted mean of functional traits by using fixed area plots. In addition, we calculated the rarefied richness and the evenness of all taxa, β-diversity and its turnover and nestedness components. After controlling for sampling efforts, we still found that the island area had a significant effect on biodiversity indices, except for plant abundance. Turnover components are more important than nestedness components in local community composition. However, nestedness components between islands increased with increasing differences in island area. Species diversity at higher trophic levels (insects) were more sensitive to habitat loss than plants. For insects there were fewer species with low dispersal ability on smaller islands than on larger islands and diversity of species with low dispersal ability was more sensitive to habitat loss than that of good dispersers. Our results strongly support the 'ecosystem decay' hypothesis. The demography of species is affected by trophic levels and dispersal ability and these species' characteristics should be considered together. Our results suggest that the impact of habitat loss on biodiversity loss may be larger than that of passive sampling. On small islands, the species at higher trophic levels or with lower dispersal ability are at higher risk of extinction in the face of habitat loss. This highlights the need to consider the trophic interactions and the dispersal limitation of the species in order to conserve continuous habitats.

Species turnover shapes the effects of habitat fragmentation on specialization of tri-trophic interaction networks

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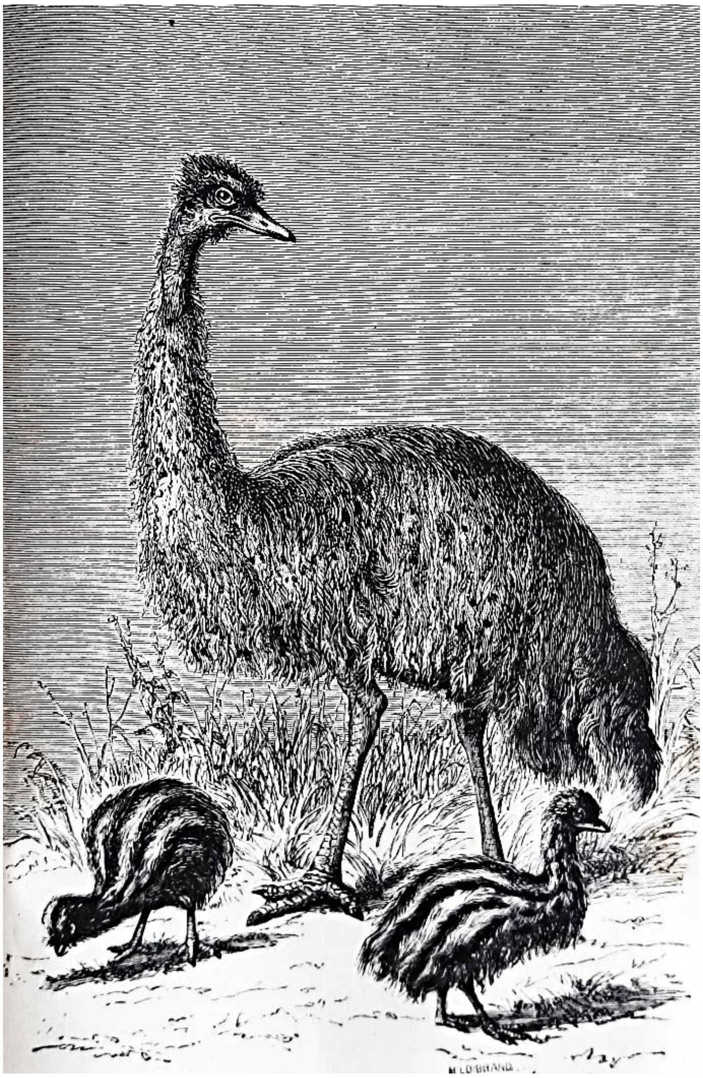
Habitat fragmentation is rapidly altering interactions among species worldwide. As an 'early warning' of community change, many studies have reported how specialization responses to habitat fragmentation, but the mechanisms underlying the effects of habitat fragmentation on level of specialization across multiple types of trophic levels have rarely been studied. Using an unprecedented dataset consisting of 2670 observations of tri-trophic interactions among plants, sap-sucking aphids and honeydew-collecting ants on 18 fragmented islands in the Thousand Island Lake, China, we constructed antagonistic plant-aphid and mutualistic aphid-ant networks. For both antagonistic and mutualistic networks, we tested the effect of habitat fragmentation on network specialization and explored the factors influencing specialization among islands. We found that both types of networks were more specialized on small islands, while only the mutualistic aphid-ant networks increased in specialization with increasing island isolation. Turnover among interacting species led to dissimilarity between both networks primarily, but interaction rewiring among shared species also played a role in the variation of network specialization. Furthermore, island area and isolation affected the specialization of the two networks through a bottom-up effect of plant community composition on aphid community composition. Our study is the first to explore how habitat fragmentation alters network specialization across different interaction types, and the effects of connections across multiple trophic levels on network specialization. Our results present a clear picture of the forces shaping interaction structures and community assembly and provide the possibility of predicting their possible variation in the context of global environmental change.

Evolution of Islands and Their Biotas

Contributed Talks



(From: L. Figuier, Vita e costumi degli animali: Gli uccelli. Fratelli Treves, Milano, 1881)

In solving the paraphyletic problems of Asian ranid frogs genus *Huia* (Amphibia: Ranidae)

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Prior our study, five species of ranid frogs genus *Huia* (*H. cavitympanum*, *H. masonii*, *H. sumatrana*, *H. modigliani*, and *H. melasma*) were recognized but multiple studies have demonstrated that *Huia* is not a monophyletic group. For decades, no studies have provided adequate systematics solutions, leaving the genus to languish in classification that is evolutionary incoherent. Through extensive fieldwork in Java and Sumatra, we generated most comprehensive taxon sampling of *Huia*. We then analyzed four mitochondrial DNA and two nuclear DNA markers in conjunction with morphological data from tadpoles to resolve the systematics of *Huia* under the framework of integrative taxonomy. Confirming the previous hypotheses, *Huia* was revealed as a paraphyletic group. Type species *H. cavitympanum* was the sister lineage to the genus *Meristogenys*, while the remaining members of *Huia* formed a monophyletic group that was sister to the *H. cavitympanum+Meristogenys* clade. Additionally, our extensive geographic sampling revealed multiple highly divergent, undescribed lineages in Sumatra and Java. By integrating molecular and morphological data from tadpoles, we provide evidence to justify the retention of the genus *Huia*, which now constitutes a monotypic genus consisting of the species *H. cavitympanum*. To avoid paraphyly, we propose a new genus to accommodate the remaining members. This study highlights the important of expanded geographic sampling and the utility of tadpole morphology to diagnose lineages that are otherwise hard to differentiate as adults.

Tempo and mode of diversification in red devil spiders (Araneae: Dysderidae) from the Canary Islands

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Adaptive radiations have played a key role in our current understanding of species evolution, but few common underlying patterns have been found to describe this process. Previous studies examining the mode in which species diversified, how diversification rates shifted through time, and how ecological specialization influenced both aspects, have yielded mixed results. To gain further insights into the diversification process, additional model systems involving alternative ecological settings are needed. Here, we present the results of a study aimed to unravel the diversification of the species rich genus *Dysdera* (red devil spiders) in the Canary Islands. These species exhibit remarkable phenotypic variability in their mouthparts, which is related to different levels of tropic specialization to predate on isopods. Specifically, we used phylogenetic comparative methods to explore patterns of linage diversification and assess the role of trophic specialization as a driver of species diversification. Additionally, we used climatic variables, occurrence data and geometric morphometric data to unravel the underlying mode of speciation by means of joint species distribution models and age-range correlation methods. Our results show that Canarian red devil spiders underwent an early burst of diversification, followed by a slowdown of diversification rates, which is a hallmark of adaptive radiation processes. We also found evidence that trophic traits shaped diversification, with specialist species exhibiting higher rates of speciation. However, trophic traits may not have been the sole or primary driver of diversification. Finally, our analyses suggest that speciation occurred mostly in allopatry, with secondary sympatric distribution following range expansion.

Insular speciation and influence of the environment on the phenotypical traits in the perennial species of the genus *Solenopsis* C. Presl

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The genus *Solenopsis* C. Presl belongs to subfam. Lobelioideae (Campanulaceae) and is currently represented by 9 taxa, which can be clearly differentiated for habit and flower structure in two well-distinct groups. The first one includes only two annual species with caulescent or subcaulescent habit and flowers with corolla provided by lobes slightly divaricated at the top, while the species belonging to the second are generally perennial and show stemless habit with leaves all arranged in basal rosetta and flowers with corolla provided by lobes markedly patent at the top. The taxa belonging to this second group are restricted to the Mediterranean area, showing their maximum degree of diversity in the larger islands, such as Sicily, Sardinia, Crete, Corsica, Cyprus, and Majorca. On each island, there is at least one strictly endemic species, while only a few taxa are shared by more than one island. Therefore, *Solenopsis* represents an interesting example of a genus with evident phenomena of vicariance in the Mediterranean islands and with a sporadic presence in continental areas. This contribution analyzes the species currently known from a taxonomic point of view and examines the relationships between ecological factors (climate, soil and habitat type) and morphological characters, such as the width of the basal rosette, plant height, leaves size, length of corolla, calyx, capsule and seed size and specific leaf area (SLA). The aims of this study are to determine if some morphological traits are significantly influenced by the environment and if it is possible to group the perennial *Solenopsis* species according to their ecological preferences along a geographical gradient.

Integrative taxonomy provides new evidence of cryptic diversity: Diversification of *Leptotrichus* Budde-Lund, 1885 (Oniscidea, Porcellionidae) on Cyprus

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Porcellionidae are one of the most diverse families of terrestrial isopods (Oniscidea), comprising more than 330 species in more than 19 genera mainly distributed in tropical and temperate zones around the globe. The genus *Leptotrichus* includes 10 species and one subgenus, and it is morphologically characterized by the shape of the cephalon. Cyprus is the third largest island within the Mediterranean, it has a volcanic origin (first appearance above sea level ca. 20-15 Mya), and it is composed of two mountain ranges, that correspond to the two paleoislands that comprised Cyprus until mid- to late Pleistocene, Troodos at the central-western, and Pentadaktylos at the north-northeastern part of the island. Until today, only *L. kosswigi* and *L. naupliensis* were recorded from Cyprus. A large collection from many habitats along the island revealed the presence of new *Leptotrichus* species. In order to explore the genetic diversity within the island and evaluate the morphology-based taxonomy of the species in the genus, three mitochondrial (COI, 16S and 12s) and one nuclear (protein coding Sodium-Potassium Pump, NaK) markers were sequenced. In addition, genome-wide ddRAD sequencing was conducted to evaluate the population structure of the studied species. Morphological and molecular data confirm the taxonomic validity of both *L. kosswigi* and *L. naupliensis*. Two distinct genetic clades based were revealed in the case of *L. kosswigi*. Our results are not in line with recently identified diversification patterns of *Armadillo* and *Schizidium*, where the two mountain ranges clearly influenced the patterns of these genera. The present work stresses the importance of integrative approaches in Oniscidea systematics in order to gain a better understanding of the evolutionary dynamics in terrestrial isopod lineages and for a more efficient species delimitation, using also all other available evidence, such as paleogeography.

Biogeography, ephemeral population dynamics and repeated-phenotypic evolution in the Cape Verdean Darwin's sparrow (*Passer iagoensis*)

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The Cabo Verdean endemic sparrow (*Passer iagoensis*) was first collected by Darwin during the Voyage of the Beagle and remains an emblematic species of the archipelago. This species inhabits a diverse range of environments on the islands, from arid lava regions to high-elevation forests, and gaining insight into its population structure and speciation dynamics is of great value. In this study, we sampled, phenotyped, and sequenced over 300 genomes from all major islands and islets in Cape Verde to analyze the biogeographical patterns and population structure associated with environmental variation. Our findings suggest that the biogeography of this species is complex and not linked to specific environmental or biogeographical patterns. Additionally, using the ancestral recombination graphic, we found evidence that the age of genomic variants predates the calculated colonization of the archipelago. This discovery suggests that phylogenetic approaches may be biased by ephemeral population dynamics. Furthermore, we identified a population with signatures of selection in the genes HMG20 (beak size) and ALX1 (beak size) on the small islets of Rombos. These genomic signatures are similar to the selection signatures found in the Galápagos finches, and concordant with phenotypic data. These results provide valuable insights into the evolutionary history of the Cabo Verdean endemic sparrow and highlight the importance of further research on this iconic species.

High throughput genotyping of *Micromeria* Benth. (Lamiaceae) in the Canary Islands reflect species syngameon dynamics in different stages of species diversification

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Hybridization can promote adaptive radiation by increasing standing variation and consequently the ability of an organism to adapt to new conditions. In oceanic islands, this mechanism may be valuable in counteracting founder effect through the admixture of lineages arriving to an archipelago by independent colonization events. The resulting species would evolve connected by geneflow in what is known as species syngameons. This is the case of genus *Micromeria* (Lamiaceae) in the Canary Islands where previous genotyping studies have shown that this mechanism shaped the distribution of both neutral and adaptive genetic diversity. So far, for phylogenetic analyses, nuclear variation of only a few individuals per species could be included, causing difficulties to infer the extent of gene flow between species. In the present study, we have overcome this limitation by using 6000 bp of chloroplast genome and 23 nuclear intron loci across several populations per species of *Micromeria* to assess phylogenetic patterns that might indicate the establishment of species syngameons. Both gene- and species tree approaches were implemented using ASTRAL and RAXML, respectively, and the resulting patterns were compared among loci and marker systems. Trees combining information from all loci are congruent with species delimitation, which is not the case for gene trees. Chloroplast haplotypes were shared among the Islands of Tenerife and Gran Canaria, some of the most divergent lineages in the archipelago. Concerning nuclear variation, different samples of the recently diverged species *M. herpyllomorpha* from La Palma presented haplotypes from different islands. Haplotype sharing between species may be a signal of introgression resulting from the establishment of species syngameons. Given the different evolutionary rates of chloroplast (slower) and nuclear introns (faster), they may reflect introgression events that happened in different stages of *Micromeria* diversification.

The extension of the taxon cycle model to island plants: insights from the Canarian flora

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The taxon cycle paradigm has been applied in several insular areas (Caribbean, Melanesia, Macaronesia, Polynesia) for explaining the progressive range contraction and fragmentation, and consequent diversification and population decline path towards species vulnerability, and eventually, extirpation and/or extinction happening to localized island populations in interior habitats, as a consequence of the pressure exerted by a subsequent island colonization of marginal open habitats by a more generalistic species. So far, the taxon cycle been applied to a few vertebrate (lizards, birds) and invertebrate (ants, butterflies, etc.) groups but never to plants. In this work we investigate to what extent the model can also be extended to plant species using the Canary Island's flora, well known for its high species diversity and endemicity, as a model system. With this aim we have defined four stages in the cycle: S1 (widely distributed Multiple Island Endemics, MIE); S2 (restricted but non-threatened MIE); S3 (non-threatened Single Island Endemics, SIE) and S4 (threatened species, whether MIE or SIE). We found patterns consistent with the following classification of responses: i) the classic path of range contraction, fragmentation, diversification and population decline after the colonization of a different lineage within the same genus (*Echium, Helianthemum, Limonium* and *Lotus*); ii) a similar pathway without the colonization of a new lineage, where one or several of the species of the original lineage became widely distributed generalists (*Aeonium, Argyranthemum, Pericallis, Sonchus*); iii) the rarity of all the species within a lineage despite the lack of generalists or new colonists within the lineage (*Cheirolophus, Crambe*) and, finally, iv) the failure of the taxon cycle paradigm, because of the failure of some widespread MIE generalistic taxa to contract their range and become isolated (*Kleinia, Laurus, Pinus, Plocama*).

The role of song in restricting gene flow among locally adapted populations of the Common Chaffinch on the island of La Palma

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Understanding the speciation process is one of the most pressing questions in evolutionary biology. In songbirds, vocalizations are important in individual and species recognition and are crucial in sexual and social communication. Populations that diverge in song may fail to recognize each other, leading to assortative mating and, potentially, speciation. Therefore, song may constitute a premating barrier to reproduction. The Common Chaffinches from La Palma (Canary Islands, Spain) constitute a clear case of recent lineage formation, with populations that inhabit pine forests diverging genetically and morphologically from cloud forest populations. However, song characteristics of both populations have not been studied, so the role of song in their divergence into different populations and maintenance as distinct remains unclear. We aimed to characterize and quantitatively compare acoustic traits between populations in the two habitats, test whether differences in acoustic traits correlate with environmental variables at macro and micro scales, and test whether their song differences act as a behavioral isolating mechanism. We recorded songs of both populations along their distribution ranges, examined the sonograms, and measured bioacoustic variables related to frequency and time. We quantified the habitat characteristics across their distribution ranges using general environmental variables and habitat variables measured in the field. Additionally, we conducted playback experiments in which songs from the same or different habitats were broadcasted and the reaction of the individual was registered. We found differentiation of the songs of individuals from the two types of forest, with results revealing a negative correlation between minimum frequency and tree cover percentage. Preliminary results indicate that birds do not appear to react significantly differently to same-habitat or different-habitat songs. Thus, song differences in minimum frequency seem not to be strong enough to prevent behavioral discrimination against songs from individuals living in the other type of forest.

Plasticity in lizards from small islands

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Islets, even when close to the mainland, can be very selective for small vertebrates such as the lizards. The unpredictability of weather, food resources, water and predators can lead to adaptive responses in short time. The ability to evolve in few generations may not include genomic variations, open up to the hypothesis of evolutionary plasticity. Plasticity can save from extinction, mainly when population is not possible to move away. Insular lacertids are ideal models to investigate the variation expressed in phenotypes according to selection and the spatial restriction imposed by small islands. In our contribution we highlight how the *Podarcis siculus* is able to face the challenges imposed by selection on small islands through a plasticity involving morphology, reproduction, behavior and the gut microbial community. In addition to data collected on the phenotypical variations, we considered also the regulative mechanisms through annotated transcriptome sequences in brain and testis. This highlights how adaptive traits can arise from differential gene expression rather than genomic variation. This could be also corroborated by our data on speed of evolution in the population of lizards from Faraglione of Capri. An extraordinary ability to re-adapt in a short time was observed also for gut microbiota of insular lizards under unexpected environmental changes. These studies improved the knowledge of evolution pathway in the insular lizard populations, and represent the basis for better placing the diversity of this species in an adequate conservation perspective.

Living on a rock: genomics of the critically endangered Aeolian wall lizard

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Small populations give a unique opportunity to investigate the relative roles of drift and selection in evolution. In particular, small populations can show an accumulation of deleterious mutations (the genetic load) due to the strong effects of drift. The Aeolian wall lizard *Podarcis raffonei* is endemic to the Aeolian archipelago, located in the Mediterranean Sea, North of Sicily. The extremely restricted distribution range includes two small islets (La Canna, 940 m^2, and Strombolicchio, 3,070 m^2). Here, we analysed the genomic variation pattern and the genetic load in these two small populations, and compared them with those observed in the sister species *Podarcis waglerianus* (the Sicilian wall lizard), where the distribution range and the population size are much larger. A newly assembled genome was generated for the Aeolian wall lizard, and whole genomes were resequenced for ten individuals each from La Canna and Strombolicchio and for ten individuals of the Sicilian wall lizard. The Aeolian wall lizard shows a uniquely low level of polymorphism, especially for the La Canna population with the lowest value of genome-wide heterozygosity documented in vertebrate species (3.4×10^{-6}, i.e. one SNP every 300 kb). Both individuals from La Canna and Strombolicchio islets show exceptionally high levels of inbreeding (FROH=0.99 and 0.67, respectively). Genetic load estimates based on annotation and evolutionary conservation revealed an accumulation of deleterious mutations in homozygosis for the Aeolian wall lizard when compared to the Sicilian wall lizard. Despite the much lower population size and genomic variation in La Canna compared to Strombolicchio, their level of genetic load is comparable, suggesting a maximum level of tolerable genetic load in these isolated populations.

Are islands really special? Time scaling and evolutionary rates on islands

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Islands are often considered special due to their tendency to exhibit rapid evolution and speciation. This idea, however, is potentially confounded by the ubiquitous scaling of evolutionary rates. Rates of molecular evolution, trait evolution, speciation, and extinction are all time-dependent, with the fastest rates observed over the shortest time scales. Islands, then, should show elevated rates simply due to their young age. I discuss the relationship between evolutionary rates on islands versus mainlands in the light of rate scaling. I also show methods to determine which island radiations have particularly fast rates given their age.

Charr-lock Holms: Genetic clues on how to grow large and become a fish eater

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Ecological specialisation is a widespread phenomenon in natural populations, often arising from standing phenotypic and genotypic variation through niche shifts, ecological sexual dimorphism and a combination of both. A prominent example of ontogenetic shift is the transition to piscivory in fish. Such diet shift requires the physical capability of preying on fish, which is directly dependent on the individuals body size. The mechanisms behind diet shifts and increased body sizes are often complex and can depend on numerous factors such as the genetic and physiological capabilities to grow, the degree of prey availability and the environmental conditions allowing the predators access to the ecological opportunity. The Arctic charr in Thingvallavatn (Iceland) is a young evolutionary system undergoing ecological specialisation and is a great system to study the transition to piscivory. Four phenotypic morphs belonging to three genetic clusters coexist in the lake. Two of these morphs, a small planktivorous (PL) and a large piscivorous (PI), although phenotypically very different, belong to the same genetic group. Despite modest genetic differentiation between the PL and PI morphs, FST outlier analysis showed differences in isolated regions of the genome. The most notable FST outliers were located on LG2 and spanned the region of Glypican 6, a protein coding gene which in humans is involved in growth control and cell division. In zebrafish, it shows both maternal and zygotic expression throughout development.

Breeding system of flowering plants in Izu-islands

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The hypothesis that long-distance dispersal to oceanic islands selects for uniparental reproduction has been debated for over half a century due to the inconstancy with the high ratio of dioecious plants found on some oceanic islands. Some studies report higher proportions of self-compatibility in island populations than in mainland populations, while others report higher proportions of dioecy in islands. To understand the evolutionary trend on islands, a comparison of reproductive traits between source and island populations focusing on the lineages could work as well as the comparison of the proportion of self-compatible species in the flora. This presentation provides an overview of such comparative studies between oceanic islands and mainland Japan, particularly in Izu-islands. Izu-Islands, relatively close to the mainland, are ideal for comparative studies. The pollinator fauna in the Izu-Islands lacks bumblebees and large swallowtail butterflies are less-density. Breeding systems in five taxa between Izu-islands population and the corresponding mainland populations have been reported. In *Campanula*, *Rhododendron*, and *Clerodendrum*, the island populations exhibit traits associated with self-fertilization more than the mainland populations, while *Weigela* and *Lilium* do not (Inoue 1993, Mizusawa et al. 2014, Nakajima et al. 2018). The maintenance of entomophily in these five taxa suggests outbreeding has adaptive significance even in self-compatible island populations. Indeed, inbreeding depression has been suggested in self-compatible islands *Campanula* and *Clerodendrum* based on allozyme or microsatellite analysis (Inoue 1993, Mizusawa unpublished). Given these studies, it may be appropriate to consider self-compatibility and selection for outcrossing can coexist in islands. S-allele polymorphism and characteristics of flower morphology in Izu-islands will be also discussed.

Functional island biogeography through time

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The accumulation of functional diversity in communities is poorly understood. Island biogeography models make predictions for how such diversity might accumulate over time, but these have rarely been tested in empirical systems. In this multiscale study of land snail communities on 10 oceanic archipelagos, we test hypotheses of community assembly as related to the accumulation of species and functional diversity. We find support for the hump-shaped curve of accumulation of species richness over time, with depauperate snail faunas on young islands, increasing species richness on mid-age islands and low species richness on older islands. Given their species richness, we find that functional diversity is lower than expected on young islands, matching predictions on mid-age islands, and unpredictable on older islands. We also find that island age is a significant predictor of the region of the morphospace occupied by snail species. We conclude that consistent patterns of functional diversity in early community assembly and species co-existence indicate a common role for habitat filtering, ecological opportunity and competition in a range of island systems, whereas patterns of species richness appear subject to archipelago-specific effects.

Investigating the relationship between macroevolutionary processes and microendemic ranges in new Caledonian leaf-beetles

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The biota of New Caledonia is highly endemic and diverse, and most species can be considered microendemic, a condition indicating their relatively small ranges. Microendemicity characterizes many taxonomic groups in New Caledonia suggesting the possibility of similar factors influencing species distributions. In this work we focused on potential intrinsic factors related to microendemic distributions. Specifically, we have used a multifaceted approach to study the diversification dynamics and the geography of speciation of two endemic genera of leaf beetles in New Caledonia, *Taophila* and *Tricholapita*, which are distributed along the main island of Grand Terre and most species have narrow ranges. We found a decrease in diversification rate consistent with a protracted speciation model potentially intensified by the combined effect of several ecological and environmental factors. Climatic and geological changes during the Cenozoic probably conditioned several cycles of allopatric speciation leading to the rich diversity of the studied genera. Moreover, we did not find a correlation between species ages and ranges. Ecological interactions and the complex geographic features of the island possibly contributed to the origin of species, but also to maintaining small ranges after speciation. Thus, microendemicity seems to reflect in this case a mature state of the system rather than a temporary condition post-speciation.

Diversification of the Common Chaffinch upon colonization of Macaronesia

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Avian radiations in archipelagos provide ideal systems for understanding the relative roles of geographic isolation and selection in the process of speciation. The common chaffinch (*Fringilla coelebs*) is a widespread Eurasian species that colonized the Atlantic archipelagos of the Azores, Madeira and the Canary Islands from the continent, resulting in a species-level radiation. The sequential colonization route has led to a reduction of genetic diversity at each step due to consecutive founder events. On the island of La Palma chaffinches expanded their range from the humid laurel forest to the dry pine forest. We explore whether this habitat shift has resulted in evolutionary divergence between locally adapted populations. Birds in the two habitats show significant differences in diet and plumage coloration, and morphological differences are consistent with ecomorphological predictions. A genome-wide survey using SNP loci revealed that neutral genetic structure is consistent with geography, showing significant isolation-by-distance and suggesting markedly restricted dispersal despite high dispersal capacity. Genome-Wide Association Study (GWAS) and Genotype-Environment Association (GEA) methods revealed numerous loci involved in local adaptation distributed across the genome, and a redundancy analysis (RDA) indicates that populations in the two habitats diverge at loci associated with vegetation greenness (NDVI). Among the candidate genes we found some involved in morphological development, plumage coloration and metabolism. Analysis of whole-genome variation revealed habitat-specific selective sweeps. Our results suggest a strong role for polygenic selection in driving local adaptation in chaffinch populations on La Palma, a promising insular model for studying the evolutionary mechanisms of adaptive divergence.

Colonization, diversification and speciation of the genus *Hipparchia* (Lepidoptera, Nympalidae) in the Canary Islands

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The Canary Islands make for a fascinating archipelago given their volcanic origin and complex geological history. They are home to many endemic taxa, which display a variety of colonization and diversification patterns. In this study, we focused on the butterflies of the genus *Hipparchia*, which are present in five of the seven main islands of the archipelago (Gran Canaria, Tenerife, La Gomera, La Palma and El Hierro). We used both mitochondrial and nuclear loci in order to elucidate the taxonomic status of the insular populations. Additionally, we performed chronophylogenetic and biogeographic analyses to explore the mode and timing of the colonization of the islands by these butterflies. Finally, taking advantage of our success in producing sequences from the elusive *Hipparchia tewfiki*, we explored the Canarian lineages position within the subgenus *Pseudotergumia*. Our results support the presence of single-island endemics, as no lineage is found in more than one island. Surprisingly, they suggest that the insular lineages are sister to the rest of the subgenus rather than directly related to *H. fidia*, which is the closest geographically. Additionally, the chronophylogenetic analysis shows that the initial colonization event happened ~5.4 Mya and that the remaining islands with sufficient altitude —apparently an ecological requisite— were colonized soon after that. Interestingly, the islands that emerged later on, were almost immediately colonized by these butterflies. This result, coupled with the apparent lack of recent admixture, suggests the existence of another type of barrier to gene flow beyond spatial isolation, and further supports the specific status of the five insular lineages. Our taxonomic proposal, together with the extremely limited range of some of the insular lineages, raises the importance of each population regarding future conservation efforts in the area.

Multi-species phylogeography and genetic diversity of flora in the Ryukyu Islands, Japan

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It is believed that geohistorical events have strongly influenced the distribution of organisms in the Ryukyu Islands. In particular, two major geographical gaps between the islands that formed millions of years ago (the Tokara and Kerama gaps) are thought to have had a strong impact on the distribution and population genetic structure of many plant species. However, the effects have only been investigated for some species, and a comprehensive understanding of the vegetation history has not been achieved. In this study, we analyzed the population genetics of the multiple plant species distributed in the Ryukyu Islands and clarified their molecular phylogeography and distribution of genetic diversity. We selected all six species of Fagaceae distributed in the area, along with mulberry and bamboo species, as widely distributed and often dominant forest plant species in the islands. Population samples were collected from 12 islands throughout the region, and DNAs were extracted from them. Genome-wide SNP analysis was conducted using the multiplexed ISSR genotyping by sequencing (MIG-seq) method. Phylogeographic analysis revealed that the two geological gaps affected the formation of population genetic structures in the Ryukyu Islands; however, the degree of the effect seemed to differ depending on the dispersing ability of each species. Additionally, the results of population dynamics estimation suggested that their genetic structure was strongly influenced by past climate change. We also presented examples of vegetation formed by artificial long-distance transplantation. Based on population genetic data, we illustrate a hotspot of genetic diversity in the area. Our study demonstrates that genome-wide DNA analysis targeting multiple species is an effective method for clarifying the formation and actual state of biota in island ecosystems.

Phylogeny, geology and ecology: reconstructing the assembly of island biological communities in a complex world

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Island communities can be composed of various lineages. Some of these lineages may be endemic, others widespread; some may have radiated and others may be composed of just one species. But current diversity is just a snapshot: many species and lineages may have previously thrived on the island and later gone extinct, and islands today can look very different than they did millions of years ago. What can the extant biota tell us about the way island communities are assembled over evolutionary time scales in the context of extinction? In this talk, we will discuss how phylogenetic data of island species, paleogeographic reconstructions, trait evolution and biotic interactions are increasingly being incorporated into dynamic models of island biogeography. While we find that increased model complexity can lead to more realistic reconstruction of past processes in some cases, in others we find that simple models can perform surprisingly well. We will illustrate this using empirical case studies from angiosperms, arthropods, and vertebrates from a variety of continental and oceanic islands worldwide.

Progressive spread of an ancient inversion polymorphism blends the role of within-island evolution and inter-island colonization along a parallel Galápagos beetle radiation

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We here study a progressive parallel adaptive radiation of caterpillar-hunter beetles (*Calosoma*) at the Galápagos. Beetles show wing reduction at high altitude on all major islands of the archipelago, and the magnitude of within-island phenotypic and genetic divergence between high- and lowland ecotypes follow the island chronosequence. Using whole-genome resequencing and restriction site-associated DNA sequencing data we inferred the genomic basis of this gradual divergence and illustrate that a mixed contribution of inter-island dispersal and within-island evolution has shaped parallel species communities across the archipelago. Results revealed that the genomic regions underlying the repeated divergence entail massive chromosomal inversions, whose origin could be traced back to the initial high-lowland divergence on the oldest island. Highland alleles subsequently spread to younger islands through dispersal of highland individuals as well as dispersal of lowland individuals carrying introgressed highland alleles and thereby facilitating in-situ evolution. In conclusion, while the roles of in situ evolution versus colonization as drivers for repeated adaptation are often viewed as opposing mechanisms, our results urge to relax this dichotomous view. Rather a complex interplay between colonization and introgression gave rise to this parallel beetle radiation at the Galápagos. These results enhance our understanding on the molecular underpinnings and rapid evolution of island biodiversity.

Evolutionary syndromes in island animals: a progress report

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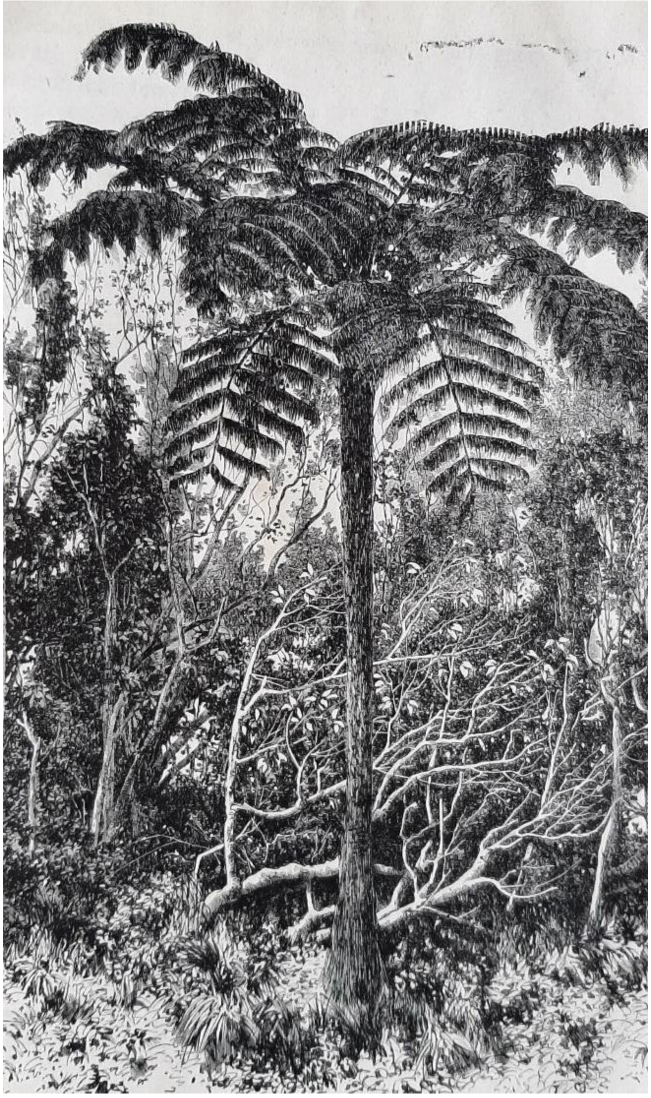
We review recent literature on island evolutionary syndromes with particular focus on animal syndromes. Increasingly, efforts to examine these syndromes involve comparative analysis of multiple study systems and taxa, providing a stronger basis for statistical inference than previously available. We provide a synthesis of the levels of support to be found in the literature for evolutionary syndromes that have been postulated for island animal species. We briefly consider the link between these syndromes and vulnerability to anthropogenic change on islands.

☙ Evolution of Islands and Their biotas ❧

Posters



(From: L. Figuier, Storia delle piante. Fratelli Treves, Milano, 1882)

Evolutionary genomics of adaptive radiations on islands

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Adaptive radiations have been central to our understanding of speciation. Despite this central role, most inferences have come from a limited set of study systems such as the cichlids from the African Lakes, *Heliconius* butterflies and Darwin's finches. In this contribution, I review the literature for insular adaptive radiations, uncovering ~150 hypothetical adaptive radiations on islands. These radiations exist in a broad range of taxonomic groups, archipelagos, geographical ranges and substantially vary in the number of species. The variation in rate and number of species formation is linked to the ecological forces promoting differentiation of ecomorphs, and insular traits such as the age of the archipelago. This represents a first step to map and foster interest in insular adaptive radiations, and I discuss the potential of these systems in helping us understanding the process of speciation.

Historic plant communities of the coastal lowlands of Mauritius as a guide for restoration of the northern off-shore islands

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Information on the historic plant communities in Mauritius is required to help guide on-going ecosystem restoration programmes on several off-shore islands. Of particular interest is information concerning former giant tortoise-driven grazing climax communities and also the presence/extent of hypothesized former palm woodland (de Boer 2014; Cheke and Hume 2008). Unfortunately, the off-shore islands do not support the wetland habitats required for the preservation of sedimentary records for palaeoecological assessments. However, palaeoecological records from wetlands in the coastal lowlands of northern Mauritius have potential to be used as proxy records for the off-shore island communities. This poster presents initial results of eDNA metabarcoding analyses from sedimentary records obtained from three coastal sites in Mauritius, spanning the historic period. It demonstrates the potential of sedimentary ancient DNA (sedaDNA) analyses to be used in conjunction with traditional palaeoecological assessments (e.g., fossil pollen, plant macrofossils) to reconstruct the historic lowland plant communities of Mauritius.

Cognition and personality in island lizards

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Islands differ considerably from mainland habitats in a series of biotic and abiotic factors, and organisms often respond to this variation with a striking suite of phenotypic changes, often referred to as "the island syndrome". While morphological, physiological and life-history components of the island syndrome have received considerable attention, much less is known about how insularity affects behavioral aspects of the phenotype, such as personality and cognitive traits. This is unfortunate, because many characteristics of insular environments (e.g., relaxed predation and interspecific competition, high densities, limited resource availability) are likely to select for behavioural shifts; an important component of the island syndrome therefore remains underexplored. In this study, we compared multiple aspects of animal personality (aggression, boldness, neophobia) and cognition (spatial and reversal learning, inhibitory control and problem-solving) in eight mainland and island populations of the Aegean wall lizard (*Podarcis erhardii*). We also tested whether personality–cognition covariance differs in mainland and island lizard populations.

Diversification dynamics in Caribbean rain frogs (*Eleutherodactylus*)

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Adaptive radiation is proposed to play a key role in generating differences in species richness among lineages and geographical regions. Due to the importance of ecological divergence in adaptive radiation, species richness is predicted to be influenced by equilibrium diversity dynamics, although the concept continues to generate much debate. An additional important question is whether radiating clades have intrinsic biological characteristics that make them particularly prone to diversify. We tackle these questions by analysing (i) the temporal patterns of diversification of Caribbean *Eleutherodactylus* frogs, and (ii) assembly of the complete native anuran community of the Caribbean archipelago (197 species), testing for the presence of equilibrium dynamics and whether diversification patterns of *Eleutherodactylus* differ from those of the rest of the Caribbean anurans. Diversification rates follow the predicted pattern of rapid diversification early in the radiation which gradually decreases towards the present. *Eleutherodactylus* diversification is significantly faster than that of the Caribbean anuran community, and although equilibrium dynamics influence richness of all Caribbean anurans, *Eleutherodactylus* shows higher carrying capacity. Our results indicate that ecological opportunity per se is not sufficient for adaptive radiation and that diverse lineages present intrinsic characteristics that enable them to make the most of available opportunity.

Speed of evolution in melanic insular lizard

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Some lizard populations living on small islets show the Reversed Island Syndrome (RIS) traits: drastic phenotypic changes in body shape, skin coloration, age of sexual maturity, aggressiveness, and food intake rates. We investigated the timing and mode of evolution in an *ad hoc* model system of three lizard populations: wild-type lizards from the mainland, insular lizards from a big island (Capri, Italy), both *Podarcis siculus siculus* not affected by the RIS, and a lizard population from an islet (Scopolo) undergoing the syndrome (*P. s. coerulea*). We assessed the rate of molecular changes on complete mitochondrial genomes for each population to reconstruct the phylogeography and estimate the divergence time between island and mainland lizards. Molecular data were compared to geological pattern and slit time dating. Interestingly, we found the lowest mitochondrial mutation rate in Scopolo lizards despite the phenotypic changes achieved in approximately 8,000 years. This hypothesis implies freezing of the mtGenome in which we observe a strong selection on coding sequence, suggesting the pivotal role of plasticity in the population affected by RIS. Even the analysis of single nuclear genes involved in the phenotypic variation (melanization, Melanocortin receptor 1) highlights variations in expression gene level rather than structural mutations. This increase in melanocortin receptor RNA corresponds to a significant increase in agonist (alpha-Melanocortin Stimulating Hormone) in plasma of insular lizards under RIS.

Stepping-stone colonization of *Hydrangea macrophylla* (Hydrangeaceae) on the Japanese oceanic islands: is gradual loss of dispersal ability underway?

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In oceanic islands, evolutionary events caused by the geographical barrier and unique environments between insular and continental species are known as the island syndrome. Although the loss of seed dispersal ability in insular plants is considered one of the typical examples of the island syndrome, the process underlying this evolutionary process remains poorly understood. In this study, we focused on *Hydrangea macrophylla* (Hydrangeaceae), the endemic species distributed in the Pacific side of the Japanese mainland Honshu, the Izu Islands, and the Bonin Islands. The Izu and Bonin Islands, which are located 25-250 km and 1,000-1,200 km far from the mainland, are oceanic and linearly extending from north to south. Considering the linear configuration of these islands like stepping-stones, *H. macrophylla* might have gradually lost its seed dispersal ability during the migration from north to south. Hence, this study aims to clarify the process of island colonization and the associated loss of seed dispersal ability in *H. macrophylla* on the islands. Population genetic analyses based on the whole genome re-sequencing data indicated distinct genetic differentiation among island populations, suggesting that *H. macrophylla* migrated from north to south on stepping-stones. In this presentation, we examine the divergence time and population dynamics of the island populations, providing a more detailed evolutionary history. In addition, we quantify the seed morphology of the island populations and discuss the effects of the distance from the mainland and the isolation period of the populations on seed dispersal ability.

Discovery of cryptic plant lineages in a biodiversity hotspot, New Caledonia, through genome-wide DNA analysis

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New Caledonia is one of the world's biodiversity hotspots, known for its highly endemic biota. Even today, new species continue to be discovered, and there are also many groups of species whose phylogenetic relationships have yet to be clarified. However, the active mining of nickel ore, frequent forest fires, and biological invasions threaten precious natural ecosystems. Therefore, we combined efficient genetic analysis with conventional plant taxonomic surveys to identify unknown cryptic plant lineages and genetically unique local populations. As target genera, a comprehensive population sampling was conducted for the genus *Oxera* (Lamiaceae) and ongoing for the genus *Acropogon* (Malvaceae). Both are expected to include some cryptic lineages. We used the multiplexed ISSR genotyping by sequencing (MIG-seq) method to detect genome-wide SNP data and analyze phylogenetic relationships. Based on the genetic data from 1370 samples covering all species of the genus *Oxera*, we clarified the phylogenetic positions of all species and identified several new taxa. For example, a different genetic group was discovered based on phylogenetic and population genetic analysis, and its morphological identity was also studied through field observation. The sampling and analysis of the genus *Acropogon* are ongoing; however, new findings have already been made based on the analysis of about 200 samples. The goal of this research is not only to contribute to the conservation of local biodiversity in New Caledonia but also to build a foundation for contributing to biodiversity conservation worldwide, especially for unique island ecosystems, through population genomics analysis technology.

Diversity and biogeography of the terrestrial Isopoda (Crustacea, Oniscidea) from the Mascarene Islands, western Indian Ocean

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Terrestrial isopods (Oniscidea) comprise more than 4,000 species in 38 or 39 families distributed in almost all types of terrestrial habitats. A large number of Oniscidea occurs on oceanic islands, many of which are still poorly investigated. The Mascarene islands (Mauritius, Rèunion, Rodrigues, and Cargados Carajos) are located in the southwestern Indian Ocean, between 700 and 1,500 km east of Madagascar, have a volcanic origin, and never connected to each other or to any other land mass. Réunion is the largest island (2,500 km^2), followed by Mauritius (1,900 km^2), Rodrigues (110 km^2), and Cargados Carajos (1.3 km^2). A large collection of Oniscidea from Réunion, Mauritius and Rodrigues have been examined. The number of species from the Mascarenes increased from 32 to 53. Mauritius with 37 species is the richest, followed by Réunion (24), Rodrigues (5) and Cargados Carajos (3). Most of the species are widespread in the tropical area, especially in the lands encompassed by the Indian Ocean, and possibly arrived passively or introduced with human activities. One genus of Armadillidae and eight species are new to science, and a total of 20 species are apparently endemic to the islands (15 on Mauritius, four on Réunion and one on Cargados Carajos). The genus *Pagana* (fam. Trachelipodidae) and the new genus *Cisnetia* (Armadillidae), with seven species each, are endemic to Mauritius and Réunion. Five new troglomorphic species in the families Styloniscidae, Philosciidae, Trachelipodidae and Armadillidae are recorded from lava caves. The larger number of species present on Mauritius compared with Réunion most probably depends on the older age of the island (Mauritius ca. 8 Mya vs. Réunion ca. 2 Mya). The small number of species recorded from Rodrigues and Cargados Carajos is certainly due to the lack of intensive investigations on those islands.

How to solve the "Island Paradox"? Integrating genomics, functional morphology, and wall lizards

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Although often genetically impoverished due to founder effects, inbreeding, genetic drift, and sequential bottlenecks, island populations tend to reach high densities and adapt to the local environment. This is paradoxical because low allelic diversity can lead to inbreeding depression (reduction in fitness due to deleterious recessive alleles), and, on a longer timescale, to reduced genetic adaptability of populations. How and why do island populations, despite low genetic diversity, survive, adapt, and thrive? A first possibility might be that low heterozygosity does not translate into inbreeding depression through the purging of deleterious variants. Alternatively, the fitness consequences of inbreeding may be bearable under mild selection regimes typical for islands. However, evidence that either of these mechanisms is at work in wild island populations remains scarce. Populations of the Italian wall lizard, *Podarcis siculus*, constitute an interesting system to study and unravel the "Island Paradox". The species is native to the mainland of Italy but also occurs on several islands in the central Mediterranean, where it shows extraordinarily high densities despite reduced levels of genetic variability and increased homozygosity. In this up-and-coming project, we aim to shed light on the mechanisms of the island paradox using *P. siculus* as our study system. Specifically, we will determine the demographic history and genetic diversity levels of the island and mainland populations using state-of-the-art genomics, as well as characterize the levels of inbreeding depression on the islands with extensive functional morphological approaches. In addition, we will investigate whether purging of highly deleterious alleles may have alleviated the burden of inbreeding depression using both genetic and phenotypic insights. Lastly, we will quantify whether relaxed selection may mask the detrimental effects of inbreeding. By employing this integrative approach, we aim to elucidate why and how island populations survive and adapt, despite their low genetic diversity.

Heterostyly in the Japanese islands

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Heterostyly is a genetically controlled floral polymorphism that promotes outbreeding. Lower proportion of heterostyly is known from many oceanic islands, which is regarded as one of the island syndromes, yet there has been not enough data to support this tendency. Japanese islands consist of more than 6800 islands, including both oceanic and continental islands, stretching in cold, temperate, and subtropical climates. Although many studies on heterostyly have been done in Japan, no comprehensive analyses are available. Here I present a review of heterostyly in the native flora of Japan, and I tested the difference in the occurrence of heterostylous species among subgroups of islands. Then I also tested the difference in growth forms and dispersal modes between northern and southern part of the Japanese islands. After a careful examination of the literature, about 0.7% of the Japanese flora was recognized as heterostylous, which is slightly lower than the world estimate. There was no significant difference in the occurrence among three geographical areas (cold, temperate, and subtropical island groups). Woody and zoochorous species prevailed in the southern islands, which reflected the occurrence pattern of heterostyly in the world. Evolutionary modification of heterostyly and perspectives in the study of heterostyly on islands is discussed.

Evolutionary syndromes in and involving island plants: a progress report

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We review recent literature on island evolutionary syndromes with particular focus on plant syndromes. Increasingly, efforts to examine these syndromes involve comparative analysis of multiple study systems and taxa, but for some proposed plant syndromes, the comparative basis is rather limited. We provide a summary of the levels of support to be found in the literature for around 18 evolutionary syndromes that have been postulated for island plants and also consider four proposed syndromes involving plant–animal interactions.

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