



Book of Abstracts

BIODIVERSITY CHANGE IN THE ANTHROPOCENE

PRIORITIES FOR RESEARCH

A dynamic and open discussion on one of the
major issues of our time

Edited by:

Ernesto Azzurro
Lucia Bongiorno
Lucia Cherubini
Paola Pollegioni
Diego Fontaneto
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Fano Marine Center - Fano (PU), Italy, April 10th-11th 2024



NATIONAL
BIODIVERSITY
FUTURE CENTER

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Our Symposium

Dear colleagues, we are more than happy to present the Book of Abstracts for the Symposium entitled "*Biodiversity Change in the Anthropocene: Priorities for Research*" a national meeting organized by the CNR-Istituto per le Risorse Biologiche e le Biotecnologie Marine (IRBIM) and CNR-Istituto di Ricerca sugli Ecosistemi Terrestri (IRET), in collaboration with the Fano Marine Center, Lifewatch Italy and the National Biodiversity Future Center. This Symposium was conceived, ideated and scientifically supported by the Working Group Biodiversity of CNR, which was formally established in May 2021 as a network of researchers aimed at enhancing Italian research on biodiversity.

The detrimental impacts of recent human activities, particularly intensified by the "great acceleration" of the past decades and the resultant habitat destruction, are starkly evident through both local and global extinctions, as well as widespread biodiversity changes. These changes, occurring in what is often referred to as the Anthropocene, reflect significant human influence on the planet, even though this term has not been officially recognized as defining a new geological era. These shifts are increasingly observed not only by scientists but also by the general public and economic sectors reliant on natural environments. This growing awareness underscores the critical need for concerted efforts to mitigate these effects and safeguard the planet's biodiversity for future generations. With the launch of the European Green Deal, the European Union has finally recognized the fundamental role of the environment and placed biodiversity at the center of economic recovery actions following the COVID-19 pandemic. Today, biodiversity is not only a subject of scientific research but also a major topic of debate in the political and economic arenas worldwide.

Two years ago, on November 3rd 2022 the amendments to Articles 9 and 41 of the Constitution have been approved, introducing the protection of the environment, biodiversity, and animals among the fundamental principles of the Italian Constitution.

Article 9 is part of the Constitution's "fundamental" articles. It previously included protection for the nation's landscape and historical and artistic heritage; with the reform, it assigns to the Republic the responsibility to also protect the environment, biodiversity, and ecosystems, explicitly stating a principle of protection for animals.

The amendment to Article 41, on the other hand, establishes that health and the environment are paradigms to be protected by the economy, on par with security, freedom, and human dignity. The revised article also stipulates those institutions, through laws, programs, and controls, can guide public and private economic initiatives not only toward social goals but also environmental ones.

Under these premises and together with a large number of participants, the Symposium fueled active discussion, by concise presentations delivered dynamically. A strategy which maximized participant interaction and the exchange of experiences and perspectives on the topic.

The congress was opened by a Keynote speech of Grégoire Dubois – *Head of the Knowledge Centre for Biodiversity (KCBD) at the Joint Research Centre of the European Commission JRC di Ispra (VA)* - entitled "Reverting biodiversity loss by 2030: all for one policy and one for all policies!"

Each brief contribution, accompanied by an extended abstract, was presented in alignment with one of the Symposium's four thematic areas:

- I. Examples of change
- II. Forecasts of change
- III. Tools, actions, and management of change
- IV. PhD spot session, dedicated to PhD students

The information gathered during the congress served as the foundation for discussions in four thematic sessions and shaped the meeting's final outputs based on a defined strategy. The outcomes of these discussions are summarized in this book at the beginning of each session, followed by the abstracts of oral presentations and poster abstracts, all formatted to one page. Collectively, the abstracts included in this volume represent a wide range of studies, experiences, and perspectives from Italian experts focused on changes in biodiversity. A distinguishing feature of this Symposium is its facilitation of dialogue among scientists across terrestrial, marine, and freshwater domains. Together, these contributions highlight a number of research subjects and priorities aimed at mitigating biodiversity loss and promoting sustainable ecosystems. Within the limits of a national congress, we trust that this collection will serve as a constructive experience to stimulate collaborative efforts and innovative approaches to understand the unprecedented changes in biodiversity driven by human activities and finally safeguard the intricate web of life that sustains our planet and our species.

The Editors of the Working Group Biodiversity
of the National Research Council

Organization of the Symposium:

Scientific Committee: The scientific committee of the Symposium is constituted by the CNR's "Biodiversity" Working Group (GdL), which was established following an idea discussed during the online workshop organized on the activities of the CNR-Dipartimento Scienze del Sistema Terra e Tecnologie per l'Ambiente (DSSTTA) in March 2021 and formally instituted on May 22, 2021. The "Biodiversity" GdL forms a network to enhance Italian research on biodiversity and is composed of fifteen researchers from various CNR Institutes and members of the CNR-Dipartimento Scienze del Sistema Terra e Tecnologie per l'Ambiente (DSSTTA) staff.

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Local Committee: The Local Organizing Committee managed all logistical aspects, including venue selection, catering, and accommodation for attendees. They facilitated communication with participants, promoted the event to attract attendees, and ensured smooth on-site operations.

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Technical support: A group of technicians of CNR-Istituto per le Risorse Biologiche e le Biotecnologie Marine IRBIM handled all technical aspects, including live streaming of the congress, videography of presentations, video projections, and the evaluation of proposals using a metering system.

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Communication: Annalisa Iadanza (CNR-Dipartimento Scienze del Sistema Terra e Tecnologie per l'Ambiente DSSTTA) coordinated the communication activities of the Symposium

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Session #1 – The examples of change

Moderators: Tiziana Di Lorenzo & Davide Sogliani

Summary of the thematic session

Theme 1 has unveiled a rich and complex fresco of biodiversity changes emerging in the current era of environmental modifications. Through the voices of the speakers, our journey began in the Mediterranean islands, traversed the vibrant fishing zones of our seas, and landed along the Adriatic coasts. We then sailed along the rivers of the plains and the water flows of intensely cultivated areas, ultimately reaching the green oases of protected areas and the urban fabric of our cities. A canvas of biodiversity changes was painted, encompassing marine, freshwater, and terrestrial plants and animals, while also highlighting the crucial role of pollen and microbial communities. The role of climate changes was emphasized, illuminating how critical variations in biodiversity are often the result of climatic dynamics and anthropogenic pressures. The plenary discussion emphasized the need for a multidisciplinary and inclusive approach that acknowledges local peculiarities of biodiversity changes and integrates them into a broader systemic framework. The pressing need to bolster traditional taxonomic skills complemented by molecular research resonated during the discussion of the Theme 1. This integration is essential for a more comprehensive understanding and effective conservation of biodiversity. Additionally, Natural History museums have emerged as key players in data conservation and in providing historical data that can be analyzed to track changes in biodiversity over time. There is a crucial need to integrate all museums into a unified national system and network to enhance collaboration among scientists. Sharing data on biodiversity changes is a primary desideratum and goal in the current context, where the perception of biodiversity changes, which previously extended beyond human life expectancy, is now rapidly accelerating. This integration will facilitate more effective monitoring and response strategies to cope with biodiversity shifts. The call for collaboration among scientists, policymakers, and communities, to protect biodiversity for future generations through a holistic One Health vision, resonated strongly, underscoring the urgent need to integrate historical, current, and projected data into the development of targeted conservation strategies. This involves recognizing the necessity to simplify specialized jargon that often complicates communication between scientists and non-scientists. For instance, social media could play a role, and citizen science has been widely recognized as a contemporary and effective tool for tracking biodiversity changes while keeping the general public involved. Theme 1 has sparked significant reflection on how to enhance our understanding of biodiversity changes. Young scientists are viewed as valuable resources that should be nurtured. Technological innovations may be featured at the next symposium to support this goal, while ensuring that taxonomic training is consistently emphasized and included. An urgent call has been made to develop an action plan that positions biodiversity research at the core of environmental management policies and climate change adaptation strategies, emphasizing ecosystem resilience and the conservation of endangered species. Interdisciplinary synergy is underscored as a pivotal element to effectively address the challenges posed by the climate crisis and biodiversity loss, steering us toward a sustainable future.

Witnessing 50 years changes of the Decapoda assemblage in the Pomo pit (Adriatic Sea)

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Short summary: The dramatic changes in the composition of the benthic Decapoda community, recorded in 50 years monitoring of the West Pomo pit trawling ground are discussed with reference to fishery, biodiversity and oceanography of the area.

Keywords: Crustacea Decapoda, Monitoring, Benthic community, Fishery, Parasite, Adriatic Sea

I. BACKGROUND

The meso-Adriatic depression (Pomo pit) is the main Nephrops ground in the Adriatic GSA 17. Exploitation of its resources started only after the World War I, when the mechanization of fishing vessels made possible bottom trawling at its depths (200–260 m). Fishing effort peaked by the end of the past century with depletion of resources and since 2015 the area is under a special management regime. Its biota is influenced by the periodical renewal of the near-bottom water masses of the depression with cold oxygenated waters, originated in winter in the North Adriatic, and flowing southward.

MATERIALS AND METHODS

Data on the Decapods assemblage have been gathered from the analysis of the catches of scientific bottom-trawl hauls made, for 50 years, in the frame of various fishery investigations. Landings auctioned in the gross-market of S. Benedetto del Tronto, home port of a large number of trawlers fishing in the area, have also been examined.

II. RESULTS

The Pomo megabenthic community in the early 1970's was dominated by *Nephrops norvegicus* and *Munida intermedia* (Fig. 1A). In the gross-market of S. Benedetto del Tronto, 500 t of *N. norvegicus* were yearly auctioned in the mid 1960's, but were less than 150 t already in the years 2000–7, and are now around 10 t (Fig. 1B). The quantities of the shrimp *Parapenaeus longirostris* caught by the trawlers on the same grounds, present an opposite trend, with a maximum of 140 ton auctioned in 2018 (Fig. 1B). Prior to 2003 the small quantities landed were not separately recorded in the statistics of the market. It is worth to note that in the 1990's in our scientific sampling the shrimp never exceeded 5 specimens/hour trawling.

The abundance of squat lobsters (Munididae) in the Pomo pit was already reported by the “Hvar fishery expedition” conducted in 1948–49. At least until the year 1998 *Munida intermedia* was the only squat lobster present in the area. Scientific trawling could not be carried out again until June 2003, when we had the surprise to collect a second species – *Iridonida speciosa* (= *Munida ruttianti*) – that already outnumbered *M. intermedia*. Nowadays *M. intermedia* and its parasites are no longer present in the West Pomo pit, replaced by *I. speciosa* (Tab. I).

Plesionika heterocarpus, first reported in the Pomo pit only in 1972, from few ovigerous females, currently makes about 15% of the biomass of Decapod benthic community.

III. DISCUSSION AND MAIN CONCLUSIONS

Most relevant changes were observed in the years following the oceanographic event known as “Eastern Mediterranean Transient” and they seem consequence of the synergic action of fishery and “global change”. The high fishing effort affects, more severely, *N. norvegicus*, a long-lived, slow growing species, whereas the global warming may favor spreading of *P. longirostris*, and also affects characteristics of the near-bottom waters. The importance of a regular monitoring of biodiversity and environment of this area results crucial.

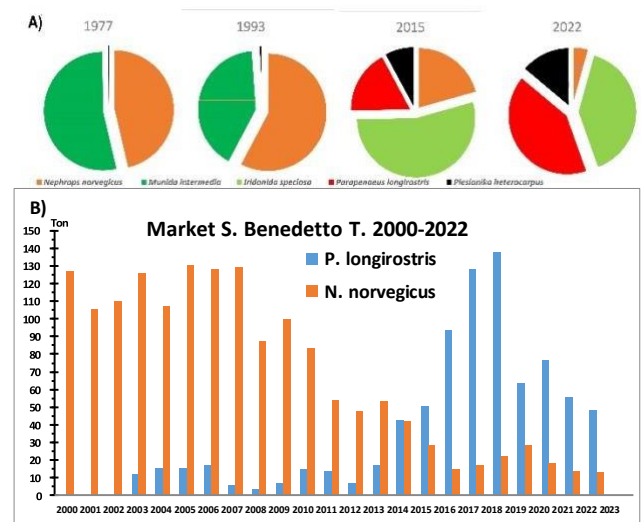


Fig. 1. A) Relative abundance of dominant species in the Decapoda assemblages in selected years; B) Quantities of *N. norvegicus* and *P. longirostris* auctioned in the S. Benedetto del Tronto gross-market.

TABLE I. ABUNDANCE OF *MUNIDA INTERMEDIA* \ *IRIDONIDA SPECIOSA*, AND PREVALENCE OF THEIR PARASITES IN THE PERIOD 1993–2022

Year	1993	2003	2005	2015	2022
N. <i>Munididae</i> examined	3462	728	3776	5736	1096
<i>M. intermedia</i>	3462	186	397	1	0
<i>I. speciosa</i>	0	542	3379	5735	1096
<i>M. intermedia</i> with Rhizocephala (%)	14.0	24.7	30.2	0.0	--
<i>M. intermedia</i> with Bopyridae (%)	0.6	1.1	1.1	0.0	--
<i>I. speciosa</i> with Rhizocephala (%)	--	0.2	0.03	0.0	0.0
<i>I. speciosa</i> with Bopyridae (%)	--	0.6	0.3	3.2	4.2

Biodiversity loss in small low land rivers: an historical perspective

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Short summary: Historical trends (i.e. last 50 years) of biodiversity loss in small, lowland rivers of the Po plain was demonstrated for invertebrates, vegetation and fish. Taxonomic and functional approaches were applied to disentangle the most influent drivers of changes.

Keywords: Lowland rivers, Climate change, Exotic species, Po plain, Functional diversity, Taxonomic diversity

I. BACKGROUND

Freshwater ecosystems are among the most threatened bioma on Earth and suffer the most relevant loss of biodiversity. Lowland rivers are among the last hot-spots

of biodiversity in highly cultivated plains, such as along the

Po river, Italy. Yet they are commonly excluded by the WFD monitoring. This study, currently ongoing, aims at:

- 1) highlighting historical biodiversity for trends invertebrates, vegetation and fish by adopting taxonomic and functional approaches;
- 2) disentangling the most influent drivers of changes.

MATERIALS AND METHODS

Available biodiversity census data from the '50s to 2018, covering the central portion of the Po plain, were collected from historical documents, and integrated with present censuses. Trends were disentangled at population level (flagship, rare species) and at community level, either by using biotic indexes, community ecology analysis (e.g. rarefaction analysis) or functional diversity (e.g. functional richness, dispersion). Main drivers datasets (i.e. climate change, exotic species spread, habitat quality) were also created and related to biodiversity trends by means of linear mixed models.

II. RESULTS

Clear negative trends for vegetation, invertebrates and fish biodiversity were highlighted at each level of biological complexity (Fig. 1), particularly in the last 20 years. Negative trends determined a pervasive scarce ecological status of these ecosystems.

For fish, reduction of functional diversity was bound to increasing temperatures (Tab. I), which also led also to a shift of generalist and dominant species. Increasing functional dispersion was related also to the introduction of new ecological traits brought by expanding exotic species.

III. DISCUSSION AND MAIN CONCLUSIONS

A dramatic loss of biodiversity is occurring in the freshwater hot-spots of biodiversity of lowlands. Climatic changes can erode the niche exploitability for functionally key species (predators), and potentially causing top-down effects on ecosystem stability (Stefani et al., 2020).

Temperature changes may induce abundance shift of dominant traits, and hence loss of functional redundancy.

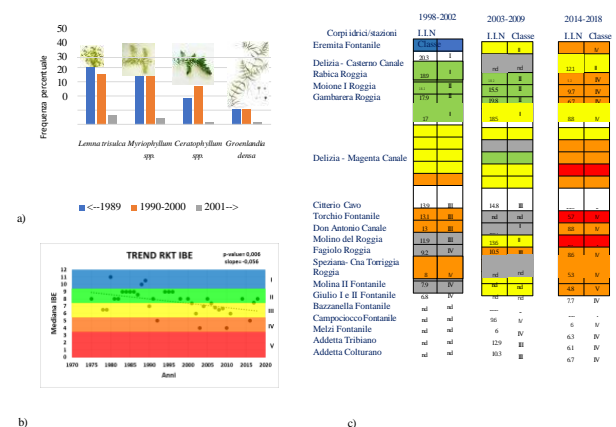


Fig. 1. Historical trends of biodiversity descriptors for: a) vegetation (single taxa occurrence); b) invertebrates (IBE); c) fish (Indice Ittico).

Predictor	Response	Slope coefficient (p-value)		Non-quantile models
		Lower quantile (20%)	Upper quantile (80%)	
Temperature trend	SESF _{ric}	-0.167 (0.527)	-2.140 (<0.001)	-
	SESF _{dis}	0.937 (<0.001)	2.329 (<0.001)	$\beta_1 = 1.310, (p < 0.001)$
	U	0.014 (0.239)	0.056 (0.014)	-

TABLE I -. SIGNIFICANT RESPONSES OF FUNCTIONAL DIVERSITY TO TEMPERATURE TREND AND EXOTIC SPECIES (IN BOLD); SLOPE COEFFICIENTS ARE REPORTED TOGETHER WITH P-VALUES (IN BRACKETS). B1 IS THE ESTIMATED SLOPE COEFFICIENT.

However, other drivers are likely to act simultaneously, such as exotic species or habitat quality (Stefani et al., 2024), and their contribute needs to be assessed accurately.

ACKNOWLEDGMENT

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Indicators of fast biodiversity changes in hard bottom communities along the Apulian Coast

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Short summary: Changes in benthic communities along the Apulian coasts in term of dominance and in species composition can be observed. Here example were given using species of marine Annelids of the Family Sabellidae, for which we have good distributional data, as indicators of these changes.

Keywords: Sabellidae, Annelida, *Branchiomma*, *Bispira*, species adding

I. BACKGROUND

The Apulian coast has been extensively examined in the last 40 years, being the subject of in-depth faunal studies, especially concerning the Sabellidae family. In recent years they have provided much of the material to produce reviews of several genera. During the time of study several faunistic changes could be recorded, especially concerning the genera *Bispira* Krøyer, 1856 and *Branchiomma* Kölliker, 1858. Sabellids are filter feeders tubicole marine worms ranging from few mm to 50 cm in length. They possess a colorful and showy branchial crown which makes these worms appreciable subjects for underwater photography. When they are very abundant they act as habitat formers [1] and this, coupled with their feeding action, makes these worms ecologically important.

MATERIALS AND METHODS

Most of the dated collections were relative to material coming from monitoring works [2], but during the last years extensive sampling focused on sabellids were performed by SCUBA diving in different habitats, along the Apulian coast.

II. RESULTS

The species of *Branchiomma* present along the Apulian coasts before the year 2000 were only *B. bombyx* (Dalyell, 1853) and *B. lucullanum* (Delle Chiaje, 1828) (Fig. 1A), commonly found on hard bottom with algal cover. During the last years the second species become rare along all the Italian coasts. By contrast, in 1988, the alien species *B. luctuosum* (Grube, 1870) was recorded in the region, and in 2012 a second alien, *B. bohollense* (Grube, 1878), appeared, both having tropical affinity. At first, they colonized the confined areas in Taranto area, but at present are widely distributed along the Salento coast, mixed with another smaller introduced taxa: *B. bairdi* (McIntosh, 1885).

As far as the genus *Bispira*, until the year 2010 the only species present in the waters of the Apulia region was the historical species *B. mariae* Lo Bianco, 1893, a very large form easily recognizable underwater. In 2015 a *Bispira* species never recorded before was collected in Otranto area, closely related to *B. viola* (Grube, 1863), suggesting the presence of a complex of species with tropical affinity. Today, these taxa are becoming increasingly abundant, especially one of them (Fig. 1).

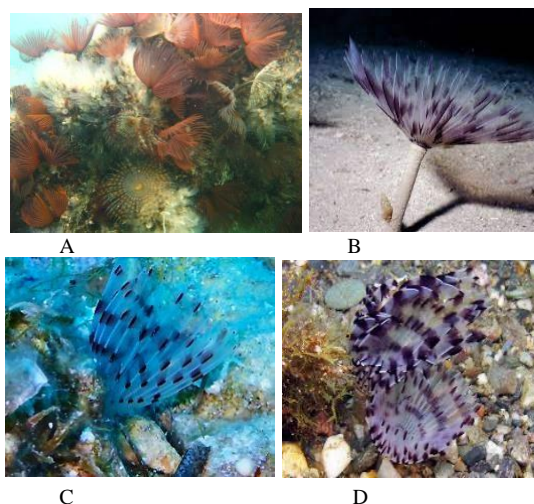


Fig. 1. A. *Branchiomma luctuosum*; B,C,D *Bispira viola* complex.

III. DISCUSSION AND MAIN CONCLUSIONS

Although the environmental changes that have occurred over the last 50 years appear significant, the period considered is probably too short for evolutionary responses at community level to be highlighted. However, some biodiversity changes were recorded along the Apulian coast in term of dominance and species composition of some sabellid taxa. At the moment their presence simply increased the diversity of the area and no competitive exclusion with autochthonous species has been observed. As far as the forms of the “*Bispira viola* complex” are concerned, these were not present in the past as the area under examination has been always finely investigated, but since their appearance there was a steady increase in abundance throughout the area, noticeable from year to year. All the introduced taxa are of tropical affinity, but taxonomically still unknown. For this reason, for the moment we define them as cryptogenic forms.

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Non-random extinction patterns of mammals in cities across two centuries

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Short summary: The fast rate of replacement of natural areas by expanding cities is a key threat to biodiversity in the Anthropocene. Here we used a long-term dataset on mammals from two of the most ancient cities in Europe (Rome and Florence) to document trait-based changes in mammalian assemblages due to local extinctions and colonization events over two centuries. Besides shedding light on the role of traits in urban environments, we also highlight the importance of long-term monitoring in highly dynamic areas such as cities.

Keywords: Extinction, Habitat, Mammals Resampling, Urban wildlife

I. BACKGROUND

Many wild species thrive in urban environments, with increasing amounts of scientific literature focusing on ecological processes that shape urban wildlife, such as the so-called urban filter [1]. Besides few clear patterns in species dynamics in cities, most literature on the topic is focused on few taxonomic groups, leaving huge gaps in our ability to understand, and possibly overcome, extinction processes in cities. Most papers on urban wildlife focus on birds and carnivores, with few studies following multi-taxa approaches [2]. Here we use the cities of Rome and Florence, and their mammalian faunas, as a model system to define patterns of local extinction and persistence within large urban areas, testing the hypothesis that past spatial spread and association to different habitats may drive the fate of species at local level.

MATERIALS AND METHODS

We conducted a systematic search and collection of mammal records from Rome and Florence (central Italy), including all records from either scientific or grey literature, as well as those from citizen science platforms (iNaturalist.org). We then organized data into three checklists, corresponding to the three main periods describing the urban development history of most Italian cities. For each recorded species, we calculated indicators of spatiotemporal persistence in each area, and we assigned each taxon to a favored habitat type. We then used mixed regression to model the probability of extinction as a function of ecological preferences and historical species' local spread.

II. RESULTS

We retrieved 6,342 and 1,297 records of mammals from Rome and Florence, respectively, spanning from year 1832 and 1896 to 2023, and belonging to 63 species. Trends of spatial spread through time were consistent across taxonomic orders, with few exceptions related to Chiroptera and Rodents. Species associated with wetlands and less widespread across each city showed significantly higher probability of extinction (Fig. 1).

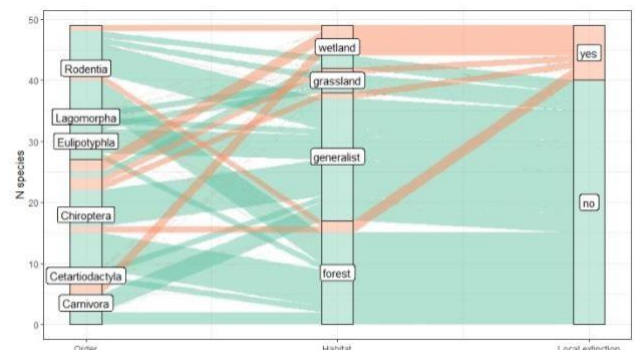


Fig. 1. Alluvial plot depicting the numbers of mammal species that went locally extinct in the urban areas of Rome and Florence between 1832 and 2023, according to taxonomic order and favored habitat type.

III. DISCUSSION AND MAIN CONCLUSIONS

Understanding extinction in human-modified environments is key to protecting wildlife, particularly in the Anthropocene and its associated spread of urban areas worldwide. Here we documented two centuries of mammal extinctions from two of the most ancient urban areas of Europe. Several species have in fact gone locally extinct within each of the considered urban areas, with such disappearance being disproportionately likely to involve species associated with wetlands. The species' turnover we detected suggests that time-series analyses are essential to reveal how trait-based filtering of species in cities may occur at different temporal scales. Understanding species' dynamics is a key asset for wildlife conservation, and for the development of wildlife-friendly and sustainable cities in the future.

ACKNOWLEDGMENT

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Anthropogenic Pollution enhances natural transformation with extracellular DNA in aquatic ecosystems potentially favouring the spread of antibiotic resistance genes

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Short summary: This study investigates the impact of anthropogenic pollution on microbial communities. We found that the richness of microbial communities and the resistome were higher in heavily polluted waters. Additionally, anthropogenic pollution significantly influenced the natural transformation of extracellular DNA.

Keywords: Extracellular DNA, Shotgun Sequencing, Resistome, Anthropogenic Pollution

I. BACKGROUND

Aquatic ecosystems play a crucial role in the spread of antimicrobial resistance [1]. While intracellular DNA has been thoroughly studied to understand the impact of human activities on the dissemination of antimicrobial resistance genes (ARGs), extracellular DNA is often neglected. In this study, we conducted field investigations and experiments to assess the influence of human activities on water microbial communities, their associated resistome, and the spread of ARGs.

MATERIALS AND METHODS

We collected samples from effluents of three wastewater treatment plants (WW) and three lakes (LW). We extracted both intracellular DNA (iDNA) and extracellular DNA (eDNA), analyzing the microbial community composition and resistome by shotgun sequencing. Additionally, we conducted an experiment to assess the impact of anthropogenic pollution on the uptake of eDNA (Gfp-plasmid carrying ARGs) by natural transformation, detected by qPCR.

II. RESULTS

a. Field study

Richness of the microbial community and of the resistome (comprising high-risk ARGs) was higher in WW than in LW samples with iDNA generally showing a higher diversity than eDNA (Fig.1). Several ARGs were associated to mobile genetic elements (mainly located on plasmids (Fig. 1).

b. Experimental study

The anthropogenic pollution positively influenced the uptake of eDNA (Gfp-plasmid carrying ARGs).

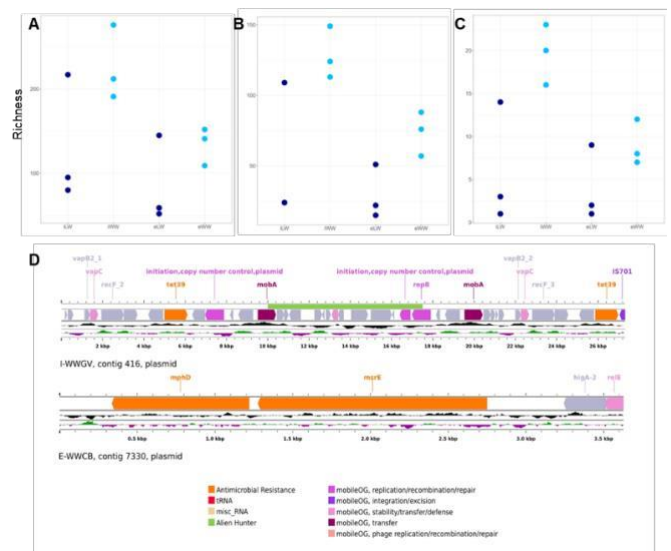


Fig. 1. Richness of A) microbial community, B) resistome and C) high- risk ARGs; D) linear representation of ARG-containing contigs and mobilome genes (focus on the contigs showing the presence of ARGs in two bins).

III. DISCUSSION AND MAIN CONCLUSIONS

Our findings highlight the substantial impact of anthropogenic water pollution on the diversity of the whole microbial community, along with the associated resistome. Additionally, our results offer an experimental evidence of the contribution of anthropogenic pollution to the spread of ARGs via horizontal gene transfer.

ACKNOWLEDGMENT

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Historical trends of Elasmobranch Populations in the Central Adriatic Sea

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Short summary: Combining social data, extracted from LEK and social media platforms, to scientific databases such as STECF, is an effective approach to reconstruct trends of population of threaten species, including elasmobranchs.

Keywords: Adriatic Sea, LEK, FDD, Social media, Elasmobranchs, Abundance trends

I. BACKGROUND

The Mediterranean basin is a hotspot of biodiversity for chondrichthyans, hosting over 80 species, but it is also one of the world's regions facing the highest risk of extinction: more than half of the evaluated species are under threat, with almost a third of them fished close to the level of extinction [1]. Within the Mediterranean, the Adriatic Sea is the most exploited and impacted sub-basin [2] with detrimental effects for elasmobranch species. Through a multidisciplinary approach, the current study analyzes the trending of population of 13 common species of elasmobranchs in the central Adriatic region, over a period of 45 years.

MATERIALS AND METHODS

Data has been analyzed by means of three different approaches, integrating scientific and social science data: *i*) Local Ecological Knowledge (LEK) of fishers through interviews with local fishermen, to reconstruct long-term species population trends; *ii*) Fishery Dependent Data (FDD) from STECF, to analyze species trends through catch landings; and *iii*) Social media platforms data extraction to determine distribution of species (including rare species). LEK data has been analyzed through breakpoint analysis and heatmaps; STECF data has been analyzed by doing a scatter plot, and statistically analyzed; sighting of species on media platforms have been transferred to a bubble map. All data has been analyzed with R software.

II. RESULTS

a. LEK data

A total of 60 interviews were conducted to professional fishermen with at least 10 years of experience. Fishermen reported an increase of four species, (*Raja asterias*, *Raja miraletus*, *Myliobatis aquila*, *Pteroplatytrygon violacea*), a fluctuation of two (*R. clavata* e *Mustelus mustelus*), and a decrease of five other species (*Galeus melastomus*, *Prionace glauca*, *Scyliorhinus canicula*, *Squalus acanthias*, *Torpedo marmorata*) (Tab. I). Information on most of the species abundances date from the 70s.

b. STECF data

The analyzed data covers a period from 2013 to 2022 and includes data from 12 out of the 13 species studied. FDD showed an increase of catches of six species (*R. miraletus*, *R. clavata*, *M. mustelus*, *S. canicula*, *S. acanthias*, *T. marmorata*), while five showed a decline (*G. melastomus*, *P. glauca*, *R. asterias*, *M. aquila*, *P. violacea*) (Fig. 1).

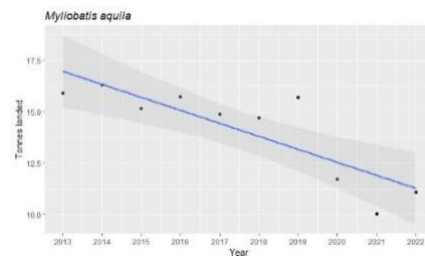


Fig. 1. Trend of the eagle ray *myliobatis aquila*, as an example of declining species from STECF data for GSA 17.

c. Social media

Social platforms showed the spatial distribution of 10 of the species studied, plus some other rare/occasional sightings including also *Isurus oxyrinchus*, *R. polystigma*, and *Aetomylaeus bovinus*.

III. DISCUSSION AND MAIN CONCLUSIONS

Analyses on LEK and FDD for 13 species showed differing trends in seven, while five concurred (with data for one species solely in LEK). LEK has been particularly useful for some species lacking sufficient data such as *P. violacea*, as while STECF data for this species only covered two years of tones landed, LEK data revealed a trend extending back to 1962. Moreover, social platforms can be useful for information on sightings/distribution of elasmobranchs, including species considered rare in the study area, such as *Cetorhinus maximus* and *Carcharodon carcharias*. Conversely, LEK focuses mainly attention on commercial species, and both LEK and social data may be subject to possible misinformation. This multidisciplinary approach could tackle gaps in scientific knowledge by adding the social dimension, providing a comprehensive view of the temporal changes in abundance of the species of interest, specially at regional scale. This approach is highly useful due to the lack of data on some of the species, and the level of threat of elasmobranchs in the Mediterranean Sea.

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Mass mortality event of the Mediterranean mussels (*Mytilus galloprovincialis*) in the middle Adriatic: potential implication of climate crisis on marine ecosystem

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Short summary: We have recently analyzed the potential causes of a massive die-off of Mediterranean mussels observed along the Piceno coast in the summer of 2022; we propose that the combination between the heat wave and the reduced river runoff acted synergistically as deleterious stress factors, generating unsustainable local living conditions for this species.

Keywords: Mussel die-off; Food availability; Marine heatwaves; Adriatic Sea; Climatic crisis; Synergistic effect

I. BACKGROUND

The climate crisis is a global threat to species, biodiversity, and ecosystems; it affects individual organisms and their interactions with other species and habitats, thus altering ecosystem functions and structure [1]. The aim of our study was to propose potential causes and foresee ecological consequences of a Mass Mortality Event (MME) of the Mediterranean mussel (*Mytilus galloprovincialis*) observed along the Piceno Adriatic coast (Marche Region, central Italy) at the end of the summer of 2022.

MATERIALS AND METHODS

The pre- and post-summer 2022 status (mussels percentage covers) was assessed in a natural reef of the Piceno coast (SCI IT534022; Site I). Other three sites close to the Site I were monitored using observational methods which included visual surveys for qualitative inspection. To detect marine heatwaves (MHWs) occurred in the last decade, we performed a proper climatic data analysis considering a long-term local climatology [2]. Data regarding the loss of productivity were also obtained for local mussel farms.

II. RESULTS

We observed a dramatic disappearance of Mediterranean mussel beds that, previous to the summer 2022, had covered the rocky substrates. In the natural reef, the mean percentage of substrate covered by mussels dropped from $81.6\% \pm 16.3$ SD to 0% in little more than two months (Fig. 1).

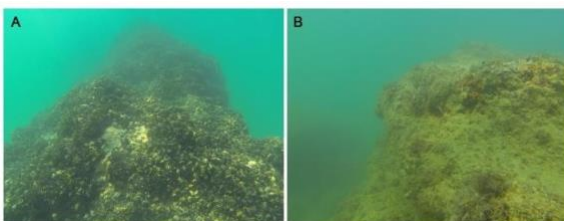


Fig. 1. Pre (A) and post (B) summer 2022 rocky substrate covered by mussel beds in the natural reef.

This phenomenon, which affected both intertidal and subtidal zones, was observed after June–August 2022, when four MHWs hit the western Central Adriatic coast. Water temperatures reached 30.6 °C, and during the last

MHW (July 25–August 7), remained above 29.5 °C for 14 days and above 30 °C for 10 days. There was a 30% drop in mussel production recorded after the summer of 2022 in the mussel farms located in and near the study area.

I. DISCUSSION AND MAIN CONCLUSIONS

The 2022 MHWs were caused by the high air temperatures recorded at the end of June along the middle and upper Adriatic Italian coast. Indeed, July 2022 was the hottest July in the last 50 years [59]. During 2022, the Po River reached the absolute minimum of the last 200 years, with a flow of 104 mc/s on July 24th at the Ferrara- Pontelagoscuro hydrometric station. The chlorophyll-a was always much lower than the average of the period from January to August 2022 in the mid-Adriatic Sea. Based on our field survey and climatic data analysis, and also considering previous findings on *M. galloprovincialis* tolerance under certain stress conditions, we suggest that the MME observed in the summer of 2022 was likely due to prolonged anomalously warm water combined with reduced nutrient supply.

ACKNOWLEDGMENT

This study was recently accepted in Diversity (ISSN 1424-2818). We would like to thank the “Autorità di bacino distrettuale fiume Po” for the historical flows of the Po River data provided, and the Mediterranean Aquaculture Association (AMA) for both the mussel productivity data and for sharing their experience on mussel farming and techniques.

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Mining social networks to track the irruption of a boreal seabird in the Mediterranean

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Short summary: In an era of rapid climate and environmental changes, reporting on uncommon wide-range animal movements may help to depict potential carry-over effects at the population level. In winter 2022–2023, a typical seabird of the North Atlantic, the razorbill *Alca torda*, irrupted in unusual large numbers in the Mediterranean. Mining social networks, we estimated the spatio-temporal progression of the irruption event and reported first data on the foraging habits of razorbills, at regional level.

Keywords: Auks; Citizen Science; Diet; Irruption; Mediterranean Sea; Razorbill

I. BACKGROUND

Climate changes are inducing increasing surface water temperatures and frequent extreme events, with negative effects on seabird communities. In winter 2022–2023, an exceptional irruption of razorbills *Alca torda* occurred in the Mediterranean Sea [1]. We estimated the relative magnitude of the irruption, reporting first data on the diet of irrupted razorbills. We also discussed the causes that may have triggered the phenomenon at regional level.

MATERIALS AND METHODS

We conducted a data-mining campaign on social networks to collect data on the occurrence of razorbills in the central Mediterranean, in winter 2022–2023. To examine *in situ* spatial distribution of razorbills, we used a 50x50 km vector polygon grid shapefile of the European Environment Agency (EEA). A cell grid was considered “occupied” if at least one observation was included. Foraging habits were estimated *i)* by identifying beak-transported prey items from photos/videos and *ii)* via stomach content analysis.

II. RESULTS

A. Observations and origin of records

Nine Italian regions were interested by the irruption (n=238 records). The highest number of individuals (n=747) was recorded on 27 November 2022 in Liguria. Thirty-one records were in Tunisia, Algeria, Corsica, Malta, Libya and Greece (Fig. 1), the others in Italy. The irruption followed a North-to-South direction. In winter of 2023–2024, another irruption occurred, albeit with smaller numbers (20 records) and in the opposite direction (South- to-North).

B. Foraging habits and ingested plastic

We analyzed 32 pictures, 7 videos and 7 dead individuals. Overall, 12 fish prey were identified. Razorbills fed on small-medium sized fish species from the neritic zone (e.g. *Belone belone*, *Trachinotus ovatus* and *Engraulis encrasicolus*). The dead individuals mostly had empty stomachs, consistently with low weight and fat levels. In 3 dead individuals, the presence of plastic items (n=41) was detected in stomach content, gut, liver and pectoral muscle.

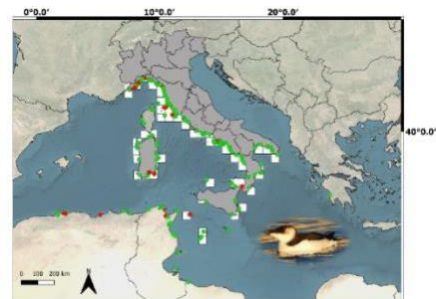


Fig. 1. Razorbill observations during Nov-Dec 2022 in the central Mediterranean area. Green dots are for alive and red for dead individuals. For Italy, the 50x50 km vector polygon grid was used (white squares).

III. DISCUSSION AND MAIN CONCLUSIONS

An unprecedented massive irruption of hundreds of razorbills occurred in the central Mediterranean Sea in the winter 2022–2023, likely triggered by Atlantic storms. Irrupted razorbills have been detected underfed/dead. Social media allowed tracking the irruption in *real-time*. Monitoring peculiar movement patterns of birds in response to severe weather is key for understanding the extent of carry-over effects on animal populations.

ACKNOWLEDGMENT

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Three millennia of changing plant biodiversity revealed by fossil pollen

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Short summary: This paper investigates the impact of past climate and anthropogenic activities on plant biodiversity in Central and Southern Italy using palynology. The goal is to develop conservation strategies for national protected areas.

Keywords: Palaeoecology, Central and Southern Italy, Late Holocene, Pollen analysis, Palaeoclimate, Human pressure

I. BACKGROUND

The Mediterranean region experienced important climatic anomalies during the last thousands of years, which impacted not only on vegetation but also on the land use by man. Among these fluctuations, the most impacting were the so-called Homeric Climatic Oscillation (8th – 6th cent. BC), the Roman Climatic Optimum (2nd cent. BC – 5th cent. AD), the Medieval Warm Period (mid-10th – mid- 13th cent. AD), and the Little Ice Age (15th – 19th cent. AD) [1]. In Italy the prolonged changing climate may have altered the natural and cultural dynamics, causing shifts in plant distribution and community composition. Our research aims to detect changes in plant biodiversity by comparing palaeoecological records obtained through pollen analysis.

MATERIALS AND METHODS

We collected ten pollen records from lakes of Central and Southern Italy covering the last three millennia with an average temporal resolution of max 100 years and ¹⁴C-age control (Fig 1). Data were provided by the authors or obtained from the Neotoma Paleocology Database (<http://www.neotomadb.org>) [2]. The age–depth models of the selected sequences were developed through the Clam package (version 2.5.0) of R software for the purpose of this study. Secondly, we applied multivariate statistical analyses to arboreal pollen data to assess changes in forest composition and structure resulting from changing climatic conditions during the investigated time span.

II. RESULTS

Our results show different palaeoecological scenarios in terms of qualitative and quantitative reconstructions. In particular, regional trends of forest ecosystems are attested with alternating changes in forest biomass and biodiversity.

III. DISCUSSION AND MAIN CONCLUSIONS

We stress how fluctuations of forest biomass are driven not only by palaeoclimatic conditions, but also by cultural developments. The imprint of human pressure on the landscape especially affects regional biodiversity in

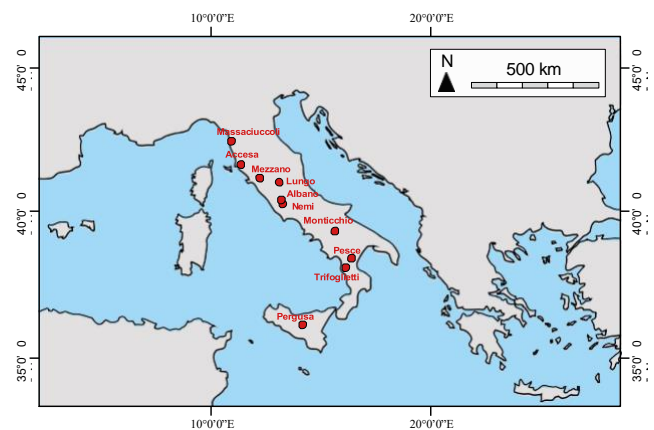


Fig. 1. Distribution of Holocene pollen records considered in this study.

relation to the level of economic activities from the pre-classical times to the Modern Era. Past natural and cultural dynamics represent an essential base for the contemporary studies and conservation of biodiversity in the Italian protected areas.

ACKNOWLEDGMENT

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The fate of cold-water species in a warming hotspot: the case of *Micromesistius poutassou* in the Adriatic Sea

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Short summary: This study updates blue whiting data in the Adriatic Sea and compares specimens collected in the Pomo Pits area with a time shift of 35 years to investigate the potential causes behind its decline over the last decades. Our findings reveal a reduction in growth performances that may be linked to climate-induced modifications of temperature and circulation patterns in the area.

Keywords: Adriatic Sea, Pomo Pits, Climate change, Growth, Blue whiting, Cold-water species

I. BACKGROUND

Understanding how environmental conditions affect fish populations is essential to address fishery management under climate change [1]. In the rapidly warming temperate regions, such as the Adriatic Sea, cold-water species are expected to be the most vulnerable, although little is known about their status, as in the case of the blue whiting Adriatic population, which is here investigated.

MATERIALS AND METHODS

Blue whiting specimens were collected from the western side of the Pomo Pits between 100 and 250 m using a bottom otter trawl in two different periods: 1985–1986 and 2020–2021. After taking individual biometric measures, the sagittal otoliths were extracted and age readings were performed by soaking them in water over a black surface under reflected light. Age estimates and individual length data were used to fit VBF growth models.

II. RESULTS

The total number of specimens analysed was 193 in 1985–1986 and 453 (173 females, 261 males, 19 unsexed) in 2020–2021. The length-frequency distributions were different in the two sampling periods, showing a higher proportion of large individuals (> 28 cm TL) in 1985–1986. The 1985–1986 sample showed higher asymptotic length (L_{∞}) and growth performance index (ϕ') but lower growth rate (k) compared to 2020–2021 (Tab. I).

TABLE I. VON BERTALANFFY AND POPULATION PARAMETERS

	Size range (cm)	Age range (years)	L_{∞} (cm)	k	$t0$	ϕ'^*
1985–1986	12–38	0–8	31.11	0.95	-0.22	3.06
2020–2021	6–32	0–9	25.63	1.31	-0.06	2.94

*Growth performance index

The mean length-at-age was higher in 1985–1986 for all the age classes, suggesting a faster growth across the entire life span (Fig. 1). On the other hand, the proportion of old specimens (> 4 years) was higher in 2020–2021.

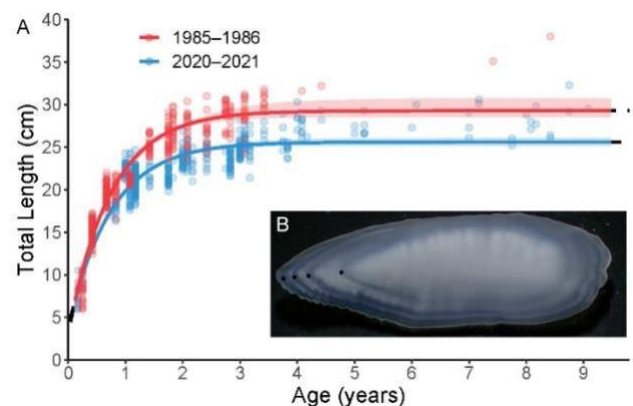


Fig. 1.A) Von Bertalanffy growth curves for *Micromesistius poutassou* sampled in 1985–86 (red) and 2020–21 (blue); 1.B) Sagittal otolith of *M. poutassou* (distal side up) under reflected light showing four annuli (dots).

III. DISCUSSION AND MAIN CONCLUSIONS

The decrease in growth performances and size together with the decline in the Adriatic landings support the idea of a poor health status for the blue whiting population in the Adriatic Sea. The lack of recovery signals after the 2015 restrictions in the Pomo Pits may indicate that unfavourable environmental conditions, and in particular warmer temperatures, interfere with the metabolic processes of this species. Considering that the Adriatic Sea shows one of the highest sea warming trends over the last decades [2], further studies should evaluate the species' vulnerabilities and understand whether the changes observed in cold-water species can be alarm bells for the entire ecosystem.

ACKNOWLEDGMENTS

The research leading to these results was conceived under the International Ph.D. program “Innovative Technologies and Sustainable Use of Mediterranean Sea Fishery and Biological Resources”.

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“API IN CITTÀ” Project

Monitoring by bees (*Apis mellifera*) of biodiversity and some pollutants of health interest in urban environments

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Short summary: Bees are fundamental insects for biodiversity and the protection of ecosystems and can be used as bioindicators: "sentinels" capable of providing information on the health of the environment.

Keywords: Bioindicator, Monitoring, *Apis mellifera*, Biodiversity, Air quality

I. BACKGROUND

This project is inspired by the pre-experience gained by the Carabinieri with the Federazione Apicoltori Italiani (FAI) in the city of Rome, which is extended to 60 monitoring sites distributed throughout the country. The project proposal, in line with Ministero dell'ambiente e della Sicurezza Energetica (MASE) initiatives on biodiversity conservation, envisages the use of bees as urban bioindicators.

The installation of beehives on the roofs of cities is a strategic and natural tool for understanding the health of the environment that surrounds us.

The monitoring takes place at the headquarters of the 14 Comandi CC Forestali Regionali, in addition to Matera, in the offices of 27 Reparti CC Biodiversità, 17 Reparti Parco Nazionali and the Istituto Superiore di Sanità (ISS) (Fig.1), with the aim of establishing a real detection network on the presence of urban pollutants of high scientific value and to protect health.



Fig. 1. Relocation of the stations throughout the country.

MATERIALS AND METHODS

Each monitoring station will consist of three hives, one of which will be high-tech equipped with electronic sensors for remote verification of the health of the hives (Fig. 2).

Samples of biological material will be collected which will then be analyzed by detecting the concentration of:

- Polycyclic aromatic hydrocarbons (PAHs),
- Polychlorinated biphenyls (PCBs);
- Polychlorinated dibenzodioxins (PCDDs);
- Polychlorinated dibenzofurans (PCDFs).

The concentrations of the main pollutants PM10 and PM2.5, organic pollutants (PCDD/F, PAHs and PCBs), inorganic pollutants (metals and metalloids) and sedimentable dusts PCDD/F, PAHs and PCBs will also be analysed.

At the same time will be the characterization of the

environmental context of the monitoring sites, through the definition of the potential vegetation, ecological dynamics, analysis of environmental parameters, microclimate, state of the flora-fauna component, characteristics of surface and groundwater, analysis of the feeding behavior of local wild pollinators, analysis of their interactions with habitats, analysis of the availability of land use classes. Finally, a training course was held for the designated military personnel who will provide for the care and well-being of the bees.



Fig. 2. beekeeping station with sensors

II. RESULTS

The harvest of the biological samples to be subjected to analysis is underway and the significant results will be available from the end of the 2024.

III. DISCUSSION AND MAIN CONCLUSIONS

The bees will control the presence and concentration of pollutants in the area they explore to forage. It will therefore be a widespread monitoring that will be able to provide useful information for researchers and integrate the network of ARPAs that today carry out a punctual and non-widespread control of the "poisons" of cities. Two samples will be taken per month for a total of 1,200 analyses per year.

Finally, the palynological analysis of the pollen collected by the bees present in the hive will provide valuable information on the biodiversity of urban centers, highlighting, on the one hand, the richness of the city's flora.

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Patterns and changes of island plant diversity in Mediterranean Islands

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Short summary: We present the first outlook of the plant diversity of Mediterranean islands based on all the data available from the major data repositories and the start of a resurvey project aiming dedicated to detect the changes in plant species diversity in 72 small islands.

Keywords: Big Data, Biodiversity, biogeography, conservation biology, island ecology, macroecology

I. BACKGROUND

Human activities are causing unprecedented changes in ecosystems. Islands are special places for biodiversity and endemism, and are suffering ecosystem degradation and species extinctions [1]. Including island targets in biodiversity policies is therefore fundamental. Thanks to big data resources, we face new opportunities of analyzing spatial and temporal trends of biodiversity also on islands. We present here the first comprehensive outlook of plant diversity on Mediterranean islands by using three major databases and the launch of a resurvey project dedicated to quantify the changes in plant species diversity in small islands during the last 30 years.

DATA AND METHODS

We assembled vascular plant checklists for all the Mediterranean islands for which species occurrence data are stored in EVA, GIFT and GBIF. The assembled data set was subjected to taxonomic harmonization, and Island Species Area Relationships was calculated for the three datasets and the pooled one. We also searched for potential bias introduced by the datasets, by comparing the species and family pools for each island. A set of small (0.01 - 1.00 km²) islands with high-quality historical data was selected for being resurveyed in 2024.

II. RESULTS

We obtained data for 752 islands. GBIF data are limited to 1 to 5 occurrences for 205 islands. GIFT checklists are more complete than EVA and GBIF ones. The pooled dataset provided a cumulative checklist of 8628 species, belonging to 198 families. *Asteraceae* (1113 species), *Poaceae* (590 species), and *Fabaceae* (576 species) are the most abundant families. Islands Species Area Relationship (Fig. 1) with GIFT and Pooled datasets have the highest R² values (respectively, 0.8 and 0.79).

The 72 small islands selected for resurvey in 2024 (Fig. 2) were those for which high-quality plant diversity data dating back at least 30 years are available to allow a resurvey in 2024.

III. DISCUSSION AND MAIN CONCLUSIONS

Island species pools are best described by relying on data originated by pure floristic checklists, such as those provided by GIFT. However, the combination and homogenisation of data from different data sources significantly improve species richness estimation. When using different datasets for a floristic purpose, one should be aware of the reduced variability captured by databases

based on preferential sampling. The outlook emerging is that the amount of plant diversity hosted in the Mediterranean islands is impressive and most of the species are limited to one or very few islands.

The number of islands for which high-quality data to allow for a species composition resurvey is good and spatially distributed, allowing to get a picture of the changes in species diversity experienced by these islands in the last three decades.

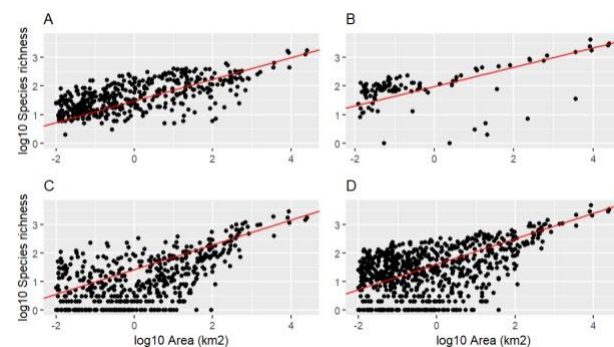


Fig. 1. Island Species Area Relationships obtained for plant species of Mediterranean islands, according to the source datasets: EVA (A), GIFT (B), GBIF (C), and pooled (D).



Fig. 2. Small islands with high-quality data on plant species diversity dating back 30 years and subject to resurvey action in 2024.

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Considering climate-induced sex-based differences to mitigate biodiversity loss

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Short summary: The response of living organisms to climate change can depend on biological sex. This new understanding is essential to improve climate adaptation and mitigation strategies. Researchers are called to consider sex in field and laboratory research.

Keywords: Sex analysis, Community ecology, Intraspecific variability, Research design and methods

I. BIOLOGICAL SEX OFTEN OVERLOOKED

In the Anthropocene, effective strategies for reversing the loss of biodiversity rely on knowledge of how marine organisms, populations, and communities respond to environmental change. A fundamental but often overlooked biological characteristic of organisms is sex, which is distinct from sociocultural gender. Sex describes differences in sexual characteristics within living organisms that go beyond their reproductive functions and affect appearance and physiology, neuroendocrine, behavioral, and metabolic systems [1]. Although integrating sex into research design and analysis has produced new insights and solutions in biomedicine, artificial intelligence, and other disciplines, this has yet to occur for marine biology. Here, drafting from examples from [2,3] and initial evidence from the Mediterranean Sea, we argue that studying sex-based differences from organisms to populations and communities may generate new insights into resilience and vulnerability to climate stressors that may otherwise not be recognized.

II. WHY SEX MATTERS

Sex as a key biological trait

Through a review of marine biological research into sex-based differences we revealed that sex broadly affects the morphology, physiology, behavior, and distribution of organisms and populations across taxa, with evidence of sex-specific differences in survival to thermal stress, timing of biological mechanisms, and energetics [2]. Sex analysis is most commonly applied at the scale of organisms and populations, but not communities. In 90% of studies that explicitly considered biological sex, physiological, morphological, and behavioral mechanisms were found to be influenced by sex.

Sex-specific responses to climate-change

The response of aquatic and terrestrial organisms to climate change can depend on biological sex [3]. At the organismal level, individuals can display sex-specific responses to climate stressors that affect body size, growth rates, and other life-history traits that influence reproductive output and population dynamics and persistence. Population sex ratio can also change as an effect of different thermal performance between males and females. Females and males tend to respond differently to climate-induced environmental changes in species where females and males have different energetic requirements, foraging behaviors or habitat preferences. Consequently,

sex-specific sub-population responses to climate change can impact meta-population dynamics by disrupting interactions between sexes.

Community-level consequences

Sex-specific responses at the species and population levels may impact community dynamics and energy transfer throughout food webs, with consequences for the benefits that humans derive from ecosystems. Sex can be one of the driver of community variability to be investigated among others, like body size. Trait-based ecology has investigated how trait variability drives community stability. Sex is a major source of individual heterogeneity in communities, and can be used to explain species interactions and intra-specific interactions.

III. TAKING ACTION TO REVERSE BIODIVERSITY LOSS

A key challenge is to unravel the interactive effects of sex and climate change at the individual and population levels and the cascading effects on communities. This new understanding is essential to improve climate adaptation and mitigation strategies. Researchers can address the many unanswered questions about biological mechanisms influenced by sex and climate change across species and systems. Researchers have begun to show that climate change can induce sex-specific responses both in the presence and absence of pre-existing sex-specific physiological, metabolic or behavioral differences.

To facilitate further integration of sex into biological research, we synthesize current approaches, discuss methodological and logistical challenges, and lay out guidelines for future research.

ACKNOWLEDGMENT

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Biodiversity changes in the Mar Piccolo of Taranto (southern Italy, Mediterranean Sea): alien species

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Short summary: The long-term observations carried out on plankton and benthos organisms from the Mar Piccolo of Taranto proved useful for the detection of alien species, which noticeably changed the basin biodiversity in the last 100 years.

Keywords: Alien species, Mediterranean Sea, Phytoplankton, Seaweeds, Transitional waters, Zoobenthos

I. BACKGROUND

The Mar Piccolo of Taranto (MP) is a transitional water system deeply studied both from a chemical-physical and biotic point of view. The first studies on the benthic communities date back to the Twenties for seaweeds, and Seventies for invertebrates. Studies on phytoplankton and particularly on harmful species started on 1938 [1]. Since 2011, the basin is a site of the Italian Long Term Ecological Research (LTER) network, so systematic seasonal observations are carried out. Special attention is paid to alien species, which are increasing since the Eighties [2].

MATERIALS AND METHODS

Phytoplankton observations dates back to the end of eighties, but seasonal samplings have been carried out since 2016 in five coastal stations. Three replicates were collected in each station. All the material included within metallic frames 50x50 cm was scraped and brought to the laboratory for sorting and taxonomic identification. Macrofauna associated to macroalgae has been sorted starting from 2022 to 2023. Phytoplankton monthly samplings, conducted using a Niskin bottle, began from 1991, although not continuously, in two stations located approximately in the center of the First and Second Inlet of the MP (Fig. 1).

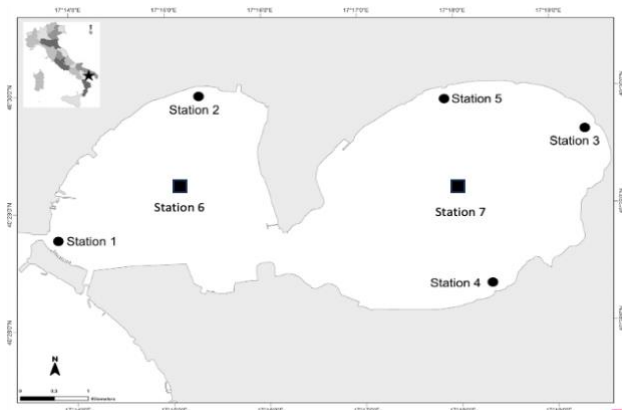


Fig. 1. Map of the Mar Piccolo of Taranto with the location of the benthos (Stations 1-5) and plankton (Stations 6-7) sampling sites. In the frame, the location of Taranto in Italy (modified from [3]).

II. RESULTS

Concerning seaweeds, in the period 2016-2023, 13 alien species were identified. However, only eight reached high biomass values, with a very variable yearly trend. A clear difference among stations was observed, and none of them

was present in all the sampled stations. The Rhodophyta *Hypnea corona* Huisman & Petrocelli reached the highest biomass values ever ($11.2 \times 10^3 \text{ gm}^{-2} \pm 336.7$) and was present at three stations. As regards macrozoobenthos, six alien species for a total of 227 individuals were identified. The macroinvertebrate composition was dominated by Mollusca, with *Arcuatula senhousia* (Benson, 1842) and *Pinctada radiata* (Leach, 1814), while *Paracerceis sculpta* (Holmes, 1904) was the dominant species among Crustacea. Significant differences in the macrozoobenthic density and biomass among the stations and the seasons were observed during the study period ($p < 0.05$). In recent years, as regards phytoplankton, four alien species were recorded. These species are all potential producers of biotoxins: the diatom *Pseudo-nitzschia multistriata* (Takano) and the dinoflagellates *Lingulodinium polyedrum* (Stein) Dodge, *Ostreopsis ovata* Fukuyo, *Prorocentrum cf. shikokuense* Y.Hada. They never reached particularly high concentrations.

III. DISCUSSION AND MAIN CONCLUSIONS

These observations demonstrate that the MP is highly exposed to the introduction of alien species, like all the transitional water systems with aquaculture activities. The trend observed among all the phyla shows that the basin seems to have an inner buffer that controls the alien species establishment reducing their invasiveness, confirming what already observed on some seaweeds in previous years [3]. However, the continuous monitoring of these species' behaviour is crucial since both new species can easily be introduced and those already present can suddenly become invasive if environmental conditions keep changing.

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Climate change and risks to bivalve biodiversity

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Short summary: Evaluation of the heat waves exposure effect on Pacific oyster (*M. gigas*), mussel (*M. galloprovincialis*), and clam (*C. gallina*) performances. The present study could contribute to identify which species is most at risk in the modern era.

Keywords: Heat waves, Thermal stress, Pacific oyster, Mediterranean mussel, Stripped venus clam

I. BACKGROUND

Many bivalve molluscs are endangered by climate change, even those farmed and of great commercial interest. Predictive models show there will be more frequent, intense and lasting heat waves (HW), which could reduce the shellfish production. But, how the increase in water temperature affects the physiological state of bivalves, putting biodiversity at risk, is still little known.

MATERIALS AND METHODS

Three animals particularly present in Italy, the Pacific oyster (*Magallana gigas*), the striped venus clam (*Chamelea gallina*) and the Mediterranean mussel (*Mytilus galloprovincialis*), were exposed to a heat wave of 28°C for 30 days, as expected for the northern Adriatic in the coming years, then a series of stress indicators were evaluated. Biometric, physiological parameters were assessed for all of them. For the oyster has been quantified also the gene expression of heat shock proteins; while for the clams has been evaluated the ability to survive at air and the synthesis of *HSP70*; finally for the mussels, the performances of the byssus have been evaluated, as quantity, structure, production of collagen, resistance and deformation to the traction.

II. RESULTS

What emerged from the studies is that, over 10 days of high temperature, the oyster metabolism is adversely affected, proved by loss in weight, in energy resources, reduction of nutrient absorption and pulp yield, as well as an over-expression of *HSPs*. Clams, on the other hand, beyond the heat wave, remain slightly affected, using the energy resources of hepatopancreas to respond to stress but increasing the ability to survive at air and inhaling the synthesis of *HSP70*. Even for mussels, the prolonged duration of heat wave over 10 days most affected the metabolism, with an intermediate response compared to the two molluscs mentioned above: no reduction in pulp yield but in the energy resource compromises other aspects, such

as air survival and byssus performances with less threads, altered structure and less strength.

III. DISCUSSION AND MAIN CONCLUSIONS

From a shellfish aquaculture point of view, the HW effects on oysters may suggest a reduction in productivity and salable products, as well as for mussels. While clams' remarkable thermal resistance highlights their suitability for the sector. Placing the tested animals on a decreasing scale of heatwave damage, the most affected bivalve was definitely the oyster. In second place could be placed the mussel and finally, there is the clam, which emerged as the animal most resistant to this type of stress. This ranking can help to define which shellfish species is most at risk due to climate change and which requires more preventive and adaptive action. It is clear therefore that extreme climatic events are disturbing and will change biodiversity, going to eliminate the most sensitive species and selecting instead the most resilient.

ACKNOWLEDGMENT

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New gastrotrich species were found, but what is happening with old ones?

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Short summary: The reinvestigation of three Italian freshwater biotopes and a marine beach showed a marked change in the diversity of gastrotrich populations in freshwaters and a negligible variation in the marine habitat. A working hypothesis links this shift to climate change, resulting in the emergence of previously undetected rare species and a decline in formerly dominant taxa.

Keywords: Biodiversity, Change, Gastrotricha, New species

I. BACKGROUND

Gastrotrichs are microscopic (0.1-3.0 mm) free-living, aquatic worms with a meiobenthic lifestyle. The Italian gastrotrich fauna is one of the best-known worldwide, although studies on freshwater taxa are dated. The most recent taxonomic research involving the Italian freshwater gastrotrich dates back 25 years, while three freshwater species have been used in a phylogenetic study in 2013 [1]. In the framework of the NBFC-PNRR project, we are revitalizing the investigation of Italian freshwater gastrotrichs using the Next Generation Taxonomy approach based on innovative morphological and genomic observations.

One of the first goals was to investigate biotopes near our home institution to retrieve species discovered earlier and perform genotyping. We also sampled a marine location on the Tuscany coast, known to host species relevant in parallel phylogenetic studies.

MATERIALS AND METHODS

We sampled three freshwater lakes near Modena (St. Anna, Sassomassiccio, and Pratignano) and the marine beach of Mortelliccio (GR) using consolidated techniques (Tab. I) [2]. Morphological analysis was conducted on living specimens using DIC optics under a Nikon Eclipse Ni-U microscope. Specimens of selected species were processed for whole genome amplification and sequencing for future genetic identification.

II. RESULTS

The new investigations showed that species composition was markedly changed in freshwater habitats (Tab. I), including the finding of a species new to science which is being formally described. Meanwhile, several species were the same as in past in the marine biotope. Change in the number of species recorded in the past vs present research was expected due, for example, to the sampling effort often being cumulatively higher in the past. However, what appears most interesting is the finding of previously unreported taxa, especially in freshwater biotopes.

Considering also old, unpublished records, reinvestigation of the chosen Italian biotopes showed substantial changes of gastrotrich diversity in freshwater habitats within last 10-45 years, while change in the marine habitat (reinvestigated after 23 years) was partial (see details in Tab. I).

TABLE I INVESTIGATED FRESHWATER (F) AND MARINE (M) HABITATS AND NUMBER OF SPECIES FOUND OVER TIME

Biotope	Old data	New data	Remarks
Pratignano (F)	to 2013 12 spp	2023, 17spp	only 4 spp match old data
Sassomassiccio (F)	to 2012, 19 spp.	2023, 11 spp	community highly changed
St. Anna (F)	to 1977, 8 spp	2022, 8 spp	community fully changed
Mortelliccio (M)	to 2000, 22 spp	2023, 10 spp	all 10 spp match old records

III. DISCUSSION AND MAIN CONCLUSIONS

Advances in industrial development and other human-associated activities are known to cause radical changes to the biodiversity in many habitats; however, variation also occurs in apparently pristine biotopes, as it was shown in small-scale comparison data here. This calls for further investigation, taking into account multifactorial analysis that can explore the causes affecting the rapid changes of species compositions in different habitats. Intriguingly, some habitats are more resilient than others (e.g., the marine habitat in this case), questioning whether this is related to species adaptation to specific environments or with abiotic factors. A working hypothesis connects the relatively swift shift in species composition of freshwater gastrotrich communities to climate change. This may have led to the increase in rare species that were previously undetected and a decline in old dominant taxa.

ACKNOWLEDGMENTS

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Structural complexity and ALDFGs assessments in the upper mesophotic of the Portofino MPA: implications for future conservation strategies

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Short summary: The upper coralligenous of the Portofino MPA is severely threatened by fishing litter, mainly affecting vertically structuring species such as the red gorgonian *Paramuricea clavata*, thus reducing the overall structural complexity of this habitat.

Keywords: Marine animal forests, Key species, Biodiversity, Artisanal fishing, Mitigation strategies

I. BACKGROUND

Coralligenous, a typical Mediterranean mesophotic habitat, is considered the second biodiversity hotspot in the basin. Nonetheless, it still lacks effective conservation measures, as well as a shared approach to assess its environmental status, with fishing impacts being one of the main contributors to its rapid degradation [1,2]. In this context, the present study aims to characterize the upper coralligenous habitats in the Portofino marine protected area (MPA) (Ligurian Sea, Italy) by comparing the benthic assemblages and the so-called “abandoned, lost or otherwise discarded fishing gears” (ALDFGs) at two bathymetries.

MATERIALS AND METHODS

Thanks to technical divers, video-transects at 35 m and 50 m depths at four sites were recorded. From each transect, 10 frames were randomly selected (0.15 m²), and organisms identified to the lowest taxonomic level possible. To assess the overall structural complexity, identified organisms were assigned to one of the six structural descriptors described by Valisano et al. [2]: nude substratum (NS), non-crustose coralline algae (nCCA), crustose coralline algae (CCA), encrusting epibenthic fauna (EPI I), massive epibenthic fauna (EPI II), and branching epibenthic fauna (EPI III). Additionally, all ALDFGs were detected and quantified in each transect, also recording the affected taxa as well as the type of damage.

II. RESULTS

A total of 86 taxa were identified, belonging to 8 phyla and 28 orders. Significant differences were found in the community composition and structural complexity between 35 and 50 m depth (PERMANOVA, $p < 0.001$). An increasing area coverage of EPI III and EPI II was recorded with depth, being the red gorgonian *Paramuricea clavata* the dominant taxon in the assemblages (0.4 – 6.6 colonies/m²). Overall, 120 ALDFGs were observed along the transects, represented exclusively by fishing lines, with 42.5 % found at 35 m and 57.5 % at 50 m. The most impacted organism were *P. clavata* (42 individuals), and erected bryozoans (12), while the most recorded damage type was “entanglement” (60) (Fig. 1).

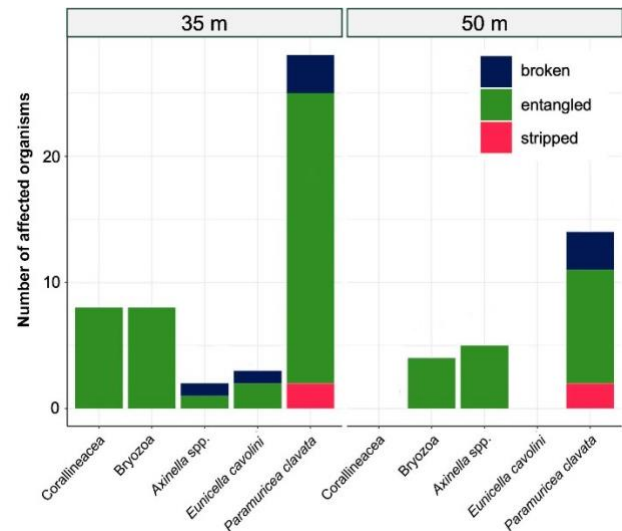


Fig. 1. Bar plot representing the number of individuals per taxa affected by ALDFGs at 35 and 50 m depth.

III. DISCUSSION AND MAIN CONCLUSIONS

The overall lower density of this species compared to previous studies (e.g., [3]), together with the impact caused by the fishing lines found along the transects, highlight a trend of loss of habitat complexity, increasing the habitat fragmentation and the urgent need for tailored conservation measures.

With the unfolding of the current climate crisis, the warmer temperatures reaching down the water column and the cumulative impacts of fishing activities degrading mesophotic rocky habitats, future MPAs needs to be implemented including mesophotic depths, thus contributing to Target 3 of the “30x30 targets” of the Global Biodiversity Framework agreed upon at the COP15.

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Changes and extinction of Mediterranean marine species in the last decades: an example with Hydrozoa

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Short summary: Today, the tendency to examine changes in biodiversity is essentially based on the introduction of new species, while the stability of the present biodiversity in an area with the possibility to track the extinction of some taxa as a response to the pressure of anthropogenic activities, including climate change, is rarely investigated. Here, the marine Hydrozoa are analyzed as the total number of species in the Mediterranean Sea to observe the changes during the last decades. Distribution in space and time is then analyzed considering a very important habitat as the seagrass *Posidonia oceanica* meadows.

Keywords: Biodiversity, Hydrozoa, Disappeared species, *Posidonia oceanica*, Mediterranean Sea

I. BACKGROUND

Data on biodiversity changes during time are mainly based on the addition of new introduced taxa, with a scarcity of well-documented cases of marine invertebrate extinction in the environment. An example is here reported considering the Hydrozoa which constitutes one of the best-known marine invertebrate taxa, and which can be considered a good indicator of marine biodiversity, being widely represented in both plankton and benthos and showing significant responses to climate change.

MATERIALS AND METHODS

The Mediterranean species analysis of Hydrozoa is available in Gravili et al. [1], where temporal and spatial distribution recorded by the scientific literature was analyzed within a threshold of about 40 years, adapting a paleobiology method to analyze cases of putative extinction in recent species. Moreover, an analysis within the *Posidonia oceanica* meadows is available in Gravili et al. [2].

II. RESULTS

The results from Mediterranean Hydrozoa species analysis represent the only work with the application of this type of approach. As in all the other groups, the number of species is continuously updated, and many new reports are labeled as NIS (non-indigenous species). Many of the species reported in the past have not been recorded in recent decades. The use of the Confidence of Extinction Index [1] made it possible to identify extinct species or cases of probable extinction. The largest contingent of the 53 missing species (Fig. 1) is endemic to the Mediterranean (18 species, 34%), followed by boreal ones (10 species, 19%), 15% (8 species) is Mediterranean-Atlantic; the Indo-Pacific and circumtropical contingents are represented by 6 species each (11%), followed by the cosmopolitan contingent (2 species, 4%), 4% (2 species) are non-classifiable, and 1 tropical-Atlantic species (2%).

The temporal analysis of hydroids' species living on *P. oceanica* showed an opposite trend, with an increase of 30% of species if compared to the previous lists. This is also probably due to contribution of recent data obtained in

a unique condition: the *Posidonia* at volcanic CO₂ vents where the group showed a clear tolerance to low pH levels.



Fig. 1. *Tricyclusa singularis* (Schulze, 1876) After the original description by Schulze (1876) in the Gulf of Trieste the species has never been recorded again from the Mediterranean Sea.

III. DISCUSSION AND MAIN CONCLUSIONS

Historical marine biodiversity datasets for past reconstruction and recent evaluation of biodiversity and ecological patterns are limited for several reasons: the lack of quantitative data, the taxonomy of many species recently updated with the description of new taxa or the difficulty of relocating ancient names of toponyms to track detailed species' occurrence. This was possible in the analysis of Hydrozoa which revealed a high number of species that disappeared. Several features of species contribute to their disappearance (such as their population turnover, trophic level, range and distribution, commonness and/or rarity). The scarcity of well-documented cases of extinction in the marine environment is a problem for dealing with the invertebrates.

The Mediterranean Sea, characterized by a high rate of endemism, is predisposed to local extinction because it is much smaller than the open ocean and almost closed, responding more quickly to environmental change.

Lastly, the strictly typical hydrozoan epiphytic population of *P. oceanica* confirms that these organisms represent some of the invertebrates able to survive in view of the future scenario of ocean acidification.

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Biodiversity changes and economic implications

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Short summary: The current problems of shellfish farming in the Taranto area (Ionian Sea) are reported. The area once considered the kingdom of mussel farming in Europe, is at present experiencing serious problems in the production. Most of the problems arise from pollution but at present are especially linked to climate change. The possibility of cultivating an alien species is being considered.

Keywords: Mussel farming, Biodiversity changes, Fouling, Mediterranean Sea

I. BACKGROUND

The Taranto Sea system is one of the most important and human-influenced coastal marine ecosystems in the Apulia region (southern Italy). It was one of the most important areas in Europe for Mediterranean mussels *Mytilus galloprovincialis* (Lamarck, 1819) production, and mussel farming was one of the main economic activities of the local population. Since 2006, a decrease in the production has been observed, coupled with a decrease in the quality of the product. This was most likely due to the relocation of some sewage discharge out of the Mar Piccolo to reduce bacterial load, which, in turn, reshaped the trophism of the system. Moreover, in recent years, several mass mortalities of mussels have occurred in the Taranto area due to recurring summer heat waves [1].

MATERIALS AND METHODS

The fouling composition was followed in the area of the Mar Grande (Fig. 1.A) from the year 1970 [2]. The growing of *M. galloprovincialis* was studied for three cycles in the years 2021-2023 [1]. The growing and abundance of the alien species *Pinctada radiata* (Leach, 1814) was studied in suspended collectors placed in the same long line system during the years 2022-2023.

II. RESULTS

The Taranto Seas are characterized by distinctive fouling communities, dominated mainly by filter feeder species [2]. The area is also considered a hot spot of alien biodiversity. Alien taxa increased in time and since 2014, a lot of additional introduced species have been recorded, including the mollusc *P. radiata* of tropical origin (Fig 1.B). Over the last few years this species started to become very abundant and we were able to obtain some data on its life cycle and reproduction in the area.

One year after the installation of collector ropes (April 2022), oysters had settled in high densities (with a maximum of 468.8 ind./m). The size classes compatible with sexual maturity were the most represented in the following sampling (July). The last sampling (October) (Fig. 1.C) showed that a large amount of spat had settled, as a consequence of a spawning event of the ripe cohort; in fact, most of the oysters in the previous sample were ripe.

It appears that *P. radiata* exhibits a peak in reproductive activity in the summer months.

During the years 2021 and 2023, *M. galloprovincialis* did not reach the required size for commercialization as almost all mussels in the farm died during a mass mortality event due to anomalously high temperatures in summer.

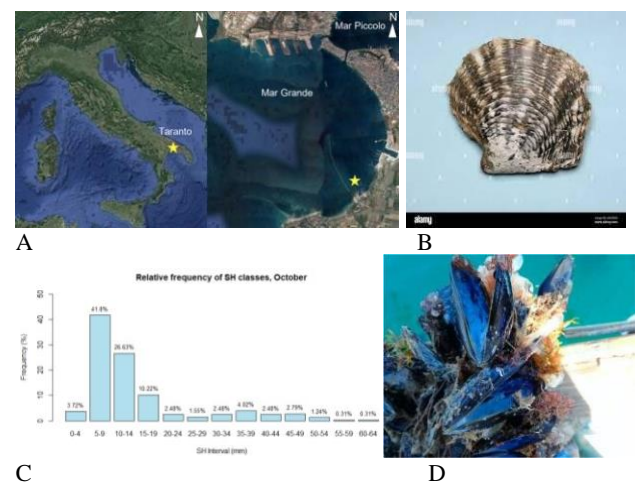


Fig. 1. A: Map of the study area; B: The oyster *P. radiata* C: size distribution of *P. radiata* in October 2023). D: Dead mussels.

III. DISCUSSION AND MAIN CONCLUSIONS

At present, in the Mar Grande, *M. galloprovincialis* is unable to reach a suitable size for marketing in a short time due to the oligotrophy of the waters. Therefore, the area can be utilized only for recruitment or keeping the organisms before the marketing. Furthermore, in recent years there have been crises of prohibitive summer temperatures which have led to the death of almost all mussels. By contrast, during the same period of study, the introduced species *P. radiata* had its summer reproductive event which resulted in an exceptional recruitment. If handled with caution and appropriate safety precautions, the cultivation of this alien species could hold great promise for the future of sustainable aquaculture.

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Response of meiofauna on vermetid reef to increasing temperature and the buffer effect of canopy-forming algae

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Through a field colonization experiment, we evidenced the negative effect of the increasing temperature on meiofaunal community associated with a vermetid reef and the effectiveness of the canopy-forming algae in buffering the impacts of future climate conditions

Keywords: Meiofaunal community, Biogenic reefs, Macroalgae, Climate change, Mediterranean Sea

I. BACKGROUND

The organisms living in the intertidal are particularly prone to the effects of climate changes [1]. Vermetid reefs play an important role in structuring benthic fauna along coastlines and the presence of canopy-forming algae can facilitate the colonization of organisms ameliorating physical conditions [2]. We investigated the simulated climate change impacts on vermetid reef meiofaunal community and the ability of the macroalgal canopy to buffer thermal stress.

MATERIALS AND METHODS

In a field experiment, along the northwestern coast of Sicily, we placed 30 geopolymer concrete discs with a topographic design on a vermetid reef (Fig. 1). The temperature was manipulated by using white (Ta) and black (T+) PVC frames, placed around the discs. Each treatment (Ta and T+) and control (CTRL; no frame) was replicated in the presence (+C) and absence (-C) of the algal canopy (*Cystoseira sp.*). After 35 days the discs were collected, the vegetation coverage on the discs was assessed by a photo analysis, and meiofauna associated with each disc and with the algal canopy were extracted and identified. The temperature at colonization substrates was monitored by an infrared thermal camera and thermo-loggers.

II. RESULTS

A. Substrate vegetation coverage and temperature

Under the algal canopy, the discs were significantly less vegetated compared to those placed on the bare reef ($p < 0.001$). The temperatures on the T+ discs, recorded during the diurnal low-tide periods, reached maximum values $\sim 3^\circ\text{C}$ higher than those on the Ta and CTRL discs. On the substrate under the algal canopy, the temperature variation was lower ($0.2 - 0.7^\circ\text{C}$) than on the bare substrate.

B. Meiofauna

The results revealed significantly lower abundances ($p < 0.05$) of the total organisms and the major meiofaunal taxa (i.e. nematodes and copepods) on T+ discs compared to the others, but only in the absence of algal canopy. The community composition also changed significantly among treatments ($p < 0.001$). The meiofaunal colonization, regardless of the T treatment, was significantly higher on -C discs than on +C discs ($p < 0.001$). High abundances were also found on the algal canopy, enclosing the discs.

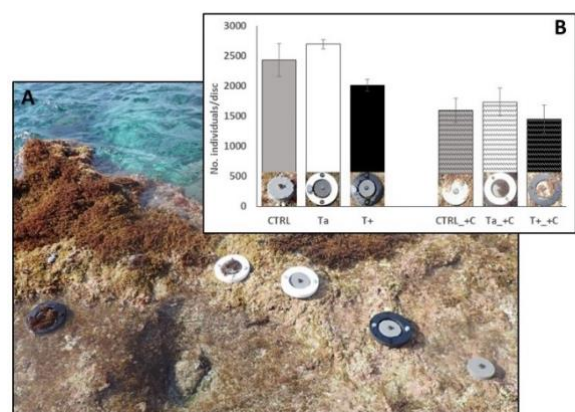


Fig. 1.A) Discs with white (Ta) and black (T+) PVC frames and without frame (CTRL) deployed along the vermetid reef during the experiment under the algal canopy (+C) and on the bare reef. 1.B) Meiofauna abundance (mean ind \pm SD) in each experimental treatment

III. DISCUSSION AND MAIN CONCLUSIONS

Our results highlighted that changes in the temperature may significantly affect meiofaunal communities associated with this intertidal bioconstruction. Despite the macroalgal canopy performs a negative control on the understory algal coverage, reducing the meiofaunal abundance on the artificial substrates, it appeared to provide additional substrate for colonization and to protect meiofaunal organisms from thermal stress. Given the usefulness of meiofauna as a proxy of benthic biodiversity alterations [3], this work demonstrated the importance of considering the interplay among biotic and abiotic factors to understand the response of marine organisms to environmental changes.

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How anthropogenic actions affect gastrotrichs diversity in Italian freshwaters

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Short summary: Data Analysis of the Italian freshwater gastrotrichs shows that the diversity of these animals does not depend on the natural or artificial origin of biotopes but rather on human exploitation of water bodies.

Keywords: Benthos, Biodiversity, Gastrotricha, Distribution, Meiofauna, Anthropogenic impact

I. BACKGROUND

Gastrotrichs are microscopic benthic animals virtually found in all water bodies. To date, over 890 species distributed in 71 genera, 18 families, and two orders are known, 376 of which live in freshwater environments. Many of those are also found in Italy. We created an interactive GIS-based web map to collect information about their diversity and distribution in Italian freshwater biotopes [1]. Using this information, we could identify the natural and artificial (human-made) settings, compare the diversity and species abundance of gastrotrichs in those contrasting sites, and explore if and how human activities may impact gastrotrich biodiversity.

MATERIAL AND METHODS

The data about gastrotrich diversity across the national inland-water biotopes were gathered from the interactive web map of the Italian freshwater Gastrotricha (<http://gastrotricha-gis-italy.unimore.it/>). Information regarding the origin of the biotopes and their possible exploitation by humans was obtained from the original papers. Those data were organized in a matrix used for the statistical analysis (Mann-Whitney test), performed with Past software (version 4.03). We used 47 natural and 19 artificial sites for building the matrix. First, we compared natural and artificial sites, and then we compared the exploited and non-exploited sites, whether they were natural or artificial.

II. RESULTS

A total of 92 gastrotrich species, belonging to 17 genera and three families, have been found in Italy over 239 years during which 81 biotopes across nine regions have been investigated. About a quarter (19) of the water bodies hosting gastrotrichs have fascinating anthropic origins. Some were created for irrigation and sport fishing; others were intended to beautify gardens or parks and grow plants in botanical gardens; le Polle was created for artificial snowmaking, whereas St. Anna lakes are abandoned quarries. Arguably, the most striking origin is that of Mount Bondone's Viotte, small basins unintentionally created by the explosion of artillery charges during World War I subsequently filled with rainwater. Some of the above freshwater biotopes are now not disturbed by human action, but most are still subject to severe anthropic impact.

Among the artificial biotopes, five are the type localities for one or more species, and four sites host one or more species endemic to Italy. Two artificial biotopes host

a higher number of species compared to the national average (St. Anna Lakes, 8 spp.; Mount Bondone Viotte 2, 11 species; Italy: 5.33 ± 6.13 species per locality); in six biotopes, the number of species (3-6 species) is within the national average while in the remaining 11 sites, the number of species is below the mean (1-2 species). Statistical analyses show that, as a whole, biotopes of natural and artificial origin do not have significantly different numbers of species ($p = 0.21$). However, we found that the current human exploitation of the water bodies significantly affects the diversity of gastrotrich communities ($p = 0.0073$).

III. DISCUSSION AND MAIN CONCLUSIONS

Our results show that the number of gastrotrich species does not depend on the origin of the water body; in fact, the artificial basins considered here host a number of species (1-11 species) in line with the numbers observed in the natural settings (1-18 species), and statistical analysis confirms this claim. Thus, anthropogenic action cannot be considered an adverse driver of biodiversity in this case; on the contrary, human action has created new niches colonizable by different meiofaunal species. On the other hand, current human use of the water body is a crucial factor influencing biodiversity. Water bodies being heavily exploited by humans (e.g., fishing lakes, irrigation lakes, etc.) show lower numbers of species than those that are virtually non-exploited (e.g., Astroni Lake, Tovel Lake, etc.) Based on these findings, human activities strongly impact gastrotrichs communities in both positive and negative ways. On the positive side is creating new colonizable habitats, while on the negative side is reducing the number of species.

Particular attention should be paid to the management of relevant biotopes for conservation, such as the type localities and the ones hosting endemic species.

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In the Anthropocene clams do not die but resist!

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Short summary: The ability of the bivalve *Chamelea gallina* to withstand the high fishing pressure is to be found in its biological traits and is encoded in its genome, combined with the adoption of more restrictive and effective management measures over time.

Keywords: Striped venus clam, Fishing effort, Biological traits, Age & growth, Reproductive cycle, Survivability

I. BACKGROUND

In the early 1970s the introduction of technological innovation in the harvesting of the striped venus clam (*Chamelea gallina*) through the development of hydraulic dredges, led to a steep increase in landings and fishing effort also due to the poorly managed fishery sector. However, starting from the early 1990s to nowadays co-management systems, based on effective and more restrictive measures (e.g. fishing closure, seeding, repopulation, rotation, quota and fishing days' reduction, MCRS, AIS implementation), had evolved over time to manage sustainably such an important economic resource. Therefore, the life history traits of *C. gallina* (age and growth, reproductive cycle, size at sexual maturity, reburial ability, survivability of damaged and undamaged shells) where here investigated, as a prerequisite for appropriate resource management is to have a sound knowledge of the biological traits of the target species.

MATERIALS AND METHODS

Different biological traits of *C. gallina* were investigated collecting all the samples and conducting tests in the Maritime District of Ancona (western-central Adriatic Sea). Age and growth were analyzed using a shell sectioning technique to identify annual growth rings defined as the set of an opaque (carbonate matrix) and translucent (carbonate-organic matrix) increment visible on the shell cross-section. The reproductive cycle, as well as size at sexual maturity and partial fecundity were investigated by microscopic, histological and video analysis techniques, and were correlated with the variation of some environmental parameters (i.e. bottom seawater temperature and Chl-a).

To test for the reburial ability of the species in laboratory tanks all the environmental conditions were mimicked and shots were taken every 30s by placing go-pro cameras outside the tank. Finally, survivability of undamaged clams was tested both in the laboratory (135 clams, 21 days) and at sea (320 clams, 15 days), whereas for damaged clams only tests in sea cages were conducted (262 clams, 21 days).

II. RESULTS

Shell growth analyses showed that growth is slower in the cold season and in older specimens, highlighting a very fast growth in the 1st year of life (of 14-15 mm TL), whereas in the 2nd year of life (of 21-22 mm TL) the growth rate had more than halved already.

Concerning the reproductive cycle of *C. gallina* it was found that its breeding season is driven by rises in seawater temperature (from 20.6 ± 2.2 to 25.8 ± 1.5 °C) and Chl-a concentration which peaked in June (4.6 ± 1.9 mg/m³), and that its spawning period lasted from early-spring to late-summer (March-September). Size at sexual maturity was reached very early in the life cycle at about 12 mm TL. As regards partial fecundity – the number of mature oocytes potentially released by females with ripe gonads in a single release event – varied in relation to shell size ($PF = 3.01 \times 10^4 TL - 5.21 \times 10^5$).

Reburial tests showed reburial times (T50 and T90) of about 4 h (CI+ 4.4, CI- 3.6) and 8 h (CI+ 8.2, CI- 7.7), respectively, nevertheless by 21 h 100% of clams had reburied inside the sediment. Survival tests highlighted a high survival rate of the species independently from the kind of treatment (tank or sea cage) and clam condition (damaged or undamaged) see Tab. I.

TABLE I. STRIPED VENUS CLAM SURVIVABILITY

Treatment	Clam condition	N beginner	N survivors	Overall survivability
LAB TANK	UND	135	128	94.8%
SEA CAGE	UND	320	308	95.5%
SEA CAGE	DMG	262	203	93.8%

*UND: undamaged, DMG: damaged

III. DISCUSSION AND MAIN CONCLUSIONS

The ability of the Adriatic clam stocks to withstand the past and present strong fishing pressure is due to its high reproductive plasticity, natural resilience [1] and high level of genetic diversity [2] which confer to this species a good adaptive potential to face the environmental perturbations. All these, combined with the effect of management measures (closed areas/seasons, quota, MCRS) and technical constraints on the gear and the sieve on board allowed to keep on average the fishery sector always productive over time.

ACKNOWLEDGMENT

Samples were collected within the Data Collection Framework (DCF) set out in Regulation (EU) 2017/1004.

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Monitoring environmental changes with old collections and field data: a case study in Verona

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Short summary: This abstract presents the results of the comparison between historical data obtained from *Orchidaceae* specimens in the herbarium VER collected across the province of Verona and field data from recent times. The study focus on highlighting the effects of the climate and land-use changes on the examined species.

Keywords: *Orchidaceae*, Herbarium, Historical collection, Biodiversity changes, Province of Verona

I. BACKGROUND

The Veronese territory has a long tradition of floristic investigations and has wide variety of habitat, from the Po Valley to the mountain range of Mount Baldo. All this allows to compare the historical situation with the current one. The choice of the taxonomic group to be examined fell on the *Orchidaceae* given that the specimens in the herbarium of Verona (VER) belonging to this family were entirely digitized. Furthermore, it is a sensitive group to environmental variations and deeply observed to this date. In addition to the herbarium data, around 12.000 field records observed by Associazione GIROS Sezione Monte Baldo and Natural History Museum of Verona are evaluated.

MATERIALS AND METHODS

During this study, specimens in the general herbarium (VER) from the middle of the nineteenth century onwards, were digitised and georeferenced. The beginning of the recent period corresponds with the launch of the field surveys made by the Botanical Department of the Museum. The majority of the recent records was provided by GIROS Sezione Monte Baldo archive; these records were noted on the field through GPS with punctual coordinates.

The province of Verona was divided into geographical areas following Bianchini and Di Carlo [1], simplifying the zones corresponding with Mount Baldo and Lessinia.

For each area, it was made a comparison between the *taxa* distribution during historical times and its current state.

II. RESULTS

The data extracted from the general herbarium (VER) comprise 895 specimens belonging to 63 different *taxa* of *Orchidaceae* collected in the province of Verona. The analysis of these records highlighted the presence of 502 historical specimens (period 1800 - 1960) and 393 recent ones (period 1961 - 2024). As shown in Fig. 1, the historical data are gathered in the sites located on the Mount Baldo and Lessinia, while the plain zones are less represented. As for the recent specimens, they're also situated on the mountains but what stands out is the lack of data in the lowlands.

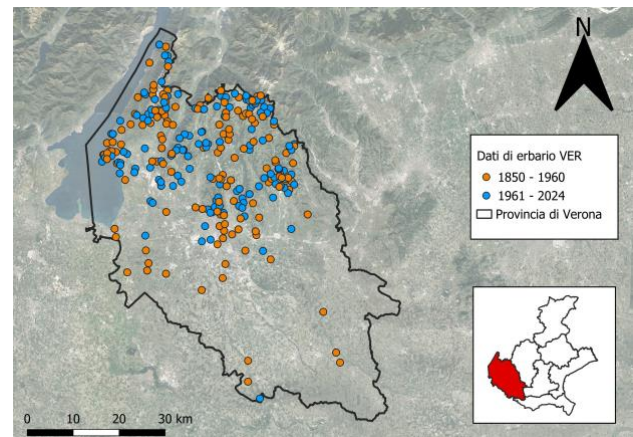


Fig. 1. This figure shows the data obtained from the specimens of the general herbarium (VER) regarding the province of Verona. Orange dots indicate orchids collected during the historical period, while light blue ones those gathered in recent times.

III. DISCUSSION AND MAIN CONCLUSIONS

The distribution of the recent herbarium specimens shows the decrease of plain species during the last decades, compared to the identified historical period. This is likely due to heavy land-use change resulting from intense anthropization in the Po Valley.

Studies on further implications of contemporary biodiversity changes will be performed using additional data provided by Sezione Monte Baldo of GIROS. A detailed comparison will be conducted to evaluate the variation in terms of number of species regarding each geographical area of Verona. Additionally, the elevation of each record will be examined in order to inspect the possibility of an altitude shift in response to the ongoing changes. The detailed analysis of the state of conservation of orchids once present in the lowlands, focusing on their habitat suitability, will instead allow to examine which habitat underwent the most significant modifications after the intense increase of anthropization of the Veronese plain.

ACKNOWLEDGMENT

We are grateful to Associazione GIROS Sezione Monte Baldo for the provided data and the cooperation.

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Sudden expansion of the Blue Crab (*Callinectes sapidus*) in the Northern Adriatic Sea

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Short summary: The Blue crab is an invasive species in the Adriatic Sea whose first occurrence in the SoleMon beam-trawl survey was in 2020. Three years later the Blue crab was caught in hundreds of specimens. We provide some data exploration to show the remarkable expansion of this species, along with some insights on its relationship with salinity.

Keywords: Blue crab, Invasive species, Machine learning, Spatial expansion, Adriatic Sea

I. BACKGROUND

The Blue crab (*Callinectes sapidus* Rathbun, 1896) is an invasive species in the Adriatic Sea [1]; it is a voracious predator that menaces the resilience of the food web. SoleMon survey recorded its first occurrence in 2020. As for 2023 the Blue crab shows an exponential increase in density and area occupied.

MATERIALS AND METHODS

Relative abundance and biomass data used for the present analysis were collected from the SoleMon beam-trawl survey. For each year, the Carapax Length (CL) and individual weight (W) of Blue crabs were measured. Linear regressions of $\log(LC) - \log(W)$ were calculated for each year. Data on relative biomass were fitted into a Random Forest model [2], where biomass was the response variable and bathymetry, granulometry, sea bottom temperature and salinity were the predictors (data from remote sensing obtained through the Copernicus database). The model result was used to explore the relationship between the response variable and each predictor. Gridded predictions were further analyzed to extract the density contours of the 95th percentile of the annual spatial distribution.

II. RESULTS

The length, weight, and number of specimens along with density and biomass indices of blue crab captured during the 4-year survey period considered (2020-2023) are presented in Tab. I. Linear regressions, revealing a parameter $b \neq 3$, confirmed the allometric growth as previously documented in the literature.

TABLE I. MEAN (\pm SD) AND NUMBER OF THE SPECIMENS CAPTURED IN DIFFERENT YEARS.

Year	LC	W (g)	N	N/km ²	Kg/km ²
2020	60 \pm 2.8	180 \pm 48.1	2	0.993854	0.178894
2021	58	113	1	0.527265	0.059581
2022	67.5 \pm 7.7	168 \pm 65.5	15	10.5897	1.899087
2023	63.7 \pm 5.8	150 \pm 42.8	1509	762.1848	260.748

Salinity was the most important variable contributing to predicting the blue crab biomass. The response to salinity changed over the years (Fig. 1.B). The spatial analysis (Fig. 1.A) shows an expansion of the occupied in the year 2023, extending far offshore.

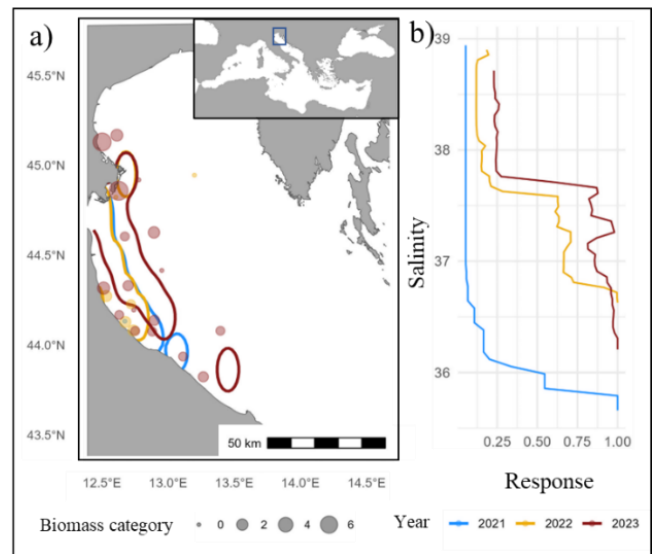


Fig. 1. A) spatial distribution of Blue crab individuals collected from the Solemon data (bubbles) and density contours of the 95th percentile of biomass predictions from the Random forest model; 1.B) response of biomass to salinity over the years.

III. DISCUSSION AND MAIN CONCLUSIONS

The overall impact of a non-indigenous species depends on its distribution, abundance, and ecological effect [3]. In the northern Adriatic Sea, the abundance of Blue crab increased in recent years [3] and its range has significantly expanded outside from brackish environment to offshore areas with higher salinity. Further monitoring will allow to understand if the 2023 outbreak was an occasional boom or the beginning of a stable colonization of the offshore areas in the Northern Adriatic Sea.

ACKNOWLEDGMENT

We are grateful to all the Solemon team.

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Finding Pinna: a survey to investigate the presence of surviving fan mussel along the Apulian coast

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Short summary: To spot fan shell (*Pinna nobilis*), a species facing a mass mortality event in the Mediterranean Sea, was the aim of the survey conducted along Ionian Apulian coast. Sixty-seven specimens, most of which of a medium size class, were detected and all of them were dead, confirming the dramatic scenario already previously observed.

Keywords: *Pinna nobilis*, Mass mortality, Mediterranean Sea, Apulian coast, Monitoring

I. BACKGROUND

The fan mussel *Pinna nobilis* is a Mediterranean endemic marine species (Bivalvia, Mollusca) inhabiting *Posidonia oceanica* meadows and hard bottoms up to 60 m depth. Since 2016, this species is experiencing a mass mortality event affecting the populations all around the Mediterranean Sea, leading to its inclusion in the IUCN's red list of endangered species. As reported by Scarpa et al. [1], the etiological agents likely involved in this phenomenon were different, suggesting a multifactorial disease. In summer 2018, populations of fan mussels inhabiting the Gulf of Taranto were interested by the mass mortality, mainly related to infection by *Haplosporidium pinnae* [2]. In the frame of monitoring this endangered species, with the financial support of Apulian Region, we aimed to investigate the bottom of a stretch of Ionian Apulian coasts in order to find *P. nobilis* individuals.

MATERIALS AND METHODS

In Autumn 2023, SCUBA divers equipped with underwater scooters, investigated linear transects (200-300 m long) at the depths of 5, 15 and 25 m at each station, except at "Secca dell'Armeleia" where only two transect at 15 m depth were conducted (Fig. 1). Along the transects, tracked with a GPS mounted on a buoy, divers performed *visual census* to detect the presence and the number of specimens of living or dead *P. nobilis*, (fragments of shells were not considered in the count). The nature of the substrates observed during the scuba activities was logged.

II. RESULTS

The total distance travelled was 15,705 m. A total of 67 fan mussels were spotted, all of them were dead. No individual was observed at 5 m depth at all sites. Dead specimens were detected mainly on coralligenous substrates and *P. oceanica* meadows. Only for 19 shells was possible to measure the total length, because many others, even though were not fragments, had the anterior or posterior part damaged. The highest number of dead fan mussels ($n = 18$) was observed at Torre Zozzoli, whereas at San Pietro Island, the site nearest to Taranto, no individuals were recorded

III. DISCUSSION AND MAIN CONCLUSIONS

The detection in the present study of only dead individuals confirms the mortality rate at 100% already reported in 2020 along the entire Apulian coast [3]. Even though the methodology used was very similar, our

observations were carried out with a higher spatial sampling resolution and, despite the adoption of much shorter transects, i.e., a lower sampling effort, the results were comparable. In fact, the number of shells found at "Lido Azzurro" and "San Vito" by Pensa et al. [3] was very close to that we found at the same localities; however, we found more dead individuals at "Torre Ovo", whereas we did not observe shells at San Pietro Island (the station 2 in the present study) where they observed 7 shells.

We might conclude as follows: i. the reported mortality rates of *P. nobilis* would appear to rule out the hypothesis of finding any living specimen; ii. the adoption of shorter transects compared to [3], have the same effectiveness, allowing to increase the survey spatial resolution.

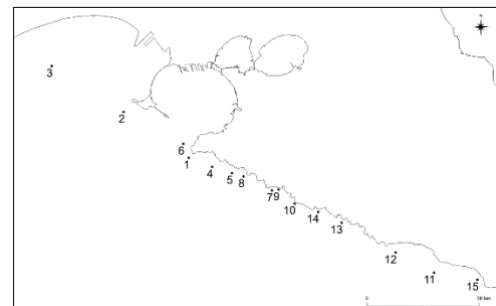


Fig. 1. Sites investigated to detect the presence of *P. nobilis* individuals. According to the numeration: 1. San Vito, 2. San Pietro Island, 3. Secca dell'Armeleia, 4. Lido Bruno, 5. Lama, 6. San Vito, 7. Mon Reve, 8. Saint Bon, 9. Lido Gandoli, 10. Saturo, 11. Le Conche, 12. Torre Zozzoli, 13. Monte d'Arena, 14. Baia d'Argento, 15. Torre Ovo.

ACKNOWLEDGMENT

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Scyphophorus acupunctatus in the Mediterranean area: distribution and phylogeography

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Short summary: The study investigates the global distribution and genetic diversity of the agave weevil *Scyphophorus acupunctatus*, a non-native invasive species that is potentially spreading worldwide. Although native to Central and North America, it is now widely distributed across the continents and poses a threat to biodiversity. The analysis emphasises the importance of understanding the origin and monitoring of invasive species to mitigate their impact on native biodiversity.

Keywords: *Agave*, Mitochondrial COXI gene, Non-native invasive insects, Population genetics

I. BACKGROUND

Crop pests are widespread worldwide, having been accidentally introduced through the intensive trade in commodities, including ornamental and crop. Curculionid coleopterans are an important threat to many cultivated species. Among those, the genus *Scyphophorus* (Coleoptera, Dryophthoridae) is one of the most widespread. This weevil is native to southern North America, Mexico and other Central American countries [1], although it has been worldwide introduced. The agave weevil is an important pest of several agave genera and species. The classification of the genus *Scyphophorus* remains controversial [2]. Currently, there are two recognised species, *S. acupunctatus* and *S. yuccae*, with no reliable information on their phylogeography. Assessing the geographical origin of non-native populations of *S. acupunctatus* may provide information for the control of plant trade and prevent new invasions. The objectives of our work were: (i) to update the distribution of the agave weevil in non-native areas with special reference to Mediterranean countries and (ii) to evaluate the phylogeographic pattern of *S. acupunctatus* and determine the origin of European populations.

MATERIALS AND METHODS

The distribution of the agave weevil in its non-native range was updated by searching for published and unpublished records in the grey and scientific literature and online databases, including citizen-science records validated by experts. Further searches were performed with photos on Social Networks and video-sharing websites. A total of 36 individual samples of *S. acupunctatus* were collected in Europe and preserved in 95% ethanol at -20 °C, before genetic analyses. Genomic DNA from all samples was extracted using QIAGEN Blood and Tissue kit, following the manufacturer's protocol. A fragment of the mitochondrial DNA Cytochrome Oxidase I (COXI) was amplified and compared with sequences deposited in the GenBank. COXI was amplified using the primers LCO1490 and HCO2198. These primers were previously used to amplify the same gene in *S. acupunctatus* from Central America for species-identification purposes.

II. RESULTS

The agave weevil was reported on all continents, except for Antarctica. Based on genetic analyses and literature, the native range of this species includes the USA, Mexico and, most likely, the rest of continental Central America. The invasive Mediterranean range of this species includes several southern European countries including Portugal, Spain, Italy, Greece and several islands such as Sardinia, Sicily, Croatian islands and Cyprus. The COXI sequences were obtained from all analysed samples. The alignment of COXI gene consists of 627–903 nucleotides for 65 individuals, including 32 from the Mediterranean area. All individuals belonged to *S. acupunctatus*, as no record of *S. yuccae* was confirmed in the analysed samples nor in any sequence deposited in the GenBank. The TCS network highlighted that the majority of introduced individuals in Italy, France, Spain and Portugal belonged to the same haplotype as in Costa Rica and Guatemala.

III. DISCUSSION AND MAIN CONCLUSIONS

This study provides the first comprehensive assessment of the global distribution of the agave weevil, examining both native and non-native ranges and assessing worldwide phylogenetic relationships. Confirmations of the species were made in several southern European countries. Genetic analyses revealed notable genetic uniformity in non-native populations, with lower nucleotide and haplotype diversity observed compared to native populations, potentially attributable to founder effects. The prevalence of a single widespread haplotype in Europe suggests either limited introduction events or a concentrated origin in Central America.

ACKNOWLEDGMENT

This work was supported by CNR through the project USEit - Utilizzo di sinergie operative per lo studio e la gestione integrata di specie aliene invasive in Italia.

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Habitat suitability widening of the Egyptian sole in the Adriatic Sea

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Short summary: The habitat suitability of the Egyptian sole in the Adriatic Sea was modeled using SoleMon survey data, along with seven environmental predictors. The ensemble model approach revealed that chlorophyll concentration, bottom temperature and grain size were the main drivers. The map of occurrence probability highlighted a widening of the species from 2011 to 2023.

Keywords: Habitat suitability, Sole, Adriatic Sea, Survey, Species distribution model

I. BACKGROUND

The spatial distribution of the Egyptian sole (*Solea aegyptiaca* Chabanaud, 1927), a cryptic and sympatric species with common sole, has been seldom investigated in the Adriatic Sea, where very few records were reported [1]. The present work aimed to study the potential habitat use of this rare species.

MATERIALS AND METHODS

Four modeling techniques were fitted in “biomod2” package in R [2] including two regression models, GAM and GLM, and two machine learning models, RF and GBM, in an ensemble model approach. Presence/absence data coming from SoleMon surveys (2011-2023) were used as response variables, while a set of seven environmental predictors were employed as explanatory variables. The predictive performance of each model was validated by True Skill Statistics (TSS). The best ensemble model was used to project present and past habitat suitability maps. Due to the scarcity of some environmental data in the southeastern part, only the SoleMon study area was considered.

II. RESULTS

a. Ensemble model results

The best ensemble model performance was obtained with the three explanatory variables listed in Tab. I. Favorable habitat for Egyptian sole was characterized by chlorophyll values higher than 0.8 mg m^{-3} , bottom temperature higher than $19 \text{ }^\circ\text{C}$, and sands or very fine silt.

TABLE I. VARIABLE IMPORTANCE (%) FOR EACH MODEL CONSIDERED

Predictors	Models			
	GAM	GLM	GBM	RF
BT	38	25	40	30
CHL	58	48	66	20
GS	54	33	19	21

* Bottom Temperature (BT; $^\circ\text{C}$), Chlorophyll Concentration (CHL; mg m^{-3}) Grain Size (GS; phi).

b. Ensemble model projections

The overall suitable areas of the Egyptian sole were concentrated in the north-western coastal waters. The comparison between past and present prediction of habitat suitability map revealed a spreading of the species during the last 13 years (Fig. 1).

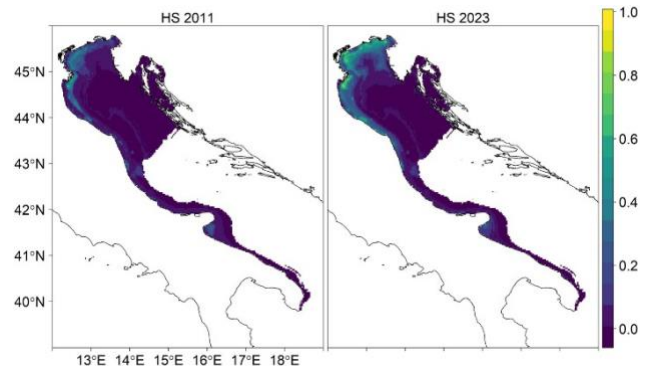


Fig. 1 Egyptian sole probability of occurrence in 2011 and 2023.

III. DISCUSSION AND MAIN CONCLUSIONS

Egyptian sole is mostly found in sandy-muddy bottoms in coastal marine and brackish waters [3]. This study showed a higher probability to find the species in eutrophic and warmer waters, which characterized inshore north-western Adriatic areas. The preference for the two kind of sediments could be explained by a change of needs during the growth. Ontogenetic spatial separation was observed, with juveniles concentrated on muddy sediments around the Po River mouth, while the adults gathered on sandy sediments (unpublished data). The application of species distribution models provided the possibility to assess the population dynamics along the time series. An increase of the suitability area was predicted during the last year. Therefore, we could hypothesize that the current sea temperature raising may positively affect the species, as also observed in the abundance data estimated from the SoleMon survey.

ACKNOWLEDGMENT

We are grateful to the SoleMon survey, carried out with the financial support of the Italian Ministry of Agriculture (MIPAAF) within the Data Collection Framework set out in Regulation (EU) 2017/1004 and multiannual programme EU MAP.

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Dynamics of microbiome colonization on artificial support in a natural gradient of water pH at Panarea Island (Italy)

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Short summary: This study investigates the dynamics of microbiome colonization on artificial support in a natural gradient of water pH at Panarea Island, Italy. Our focus looks at the influence of the acidification on benthonic invertebrates in the Mediterranean Sea and the study of the microbiome dynamics and composition of the artificial supports.

Keywords: Artificial supports, Microbiome, Core, Pioneer microorganisms

I. BACKGROUND

A naturally occurring CO₂ vent is located at a depth of 10 meters in Panarea island and it naturally acidifies seawater. For this study, three sites have been selected, corresponding to the pH scenarios of the IPCC, which predict that acidification will rise from 8.07 to 7.74 by the year 2100 [1]. In this context, some artificial nylon supports have been implanted to examine the microbial composition and colonization dynamics of these artificial supports as well as the settlement of benthic species, corals, and molluscs.

MATERIALS AND METHODS

Part of the artificial supports were sampled at 5 different timepoints, together with 1 sample of seawater (Fig. 1). DNA extraction, PCR amplification, library preparation were performed for 16S rRNA metabarcoding. Sequences were analysed for taxonomic and phylogenetic assignment; statistics and graphical representation were performed using R software.

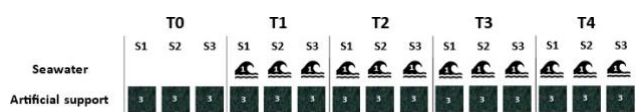


Fig. 1. Sampling scheme. T0= 48h after implantation, T1= 2 weeks after implantation, T2= 2 months after implantation, T3= 6-7 months after implantation, T4= 1 year after implantation.

II. RESULTS

By studying the dynamics of the microbial colonization, we observed a stabilization of the trend after the second sampling time. For this reason, we decided to focus on the first period to investigate the colonizer pioneer microorganisms. We identified 4 distinct groups, core and site-specific colonizer, i.e. microorganisms shared among all the sites and specifically colonizing each site, at 2 days and 2 weeks after implantation. In order to figure out the most important pioneer microorganisms as colonizer of the artificial supports, four different classes of microorganisms were considered: i) core early colonizers, as

microorganisms being able to colonize the artificial support at each site at T0; ii) site-specific early colonizers, as microorganisms specifically colonizing each site at T0; iii) core late colonizers, as microorganisms being able to colonize the artificial support at each site at T1, and iv) site-specific late colonizers, as microorganisms specifically colonizing each site at T1. According to our data, no microorganisms belonging to the first class were detected, while *Neptuniibacter* was the only microorganism belonging to the second group, being specific for Site 1. *Pirellulaceae*; *Pir4* lineage, *Haloferula*, *Filomicrobium*, *Blastopirellula*, *Woeseia* all belonged to the third group. No microorganisms belonging to the fourth group were detected.

Despite not being a core microorganism, *Sulfurovum* was identified as early colonizer, being present at S2 and S3.

III. DISCUSSION AND MAIN CONCLUSIONS

In order to describe the early colonization process, we focused on compositional dynamics of microbial communities between 2 days and 2 weeks of observation. According to our findings, early colonizers – being capable to colonize the artificial substrate after 2 days – were site specific, with *Neptuniibacter* characterizing site 1 (pH 8.07) and *Sulfurovum* characterizing sites 2 and 3 (pH 7.87 and 7.74, respectively). Conversely, after 2 weeks, the microbial communities at each sites converged, acquiring of a set of 5 core genera, mainly *Pirellulaceae*, *Pir4* lineage, *Haloferula*, *Filomicrobium*, *Blastopirellula*, and *Woeseia*, possibly keystone components for the communities stabilization.

ACKNOWLEDGMENT

We are grateful to the IEEE Computational Intelligence Society and to the Mediterranean Science Commission CIESM, which inspired the design of the current word template.

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The terrestrial macroinvertebrates of a guano-rich temperate cave – a system especially vulnerable to climate change?

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Short summary: Guano-rich caves in temperate regions host rich subterranean communities. These systems, by depending on bat guano as a key resource, may be especially sensitive to climate change.

Keywords: Guano, Invertebrates, Alpha diversity, Bats, barcoding; Conservation

I. BACKGROUND

Caves are characterized by pronounced environmental stability in abiotic conditions, including permanent darkness and the consequent lack of primary productivity. Hence, most caves depend on organic inputs from the outside, which are often scarce in temperate regions. As a consequence, temperate caves usually present low diversity and abundance of terrestrial macroinvertebrates [1]. An important exception to this trend is represented by caves hosting abundant populations of bats, where bat guano represents an important source of organic matter [2]. However, large bat colonies are rare in temperate regions, and hence this type of caves is poorly understood from an ecological viewpoint. We aimed to characterize the terrestrial macroinvertebrate assemblage inhabiting a temperate guano-rich cave and to investigate the relationship between environmental variables and structural changes in alpha diversity of the assemblage.

MATERIALS AND METHODS

We collected one year of standardized data on the macroinvertebrate assemblage occurring in the Buca dei Ladri (Tuscany, Italy), a guano-rich cave. We identified species using both morphological characters and molecular data (mitochondrial COI and nuclear 18S genes). We monitored macroinvertebrates through monthly non-invasive visual sampling in 30 sampling plots (1 m²) haphazardly distributed across the cave. In each sampling plot, we recorded the abundance of species and the main biotic and abiotic independent variables (temperature, temperature range, substrate complexity, presence of bats, dominant substrate). We modeled the association between independent variables and species diversity through linear mixed models.

II. RESULTS

We retrieved 31 species of macroinvertebrates in the cave, of which 21 occurred in the sampling plots. Species diversity was positively associated with higher substrate complexity and the presence of bats, while it was negatively associated with a guano substrate towards mud or soil substrates (Fig. 1).

III. DISCUSSION AND MAIN CONCLUSIONS

We recovered clear relationships between species diversity and the abiotic conditions of the cave (Fig. 1). The apparently conflicting negative association with a guano

substrate can be explained by the old age and subsequent low nutritional value of the historical guano deposits [2]. Collecting standardized data about poorly-studied subterranean communities is especially important in light of climate change. We speculate that these assemblages, being linked to the presence of bat guano, are particularly vulnerable to climate change. Bats make a selection based on the microclimate within roosting sites to minimize climate change adverse effects, so their distribution is likely to be changing [3]. Research on caves requires the technical support of many speleologists but, at the same time, the involvement of people also spreads a culture of knowledge and respect for the environment, thus supporting biodiversity conservation.

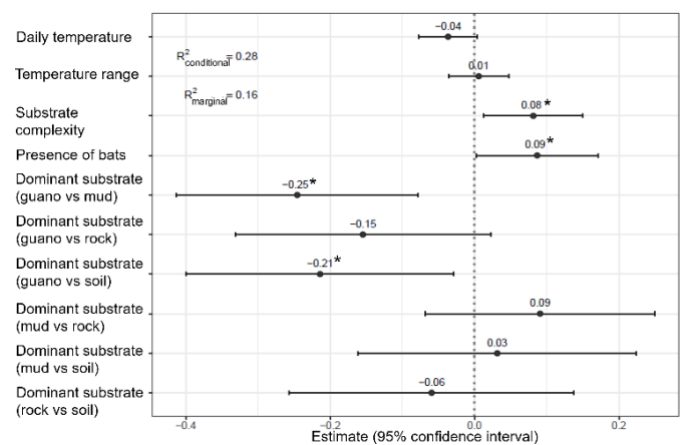


Fig. 1. Relationships between species diversity and the abiotic conditions of the cave according to a linear mixed model. Asterisk (*) highlights significant effects ($p < 0.05$).

ACKNOWLEDGMENT

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A new pine forest to save biodiversity

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Short summary: In recent years, due to climate-related environmental changes, large areas of *Pinus pinea* (L.) forest have been continuously exposed to damage by parasites, which have reduced their vigour to the point of favouring the collapse of multiple stone pine coastal forest communities.

Keywords: *Pinus pinea*, *Toumeyella parvicornis*, Remote sensing, GIS

I. BACKGROUND

Over time, due to their intrinsic habitat characteristics and the extraordinary position between protected sites and wet areas, the pine forest communities have taken on important functions ranging from the more strictly ecological-environmental to the social and economic one. In Italy, for some years, stone pine (*Pinus pinea* L.) coastal forests have been at risk of conservation due to biological adversities [1]. In particular, in 2014, the presence of the cochineal *Toumeyella parvicornis* (Cockerell, 1897) within some urban areas [2] and in various stone pine forests of Campania Region, was ascertained. The invasion by alien species is the primary factors leading to biodiversity loss [3]. Monitoring the state of the vegetation using remote sensing has highlighted the usefulness of this technique for preserving the biodiversity of the pine forest ecosystems, peculiar resource of the Mediterranean coastal belts.

MATERIALS AND METHODS

The analysis of multi-spectral images of the Copernicus Sentinel-2 satellite, was conducted on the Domitio coast Stone Pine forest, to study the spectral variation and eventually identify conditions of plant stress due to the action of pest *T. parvicornis*. In fact, in the infested trees, the insect causes a progressive yellowing of the foliage, drying out, loss of most of the needles and severe decay which, in the most susceptible pines, can even lead to the death of the plant within a few years. The use of four vegetation indices (NDVI, NDRE, NDMI, NBR) has made possible to highlight the degradation suffered by the vegetation due to infestation pest.

II. RESULTS

The results of the spectral vegetation indices (SVI) analysis combined with the field survey gave a first indication of the vegetation's response at short- and long-time intervals to the *T. parvicornis* attack.

The study showed that SVIs provide for general information on the phenological state of the canopy when a phenomenon (such as parasitic activity) able to reduce plants photosynthetic activity, is in progress. Furthermore, in terms of temporal characteristics, the study showed that it is sufficient to use even a single image per year with comparable dates, to differentiate healthy areas from wilted ones (Fig. 1).



Fig. 1. Satellite images of a sector of the study area. The images taken in 2016 (A) and 2022 (B) are compared; they allow us to make a quick visual comparison on the state of decline of the pine forest.

II. DISCUSSION AND MAIN CONCLUSIONS

In the original naturalized pine forest, the pines were associated with holm oak and with evergreen sclerophylls low scrub. The result was a mixed, stratified, uneven forest formation, which had found its own balance, giving rise to a multifaceted environment appreciated for its landscape value. All this has been lost due to incorrect silvicultural interventions and forestry policies slowly implemented or mostly absent. With the arrival and spread of parasites atypical for Mediterranean environments, a consistent part of Stone Pine forests has been degraded and locally destroyed in a few years. Of the original 400 hectares of pine forest, distributed along the coast for approximately 13 km, more than half is now completely degraded. From a long-term perspective, forest management policies should emphasize actions to reduce monospecific with the reintroduction of native forest species to mitigate parasites vulnerability and to increase biodiversity.

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Penaeus aztecus (Ives, 1891) spreads Northward, but still rare along the west side of the Adriatic Sea

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Short summary: *Penaeus aztecus*, native of the West Atlantic Ocean, has been reported several times in the Mediterranean Sea. It could compete with the autochthonous *P. kerathurus*. However, from SoleMon survey data, it is possible to notice that in the Adriatic Sea its abundance is still very low with respect to the native species.

Keywords: *Penaeus aztecus*, *Penaeus kerathurus*, invasive alien species, SoleMon survey

I. BACKGROUND

The “brown shrimp” *Penaeus aztecus*, native to the north-western Atlantic and Gulf of Mexico, was initially documented in the eastern Mediterranean Sea (Antalya Bay, Turkey) in 2010, and within an amazingly short period it has been recorded from many sites across the basin; arriving in 2013 in the Adriatic Sea. Larvae/postlarvae were likely introduced in the basin via the ballast water of transoceanic vessels [1, 2], which in general, facilitate the spread of plankton and larval stages of benthic species beyond their native ranges. The accidental introduction of invasive alien species into marine environments due to maritime activities is a global issue.

MATERIALS AND METHODS

Since 2016, photos of distinctive characteristics of the *P. aztecus* have been produced and circulated among professional fishers and fish markets, along the Italian Adriatic coast. When authors received shrimp specimens they were stored in 80% ethanol. To estimate the comparative prevalence of this species to the native homologous *P. kerathurus* in the Northern and Central Adriatic Sea (GSA 17), SoleMon survey data from 2016 onwards were analyzed. It is a “rapido” beam trawl survey conducted in the area in the fall season, to evaluate the abundance of flatfish stocks and commercial invertebrates. Approximately 60 stations are monitored every year; in each station, penaeid shrimps are identified by species, sexed, counted, and measured. In addition, a literature scrutiny was performed to detect all the Mediterranean records for this species.

II. RESULTS

In 2023, as in the previous year, no *P. aztecus* were found during the survey. But on the 9th October 2023, the authors obtained 2 shrimps found in the catch auctioned in the Cesenatico fish gross-market, by the local commercial bottom trawlers fishing around 6-8 nautical miles off shore. They were examined and identified as adult *P. aztecus* based on a set of morphological characters [2]. Both specimens were females of 35.5 and 45.8 mm of carapax length respectively. The compilation of all the records in the basin (Fig. 1) indicates a swift colonization process. This is why the species has also been nicknamed “Atlantic sprinter” [3]. However, from SoleMon survey data (Tab. I) it is evident that the abundance of the species in GSA17 is still very low compared to *P. kerathurus*.

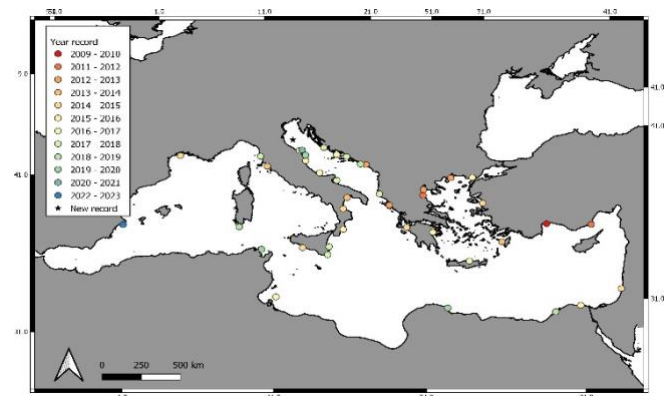


Fig. 1. Record locations of *P. aztecus* in the Mediterranean Sea (based on literature until 2023), plus the new record (star).

TABLE I. ABUNDANCE OF *P. KERATHURUS* AND *P. AZTECUS* SAMPLED BY THE FISHERY SURVEY “SOLEMON” IN THE YEARS 2016–2022.

Year	Sampled Stations*	Station positive for <i>Penaeus</i> *	<i>P. kerathurus</i> *	<i>P. aztecus</i> *
2016	74	50	1183	0
2017	70	51	1594	0
2018	68	53	2216	0
2019	68	53	1940	0
2020	58	43	932	1
2021	63	41	1062	1
2022	50	33	818	0

*Numbers

III. DISCUSSION AND MAIN CONCLUSIONS

The specimens from Cesenatico, 80 km North from previous northernmost Adriatic record, are also the northernmost record in the Mediterranean. The interplay between local climatic conditions and fishing activities targeting these valuable resources, will ultimately determine the relative abundance of each species, likely without significant alterations in ecosystem dynamics [2].

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Invasive alien arthropod species recently arrived in EU: case study at Hanbury Botanic Gardens

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Short summary: Hanbury Botanic Gardens (HBGs) represent one of the regional observatory centers of the invasive alien species (IAS) warning network in Liguria; 11 invasive alien arthropods are now present in the Gardens. Their arrival caused a loss of biological resources diversity. HBGs are committed to researching to rise integrated pest management plans that will preserve biodiversity and prevent harm and spread of alien species.

Keywords: Invasive alien species, pest, globalization, biodiversity loss, integrated pest management

I. BACKGROUND

In the Anthropocene era we are witnessing a progressive increase in trade, transport, travel, and tourism, the four pillars of globalization, which represent the main channels for the introduction of invasive alien species (IAS). They are today considered one of the main causes of biodiversity loss and species extinction [1]. This study reports the example of the Regional Protected Area and Special Area of Conservation (SAC) of the Hanbury Botanic Gardens (HBGs), as one of the regional observatory centres of the IAS warning network in Liguria.

MATERIALS AND METHODS

Invasive alien arthropod species reporting is made possible by biodiversity monitoring using pitfall and pan traps set up in the Protected Area and by visual inspections of the host plants.

II. RESULTS

Monitoring data from the 80s to today have shown the presence of 11 alien arthropods, most of Asian origin. Pests of both exotic and native plants.

TABLE I. INVASIVE ALIEN PEST IN HANBURY BOTANIC GARDENS

Invasive alien arthropod in the Hanbury Botanic Gardens			
Pest	Year of 1 st observation	Native area	Host plants
<i>Aonidiella aurantii</i> Maskell, 1879 (Hemiptera)	before 1980	Asia	Citrus spp.
<i>Unaspis yanonensis</i> Kuwana, 1923 (Hemiptera)	1987	Asia	Citrus spp.
<i>Aceria aloinis</i> Keifer, 1941 (Trombidiformes)	2003	Africa	<i>Aloe</i> spp.
<i>Cydalima perspectalis</i> Walker, 1859 (Lepidoptera)	2013	Asia	<i>Buxus</i> spp.
<i>Vespa velutina</i> Lepeletier, 1836 <i>nigrithorax</i> Buysson, 1905 (Hymenoptera)	2013	Asia	/
<i>Paysandisia archon</i> Burmeister, 1880 (Lepidoptera)	2014	South America	Arecaceae
<i>Rhynchophorus ferrugineus</i> Olivier, 1790 (Coleoptera)	2014	Asia	Arecaceae
<i>Aloephagus myersi</i> Essig, 1950 (Hemiptera)	before 2015	Africa	<i>Aloe</i> spp.
<i>Scyphophorus acupunctatus</i> Gyllenhal, 1838 (Coleoptera)	2018	Central America	Agavaceae
<i>Xylosandrus compactus</i> Eichhoff, 1875 (Coleoptera)	2022	Asia	Woody plants
<i>Xylosandrus crassiusculus</i> Motschulsky, 1866 (Coleoptera)	2022	Asia	Woody plants

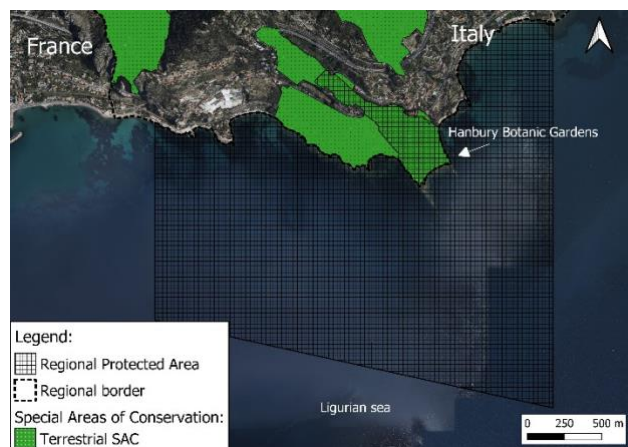


Fig. 1. Regional Protected Area and Special Area of Conservation of Hanbury Botanic Gardens. Strategic point for IAS reporting.

III. DISCUSSION AND MAIN CONCLUSIONS

Biodiversity monitoring and visual inspections are good tools for identifying IAS. Following their arrivals, HBGs invest in research to develop integrated pest management strategies that are helpful in preventing the spread of the species in nearby areas by monitoring, biological controls, and modifications of cultural practices. In addition to significantly reducing the diversity of botanical collections and, consequently, biological resources, the introduction of these arthropods has led to changes in the management of sites. Arthropods invasions are perhaps the most pervasive, underappreciated component of challenges to global development and prosperity, particularly to human health, food, clean water, resilient environments, and sustainable economies [2]. Development of sustainable IAS control methods in protected areas becomes a necessity for biodiversity conservation and global development.

ACKNOWLEDGMENT

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One hundred years of solitude: the European adder in Trentino

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Short summary: *Vipera berus* is typically associated with mountain environments. Distribution data up to 1912 were compared with recent observations (2000-2020), revealing past occurrences even at low altitudes where the species is currently absent. The presumed causes for this shift are habitat destruction and alteration due to increased human presence, as well as rising temperatures attributed to climate change.

Keywords: Species distribution, Climate change, Habitat alteration, European adder

I. BACKGROUND

Under the influence of climate change, species can shift their ranges toward higher latitudes and/or altitudes in search of suitable climatic conditions to which they are adapted.

MATERIALS AND METHODS

The historical distribution was obtained by mapping data reported by few naturalists of the 19th century but most significantly by Dalla Torre [1] who provides a comprehensive and detailed overview of the presence of the European adder in Trentino. These data were then compared to those collected for the project "Amphibians and Reptiles of Trentino" (2017-2024). The territory was divided into 10x10 km grid cells to compare the number and spatial distribution of both data sources.

II. RESULTS

For the historical distribution of *V. berus* (until 1912), 199 occurrence sites were mapped (Fig.1), covering 48% grid squares. The current distribution confirms the presence in all the main mountain complexes of the province (Fig.2), occupying 47.7% grid squares. Presently, there is a noticeable preference in altitudinal distribution, with a concentration between 1500 and 2300 meters above sea level. Particularly, a distinct peak is observed between 1800 and 2100 meters, indicating a divergence from historical trends.

III. DISCUSSION AND MAIN CONCLUSIONS

The stark contrast between modern and historical reports underscores a significant gap, largely attributed to targeted studies in recent years and to the rise of Citizen Science. Assessing distributional disparities, the configuration of occupied cells stands out as a more reliable metric. A comparison between historical and recent data (Fig.1) reveals significant distribution differences. Two key aspects necessitate evaluation: the number of occupied cells by the species and their grid placement. Notably, there are 18 new cells without historical data and 19 historical cells without recent data. However, when excluding marginal cells, a marked contrast emerges: only 8 new non-marginal cells lack historical data, while 18 historical non-marginal cells lack recent data, indicating a doubling of data gaps. This suggests a significant reduction in the

species' distribution over a century when cells are used as the unit of measurement for the occupied area, amounting to a halving of its previous range. There is a substantial contraction in distribution, notably disappearing from main valley regions (particularly the Adige Valley) and lower altitudes (Fig.2), and the species now is predominantly confined to higher elevations (Fig.1). This shift likely results from habitat destruction in valley areas due to urbanization, reclamation, and intensive agriculture, alongside the impact of global climate change leading the species, adapted to cool and humid climates, to seek higher altitudes.

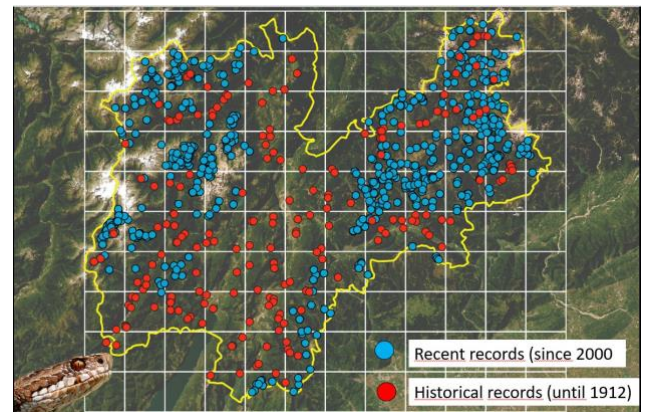


Fig. 1. Historical (until 1912) and recent (since 2000) distribution of European adder viper in Trentino with 10x10 km UTM grids.

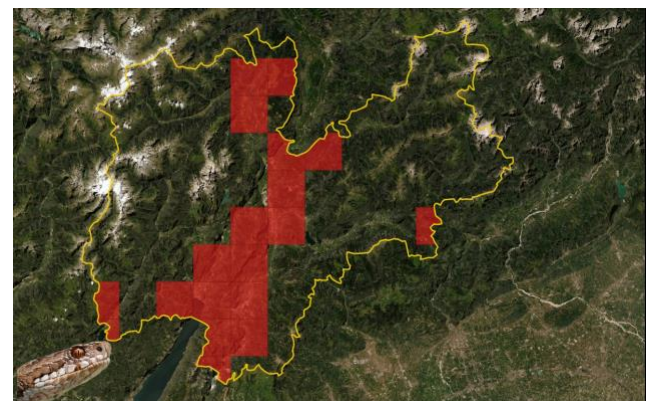


Fig. 2. Difference between 10x10 km UTM grids occupied by European adder viper until 1912 (historical data) not covered by recent data.

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New alien species associated to mussel and oyster farms in the Mediterranean.

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Short summary: This study highlighted a high diversity of assemblages associated with natural and aquaculture mussels and oysters and reported the presence of Non-Indigenous Species (NIS) never detected before in association with the mussel and Pacific oyster habitat in the Mediterranean.

Keywords: Mediterranean, *Mytilus galloprovincialis*, *Magallana gigas*, Non-indigenous species, Aquaculture

I. BACKGROUND

Mediterranean mussel, *Mytilus galloprovincialis* and Pacific oyster, *Magallana gigas* are two of the most important shellfish species farmed in the Mediterranean Sea. In addition to their economic value, the broader ecosystem benefits of these mollusks in coastal waters, including their role as ecosystem engineers, are increasingly recognized [1]. Aquaculture is one of the main vectors for the introduction and spread of non-indigenous species (NIS) in the Mediterranean Sea, which can lead to negative impacts on biodiversity and ecosystem goods and services. The aims of this research were to characterize the macrofaunal communities associated with *M. galloprovincialis* and *M. gigas*, in farmed and wild habitats in the northern Adriatic Sea with a focus on alien species.

MATERIALS AND METHODS

Mussels and oysters were collected along the coastline of the Emilia-Romagna region, from Goro to Cattolica, in May and October in farms and wild environments. For mussels three replicas were sampled at each farm and wild site and placed in 2-liter containers. For oysters, 3 replicas consisting of 5 oysters each, were sampled at each farm and wild site. The samples were sieved through two sieves of 2 mm and 0.5 mm and macrofaunal organisms were separated under the stereomicroscope, detaching also organisms attached to the shells. All specimens were identified to the lowest possible taxonomic level and counted.

II. RESULTS

A total of 149 invertebrate taxa belonging to 10 phyla were found associated with mussel clumps; of these, 36 taxa were reported for the first time associated with mussel in the Mediterranean. Regarding oyster-associated fauna a total of 103 invertebrate taxa were identified, of which only 38 taxa were known to be associated with farmed oysters. (Fig. 1).

Among the 149 taxa associated with mussels, 18 (12%) were NIS. For oysters, 18 of the total 103 taxa (17%) were non-indigenous species. Of the 18 NIS found in mussel clumps, 11 were found in farm environments, of which 5 had never been reported associated with *M. galloprovincialis* in the Mediterranean. As for oyster populations assemblages, all but one of the 18 alien species found, had never been reported in *M. gigas* habitats in the Mediterranean, 15 were found in farm environments. For the first time, the parasitism of *Gastrichaena dubia* [2] and the presence of two alien and pest species of the *Polydora* genus have been observed on the Pacific oyster [3].

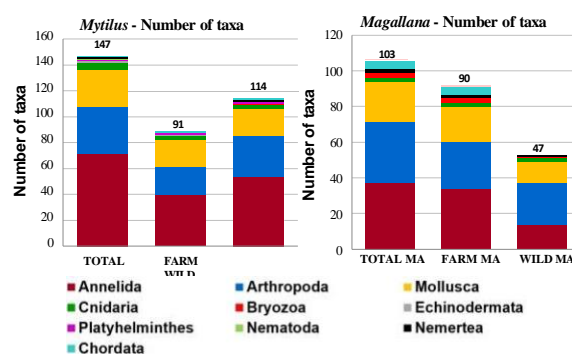


Fig. 1. Cumulative (including both sampling times) (A) total number of taxa and separately in Farm and Wild *M. gigas* population (B) total number of taxa and separately in Farm and Wild mussels' clumps.

IV. DISCUSSION AND MAIN CONCLUSIONS

The study observed a significant difference in diversity and structure of associated faunal assemblages between farmed and wild mollusks' habitats. Our results suggest not only that mussels and oysters play an important role in the spread of non-indigenous species, but also that exotic species contribute highly to the diversity of fauna associated with these natural and farmed environments in the Emilia-Romagna region, confirming the need for regular monitoring and increased research efforts in aquaculture.

ACKNOWLEDGMENT

This research was conducted within the project funded by the Emilia-Romagna Region call "Alte competenze per la ricerca e il trasferimento tecnologico" and finalized in the framework of the PhD project collaboration between University of Bologna (Department of Cultural Heritage, Ravenna) and M.A.R.E. soc. coop. a r. l. (Cattolica), in accordance with D.M. 352 of April 9, 2022, under the National Recovery and Resilience Plan (P.N.R.R.). We thank all the farmers for their support in the sampling.

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Impact of anthropogenic pathobiome on the gut microbiome of Mediterranean whales

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Short summary: The Mediterranean cetacean population is currently suffering from anthropogenic pressures resulting in their rise of gut pathobiome components.

Keywords: Cetacea, gut microbiome, 16S gene sequencing, Mediterranean Sea, Protozoan parasites, Anthropogenic stressors

I. BACKGROUND

According to their pivotal roles in marine ecosystems, cetaceans represent a valuable proxy of overall ocean health and a proper model for studying gut microbiome (GM)-host evolutionary drivers of symbiosis, considering the different feeding niches of mysticetes and odontocetes. Investigating the GM status and the distribution of pathogenic species in cetaceans could, thus, act as a key strategy to monitor the well-being of these species and of the habitats they thrive in. The Mediterranean Sea is one of the core areas for this research, since the increasing anthropic pressures along the coasts (e.g., from agriculture, animal farming, and human waste) and the aquaculture activities may enhance the rate of diseases in marine environments [1].

MATERIALS AND METHODS

The GM of 8 cetacean species were investigated through 16S rRNA analyses on both faecal samples collected in the Pelagos Sanctuary, Mediterranean Sea, and ones retrieved from literature. The DNA extraction and processing of collected samples was performed through QiaAMP DNA Stool Mini Kit (Qiagen, Hilden, Germany) and following the Illumina 16S Metagenomic Sequencing Library Preparation protocol (Illumina, San Diego, CA, USA). Parasitological analyses were performed on the collected samples searching for 3 protozoan parasites (*Blastocystis sp.*, *Giardia duodenalis* and *Cryptosporidium spp.*) through molecular and genetic characterization. Statistical analyses were performed using R software.

II. RESULTS

A. Cetacean gut microbiome profile and phylosymbiosis

Cetaceans GM differs significantly between mysticetes and odontocetes considering alpha and beta diversities, with higher microbial richness in mysticetes. The phylosymbiotic tree shows congruence between the GM diversity and the hosts' phylogenetic relationships in almost all cetacean taxa. The only weak signal was detected for the node that sees *Z. cavirostris* as sister taxon of all the other species, while the strongest phylosymbiotic signals in cetaceans can be found supporting all the sub-clades nested within the mysticetes.

B. Parasitological analyses in cetaceans

Considering collected samples (Fig. 1), the intestinal parasites were detected in 20 out of 30 collected samples. The only parasite present in mysticetes was *G. duodenalis*, also the most widespread parasite among all cetaceans, while odontocetes were parasitized by all protozoans we searched for. As for microbial community structure, no significant differences were found comparing parasitized and non-parasitized samples. The bacterial families in cetacean GMs whose relative abundance significantly shifts comparing parasitized versus non-parasitized cetaceans were Marinifilaceae, Clostridiaceae and Akkermansiaceae. The Marinifilaceae family was the only bacterial taxon overrepresented in parasitized individuals.



Fig. 1. Number of cetacean samples and marine sampling area.

III. DISCUSSION AND MAIN CONCLUSIONS

This study underlines the importance of both host phylogeny and diet in shaping the GM of cetaceans. Besides, while most samples were found to be parasitized by protozoa of possible anthropic origin, we report that this phenomenon did not lead to general GM dysbiosis, while resulting in the unbalances in specific symbiont taxa. The widespread presence of parasites of potential anthropogenic origin in the studied cetaceans and the consequent changes in the associated GM, emphasize the need to take actions to protect these important inhabitants of the Mediterranean Sea from current anthropogenic treats.

ACKNOWLEDGMENT

A special thanks to the Tethys Institute for samples collection and to the CIRCLES project.

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Stygofauna communities' diversity drivers under climate change exposure

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Short summary: The diversity of subterranean communities is closely related to the internal cave conditions, which are, in turn, affected by geographical and climatic factors. Climate change is a current threat to subterranean biodiversity.

Keywords: Biodiversity, Subterranean ecology, Climate change

I. BACKGROUND

In subterranean ecosystems, the isolation from the surface creates constant thermal conditions; therefore, subterranean-dwelling organisms typically lose physiological mechanisms to withstand temperature fluctuations. Due to this high climatic stability, caves are simplified natural laboratories for studying ecological processes [1]. However, external factors, such as ecological and climatic processes, over long time frames have an impact on subterranean ecosystems. In particular, the increasing rate of surface climate change impacts subterranean communities, threatening the long-term survival of most specialized subterranean species [2].

MATERIALS AND METHODS

Retrieving information from the Stygofauna Mundi database [3] we investigated taxonomical and functional α - and β -diversity of communities of specialized groundwater crustaceans (Amphipoda and Isopoda) inhabiting subterranean habitats in Northern Italy. We expressed taxonomic diversity as species richness within each subterranean community, after correcting the value for sampling bias. We calculated functional diversity as n-dimensional hypervolumes calculated using species traits. We modelled the influence of ecological variables (temperature annual range, elevation range, precipitations) and historical processes (distances from the sea and the glaciers during the LGM and in present days) on α -diversity patterns via regression models, while we used generalized dissimilarity models for β -diversity.

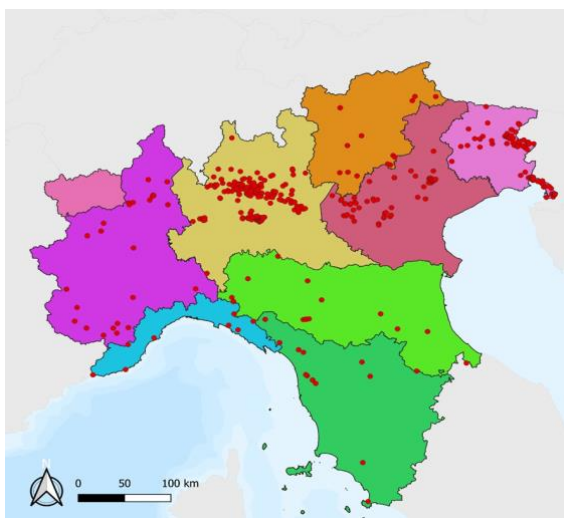


Fig. 1. Study area, highlighting the investigated administrative regions and studied communities as red dots.

II. RESULTS

Drivers of taxonomic and functional diversity

We found that diversity patterns are closer related to ecological local scale factors than to historical processes. The annual temperature range, precipitation and the presence of karstic substrates are the primary drivers of both taxonomic and functional diversity. Specifically, these significantly affect species richness as they create a broad ecological niche differentiation dependent on temperature range across the mountain and more habitat heterogeneity. This is also supported by functional diversity, which underlines how niche diversity correlates with overdispersion of functional traits. Conversely, historical processes had limited influence on diversity patterns.

III. DISCUSSION AND MAIN CONCLUSIONS

Geographical and climatic factors influence taxonomic and functional diversity of subterranean communities of groundwater crustaceans. Knowing how climate change affects the caves' internal conditions allows us to predict possible changes in their diversity. Importantly, all caves are different in shape and structure, thus each cave responds differently to climatic changes. In the future, we plan to categorize caves based on their thermal compression factor and structural aspects in order to predict their vulnerability to climate change. This will be developed within the 2022 P.R.I.N. "DEEPCHANGE", a multidisciplinary project focused on forecasting climate change impacts on subterranean alpine communities.

ACKNOWLEDGEMENTS

This study was supported by and the P.R.I.N. 2022 "DEEP CHANGE" (2022MJSYF8), funded by the Italian Ministry of University and Research, and by Biodiversa+ project "DarCo" funded by European Biodiversity Partnership under the 2021–2022 BiodivProtect joint call and co-funded by the European Commission.

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Benthic biodiversity patterns in rapidly evolving Alpine proglacial ponds (Cevedale glacier, Italy)

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Short summary: Proglacial ponds represent selective habitats that host specialized benthic eukaryotic biodiversity. The climate-driven deglaciation induces rapid ecological changes in proglacial ponds, that can result in a biodiversity loss for Alpine catchments.

Keywords: Alpine deglaciation, Eukaryotes, 18S, Benthic communities

I. BACKGROUND

Alpine headwaters are strongly impacted by deglaciation processes [1]. The climate-driven glacier melting induces the formation of proglacial lakes and ponds at an accelerated rate [2] and determines a rapid ecological evolution of newly formed water bodies and planktonic communities [3]. However, the effect of this evolution on littoral benthic biodiversity is poorly understood. We aimed at: (i) characterizing the littoral benthic eukaryotic community composition in a cluster of recently formed proglacial ponds; (ii) determining the possible effects of deglaciation processes on benthic biodiversity.

MATERIALS AND METHODS

The proglacial ponds (Z1 to Z4, Fig. 1) are located in the Stelvio National Park (BZ) between 2700 and 2900 m a.s.l., and all originated from the progressive shrinkage of the Cevedale glacier.

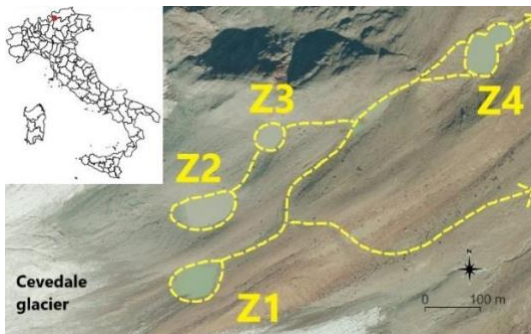


Fig. 1. Map of the proglacial study site (orthophoto 2020, downloaded from <http://geocatalogo.retcevica.bz.it/geokatalog>).

We collected biofilm samples once a month during the ice-free season in 2022 and 2023. We performed metabarcoding amplicon sequencing targeting the 18S rRNA gene, to detect eukaryotic diversity. We also collected water samples to determine the concentration of suspended solids in the littoral area and measured littoral water temperature. We completed the dataset by adding the biological samples from a clear lake, the Marmotte Lake (2706 m a.s.l. at 2.8 km from the proglacial ponds), which recently (about 40 years ago) lost the connection to a glacier.

II. RESULTS

We observed spatial environmental gradients in littoral water temperature and concentration of suspended solids (Fig. 2.A). 18S analyses showed a spatially increasing trend in α -diversity, with the highest diversity recorded in the clear lake, MA (Fig. 2.B). However, the taxonomical composition differed. For example, metazoans were represented in Z1 by only one rotifer genus, Nematode were found only at Z2 and Z4, and Tardigrades and arachnids at Z4 and MA. Copepods and ostracods were present exclusively in MA.

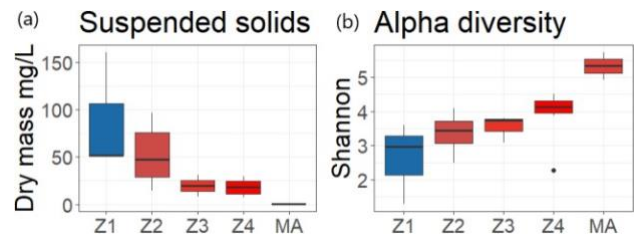


Fig. 2.A Concentrations of suspended solids in the four proglacial ponds and the clear lake; B α -diversity Shannon index for eukaryotic ASVs. Colors represent average littoral water temperature.

III. DISCUSSION AND MAIN CONCLUSIONS

Environmental gradients in suspended solids concentration and water temperature are common in proglacial ecosystems, where the glacial runoff inhibits biofilm growth in summer. Interestingly, the summer peak in suspended solids was observed only in the upstream-most pond (i.e., in contact with the glacier front). By adopting a space-for-time-substitution approach, we expect that the upper ponds will progressively shift towards clear conditions, with a disappearance of the correspondent highly selective habitats and a β -diversity loss for Alpine deglaciating catchments.

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Phenotypic plasticity in a changing ocean: the case study of the red coral *Corallium rubrum*

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Short summary: *Corallium rubrum* might reduce its size through fragmentation and branch loss to face climate change and the increased frequency of marine heat waves in the North-Western Mediterranean Sea.

Keywords: Octocorallia, Mesophotic, North-Western Mediterranean Sea, Fragmentation

I. BACKGROUND

Phenotypic plasticity is a crucial mechanism of response to environmental variability leading to an increase in the biological fitness [1]. Climate change (CC) is rapidly altering environmental parameters forcing organisms to develop specific phenotypic responses at both individual and population level, with many modular organisms known to reduce their size to face high temperatures [2]. In this work, a reduction on the number of colonies, colony size and number of apices in wild and transplanted populations of *Corallium rubrum* (Linnaeus, 1758) were documented and related to the marine heatwaves (MHWs) occurred over the last 35+years in different sites of the Mediterranean Sea.

MATERIALS AND METHODS

Photographic surveys were conducted in 4 sites to evaluate the phenotypic variation of *C. rubrum* wild populations at Isolotto (-18m, Argentario Promontory, Tyrrhenian Sea), Altare e Colombara (-30m, Portofino MPA, Ligurian Sea); and of a transplanted population at Punta Sciuscià (-32m, Gallinara Island, Ligurian Sea). The number of colonies and its variation (%) were determined for all sites. At Altare and Colombara the variation in size and number of apices was measured in 25 colonies using ImageJ software. The presence of Marine Heat Waves (MHWs) was also identified in the period 1986-2022 and related with the results of the photographic sampling.

II. RESULTS

The image analysis showed a 7% and 20% decrease in the number of colonies from 2011 (t_0) to 2021 (t_f) at Altare and Colombara (Fig. 1), respectively, and a 21% decrease from 2015 to 2020 at Isolotto. A significant reduction in colony size ($-40.0 \pm 18.1\%$, at Altare, and $-48.4 \pm 24.6\%$, at Colombara) and number of apices ($-53.8 \pm 22.9\%$, at Altare, and $-43.8 \pm 23.9\%$, at Colombara) were also recorded in each site located in the Portofino MPA (Student t test, $p < 0.05$). At the Punta Sciuscià, a mortality rate of 43% of transplanted colonies was registered in the 5-year monitoring activity. The MHWs analysis highlighted that Punta Sciuscià and Isolotto displayed the highest number of thermal anomalies, with 184 and 181, respectively, while

only 107 were recorded in the Portofino MPA. The frequency of MHWs also increased in the last decade (Kruskal–Wallis, $p < 0.05$).

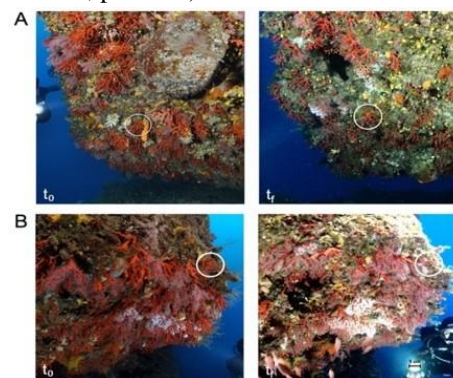


Fig. 1. Photographic survey conducted in the Portofino MPA at the sites: A) Altare and B) Colombara, in 2011 (t_0) and 2021 (t_f). White circles evidence the same colony in t_0 and t_f . The black line on the torch light indicates the reference size (5cm) used to measure the selected colonies.

III. DISCUSSION AND MAIN CONCLUSIONS

The increased frequency of thermal anomalies determined a reduction in the number of colonies of *C. rubrum* and the surviving colonies displayed a significant reduction in size. Underwater and laboratory observations suggested that red coral can undergo a fragmentation process through autotomy of the branch ends. This reorganization of the colony shape might represent an adaptive mechanisms of shallow population against rising temperatures, eventually leading to transgenerational plasticity and a bet-hedging reproductive strategy [3].

ACKNOWLEDGMENT

We are grateful to Simone Nicolini and Bruno Borelli (Reef Alert Network and Reef Check Italia) for the photographic material.

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The conundrum of extinction and incomplete taxonomy in Malagasy dung beetles

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Short summary: Oceanic island's biotas are particularly vulnerable to environmental changes. In this study, we used an integrative approach to demonstrate how taxonomic incompleteness and human impact have shaped our knowledge on Madagascar dung beetles, and species diversity in the Mascarene islands, respectively.

Keywords: Madagascar, Mascarenes, Oceanic islands, Species loss, Habitat fragmentation, Anthropogenic factors

I. BACKGROUND

The Malagasy region (Madagascar + Mascarene islands) is one of the world's 'hottest' biodiversity hotspots, and natural laboratory for studying extinction, evolutionary and biogeographic patterns. Its endemic-rich biotas are still suffering important loss because of human activities [1, 2]. Malagasy dung beetles are highly endemic (~96%) and diverse (>300 spp.), and a huge amount of data is today available. These features make dung beetles an excellent model group to elucidate the role of climate, biogeography and anthropogenic factors in species diversification and extinction in the region. In this talk, I will discuss our preliminary results in the light of human impact and taxonomic incompleteness.

MATERIALS AND METHODS

We conducted fieldworks (2007, 2021–2022) to collect target taxa for morphological and phylogenomic analyses (Mauritius, Madagascar), and to search for subfossil remains of dung beetles (Rodrigues, Mauritius). Also, museum collections were investigated. We used different approaches to study the material: (i) Comparative morphology; (ii) UCE phylogenomics; (iii) Museomics. Data was used to carry out descriptive taxonomic reviews, and perform either combined or molecular phylogenetic analyses, and biogeographic reconstructions.

II. RESULTS

We recollected multiple species belonging to the eight currently known lineages of Malagasy dung beetles.

New dung beetle tribes are described based on morphology and phylogenomic. Sediment samples yielded an extensive amount of dung beetle remains (head, pronota, elytra and legs), which we assigned provisionally to six-seven new species.

The scrutiny of museum collections allowed us to discover an extinct dung beetle species from Réunion island, as well as multiple synonyms and undescribed Madagascar species.

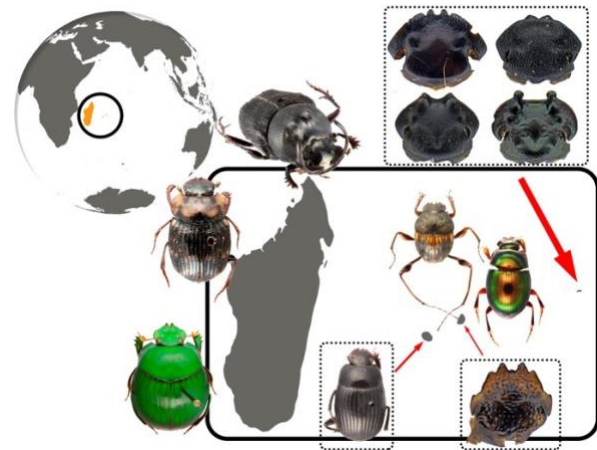


Fig. 1. Map of the findings. Dotted lines indicate extinct taxa.

III. DISCUSSION AND MAIN CONCLUSIONS

Our integrative approach suggests that poorly resolved taxonomy may have biased estimation of species diversity and extinction in Madagascar [3]. Also, morphology and molecules suggest that Malagasy dung beetle lineages must be reduced to six. The discovery of a new extinct species from Réunion island, multiple subfossils from Mauritius and Rodrigues, and the missing of one of the four forest-dweller Mauritian species, indicates that Mascarene dung beetles suffered a recent mass extinction. Overhunting and deforestation are claimed as primary causes of species loss. Museomic allowed us to clarify the systematic position of cryptic taxa, but so far DNA-archival protocols failed in retrieving acceptable sequences from subfossils. Their systematic position and biogeography are still obscure.

ACKNOWLEDGMENT

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Life in (micro)plastic: the microbial communities on different MPs and the health risk associated with them

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Short summary: The chemical properties of microplastic particles can influence the composition of the attached microbial community, selecting for antibiotic resistant and potentially pathogenic bacteria.

Keywords: Microplastic particles, Antimicrobial resistance, Pathobiome, Biodegradable plastic, Anthropogenic pollution, Plastisphere

I. BACKGROUND

In aquatic ecosystems, microplastic particles (MPs) can host a peculiar microbial community, differing in abundance and composition from the surrounding water [1], and offer an additional niche where allochthonous bacteria can survive and/or proliferate. This feature is strongly influenced by their chemical properties that hamper to consider them as a unique group of pollutants.

MATERIALS AND METHODS

MPs of different materials (conventional and biodegradable) were incubated in steel enclosures in Lake Maggiore's surface water for 43 days. We analyzed the biofilm formed on their surface investigating the composition of the bacterial community and pathobiome, and quantifying some antibiotic resistance genes (ARGs). In addition, we evaluated the dynamics of the microbial community, pathobiome, and ARGs, in a semicontinuous culture system, by incubating two types of MPs (PET and tyre wear particles, TWPs) added in different proportions to chemostats filled with 80% lake water and 20% wastewater.

II. RESULTS

A. In situ experiment

Our analysis of biofilm and planktonic bacterial communities revealed similar richness but different composition, with the communities on the different human-made materials very similar to each other (Fig. 1). Moreover, the abundance of potentially pathogenic bacteria was significantly higher within the biofilms than in the surrounding water. The tested ARGs (*bla*_{TEM}, *bla*_{CTXM}, *tetA*, *sul2*, *ermB*, *qnrS*, *strB*) showed similar abundances in the biofilms and in planktonic bacteria. The *int1* gene was more abundant in the biofilms, in particular, on Mater-Bi.

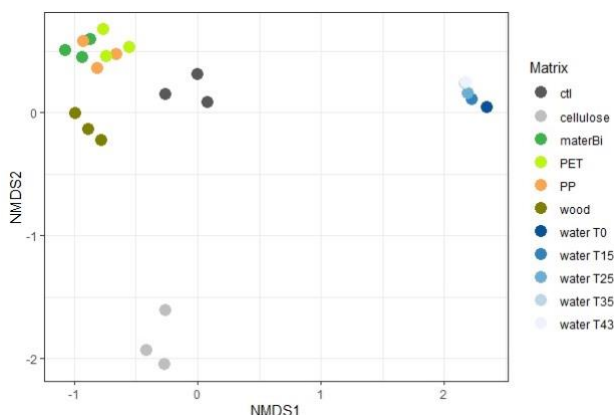


Fig. 1. NMS2 plots for the composition of water and biofilm samples.

B. Chemostat experiment

The richness of the pathobiome in the biofilm on PET was higher than on TWPs and in the surrounding water. However, the overall proportion of potential pathogens in each vessel was higher with growing proportions of TWPs, with *Acinetobacter*, *Pseudomonas*, and *Sphingomonas* dominating the pathobiome of MPs (Fig. 2). ARGs and *int1* gene did not show significant variations either on MPs or in water.

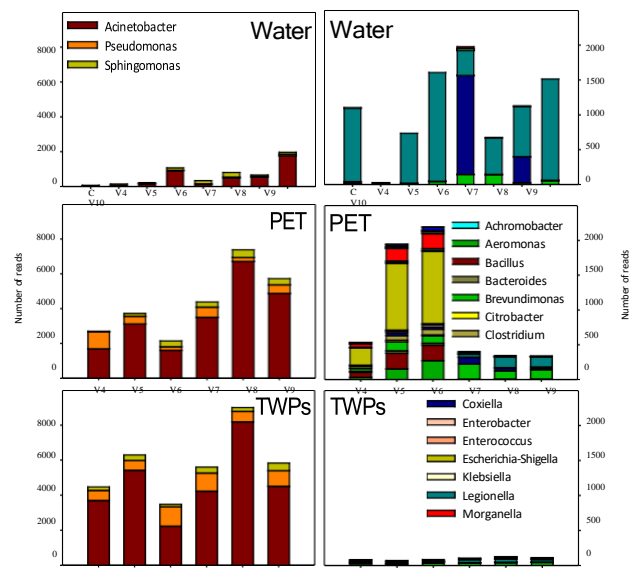


Fig. 2. Abundances of the different potentially pathogenic genera at the end of the experiment.

III. DISCUSSION AND MAIN CONCLUSIONS

Overall, biofilm on human-made polymers showed a peculiar community composition, with higher proportions of potential pathogens, a feature that is shared by both conventional and biodegradable plastics. Looking individually at the different polymers, chemical characteristics of MPs can heavily affect the pathobiome of aquatic microbial communities, offering either a refuge for allochthonous and/or rare potential pathogens or a substrate where otherwise limited bacterial groups can grow. Our results demonstrate that MPs can pose a threat to human health and underline once more the urgency for dedicated strategies to recycle plastic waste and limit their discharge into the environment.

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Session #2 – Predicting changes

Moderators: Manuela D'Amen & Stefano Mammola

Summary of the thematic session

Global biodiversity is being reshaped rapidly by anthropogenic activities. To effectively respond to this challenge and maintain ecosystem functionality in the long run and to guide conservation and management actions, we need to accurately chart trajectories of biodiversity change under natural and anthropic drivers. Predicting biodiversity change in space and time was the core topic of session 2 – "Previsioni del Cambiamento." This is a challenging task, and many different approaches exist. Assuming that the contributions within the session are representative of the research conducted in Italy aimed at forecasting biodiversity change, a positive trend emerges. Indeed, the session featured a breadth of modelling and forecasting techniques, ranging from simple correlative species distribution models to mechanistic simulations, and more. These predictive models incorporated different types of biodiversity data into the predictive pipeline (e.g., species distributions and abundances, phylogenetic information, functional traits, and ecophysiological data), along with high-resolution environmental correlates and measures of anthropogenic impacts. Also, an attempt to consider extreme and stochastic climatic events has been presented, although this remains an extremely difficult task. This picture suggests that, in Italy, researchers possess general and widespread expertise in some of the most cutting-edge approaches to biodiversity forecasting.

Despite this positive note, our thematic working group identified two future challenges. First, the goal of achieving community or ecosystem-level predictions of biodiversity change is still out of reach. The study of model species and systems may allow responding to very urgent questions, thus most research focused on single species or simplified communities. Inevitably there is a general tendency among researchers to focus modelling exercises on species that are economically important for humans or charismatic, and for which there is great data availability. On the other hand, the complexity of real-world ecosystems provides scientists with additional challenges, if accurate forecasts are aimed at. This challenge calls for renewed efforts to collect much-needed data (e.g., distribution, genetic, physiological, and biotic interactions) for neglected biodiversity groups, habitats, and processes, and to upscale our predictions to multiple ecosystem components.

The second challenge concerns translating our forecast of biodiversity change into actionable recommendations. Often, the research produces high-resolution maps of species distribution in space and time, but these are rarely taken up by stakeholders and decision-makers to inform the conservation and management of biodiversity. Moving forward, further efforts to communicate science more broadly and engage with relevant stakeholders are needed. The interaction with stakeholders could produce benefits also for the research itself, because they can provide in turn useful feedbacks to improve the modelling and forecasting of changing biodiversity.

Climate change, habitat fragmentation and biodiversity of terrestrial mammals.

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Short summary: Here we use reindeer data to show that climatic changes and instability may have determined distribution and diminished biodiversity of terrestrial mammals in the past 21 kyr, with projected changes to year 2100. We then use wolf data to show that in human dominated regions, like southern Europe, habitat fragmentation will dramatically influence biodiversity.

Keywords: Contemporary and historical biodiversity changes, Climate change, Human impacts, Habitat fragmentation, Terrestrial mammals

I. BACKGROUND

Climate-driven range fluctuations during the Pleistocene have reshaped species distribution and genetic diversity. Contemporary and future climate changes will similarly influence species. In human dominated regions, habitat fragmentation will also dramatically influence biodiversity. Yet few studies assess the impacts of climatic changes and habitat fragmentation on intraspecific genetic variation.

MATERIALS AND METHODS

Combining analyses of molecular data with time series of predicted species distributions and a model of diffusion through time over the past 21 kyr [1], we unravel reindeer response to past and future climate changes across its entire Holarctic distribution. We also use a SNP genotyping microarray to assay variation in over 48K loci in wolf-like species worldwide [2] and focus on molecular data for Southern European wolves. Finally, we use microsatellite data for 2421 gray wolves from 24 subpopulations [3] to model how allelic richness and expected heterozygosity vary at a continental scale.

II. RESULTS

Climatic instability diminished biodiversity of reindeer, with projected changes to year 2100

We found that genetic diversity is geographically structured with two main reindeer lineages, one originating from and confined to Northeastern America, the other originating from Euro-Beringia but also currently distributed in northwestern North America. Regions that remained climatically stable over the past 21 kyr maintained higher genetic diversity (Fig. 1) and are also predicted to experience higher climatic stability under future climate change scenarios. Hence, both climatic changes and instability determined distribution and diminished biodiversity of reindeer, with projected changes to year 2100.

In human dominated regions, habitat fragmentation influenced wolf biodiversity

Despite the high mobility of wolves, we found distinct hierarchical population units that correspond with geographic and ecologic differences among populations. We also determined genetic consequences of population decline and habitat fragmentation, in particular for human dominated regions, like southern Europe. Multiple axes of geographic isolation acted synergistically to erode the

genetic diversity of continental wolf populations despite the counteracting influence of long-range dispersal ability.

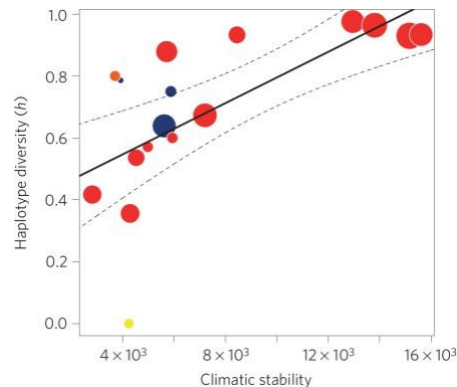


Fig. 1. Relationship between mtDNA haplotype diversity (h) and habitat stability over the past 21 kyr for the mitochondrial reindeer data set. Adapted from [1].

III. DISCUSSION AND MAIN CONCLUSIONS

Our multidisciplinary approach, combining genetic data and spatial analyses of climatic stability (applicable to virtually any taxon), represents a significant advance in inferring how climate shapes genetic diversity and impacts genetic structure. Climatic changes that happened throughout the Pleistocene and climatic instability may determine distribution and diminished biodiversity of terrestrial mammals in general. The changes we projected to year 2100 also indicate increased threats in regions with relatively warmer climate. In human dominated regions, like southern Europe, habitat fragmentation will also dramatically influence biodiversity of terrestrial mammals.

ACKNOWLEDGMENT

Project funded by the European Union - NextGenerationEU, under the National Recovery and Resilience Plan (NRRP), Project title “National Biodiversity Future Center -NBFC” (project code CN_00000033).

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Seahorses in the Anthropocene: integrated conservation gaps and trends

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Short summary: Seahorses are highly vulnerable to ongoing anthropogenic disturbances and climate change. We integrated ecological and genomic insights to assess their current conservation status and predict their resilience. We identified monitoring strategies, priority targets and provided indications for more extensive conservation programs that consider evolutionary breadth and potential.

Keywords: Conservation gap analyses, Endangered species, Evolutionary potential, Genetic erosion, Resilience to environmental changes, Species distribution modelling

I. BACKGROUND

Seahorses (*Hippocampus* spp., Fig. 1) are flagship animals inspiring numerous conservation programs. They are the first marine genus to be fully listed on the Convention on International Trade in Endangered Species (CITES) Appendix II due to their substantial vulnerability to overexploitation and habitat loss [1]. The peculiar life history of these fishes has been widely addressed through evolutionary and ecological analyses. Yet, no study has integrated current knowledge to approach species-based conservation status, including trends in abundance, diversity, and threats, hindering seahorses' worldwide effective assessment and management. Here, we bridge these gaps by taking advantage of the available geographic, ecological, and genomic (ultra-conserved elements and whole genomes [2,3]) data in the *Hippocampus* species at a global scale and present the most comprehensive study of the seahorses' conservation status to date.



Fig. 1.A. specimen of *Hippocampus guttulatus*. Picture courtesy of Fabio Russo.

MATERIALS AND METHODS

We explore seahorses' diversity patterns in space and time by using species distribution modelling, phylogenomic mapping, comparative genomic applications, and conservation gap analyses.

We consider their evolutionary history and genomic erosion including genetic load, which have been largely disregarded by current conservation policies. We investigate the degree and type of protective measures currently granted to seahorses, and the biological and ecological factors that are contributing to their existing and future extinction risk.

II. RESULTS

Our results raise questions on whether the current conservation indicators and practices are effective in preserving the present diversity and function of these iconic fishes, as well as their future evolutionary potential and ecological resilience.

III. DISCUSSION AND MAIN CONCLUSIONS

These insights provide a broad, more complete picture on the status and trends of seahorses and inform successful conservation initiatives in the face of the Anthropocene. Finally, as more diverse datasets become available in the light of the "omics" and "open-access" era, we discuss the unprecedented opportunities to address interdisciplinary studies required for proper research-based conservation, assessment, and management of biodiversity.

ACKNOWLEDGMENT

We are grateful to the scientists and citizens who publicly shared their data, and to our institutes and funding agencies for their support. This research was supported in part through high-performance computing resources available at the Kiel University Computing Centre.

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Climate change and one health: post-Vaia windthrow as new hotspot for forest zoonoses

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Short summary: Severe meteorological events related to climate change may act as additional drivers for zoonoses emergence. Using a One Health approach, we studied the changes in *Ixodes ricinus* tick abundance and rodent community composition within an alpine forest affected by Vaia storm in 2018.

Keywords: *Ixodes ricinus*, Zoonotic pathogens, Small mammals, Italian Alps, Windstorm, One health

I. BACKGROUND

Land use and climate change together with variation in wildlife communities and increased anthropisation affect the pattern of zoonotic diseases circulation as in the case of tick-borne diseases transmitted by *Ixodes ricinus* [1]. In this study, we aim to evaluate the effect of Vaia Storm on reservoir's diversity and tick-borne pathogen prevalence in an alpine area using a One Health approach. Vaia windstorm was a severe meteorological event that occurred in the North-Eastern Italian Alps in 2018 and caused the crash of 42 million trees over 41.000 hectares in few hours.

MATERIALS AND METHODS

The study area is located in the Natural Park of Paneveggio-Pale di San Martino (Autonomous Province of Trento, Italy) (Fig. 1). Twelve sites were identified in three different habitat types (post-Vaia windthrow, mixed forests, meadows) at low and high altitudinal level. In each site, in 2023 we performed (i) Capture-Mark-Recapture live-trapping of small mammals in cross-shaped grids (16 Ugglan live-traps each); (ii) tick-dragging of host-seeking ticks along 100 m transects. Bacteria and protozoa were detected in ticks using PCR-based methods combined with sequencing, while viruses were evaluated in rodent sera through Indirect Immunofluorescence Assay.

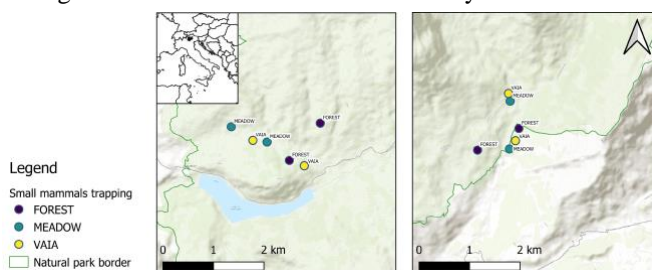


Fig. 1. Map of the study areas placed in the Natural Park of Paneveggio-Pale di San Martino (Autonomous Province of Trento, Italy). Coloured circles represent locations of small mammals and questing ticks sites (black = forest, green = meadow, yellow = Vaia windthrow).

II. RESULTS

a. Wild small mammal diversity and tick abundance

Overall, we identified 92 ticks belonging to *I. ricinus* species, 60% from Vaia and 40% from forest sites. We captured 248 small mammal individuals belonging to *Apodemus flavicollis*, *Apodemus sylvaticus*, *Clethrionomys glareolus*, *Microtus* spp. and *Sorex* spp. All species were observed in Vaia affected sites, while only three in the

forest ones. Similarly to ticks, 64% of small mammals were captured in Vaia windthrow, 20% in forests and 16% in meadows (Tab. I).

TABLE I. TICK AND SMALL MAMMAL ABUNDANCE ACROSS HABITATS

Site	Tick life stages			Total	
	Nymphs	Adult female	Adult male		
Vaia	49	1	6	56	
Forest	32	1	3	39	
Small mammal species					
	<i>Apodemus</i> spp.	<i>Clethrionomys glareolus</i>	<i>Microtus</i> spp.	<i>Sorex</i> spp.	Total
Vaia	18 (1)*	81	13	47	160
Forest	20	16	0	13	49
Meadow	10 (1)*	13	5	10	39

**Apodemus sylvaticus* in brackets, otherwise *Apodemus flavicollis*

b. Tick- and rodent-borne pathogens

We identified antibodies against Tick-borne encephalitis (TBEV) and Dobrava-Belgrade (DOBV) virus in rodents only in Vaia sites, although with very low prevalence (1/174 – 0.005% and 1/53 – 0.002%, respectively), while virus, bacteria and protozoa of ticks are under evaluation.

III. DISCUSSION AND MAIN CONCLUSIONS

After Vaia windstorm, reforestation process is ongoing. At this stage, intermediate vegetation is providing a higher vegetation heterogeneity in Vaia affected sites where several small mammal species can find food and shelters. At the same time, also ticks, probably due to suitable microclimate and adequate vegetation cover, can select those sites. Consequently, circulation of tick- and rodent-borne diseases may be enhanced given the spatial overlap of reservoirs and vectors that can maintain the pathogens in the environment. Here we contribute by suggesting the crucial impact of habitats alteration due to climate change on driving biodiversity patterns and disease risk thereafter.

ACKNOWLEDGMENT

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Future distribution of demersal fish species under the influence of climate change in a Mediterranean sub-basin

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Short summary: An ensemble species distribution model (e-SDM) was applied to the two life stages (adult and juvenile) of nine demersal commercial species in two sub-basins of the Mediterranean Sea. The approach uses past and future essential oceanographic variables and it allows determining changes in the distribution of the species in the Adriatic Sea and the North Western Ionian Sea under climatic scenarios.

Keywords: Species distribution, Climate change, Demersal community, Commercial marine species, Hot spots, Adriatic Sea

I. BACKGROUND

Climate projections for the Mediterranean Sea show a general warming of seawater associated with changes of several physical and biogeochemical variables [1]. Such oceanographic changes will affect species distribution, with potential impacts on biodiversity and fishing [2]. Predicting the range shifts of marine species under future climate scenarios is, therefore, of utmost importance to ensure appropriate management for resources already heavily impacted by several stressors. In this work, we develop an ensemble species distribution model (e-SDM) to assess the future distribution of nine demersal commercial species for their two life stages (adult and juvenile) in two sub-basins of the Mediterranean Sea.

MATERIALS AND METHODS

The e-SDM was developed using different models, namely (i) generalized additive models (GAM), (ii) generalized linear model (GLM), (iii) random forest (RF) and (iv) gradient boosting machine (GBM), by combining density data from trawl surveys and different variables such as geolocation, depth, as well as relevant Copernicus Marine Service oceanographic and biogeochemical variables (temperature, salinity, chlorophyll-a, dissolved nutrients and oxygen, particulate organic carbon, pH). We used density indices (number of individuals km⁻², N/km²) obtained during two surveys in the Adriatic and Ionian Seas in the last two decades for nine species. We then used the e-SDM to locate the hot-spots (with Getis-Ord Gi* [3]) distribution of each species in four-time windows: i) 1999-2003 'past', ii) 2014-2018 'present', iii) 2031-2035 'mid-future', and iv) 2046-2050 'far future', the latter under representative concentration pathway (RCP) 8.5.

II. RESULTS

The results show that the density of some important commercial species and their spatial distributions will change. The lost/gained/preserved areas (Fig. 1) show that no significant changes are predicted for hake and red mullet, while for Norway lobster lost areas are found in the central part of the basin. For anglerfish, the areas gained are along the northern coast of Croatia, and horse mackerel is

migrating northwards. Other species, such as the broad-tailed squid, have lost territory along the north-eastern coast of the Adriatic Sea. Overall, these first results highlight potential large changes in fish biodiversity.

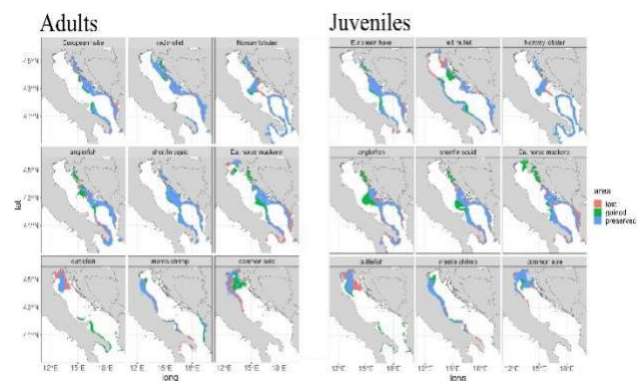


Fig. 1. area gained, lost, and preserved (see legend) for each species for the year 2050 for adults (left panel) and juveniles (right panel). Each area is composed of grid cells that do not overlap (gained), overlap (preserved), and lack (lost) Getis ord-Gi* values > 75^o percentile between the 'present' scenario and the '2050' scenario.

III. DISCUSSION AND MAIN CONCLUSIONS

Future changes in fish biodiversity, their distribution and main aggregation areas could have an impact on fishing grounds and fishing activity, thus affecting the economy of the sector in the Adriatic and Ionian Seas. Consequently, the potential changes in species distribution will require new adaptive management measures in the future, such as adaptive spatial planning with short- and long-term regulations. This could lead to the need to redefine measures such as spatial fishing bans.

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Developing a model for the expansion of *Pterois miles* in the Mediterranean Sea

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Short summary: Predicting the geographic expansion of invasive species is critical to anticipate their potential impacts. In this ongoing study, we build a spatio-temporal occupancy model for the lionfish, *Pterois miles*, one of the most successful invaders of the Mediterranean Sea. Fitting the model to observations will help us refine our understanding of the larval dispersal dynamics of the species and quantify the effect of environmental variables on colonization.

Keywords: Biological invasions, Mediterranean Sea, Larval dispersal, occupancy model

I. BACKGROUND

With the opening of the Suez Canal in 1869, hundreds of marine species native to the Red Sea and Indian Ocean gained access to the Mediterranean Sea. Referred to as Lessepsian species (after Ferdinand de Lesseps, the French entrepreneur who promoted the construction of the canal) many of these species established large, permanent populations in the eastern Mediterranean. Their spatio-temporal spread dynamics vary widely: some species develop successful populations and spread over large geographical areas, whereas others remain rare for long periods before spreading, or even fail to establish. Some species also spread further than the Easter Basin, and in few cases to the entire Mediterranean Sea. This unassisted secondary spread is mediated by dispersal in various life stages of the species (larval, juvenile, and adult) and is likely aided by ongoing climate change that brings the environmental conditions of the Mediterranean closer to species native range.

The lionfish *Pterois miles* (Linnaeus, 1758) has been one of the most rapid colonizers of the Mediterranean Sea. Predicting the geographic expansion of *P. miles* in the Mediterranean Sea is critical to anticipate and mitigate the potential impacts of its invasion on native ecosystems. To this end, we need to understand how dispersal and establishment are regulated by the availability of habitat, environmental conditions, and hydrodynamics, leveraging the documented expansion records of the species since its introduction through the Suez Canal. In this study, we seek to quantify the different role of larval dispersal and habitat suitability in *P. miles* invasion.

MATERIALS AND METHODS

We build a spatio-temporal occupancy model to reproduce the expansion of the species as a function of larval dispersal and environmental variables. The study area is discretized in grid cells representing sites ($i = 1, \dots, N$), where the species in each year can be present ($z_{i,t} = 1$) or absent ($z_{i,t} = 0$):

$$y_{i,t} \sim \text{dbern}(p \cdot z_{i,t}) \quad (1)$$

$$z_{i,t} \sim \text{dbern}(y_{i,t}) \quad (2)$$

Equation (1) states that the record of the species in site i in year t , $y_{i,t}$, is a Bernoulli random variate with parameter equal to the occupancy of site i in year t , $z_{i,t}$, multiplied by the detection probability p . Equation (2) states that occupancy $z_{i,t}$ is a Bernoulli random variate with parameter $y_{i,t}$, the occupancy probability of site i at time t , which is itself function of the site-specific annual persistence probability ϕ_i and colonization probability γ_i :

$$y_{i,t} = z_{i,t-1} \cdot \phi_i + (1 - z_{i,t-1}) \gamma_i \quad (3)$$

These site-specific persistence and colonization probability are themselves function of environmental covariates and pairwise larval dispersal probabilities between sites. Pairwise larval dispersal probabilities are calculated by simulating the dispersal of larvae of *P. miles* using a Lagrangian biophysical model [1].

The parameters of the model (e.g. coefficients of the covariates and other hyperparameters not shown in eq. 1 to 3) are fitted in a Bayesian framework using the observations of species presences, $y_{i,t}$, of the ORMEF database [2].

II. EXPECTED RESULTS

We will present the first results of the spatiotemporally explicit occupancy models to (i) identify the processes that structure the larval dispersal of *P. miles* through the spatiotemporal process of invasion; (ii) quantify the effect of environmental variables on species persistence and colonization of local sites; and (iii) account for the uncertainty deriving from imperfect species detection through explicit modelling of the observation process.

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Expected changes in life-history traits of small pelagics under climate change

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Short summary: Agent-based models based on the Dynamic Energy Budget Theory were used to simulate future temperature and food availability conditions for a population of sardine and anchovy. The aim was to reproduce expected Temperature Size Rule (TSR) patterns for small pelagics. Both metabolism and reallocation of energy into reproduction could explain reduced adult size and anticipated puberty.

Keywords: Agent-based modelling, Dynamic Energy Budget Theory, Small Pelagics, Population Dynamic, Life-history

I. BACKGROUND

Climate change impacts fish populations like sardines and anchovies in the north Adriatic Sea, where movement to cooler waters is limited. The Temperature-Size Rule (TSR)[1] suggest that higher temperatures lead to smaller adults and anticipated reproduction, likely due to metabolic constraints or adaptive energy reallocation into reproduction under suboptimal conditions. This pattern is observed also in sardines and anchovies and physiological models can help in understanding the effects in population dynamics under changing climate conditions.

MATERIALS AND METHODS

In this study, we developed an agent-based model in Julia [2], using the Dynamic Energy Budget Theory (DEB) [3] to simulate the life stages of sardines and anchovies. Both species are short-lived batch spawners with very distinct spawning times and habitat preferences. Different sets of simulations were run to resemble sea conditions in the Northern Adriatic Sea under current and future climate change scenarios to investigate direct effects on individuals' metabolism.

Moreover, we investigated the effect of perturbing DEB species-specific parameters on metabolism and allocation of energy into growth and reproduction. These simulations aimed to explore the impact of temperature and food availability on species' life-history traits and demography.

II. RESULTS

Increasing mean temperature resulted in notable decreases in mean weight and size across all age groups, along with shortened time to puberty and pronounced annual fluctuations. Interestingly, reducing the DEB K coefficient (proportion of energy allocated to growth), only at high temperature, yielded similar trends for the mean adult weight but increased average time to puberty, due to the increased intra-specific competition for food at the population level.

III. DISCUSSION AND MAIN CONCLUSIONS

The study confirms trends observed in Adriatic and Mediterranean Sea on decreasing trends for small pelagics adult size due to higher temperatures. The effect is exacerbated by limited food. Julia language facilitated simulations in making the computing time reasonable.

Currently, the increased metabolic rates due to rising temperature explained better the expected TSR patterns. The work highlights the importance of considering animal physiology in modelling fish populations under climate

change. Future research will explore spatial patterns of fish life history traits in the Adriatic Sea to understand their impact on population dynamics.

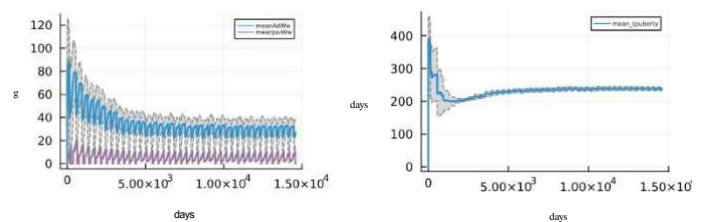


Figure 1 A-B: Temperature: 14 C. On the left, mean weight(g) of adults (blue) and juveniles (pink) during time; on the right, mean time to puberty of adults (days).

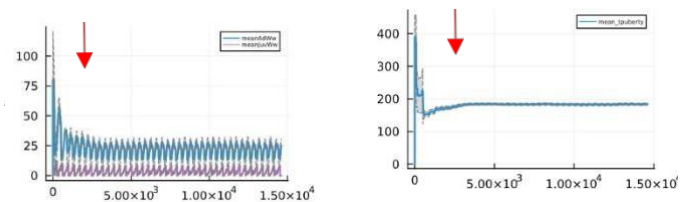


Figure 2 A-B: Temperature: 18 C and K 0.945. On the left, mean weight(g) of adults (blue) and juveniles (pink) during time; on the right, mean time to puberty of adults (days).

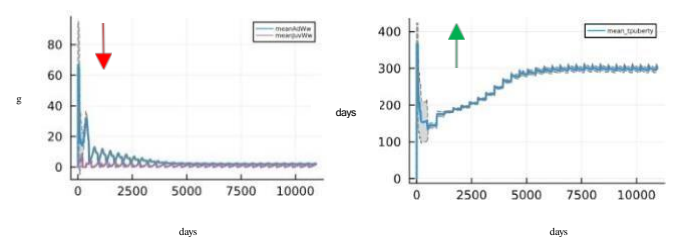


Figure 3 A-B: Temperature: 18 C and K 0.90. On the left, mean weight(g) of adults (blue) and juveniles (pink) during time; on the right, mean time to puberty of adults (days).

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Dangerous overlaps: potential impacts of seafloor litter hotspots on demersal fisheries

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Short summary: The cost of waste: overlap analysis of plastic concentrations on the seafloor and commercially important species reveals potential loss of economic productivity due to marine litter accumulation.

Keywords: Seafloor litter pollution, Fishing grounds, Commercial species, Impacts, Management

I. BACKGROUND

Seabed plastic pollution seriously threatens marine biodiversity and ecosystem functioning by damaging marine organisms and disrupting ecosystems. Litter accumulation zones may overlap with fishing grounds for commercially important species, reducing productivity and yield [1]. As no studies have been conducted on this topic, there is an urgent need to fill the knowledge gap on the impact of plastic pollution on fisheries and stock management. For these reasons, this study aimed to analyze the impact of seafloor plastic on fishing economic performance (as Gross Values Added) and on commercially important species by mapping trawl areas and identifying litter hotspots on the seafloor.

MATERIALS AND METHODS

We applied a model based on landing and VMS data to estimate the species' fishing grounds [2], and we used a random forest machine-learning technique to locate hotspots of seafloor litter [3]. Therefore, Generalized Additive Models (GAMs) were used to investigate the correlation between fishing economic performance (GVA) (response variable) as a function of seafloor litter hotspots, fishing effort, and seasonality (explanatory variables). The LPUE distributions for each species and seafloor litter were analyzed to evaluate the potential exposure risk to plastic items on a scale of 0 (low risk) to 1 (high risk) for each species. These values were used to produce an Impact Score (IS) as an indicator of the probability that a species could be affected by the accumulation of waste on the seabed, as a proxy for impact risk. Therefore, the risk of exposure was divided by the number of total cells where the species was present (LPUE values > 0), as follows:

$$IS = \frac{\text{Risk of exposure}}{\text{Total number of cells}}$$

II. RESULTS

GVA values increased with increasing fishing hours and with most of the species LPUEs until reached a plateau. Concerning seafloor litter, it was observed that GVA increased with an increase in the amount of debris up to a certain threshold (approximately 15,000 objects · km⁻²), and then GVA decreased rapidly once the amount of debris exceeded this threshold. Figure 1 highlights several areas with significant concentrations of plastic debris and high values of species abundance (LPUE). The impact scores (IS) for the key commercial species revealed that *Parapenaeus longirostris* (DPS) had the highest IS, followed by *Mullus barbatus* (MUT), *Eledone cirrhosa* (EOI), *Merluccius merluccius* (HKE), *Nephrops*

norvegicus (NEP), *Illex coindetii* (SQM), *Aristaeomorpha foliacea* (ARS), *Lophius piscatorius* (MON), *Aristeus antennatus* (ARA).

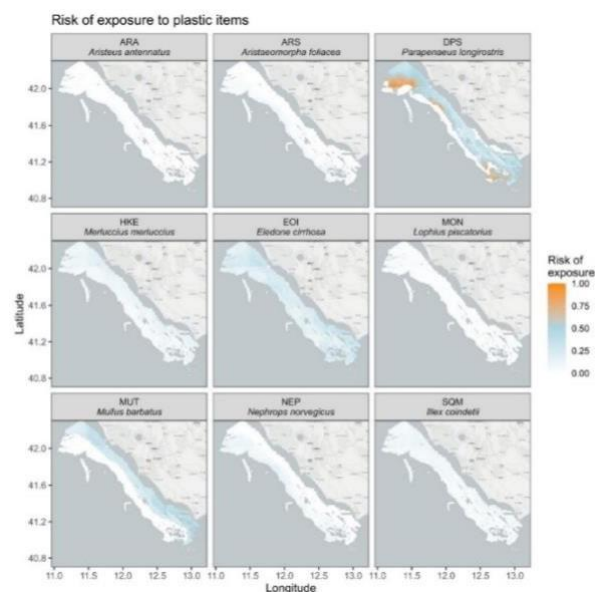


Fig. 1 Maps of risk of exposure to seafloor plastic for 9 species that are crucial for trawling in the central Tyrrhenian Sea (GSA 9). This was achieved by multiplying the LPUE of each species and the plastic litter field. The resulting maps were then rescaled from 0 to 1.

III. DISCUSSION AND MAIN CONCLUSIONS

The study shows that plastic hotspots on the seabed overlap with fishing grounds for commercially important species, such as hake, pink shrimp, or red mullet, which negatively impacts economic productivity. The implications of this problem pose a significant threat of exposure and impact to certain species. Our findings indicate that seabed plastic pollution should be recognized as a factor affecting fisheries administration and conservation approaches.

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Life without glaciers: who will survive in the changing Alps?

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Short summary: Cold-adapted Alpine plant and arthropod species are endangered by glaciers disappearing. Some ice-related landforms are acting as warm-stage refugia for these species and are pivotal for conservation and biodiversity monitoring programs.

Keywords: Alps, Cold-adapted species, Cryosphere, Ice-related landforms, Monitoring program

I. BACKGROUND

Ice-related landforms (e.g., glaciers and rock glaciers) are protected in the Natura2000 network (habitat code: 8340). Alpine biodiversity is threatened by the vanishing of these landforms and by the disappearing of cold-adapted species [1]. Recording their richness, identifying the landforms acting as warm stage refugia for them and endemic species, and selecting priority areas for their conservation, are the challenging objectives of our research activity in the Italian Alps.

MATERIALS AND METHODS

For more than 20 years, we have been investigating different ice-related landforms (glacier forelands, glaciers, and rock glaciers). Vascular plants, ground beetles and spiders were sampled at almost 700 sampling points all over the Italian Alps. In 463 sampling points, we recorded topographic (e.g., slope exposure, solar radiation) and soil (e.g., sub-surface ground temperature, grain size) variables. The obtained dataset has been analysed through spatially explicit models (e.g., GAMs).

II. RESULTS

363 vascular plant species, and 150 ground-dwelling arthropod species (52 ground beetles, 98 spiders) have been recorded. All the considered taxa showed a high percentage of species negatively linked to elevation, having none or negative relationship with ice-related landforms (these species will be “winners” in a climate change scenario, because they will probably benefit from warmer temperatures) and of species without a clear response pattern to environmental predictors (“neutral”) (Fig. 1). Overall, 17 of the recorded species resulted associated to ice-related landforms. Plants and spiders experienced the highest percentage of cold-adapted species that are linked to sites at high elevation but do not show the ability to live on ice-related landforms (“losers” in a period of glacier shrinkage) (Fig. 1). On the other hand, all the taxa also include a low percentage of “losers” found also in ice-related landforms (e.g., debris-covered glaciers, rock glaciers).

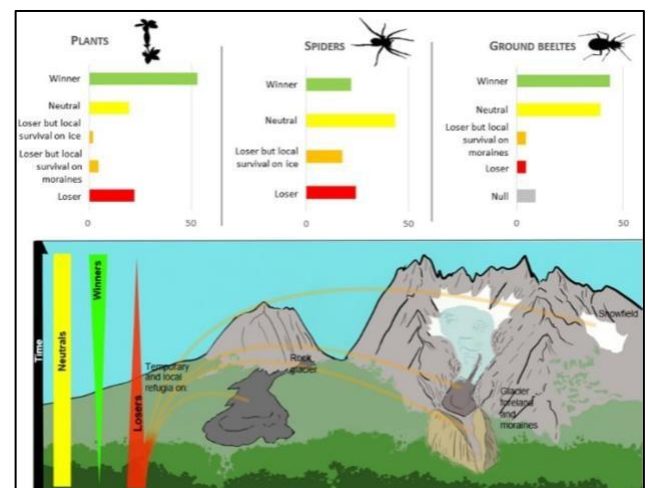


Fig. 1. Graphs show different responses of plants, spiders and ground beetles to a global increase in temperatures. The scheme at the bottom represents the general trends and possible refugia for ‘loser’ species.

III. DISCUSSION AND MAIN CONCLUSIONS

Species of vascular plants, ground beetles and spiders can be clustered into three groups based on their relationship with ice-related landforms: winners, neutral, and losers. Ice-related landforms may mitigate the extinction risk for some ‘losers’, which could benefit from landforms with a peculiar thermal profile acting as refugia (e.g., debris-covered glaciers, rock glaciers). Understanding the fate of high-altitude species in relation to the reduction of cold environments (cryosphere) is mandatory for the development of an Italian Glacial Biodiversity Monitoring Program.

ACKNOWLEDGEMENTS

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Tolerance ranges and trait-based distribution maps of the non-indigenous *Cassiopea andromeda* (Forskål, 1775) in the Mediterranean Sea

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Short summary: Temperature and salinity tolerance ranges and thresholds of the polyp stage of the scyphomedusa *Cassiopea andromeda* were determined by oxygen consumption rate, used as a proxy to assess metabolic response to sea warming. Trait-based distribution maps were created to predict its future distribution as non-indigenous species in the Mediterranean Sea.

Keywords: Metabolic response, Cnidaria, Scyphistoma, Upside-down jellyfish, Climate change

I. BACKGROUND

Global warming and the rise of seawater temperature may impact jellyfish reproduction at different stages of their life cycle. For scyphomedusae, the benthic polyp stage plays a pivotal role in securing reproductive success, long-term survival, and an additional way of dispersal across habitats and geographic regions. Yet, knowledge on the natural distribution and eco-physiological optimal requirements of the polyp stage are lacking for most jellyfish species [1]. In light of a warming Mediterranean scenario, aim of this study was to investigate the thermal and salinity tolerance range, and the potential future distribution of the upside-down jellyfish *Cassiopea andromeda* (Forskål, 1775), a non-indigenous species in the Mediterranean Sea [2]. This information will help to identify its fundamental ecological niche and foresee its distribution under current and future scenarios of climatic change.

MATERIALS AND METHODS

To project current and potential future distributions of *C. andromeda* in the Mediterranean Sea, the tolerance limits of the polyp stage to temperature and salinity were investigated under laboratory-controlled conditions, using the oxygen consumption rate as a proxy of metabolism. Responses to 15 experimental temperatures (12°C to 40°C) and 12 salinities (24 to 46) were tested by means of Pysoscience-O2 Firesting devices. Based on experimental results, Thermal and Salinity Performance Curves (TPC and SPC, respectively) were constructed.

II. RESULTS

The polyp's performance curves showed a wide tolerance range for both variables, with a higher influence of temperature on the metabolic rate in comparison to salinity. As expected from a species native of the Indo-Pacific region, *C. andromeda* showed a curve characterized by lower performances at lower temperatures. The polyps reached the maximum performance at 35.4°C, with a thermal critical limit at 39°C. Further, *C. andromeda* can

be considered a generalist species for the tested salinity range, with the maximum performance at 27.3 and a reduced performance at lower salinities.

III. DISCUSSION AND MAIN CONCLUSIONS

This is the first research on the metabolic responses of *C. andromeda* polyps to key environmental variables, increasing our understanding of the eco-physiological performance of a non-indigenous and potentially outbreak-forming, *i.e.*, invasive jellyfish species. Differently from salinity, temperature can significantly influence polyp metabolism and can be a triggering factor for the jellyfish potential distribution. So far, mapping the fundamental thermal niche of the polyp stage of *C. andromeda* unraveled a prospective wide distribution over time and space across the Mediterranean basin, and a strong invasiveness and adaptability, even under extreme environmental conditions. Such information can be crucial to develop early warning systems, to design appropriate management plans to deal with species causing negative impacts on ecosystems and human activities [3]. However, given its mixotrophic metabolism, the impact of *C. andromeda* on marine food webs and biogeochemical cycles might be ultimately beneficial to humans and ecosystems.

ACKNOWLEDGMENTS

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Factors controlling virus-prokaryote interactions, microbial diversity, and ecosystem functioning in Antarctic deep seafloor

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In the Antarctic Ocean, changes in sea-ice extent, primary production, and organic matter export to the deep seafloor are expected due to climate change. Using a replicated and hierarchical sampling approach spanning local to macro-spatial scales, we investigated two deep-sea benthic regions in the Ross Sea which exhibited distinct trophic conditions. We found that bottom-water temperature and organic matter content are the main factors influencing prokaryotes and ecosystem functioning.

Keywords: Antarctica, Deep-sea ecosystem functioning, Viral infections, Benthic prokaryotic diversity

I. BACKGROUND

Temperature is expected to increase ice melting extending ice-free periods in Antarctica[1]. These changes are predicted to raise bottom-water temperature and enhance primary production leading to a subsequent increase in C export to the seafloor[1]. These variations can affect benthic prokaryotic biodiversity, and metabolic rates potentially accelerating organic matter biogeochemical cycling with profound changes in deep-sea ecosystem structure and functioning[2]. We investigated spatial and temporal changes in deep-sea benthic prokaryotic biodiversity and virus-prokaryote interactions in Antarctic sites characterized by different trophic conditions. We also studied the drivers of prokaryotic assemblages to explore the effects of changing temperature conditions and food inputs on deep-sea ecosystems and to infer their potential response to future climate change.

MATERIALS AND METHODS

Samples were collected in the JOIDES Basin (Area B) and in the Mawson Bank (Area C), in the Southern Ocean. Organic matter quantity (OM) and degradation rates, prokaryotic and viral abundance and production were performed according to [1]. For the analysis of prokaryotic diversity, the 16S RNA gene was amplified using the primer set 515F-Y (5'-GTGYCAGCMGCCGCGGTAA) and 926R (5'-CCGYCAATTYMTTTRAGTTT) and the amplicons sequenced on Illumina MiSeq platform.

II. RESULTS

Area B showed values 5-15 times higher in OM concentration, prokaryotic and viral abundances, and production than the oligotrophic Area C. We also observed a positive relationship between microbial metabolism, trophic resources, and viral production. Despite the highest availability of proteins in Area B, Area C displayed a faster OM turnover, a negative relationship between aminopeptidase activity and OM, and a positive relationship with bottom water temperature. Differences in OM content and temperature influence the number of prokaryotic taxa and the benthic prokaryotic community

composition as the two Areas were characterized by a different degree of dominance of the main taxa.

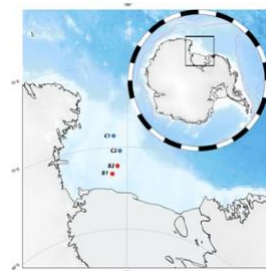


Fig. 1. Map of the Ross Sea showing the sampling Area B (Sub-area B1 and B2) and C (Sub-area C1 and C2).

III. DISCUSSION AND MAIN CONCLUSIONS

Benthic heterotrophs, including prokaryotes, are generally controlled by organic resources. Prokaryotic abundance was consistently higher where larger amounts of OM were present (Area B). The positive relationship between viral production (infection) and C production suggests that deep Antarctic viruses provide an important contribution to stimulating prokaryotic metabolism. Heterotrophic bacterial taxa in Area B are typically associated with OM-rich conditions and phytodetritus degradation processes. Conversely, taxa able to degrade complex polysaccharides are more relevant in the oligotrophic sediments of Area C. Here, the high richness of prokaryotic taxa specialized in the exploitation of refractory compounds and more efficient enzymatic digestion might cope with unpredictable inputs of organic matter maximizing the OM exploitation. We conclude that trophic resources and temperatures are the main drivers of benthic microbial communities and metabolism.

ACKNOWLEDGMENT

This study was carried out in the framework of the BEDROSE (PNRA) project.

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Thermal habitat suitability of invasive fish species: integrating physiological models and climate projections

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Short summary: The integration of physiology-based models and climate model output was used to identify a suitable thermal habitat of indigenous and non-indigenous fish species, in present-day and future climate projections. Aerobic Metabolic Scope (AMS) was used as a proxy of the fishes' fitness and sea temperature as a predictor affecting their optimal thermal window. The effectiveness of this approach was tested in European waters.

Keywords: Global warming, Invasive species, Thermal habitat suitability, Physiological model, Aerobic metabolic scope

I. BACKGROUND

The combination of physiology-based models and climate model downscaling offers a stirring perspective for the assessment of species distribution in the ocean. Here, we illustrate the outcomes of two research applications (III.A and III.B). The aerobic metabolic scope (AMS) is used as a measure of the energetic potential of fish to fuel their biological activities above those of their standard metabolic rate. This approach provides indications on the suitable thermal habitat for indigenous and non-indigenous fish species and how it varies in space and time, [1, 2, 3].

MATERIALS AND METHODS

Combining fish sightings records, physiological empirical models of AMS and oceanographic data, we (i) identify a nonlinear, physiology-based model by fitting the laboratory measurements of AMS and (ii) couple it with oceanographic data. In the following, we use specific indicators, based on AMS, to discuss the main outcomes.

II. RESULTS

A. Spreading of invasive specimens, Round goby, in the Baltic Sea

An Aptness Index (AI) describes the ratio between suitable and unsuitable thermal habitat of the Round goby (*Neogobius melanostomus*) in the Baltic Sea, between 1990 and 2021 (Fig. 1, top panel). AI >1 indicate that the percentage of suitable areas, characterized by favourable thermal conditions, is higher than the unsuitable ones.

B. Environmental fitness of competing, native and invasive, fish species in the Mediterranean basin

A Coexistence Factor (CF; Fig. 1, bottom panel) was derived, based on key features of physiology-based models of the native specie, *Sarpa salpa*, and the invasive species, *Siganus rivulatus*. CF was used to quantify the dimension of their shared thermal habitat (CF near zero; green areas), as well as habitat which are favourable for *Sarpa salpa* or *Siganus rivulatus* (blue and red areas, respectively), in present-days (left panel) and future climate projections (right panel).

III. DISCUSSION AND MAIN CONCLUSIONS

A physiology-based model, using AMS as a proxy for fish potential distribution at sea, relies on solid, reproducible laboratory experiments. Future work might aim at combining the present approach with ecological models of fish distribution, to enhance the predictive power of the outcomes.

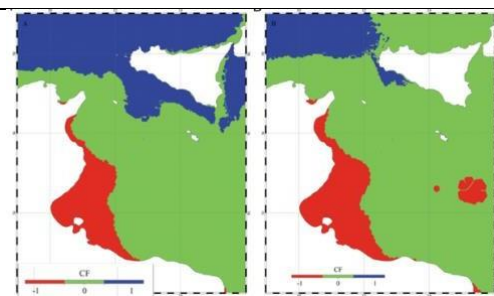
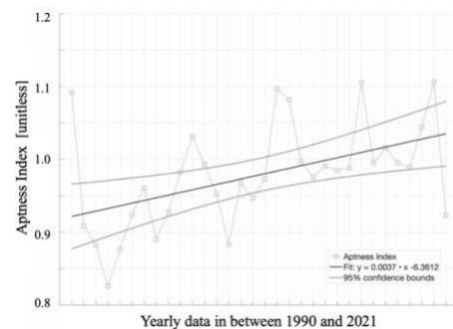


Fig. 1. Aptness Index in the Baltic Sea (top panel, Fig. 4 from [2]) and Coexistence Factor (bottom panel, Fig. 7 from [1]) in the Strait of Sicily.

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Biodiversity and fisheries in the Anthropocene

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Short summary: A fishery management strategy where bottom trawling is allowed only in selected areas with low presence of critical habitats and high catches is proposed. This strategy could balance the objectives of food production with those of biodiversity conservation.

Keywords: Precision fisheries, Impact mitigation, European policies, Spatial based management

The industrial revolutions and population growth since the 18th century have changed the relationship between humans, environment, and the other species with which they share the planet. Man's ability to exploit natural resources and transform the environment has begun to affect the ecological dynamics of the globe profoundly. All these changes suggest the advent of a new era, the Anthropocene. This process of uncontrolled transformation has essentially resulted in the degradation of marine ecosystems with a decline of biodiversity, understood as the number, distribution and abundance of living species. In this context, bottom trawling represents a controversial but interesting case study for investigating the ecological processes occurring in the marine environment, and identifying management approaches that allow for sustainable activities compatible with the needs of the era in which we live. Trawling is known to negatively impact marine ecosystems, and this impact varies depending on the nature of the biotope and biocenosis in which it operates. One of the well-known effects of trawling is the simplification of communities. Indeed, trawling removes larger individuals and species occupying the highest trophic levels, such as sharks, but also species with biological traits that are most vulnerable to the mechanical action on the sea bottom, such as deep sea corals. On the other hand, the experience of fishermen and theoretical and field research suggest that such simplification, reducing predators, may enhance food availability for species of low trophic level but

high commercial value, such as decapod crustaceans (e.g. the deep rose deep shrimp). Based on decades of experience in the field of fisheries resource assessment and management, this contribution aims to stimulate reflection on how to imagine and implement a trawl fishery compatible with sustainable use of space and living resources. This should be put into the context of an era characterized by the increasing reliance on data and advanced technologies to support human action. This approach, in analogy to what already occurs on landmass, is based on a 'dedicated' use of the maritime space in which 'anthropized' areas where fishing is permitted and primarily operates to sustain the ecosystem service of food supply, alternate with 'natural' areas where fishing activity is prohibited, aimed at regulation services (e.g. carbon fixation), support services (e.g. reproduction and recruitment), and cultural services (e.g. tourism and recreation). In other word, we advocate for a shift from a permissive fishing regime, where bottom trawling is permitted unless explicitly prohibited, to a targeted approach that allows fishing only in specific areas designated for their low prevalence of critical habitats and high fishery productivity. This specific use of the maritime space for fishing purposes presupposes an increasing involvement and responsibility of the fishers in the management of harvesting. It is believed that the proposed approach, in line with the process of maritime spatial planning promoted by the European Union, could balance the objectives of sustainability of fishing activities with those of protecting biodiversity and the marine environment that underpin EU policies.

Conservation genetics of the Italian alder (*Alnus cordata*) in the face of climate change

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Short summary: We modelled the impact of climate change on the distribution and genetic diversity of the Mediterranean endemic tree *Alnus cordata*, identifying in situ and ex situ conservation priorities for the species in its Italian distribution range

Keywords: *Alnus cordata*, Genetic diversity, Microsatellites, Conservation planning, Species distribution modeling, Climate change

I. BACKGROUND

The Italian alder (*Alnus cordata* (Loisel) Duby) is a Mediterranean endemic tree with a restricted distribution limited to southern Italian Apennines and Corsica. Under future climate change scenarios, several Mediterranean tree species are predicted to undergo range reduction and increased fragmentation [1]: in this context, a conservation strategy aimed at minimizing the loss of genetic diversity is urgently needed, for preserving their adaptation potential.

MATERIALS AND METHODS

We performed a comprehensive analysis of within- and between-population genetic diversity, at 10 microsatellite loci, in 23 *Alnus cordata* forest stands, covering the whole Italian distribution. Using 19 bioclimatic variables and CMIP6 climate projections, we mapped the current and future habitat suitability for the species with MaxEnt, and we carried out a genetically-informed conservation prioritization using the Reserve Selection analysis [2] implemented in DIVA-GIS, with the aim of identifying the minimum number of high-priority sites which are needed to preserve the overall estimated genetic diversity.

II. RESULTS

A. Genetic diversity and population differentiation

Two macro geographic areas showed the highest values for allelic richness and expected heterozygosity: Regional Park Monti Picentini and National Park of Appennino Lucano Val d'Agri Lagonegrese, with the latter also showing a high number of private alleles. We recorded relatively low levels of genetic differentiation between populations, indicating moderate to high gene flow between populations; STRUCTURE analysis identified two distinct genetic clusters, though without a clear geographic pattern.

B. Genetically informed conservation prioritization

a. MaxEnt habitat suitability modeling predicted a contraction of the distributional range for *Alnus cordata*, with the lost of some forest stands. The application of Reserve Selection procedure implemented in DIVA-GIS showed that 11 populations (~52%) are needed to preserve 100% of the genetic diversity of the species (Fig. 1), with 8 populations being classified as high-priority based on their genetic diversity levels.

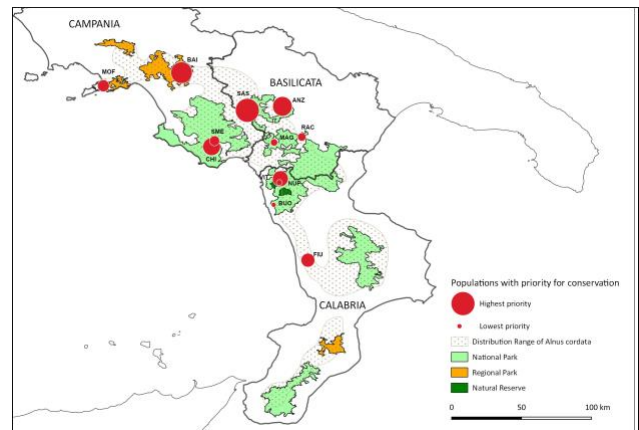


Fig. 1. Map of *Alnus cordata* populations according to their conservation priority rank, as identified by the Reserve Selection procedure implemented in DIVA-GIS based on genetic diversity data.

III. DISCUSSION AND MAIN CONCLUSIONS

Our study showed that the combination of an extensive genetic survey with habitat suitability modeling, for predicting the future distribution of species, and genetically informed spatial prioritization, allows to develop proper guidelines for the long-term conservation of Mediterranean trees and their associated ecosystems. In particular, we identified (a) high priority forest stands for *Alnus cordata* in the Italian peninsula, which should be included in an in situ conservation network, as well as (b) areas which are predicted to become less suitable for the species under future climate scenarios. Considering the first case, all the high priority sites except one (FIU) are already part of protected areas, while in the latter case, the establishment of a proper ex situ conservation program (i.e., seed bank or germplasm core collection) could allow the preservation of their gene pool even in case of habitat loss.

ACKNOWLEDGMENT

Project funded by the European Union – NextGenerationEU.

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Opposite effects of climate and land-use change on Mediterranean highland protected areas: insights from herpetofauna of Southern Italy

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Short summary: Climate and land-use/cover change are altering species distributions, particularly among amphibians and reptiles. Using climate and land-use/cover suitability models, we examined the possible effects of these threats on 27 species of Cilento (Campania). We estimated climatic suitability loss for the majority of species whereas land renaturalization may benefit them.

Keywords: Amphibians, Area of Habitat, Local conservation, Protected Areas, Reptiles, Species Distribution Modeling

I. BACKGROUND

Climate change (CC) and natural land conversion are causing drastic alterations in species distribution. Particularly exposed to these threats are amphibians and reptiles, ectothermic animals with limited dispersal ability, and Mediterranean mountain ranges, hosting numerous taxa adapted to local conditions. This is the case of Cilento, a highly biodiverse yet under-investigated area in southern Italy, protected by a National Park and 30 Natura 2000 (N2000) sites. We evaluated the possible combined impact of CC and land-use/cover change (LUCC) on 11 amphibians and 16 reptiles in the Park and the connected N2000 sites through Species Distribution Models (SDMs) and Area of Habitat (AOH) models.

MATERIALS AND METHODS

The Cilento protected areas (PAs) have a diverse topography and two major Köppen-Geiger (KG) categories: the lowland zone, with a Csa climate, primarily occupies coastal and lower elevation areas, whereas the highland zone, with a Csb climate, encompasses inland and mountainous regions. We obtained species occurrences for 11 amphibians and 16 reptiles in the PAs through decennial fieldwork, citizen science and literature¹. We developed species SDMs using an ensemble of algorithms that correlate occurrences with climatic characteristics², and AOH by categorizing land-use/cover types based on species-habitat relationships³. We obtained climate data from Worldclim (<https://worldclim.org/>) and LUCC data from Globio4 (<https://www.globio.info>) at a resolution of 1 km². We estimated climate suitability (CS) and AOH for the present and two scenarios of CC/LUCC: sustainability (SSP1-2.6) and fossil-fueled development (SSP5-8.5) and we combined the two projections to obtain consensus suitability (CS+AOH).

II. RESULTS

A. Climatic suitability and AOH for species

All SDMs performed well across the three metrics (median ROC = 0.930, TSS = 0.720, and Boyce = 0.970). Most species showed significant CS loss in both scenarios, with the greatest declines estimated for SSP5-8.5. Highland species appear to be the most vulnerable, while lowland species could gain CS. AOH showed gains or stability for all species in both scenarios. Consensus responses (CS+AOH) were mostly driven by CS (Fig. 1.A).

B. Species richness

The CS+AOH models estimated high α diversity across the study area. Both scenarios are expected to result in a significant reduction in herpetofauna diversity at lower elevations. In fact, α diversity declined significantly more

in Csa than Csb under SSP1-2.6 and SSP5-8.5 for both reptiles and amphibians (Fig. 1.B).

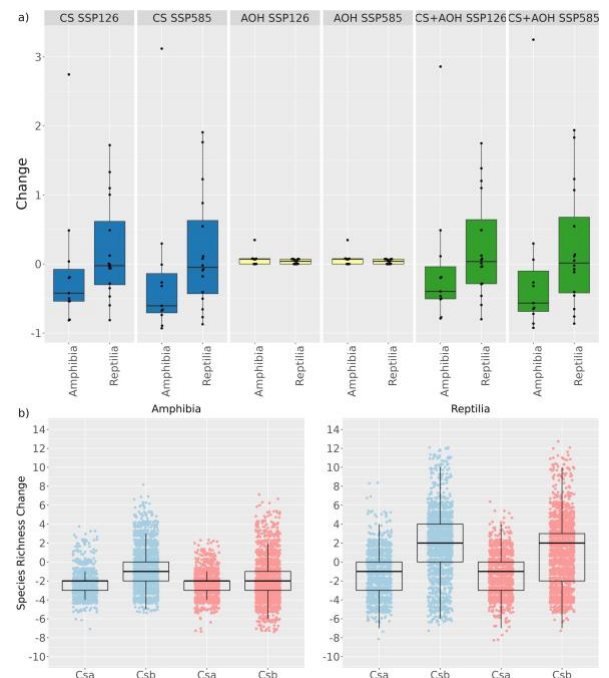


Fig. 1.A) Change in CS, AOH and CS+AOH under the two selected scenarios of CC and LUCC. 1.B) Change in α diversity per grid cell for the Csa and Csb categories under SSP1-2.6 (blue) and SSP5-8.5 (red).

III. DISCUSSION AND MAIN CONCLUSIONS

As the renaturalization of agricultural land is widespread in both scenarios, most species did not show declines in AOH due to land-use change. However, significant shifts in CS are projected for all species in both scenarios, posing a crucial challenge to their survival. Our results could inform climate mitigation projects to ensure the long-term protection of herpetofauna inside Cilento's PAs.

ACKNOWLEDGMENT

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Flying from lowlands to summits: projected effects of climate change on butterflies in Central Italy

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Short summary: Butterflies serve as essential pollinators across ecosystems and are threatened by climate change (CC). The LIFE BEEadapt project seeks to improve pollinator resilience through climate mitigation efforts in Central Italy. Using species distribution models and opposite scenarios, we assessed butterfly vulnerability to CC, informing the project conservation strategies.

Keywords: Protected Areas, Climate Change, Endangered Species, Biodiversity, Pollinators, Species Distribution Modeling

I. BACKGROUND

Diurnal butterflies are important pollinators in natural ecosystems and contribute significantly to agricultural productivity. Worryingly, a growing body of literature suggests that climate change (CC) may result in the extinction and decline of many butterfly species¹. Understanding which species and areas are most vulnerable to climate change is essential for planning conservation and mitigation efforts. The project LIFE project BEEadapt aims to improve pollinator climate resilience in four areas in Central Italy, including protected areas, natural and agro-ecosystems.

MATERIALS AND METHODS

The LIFE BEEadapt project focuses on four study areas: the Pontine plain (PP) (Latium), the Roma Natura protected areas (RNPA) (Latium), lowland/hilly areas, the Torricchio Natural Reserve (TNR) (Marche) and the Appennino Tosco-Emiliano National Park (ATENP) with buffer zone (Emilia Romagna), two mountainous areas. We developed species distribution models (SDMs) using biomod2 R package², the algorithm Maxent, and two CC scenarios by 2050: sustainable (SSP1-2.6) and fossil-fueled development (SSP5-8.5), to assess the potential impacts of CC on 114 butterflies. Species data was obtained from the Global Biodiversity Information Facility (<https://www.gbif.org/>) and bioclimatic data from Worldclim (<https://www.worldclim.org/>) at a resolution of 1 km². Model performance was assessed using the ROC, and Boyce Index³.

II. RESULTS

A. Climatic suitability for species

All SDMs showed high performance according to the ROC (median across species 0.655) and Boyce Index (0.95). We find that butterflies have a consistent vulnerability pattern at both the species and multispecies level. In the study areas, CC appears to favor lowland and generalist species, which increase their climatic suitability under both scenarios, particularly in mountains. Mountain and specialist species are expected to have reduced climatic suitability, especially under the SSP5-8.5 (Fig. 1.A).

B. Species richness

A comparable pattern appeared while examining changes in species richness in the study areas. Per cell changes in species presence were projected to be primarily negative for mountainous areas (PNATE and TNR), whereas the PP and RNPA showed more positive trends (Fig. 1.B).

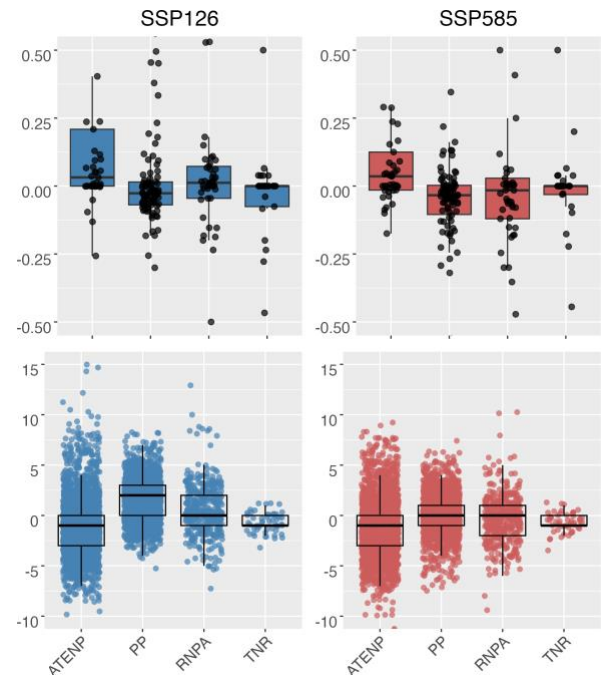


Fig. 1.A) Change in species' climatic suitability and 1.B) change in species richness in the four study areas under the SSP1-2.6 and SSP5-8.5 scenarios.

III. DISCUSSION AND MAIN CONCLUSIONS

Our findings are comparable with prior study on the effects of climate change on pollinators, which revealed similar sensitivity patterns based on species ecology¹. We provided new insights into species' potential local responses to CC, allowing to set conservation priorities and direct LIFE BEEadapt mitigation actions. Conservation measures such as habitat restoration and connectivity enhancement will be critical to the long-term survival of these butterfly populations.

ACKNOWLEDGMENT

Research funded by the LIFE BEEadapt - a pact for pollinator adaptation to climate change, LIFE21-CCA-IT-LIFE BEEadapt/101074591, <https://www.lifebeeadapt.eu/>.

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SpSpecies distribution comparison and interaction of *Clethrionomys glareolus* and *Chionomys nivalis* in a changing climate

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Short summary: Utilizing species distribution models, this study reveals a projected decrease in habitat suitability and an increased overlap in environmental niches for the Bank vole (*Clethrionomys glareolus*) and Snow vole (*Chionomys nivalis*) in Europe's changing climates, highlighting significant contemporary biodiversity changes.

Keywords: Species Distribution, Niche Overlap, Generalist Species, Specialist Species, Montane Ecology, Climate Change Impact

I. BACKGROUND

In the Anthropocene, biodiversity loss and climate change are alarming concerns, leading to accelerated vertebrate extinctions and ecosystem shifts (Ceballos et al., 2015; Pörtner et al., 2021). These changes disproportionately affect specialist species compared to generalists, reflecting the nuanced impacts of these global challenges (Clavel et al., 2011).

MATERIALS AND METHODS

This study utilized GBIF data for vole occurrences with an applied thinning to mitigate sampling biases. The study area was defined around the snow vole occurrences and bank vole data was adjusted accordingly. Environmental predictors include the Bioclim variables and ENVIREM data, with future projections modeled under the SSP5-8.5 scenario for 2041-2060. An ensemble out of a Generalized Boosted, Random Forest and Support Vector Machine Model was used in regard of TSS and AUC metrics. Predictions were made for both current and future conditions, and variable importance was assessed. Environmental niche overlap between species was evaluated, and altitude changes in the bank vole's distribution were analyzed.

II. RESULTS

The ensemble model for bank and snow voles demonstrated strong performance (AUC and TSS metrics > 0.9).

Future predictions revealed a decline in occurrence probabilities for both species (bank vole: 32.2%, snow vole: 25.5%). The most influential environmental variables were identified: for bank voles, temperature, evapotranspiration, and aridity index; for snow voles, terrain roughness.

The analysis showed increased environmental niche overlap in the future, with Schoener's D value rising from 0.423 to 0.503 and Warren's I from 0.689 to 0.764, indicating a 18.9% and 10.9% increase, respectively.

Additionally, the bank vole's altitude range is predicted to rise by an average of 56.2 m, equating to a 9.4 m per decade increase, supported by a significant t-test (p-value: 0.0002).

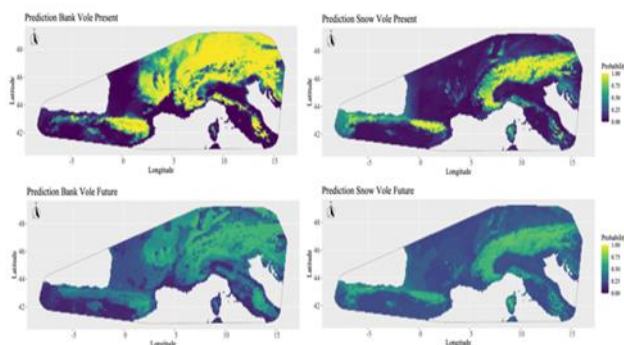


Fig. 1. Predicted model output of occurrence probability for the Bank vole (right) and Snow vole (left) for present day (top) and future (bottom) environmental conditions.

III. DISCUSSION AND MAIN CONCLUSIONS

The decline in occurrence probabilities in future climatic conditions was prominent for both species, however stronger for the bank vole than for the snow vole. With the most preeminent variables in shaping the bank vole model, reflecting vegetational growth within the ecosystem, the snow vole model was strongly drawn to the ruggedness of the terrain, which in both cases respectively aligns with the species habitat requirements. This could explain the stronger predictive change in the bank vole model as its predictors are more affected by climate change. With the observed niche overlap and elevational gains by the generalist species, study suggests interspecific competition may intensify in future, with localized effects in overlapping habitats. Overall, it predicts bank and snow voles will persist, but face habitat shifts and possible range reductions under the SSP5-8.5 climate scenario. Further refinement of the subject could be achieved by better data congruency and possible in-situ data.

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Distribution of *Caulerpa cylindracea* and *Posidonia oceanica* implementing Habitat Suitability Models

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Short summary: Habitat Suitability Models (HSMs) were implemented to characterize the distribution of *C. cylindracea* and *P. oceanica* to gain a deeper understanding of the factors driving the presence of these competing species.

Keywords: Habitat suitability model, *Posidonia oceanica*, *Caulerpa cylindracea*, Climate change, Maxent, Random forest, competing species

I. BACKGROUND

Biodiversity studies require for a detailed analysis of the habitat where marine species live since they can be affected by changes in environmental conditions. The purpose of this study was to characterize the distribution of the habitat-forming *P. oceanica* and one of its competitors: *C. cylindracea*, known for its capacity of invading different habitats and grow rapidly. Moreover, this study served as a foundation for further investigations into potential changes and adaptations of the species in climate change scenarios.

MATERIALS AND METHODS

Habitat Suitability Models (HSMs) were used to determine the areas where the species is most likely to occur. This was done by analyzing environmental variables from 1999 and 2020 and correlating them with the species' occurrences using different algorithms such as General Additive Model (GAM), General Linear Model (GLM), Maximum Entropy (MaxEnt), and Random Forest (RF).

Some of the variables considered were current velocity, salinity, sea-floor temperature, sea water temperature, nitrate, and phosphate. Additionally, the study also included bathymetry, spectral significant wave height, and wave period at spectral peak. Data were trained and tested following the spatial-block method.

II. RESULTS

The algorithms successfully distinguished positive and negative classes, with some exceptions as reported in Tab. I.

TABLE I. AUC VALIDATION METRICS

<i>C. cylindracea</i>				
	GAM	GLM	MAXENT	RF
RUN1	0.888	0.827	0.936	0.856
RUN2	0.872	0.65	0.697	0.832
RUN3	0.887	0.861	0.971	0.911
RUN4	0.534	0.626	0.535	0.467
RUN5	0.993	0.544	0.969	0.52
<i>P. oceanica</i>				
	GAM	GLM	MAXENT	RF
RUN1	0.812	0.742	0.787	0.811
RUN2	0.895	0.833	0.922	0.865
RUN3	0.824	0.791	0.769	0.723
RUN4	0.905	0.872	0.904	0.911
RUN5	0.968	0.972	0.981	0.978

The analyses permitted also to identify the variables that most influence the species' distribution (first three are in Tab. II).

TABLE II. INFLUENCING VARIABLES

<i>C. cylindracea</i>			
GAM	GLM	MAXENT	RF
pH (65%)	pH (64%)	Bathymetry (52%)	Bathymetry (27%)
Bathymetry (30%)	Bathymetry (34%)	Current velocity (28%)	Salinity (8%)
Sea-floor temperature (27%)	Sea-floor temperature (54%)	Salinity (19%)	Nitrate (6%)
<i>P. oceanica</i>			
GAM	GLM	MAXENT	RF
pH (73%)	pH (56%)	Bathymetry (33%)	Bathymetry (23%)
Sea water temperature (27%)	Sea water temperature (18%)	pH (32%)	Salinity (16%)
Bathymetry (17%)	Bathymetry (25%)	Wave period at spectral peak (18%)	Wave period at spectral peak (12%)

III. DISCUSSION AND MAIN CONCLUSIONS

The algorithms produced consistent results with some exceptions in RUN4 for *C. cylindracea*. This result is likely due to the implementation of spatial blocks, suggesting that the application of HSMs algorithms in specific areas may be influenced by the amount of occurrence points.

However, it should be noted that despite the high resolution, all the models had a good discriminatory capacity.

Bathymetry appears to be one of the most crucial variables influencing *C. cylindracea* and *P. oceanica* habitat distribution, representing a physical barrier and hindering the presence of both species at greater depth, with rare observed exceptions. Other factors that affect the distribution of *C. cylindracea* are pH, temperature, salinity, current velocity, and nitrates. *P. oceanica* distribution is driven by pH, temperature, salinity, and waves components.

To conclude, this study characterizes the habitat conditions allowing the presence of *C. cylindracea* and *P. oceanica*, providing a knowledge base to guide future investigations on the potential changes in their distribution and on their potential capability to adapt to climate change.

ACKNOWLEDGMENT

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Large-scale risks of an emergency phytosanitary action plan on regional biodiversity

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Short summary: Assessing impacts associated with the implementation of a regional phytosanitary action plan highlights a set of neglected and large-scale risks concerning a significant portion of EU-protected habitats and species in Puglia, Italy.

Keywords: Risk assessment, Agricultural policy, Natura 2000, Habitats Directive, *Xylella fastidiosa*, Conservation gap

I. BACKGROUND

Among anthropogenic pressures, agriculture is known to globally affect biodiversity and ecosystem stability, in terms of loss and degradation of habitats, species populations and ecosystem functions, thus usually requiring risk assessment procedures for plans and programs. Yet, emergency regulations are often issued without being formally evaluated through an accurate environmental impact assessment. Here, we assess the risks associated with the implementation of a phytosanitary action plan for counteracting the expansion of *Xylella fastidiosa* infection in Puglia (XAP) on protected habitats and species listed in the EU Habitats and Birds Directives.

MATERIALS AND METHODS

The XAP includes two yearly actions for the control of the primary vector of the infection, *Philaenus spumarius*: A1) soil tillage and weeding during spring to limit feeding resources of juvenile stages; A2) chemical treatments to control adult abundance on cultivated plants. Both actions are mandatory in some municipalities and recommended in the entire regional territory. Based on the best available regional cartographic information (www.sit.puglia.it), we separately quantified the overlap of land-cover classes subject to the implementation of A1 and A2 with the surfaces of EU habitats and EU species' suitable habitats occurring in the region (Fig. 1.A).

II. RESULTS

According to XAP requirements, A1 treatments affect a surface ranging between 8.6% (mandatory) and 36.1% (mandatory and recommended) of the regional territory overall. On average, these treatments lead to potential loss or degradation of 4.2 to 20.2% of the regional cover of EU-protected habitats (Fig. 1.B). Expected impacts are particularly high for 13 habitat types, namely grassland (up to 50.4%), saltmarsh (30.5%) and swamp habitats (16.2%). A1 action significantly affects 35.0% of EU-protected species, and 15.2 to 61.4 % of their overall suitable habitats, especially concerning generalist species (5.3 to 21.6%) and grassland specialists (3.1 to 21.0%). For half of the EU-listed arthropods and insectivorous species possibly targeted by insecticides, a considerable portion of suitable breeding or foraging habitat (Fig. 1.B) is potentially threatened by A2 treatments, with average impact being higher on species associated with agricultural (4.2%), riverine (3.7%) and grassland ecosystems (2.5%).

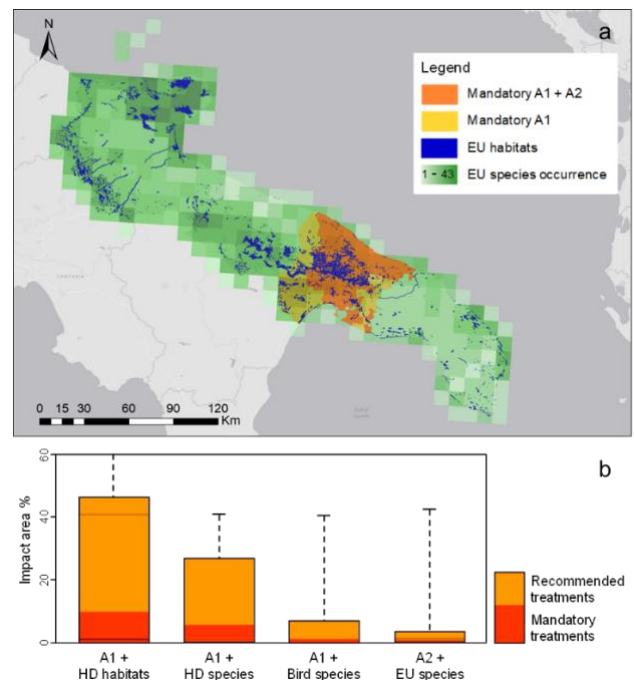


Fig. 1. A) Cartographic layers considered for the study in Puglia, southern Italy: areas of mandatory actions A1 against juvenile stages and A2 against adult stage of *P. spumarius*; regional distribution of EU habitat categories (polygons) and EU species (100 km² cells). b) Impact surface percentage of A1 on habitats and species (Habitats and Birds Directive), and A2 treatments on target species groups, either mandatory or recommended.

III. DISCUSSION AND MAIN CONCLUSIONS

The action plan issued to counteract the plant infection by *X. fastidiosa* in Puglia implies several risks potentially concerning biodiversity at a regional scale, with significant impacts on the conservation of EU-protected habitats and species. Local effects can reverberate globally for those habitats that are particularly threatened within their range, i.e. the case of temporary ponds and therewith-associated species, and for the species and habitats endemic from the region. A considerable loss and degradation of key habitats and communities may dramatically threaten ecosystem stability and functionality, e.g. in terms of breakup and imbalances within habitat networks and food webs. Considering the expected loss of ecosystem services associated with the control of pest insects, further studies should assess whether the proposed XAP regulations are effective, or potentially counterproductive, in limiting the expansion of the plant disease, at such ecological costs.

Climate change effects on aquatic invertebrates fitness, energy and resource use

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Short summary: Underground ecosystems have been explored mostly from a naturalistic point of view. The Apulian peninsula is 44.6% of karsic origin, being the first Italian region in terms of hypogean habitats. This ecosystem represents a source of ecological knowledge, that have been underestimated. The oligotrophic habitat present in caves and underground waters, is affected by climate change, and what we risk to loss in biodiversity is unknown and unvaluable. These habitats are used to stable conditions, even small variations can alter the equilibrium and result in strong selective pressure. Our study on energetic and behavioural patterns can imply further understanding also at macro- ecological context.

Keywords: Underground, Invertebrates, Metabolism, Resource use, Climate change

I. BACKGROUND

Alarmingly, groundwaters and springs are considered among the most fragile natural habitats of the world [1]. Anthropogenic-driven factors such as water pollution and climate changes can disrupt stygofauna communities and spring boundaries promoting groundwater colonization by surface animals with unknown consequences on groundwater functionality. A key role is played by the Pace of Life Syndrome (POLS), which assumes that closely related species or populations experiencing different ecological conditions should differ in a suite of metabolic, hormonal and behavioural traits that have coevolved with the life-history particularities related to these conditions [2]. The mechanistic understanding of energy and resource use by organisms at the interface between hypogean and epigeal habitats is of primary importance to predict future functioning of groundwater ecosystems.

MATERIALS AND METHODS

Sampling specimens from surficial and subterranean fauna, from different areas in Italy. The sampling campaign has been established within the framework of the PRIN 2022 STIGE-CLIMAQUIFERI. Laboratory experiments: comparative study on metabolic and behavioural patterns. First foraging behaviour assays with the use of automated video analysis. Quantification of the resource use and ingestion rate of *Speleomysis bottazzii* (model species) main species. Second respirometry assays with open flow system for the assessments of oxygen consumption as proxy of standard metabolic rate (SMR). As last comparison with data already acquired with a superficial model organism *Gammarus insensibilis*, and dormant data from the speleological societies of the territory.

II. RESULTS

Evaluation of the extent at which the POLS hypothesis can be applied across a broad range of taxonomic groups, habitat heterogeneity and lifestyle diversity by taking advantage of the peculiar metabolic adaptations of the stygofauna which will provide a comparison for a baseline estimate of metabolic rate and activity. Thanks to the limited size of the animals and their resistance to low oxygen contents, they will be easily collected and quickly transported to the laboratory from every Italian sampling site following standard protocols for live invertebrates

Fig. 1. A Map of the planned sampling points (in red). The map is taken from the map of Italian karst aquifers; in yellow are shown main karst areas and in blue main aquifers. B This figure shows one of our main model organisms *Speleomysis bottazzii*.



III. DISCUSSION AND MAIN CONCLUSIONS

The experiments will be carried out in two temporal tranches, corresponding to the two investigated seasons. This, in conjunction with the geographic distribution of the study sites, will give us the opportunity to test the effect of surface temperature fluctuations on both epigeal and hypogean populations. As empirical support for the POLS hypothesis is still mixed, advances future studies and model development. We also expect to obtain a model about niche overlap between hypogean animals and surface animals.

ACKNOWLEDGMENT

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Session #3 Tools for understanding and managing the change

Moderators: Ilaria Rosati & Flavio Monti

Summary of the thematic session

In an era of rapid climate and environmental change, understanding the factors that generate them is crucial as it can help describe and predict their effects on various spatio-temporal scales. As the volume of available data is rapidly increasing, several projects and infrastructures are developing services to better manage this information, making it accessible, available and reusable to create new knowledge. However, a common criticism that clearly emerged from the interventions of the speakers of the Session 3 "Tools for understanding and managing change" recalled the high heterogeneity and non-standardized sharing of biodiversity data at multiple levels and the fact that this fragmentation of scientific knowledge risks undermining the understanding of these changes. Therefore, the development of tailor-made tools to better understand and manage this change across multiple knowledge domains seems to be a priority. The thematic round table allowed participants to further delineate critical issues, set more urgent priorities and propose operational and synergistic approaches for the future. The discussion initially focused on the need to invest more energy in covering the knowledge gap at the taxonomic level through the integration of traditional methods and new technologies (i.e. AI, environmental DNA and barcoding, remote sensing, satellite tracking data, long-term monitoring stations) to estimate biodiversity and changes in their composition and diversity in relation to environmental changes. Lack of information on responses to changes for many functional and ecological parameters (metabolic, movement) and on different spatial and temporal scales exists. In parallel, dispersion of currently available platforms (lack of data centers, multidisciplinary hubs), lack of interoperability between the various existing platforms and paucity in powered hardware resources to process large amounts of data emerged as additional critical issues. In this sense, harmonization of data collection protocols, interdisciplinary approaches and data sharing (even in real-time) have been advocated as priorities to understand specific phenomena and ameliorate management and conservation strategies to be applied.

Among operational proposals for the future there were first of all not to lose basic knowledge of specialized figures in biodiversity monitoring programs and species identification (e.g. taxonomists) in the coming future. In this sense, new technologies should be seen as an integrative approach rather than a replacement of the former. Accordingly, investing in training plans (training/learning) and propose to integrate these highly-specialized professional figures at local, regional and European level as a recognized workforce would be a first step forward. Eventually, digital platforms dedicated to museum collections or barcoding data, as a tool accessible to all for open research, should be implemented in the future and likely converge into larger and common biodiversity gateways processing data in an automated and harmonized way.

Adopting operational synergies for the study and integrated management of invasive alien species

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Short summary: To tackle the current fragmentation of scientific endeavors related to Invasive Alien Species (IAS), a multi-disciplinary team of researchers has been convened under the framework of the USEit project, led by the National Research Council of Italy (CNR). Pilot studies focusing on different species, habitats and monitoring techniques are used to test the robustness of these approaches. This effort is generating technical and operational advice for bioinvasion research and will hopefully develop new capabilities for IAS management.

Keywords: Biological invasion, IAS, data management, FAIR, Open Science

I. BACKGROUND

Biological invasions represent one of the greatest threats to global biodiversity, with negative impacts on human and ecosystem health and on the economy of our countries [1]. Despite the ever-growing scientific interest towards this global threats, national and international prevention and control measures have been not sufficient to reverse or limit the negative impacts of invasive alien species (IAS). One of the inherent challenges is related to the diversity of species and habitats affected and to the heterogeneity of scientific evidence collected. In addition, the lack of shared monitoring strategies and the poor data management practices limit the capacity to tackle this issue using efficient management solutions [2].

To address the prevailing fragmentation in research efforts concerning IAS and to foster the creation of community-shared and integrated strategies for IAS management, a multi-disciplinary team of researchers, has been assembled by the USEit project. This team is working at enhancing capabilities for monitoring and managing IAS, with one approach rooted in the principles of the Open and FAIR (Findable, Accessible, Interoperable, Reusable; [3]) science.

MATERIALS AND METHODS

A number of actions have been carried out to gather information about existing approaches for IAS data collection and data management including: *i.* a national survey; *ii.* an extensive bibliographic review; *iii.* a workshop with IAS experts. From these efforts, guidelines on IAS data collection have been drafted and evaluated through a SWOT analysis whereas data management practices have been tested through a series of pilot studies focusing on key terrestrial and aquatic IAS.

II. RESULTS

A list of integrated and community-accepted guidelines on IAS data collection and IAS monitoring have been released along with a Data Management Plan (DMP) that describes the coordinated strategies adopted for IAS data management. The DMP ensures the good quality of the published data as well as their accurate documentation,

annotation, storage, and long-term preservation. In addition, the existing and novel IAS research data collected within the pilot studies are available through a unique access point in the LifeWatch Italy Data Catalogue that includes:

1. Distribution and abundance data of aquatic and terrestrial IAS (*i.e.* *Anadara kagoshimensis*, *A. transversa*, *Siganus luridus*, *S. rivulatus*, and *Halyomorpha halys*);
2. Satellite data of habitats invaded by *Ailanthus altissima*;
3. Stable isotope data of aquatic and terrestrial IAS (*A. kagoshimensis*, *A. transversa*, *S. luridus*, *S. rivulatus*, *Pempheris rhomboidea*, *Callinectes sapidus*, *A. altissima*);
4. DNA Metabarcoding data of mycorrhizae associated to the roots of *A. altissima*;
5. Telemetry data of *C. sapidus*;
6. Nutraceutical and elemental composition analysis of *C. sapidus*.

III. DISCUSSION AND MAIN CONCLUSIONS

The guidelines and approaches implemented for IAS monitoring and data management are aligned with international standards adopted for IAS research.

Therefore, the technical and operational solutions achieved within the context of USEit, can be used in the field of bioinvasion research within and beyond the CNR institutes working on IAS. Hopefully, this process, will also develop new capabilities for IAS management, including their potential use as an economic resource under the principles of a sustainable circular economy.

ACKNOWLEDGMENT

We are grateful to Marco Lauteri, Laura Loru, Giorgio Mancinelli, Carlo Pipitone, Giuseppe Scarcella and to all members of the USEit team.

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sRedList: A user-friendly platform for accelerating and prioritising IUCN Red List assessments

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Short summary: The IUCN Red List faces challenges due to the high proportion of outdated assessments. The sRedList platform offers a user-friendly interface to guide assessors through risk assessments, potentially reducing costs and time, improving global conservation monitoring.

Keywords: Conservation assessments, Monitoring, National Red List, biodiversity conservation, extinction risk, web application

I. BACKGROUND

The IUCN Red List of Threatened Species (RL) is a bedrock of decision-making for conservation, and global biodiversity monitoring. However, the shortage of funds and limited assessor time slows the uptake of novel data (occurrence records, species traits, and remote-sensed data) and techniques, reducing its applicability, consistency and long-term viability [1]. Here, we present sRedList, a user-friendly, interactive online platform that assists Red List assessors through a step-by-step process to estimate key parameters in a standardised and reproducible fashion.

MATERIALS AND METHODS

By bringing together RL practitioners and ecological modellers in a series of international workshops, we have designed and developed the sRedList platform, a user-friendly web-interface that guides assessors through a step-by-step procedure to assess species' extinction risk [2]. Steps include the definition of: 1) range map; 2) countries of occurrence; 3) Extent of Occurrence; 4) Area of Occupancy; 5) Population size estimate; 6) Trends in Area of Habitat over time; 7) Fragmentation; 8) Trends in human pressures within the species range over time (Fig. 1). Based on all these estimated parameters the platform returns all key parameters for RL assessment together with suggested RL categories its uncertainty.

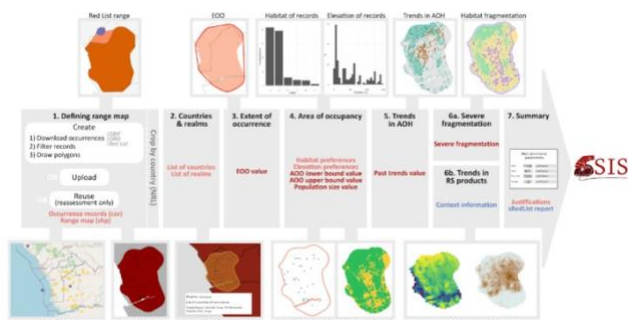


Fig. 1. Schematic workflow of the sRedList platform.

II. RESULTS

The sRedList platform (Fig. 2) has undergone an official test by RL assessors during the summer 2023, adjusted based on the comments received and launched online on

Oct. 2023 (<https://sredlist.eu/>). Two online international workshops were organized to present the platform to the RL community, which has been received enthusiastically. We are currently monitoring its usage and planning further updates to expand its functionalities.



Fig. 2. Official sRedList platform logo.

III. DISCUSSION AND MAIN CONCLUSIONS

Facilitating and streamlining the assessment procedure, the platform can reduce costs and time required to perform assessments, therefore improving our capacity to track global trends in the conservation status for multiple taxa. By eliminating technical barriers that prevent assessors from using certain data and analyses, the platform will also reduce taxonomic inconsistencies and the number of Data Deficient species. Overall, the sRedList platform has the potential to underpin the viability of the RL in the future.

ACKNOWLEDGMENT

We are grateful to LifeWatch Italy to provide the facilities and in-kind support that were key for the development of the platform.

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Artificial water bodies and amphibians

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Short summary: We disclosed that the artificial water sites (AWS) can serve as a key piece of the ecological connectivity for amphibian populations. AWS and Natural water sites have comparable values at the landscape scale, but in some areas AWS are pivotal. Furthermore, many AWS contribute by buffering the effect of climate change in the near future.

Keywords: Amphibian conservation, Climatic niche modelling, Landscape connectivity, Landscape management

I. BACKGROUND

In the Mediterranean region, amphibians, the most threatened class of vertebrates, breed in a large variety of artificial water sites (AWS), i.e., sites radically different in structure compared to natural ones (e.g., troughs, tanks).

MATERIALS AND METHODS

Using a dataset of both natural (NWS: 1006) and AWS (564), we addressed three key questions. Q1 - Are populations breeding in AWS ecologically connected with natural populations? We employed omni-directional electric circuit theory at the landscape scale to model the connectivity of the amphibian community. Q2 - Do AWS demonstrate the same effectiveness as NWS in maintaining ecological connectivity within the landscape? We assessed the significance of each site by measuring its node importance on the network. Q3 - Can AWS enable amphibian populations to persist in more extreme climatic conditions compared to NWS, thus mitigating the negative effects of climate change? We examined the climatic niche shift between AWS and NWS for each species.

II. RESULTS

A1 - We detected that the median NCF (normalized current flow, representing ecological connectivity at the landscape scale) of some sub-areas was significantly higher in NWS than AWS. A2 - From spatial layout of the graphs and of the node importance (Fig. 1) emerged: i) an uneven distribution of NWS and AWS, ii) a clustered and uneven distribution of node importance within the two water site categories. Indeed, in LUC, VOL, CIL and BAS the importance of AWS in maintaining network connectivity was central. A3 - We found significant niche variation between NWS and AWS for many species. Some species showed a broader climatic niche for in AWS compared to NWS (Fig. 2). AWS may influence the climatic niches of certain amphibian species, potentially leading to niche expansion or alteration in comparison to natural habitats.

III. DISCUSSION AND MAIN CONCLUSIONS

AWS can serve as a key piece of the ecological connectivity for amphibian populations; AWS and NWS have comparable values at the landscape scale, but in some areas AWS are pivotal. Furthermore, many AWS contribute by buffering the effect of climate change in the near future. Conservation management strategies would be strengthened by including a specific focus on human-made aquatic habitats. AWS can be a cost-effective way to increase habitat suitability and maintain connectivity

between different parts of the ecological network, increasing genetic diversity and gene flow.

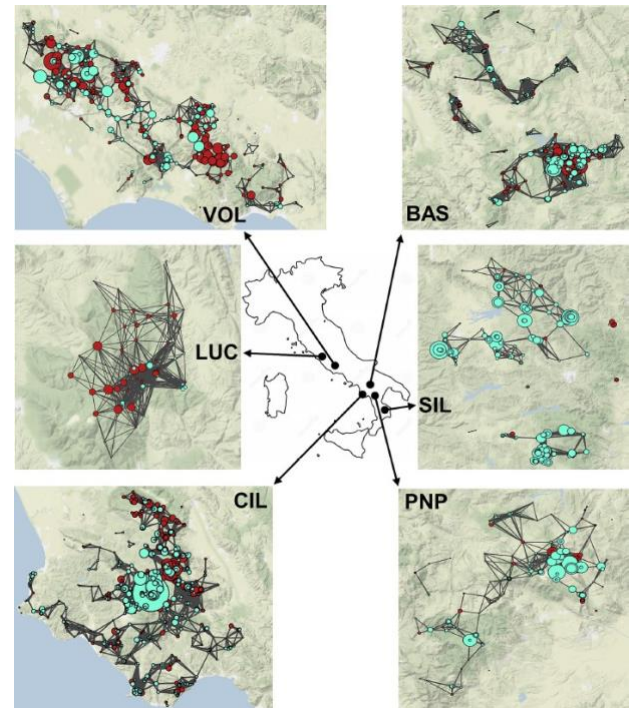


Fig. 1. Spatial layout of graphs for each study sub-area. Circles represent water sites (nodes) and lines represent edges (p connectivity > 0.2). Node size represents node importance. NWS = blue; AWS = red.

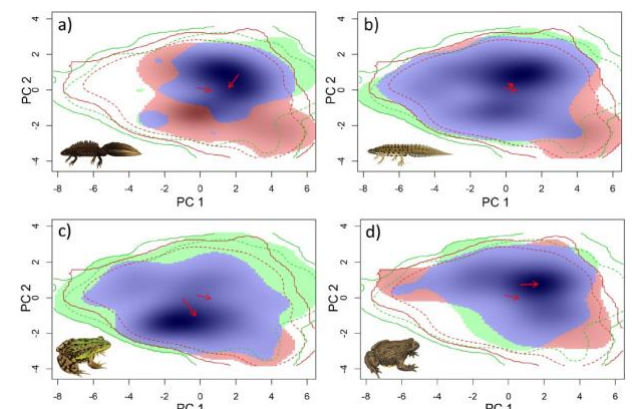


Fig. 2. Density plots representing significant niche dynamic between NWS and AWS on the first two components of the PCA space for four amphibian taxa, a) *Triturus carnifex*; b) *Lissotriton* sp.; c) *Pelophylax lessonae*; d) *Bombina variegata*. Niche dynamics are coded by colors: red = expansion, blue = stability, and green = unfilling.

Threatened ice-dwelling springtails: the need for more (unfashionable) taxonomy and field data acquisition

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Short summary: The first comprehensive description of ice-dwelling springtails of European Alps and Apennines is provided. Taxonomic knowledge of the species is the basis for monitoring biodiversity: new species are being discovered, and consistent field work is still necessary even in European habitats

Keywords: Morphology, barcoding, glacial habitats, Climate change, Cryophilic biodiversity

I. BACKGROUND

Springtails are the only group, among Alpine arthropods, that include cryophilic ice-dwelling species, i.e. adapted to survive only in direct contact to the glacial ice. Their evolutionary history is strictly linked to the glacial history. Thus, if glacial landforms disappear because of the ongoing climate change, an important portion of this biodiversity is at risk. Despite their relevance as biological indicators as ice-obligate organisms, diversity and distribution of springtails in the European mountains have been mostly overlooked. As such, their diversity is greatly underestimated, making it impossible at present to plan effective conservation efforts.

MATERIALS AND METHODS

After four years of sampling on glaciers and rock glaciers at 42 sites, we present the first comprehensive description of ice-dwelling springtails on European Alps and Apennines through an integrative taxonomy approach (morphological taxonomy and barcoding analysis using mitochondrial genes *cox1*, *16s*).

II. RESULTS

Ice-dwelling springtails biodiversity

Ice-dwelling springtails were found at 32 glacier sites in the Alps (76% of the investigated sites) and on the Calderone, the single Apennine glacier. No ice-dwelling species were found on rock glaciers and snow-patches. Usually, only one species was found in each glacier. Seven different species were found in the Alps, and one on the Apennines' Calderone glacier. Sampled species belong to three genera: *Vertagopus*, *Desoria* and *Gnathisotoma* (Fig. 1). Based on an integrative taxonomy approach, five new species were morphologically and genetically described.

III. DISCUSSION AND MAIN CONCLUSIONS

The high percentage of new species, relative to those already known, highlights the existence of a large unexplored biodiversity of ice-dwelling springtails.

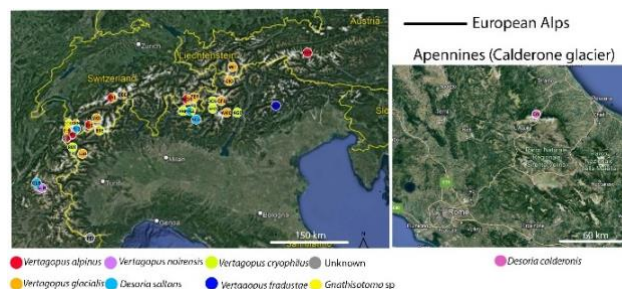


Fig. 1. Distribution of species found on European Alps and Apennines.

Probably six out of eight species found are strictly cryophilic ice-dwelling species. Moreover, the first record of the cryophilic genus *Gnathisotoma* is reported for the Alps.

Ice-dwelling springtails are at imminent risk of extinction due to the progressive vanishing of their glacier habitats. Considering the nodal role they play in trophic networks on glaciers, cryophilic species deserve to be monitored and protected. To achieve this goal, substantial work is still necessary to reveal springtails diversity and distribution on glaciers.

ACKNOWLEDGMENT

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Child's perspectives of biodiversity at land and sea

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Short summary: To evaluate their perception of biodiversity, children aged between 7 and 13 from four European countries were given a closed-ended questionnaire and asked to represent their idea of biodiversity with a drawing.

Keywords: Citizen science, Local ecological knowledge, Survey, Primary students, Education

I. BACKGROUND

In recent decades, the rapid loss of biodiversity has been paired with a growing concern about the “extinction of experience” [1]. Today's children represent the future supporters of biodiversity conservation and have the potential to influence future management choices. This study aims to investigate their perceptions of marine and terrestrial biodiversity across countries and ages through questionnaires and drawings.

MATERIALS AND METHODS

Children aged between 7 and 13 from four European countries (i.e., Belgium, France, Italy, and Spain) were administered a closed-ended questionnaire of 14 questions and asked to represent their idea of biodiversity with a drawing. The questionnaire, initially written in English and then translated into the national languages, was completed on the International Day for Biological Diversity (May 22nd, 2019). The answers were anonymous, and the only socio-demographic variables included age and gender. For the question “Have you ever heard the term biodiversity?”, the percentage of yes/no/not sure responses was calculated by country and age. For each drawing, the species richness index (S) and the number of organisms (N) were assessed. Differences in S and N between ages (7 levels, fixed) and countries (4 levels, fixed) were assessed by two-way crossed univariate PERMANOVA ($\alpha = 0.05$). Significant results were further analysed by pair-wise tests.

II. RESULTS

One thousand eighty-nine children participated in the survey: 7.16% from Belgium, 9.27% from France, 51.52% from Italy, and 32.05% from Spain. Males and females were equally in all countries. In Belgium the participants were aged 12 to 13, while in France most of the participants (72%) 10 to 11, in Italy (73%) 9 to 11, and in Spain (71%) 11 to 12. The percentage of children who have heard the term “biodiversity” increases with age, ranging from 76.5% in Spain to 100% in Belgium at 13 years old (Fig. 1.A).

Out of 952 drawings, 174 different taxa were identified, both marine and terrestrial. Mean species richness varied from 2.82 ± 0.53 (mean \pm se) at 7 years to 5.18 ± 0.22 at 11, resulting significantly lower at 7 than at other ages ($p < 0.05$), except at 9 years (Fig. 1.B). Regardless of age, the mean number of organisms per drawing was higher in France (29.55 ± 5.92) than in the other countries, reaching a minimum in Italy (10.97 ± 0.70 ; Fig. 1.C).

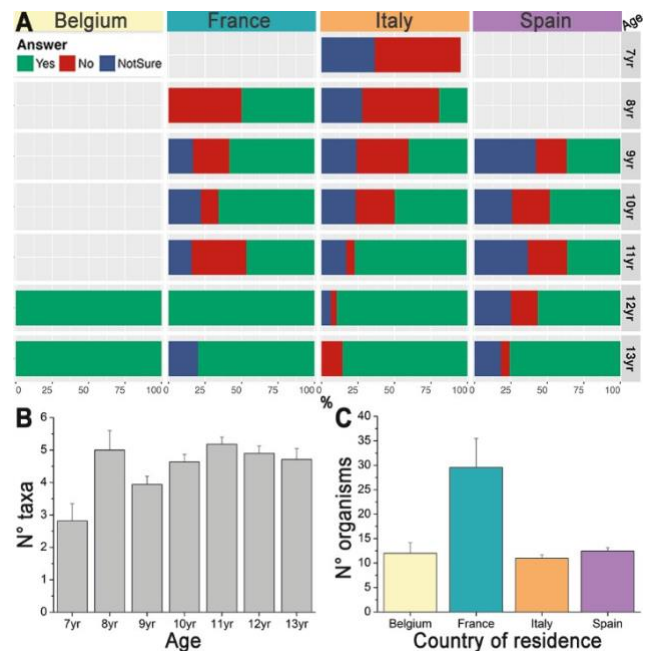


Fig. 1.A) Percentage of Yes/No/Not sure responses per country and age to the question “Have you ever heard the term biodiversity?”. In the drawings: 1.B) mean (+se) species richness per age and 1.C) mean (+se) number of organisms per country.

III. DISCUSSION AND MAIN CONCLUSIONS

Although the familiarity with the term biodiversity improves with age, a sign of greater experiential maturity in children; in the drawings, the mean number of taxa represented increases from the 7 to the 8 years and then consolidates. At the same time, French children stand out positively as the mean number of organisms represented. These results could be due to children's experiential and cultural development, willingness to draw, and interests. Drawing can be a research tool for exploring ecological knowledge in children by allowing them to freely express their perceptions, potentially becoming a steppingstone to their future involvement in participatory processes.

ACKNOWLEDGMENT

We are grateful to the EuroMarine for financially support the foresight workshop CoMBoMed, 11-14 February 2019, Ravenna.

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Maelstrom, a neural network-based multi-species approach for stock assessment

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Short summary: This paper presents a novel approach for the prediction of the impacts of fishing activities on marine resources, the estimation of Spawning Stock Biomass via a neural network multi-species model which takes account of abundance and catches data.

Keywords: Neural network, Fishery, Mediterranean, Forecast, Biodiversity

I. BACKGROUND

Stock assessment is the main tool to monitor the condition of marine resources and its exploitation, but traditional approaches often tend to focus only on fishery-related features [1]. The integration of neural networks allows the model to discern ecological patterns and relationships which cannot be made explicit by the user.

MATERIALS AND METHODS

This work has been conducted on fishery-related datasets, which are structured as yearly time series. The core engine of the model we used to analyse these data is a Recurrent Neural Network (RNN), a machine learning algorithm capable of retaining useful information from each step of the time series and utilise it to return more accurate forecast. The impact of fishing activities can be quantified by supplying a fishing mortality vector (or matrix) to the model, which is used to compute catches and abundance prevision using Baranov's catch equation. The model has been built in a Shiny app, a software-like interface developed in the R environment, which allows the user to customise the neural network parameters without having high-end developing or modeling expertise. A test run has been conducted on a single species, the Deep-water Rose Shrimp *Parapenaeus longirostris* (DPS), to assess the accuracy of the model in capturing the trend of the last 5 observed years of the time series. Two simple RNN layers have been used to perform this analysis. The forecast has been performed using the same neural network structure of the test phase, applying a flat 0.7 multiplier on a fishing mortality vector computed from the last 3 years of the fishing mortality time series from input dataset.

II. RESULTS

A. TEST PHASE

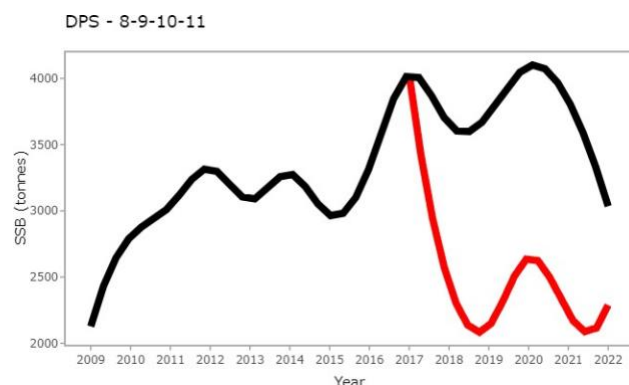


Fig. 1. Test phase on *Parapenaeus longirostris* in GSAs 8, 9, 10 and 11; observed data in black, predicted in red.

Fig. 1 shows the predicted values over the observed time series: the model captured the trend of the input dataset, even if SSB values are slightly underestimated.

B. FORECAST PHASE

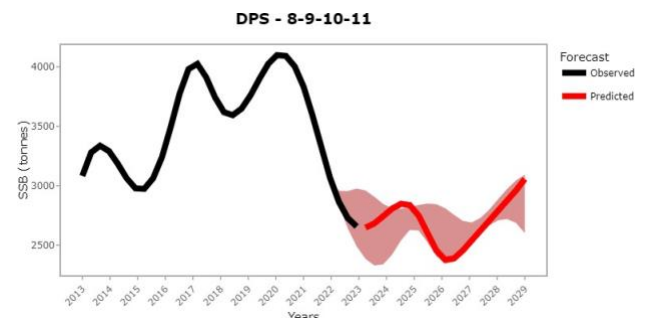


Fig. 2. Forecast phase on *Parapenaeus longirostris* in GSAs 8, 9, 10 and 11; observed data in black, predicted in red.

The resulting SSB after 7 years, as showed in Fig. 2, is 15.01% higher compared to the biomass during the last observed year, and the trend is increasing with time after a steep decrease in 2026.

III. DISCUSSION AND MAIN CONCLUSIONS

This work provides a valuable tool which can be used to underline the ecological consequences of fishing activities, both the depletion of marine resources and the community structure changes deriving from the harvesting of predominant species in the trophic web. A more accurate assessment of anthropic impacts on marine ecosystems can be one of the keys towards sustainable interactions with the environment.

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More ‘Risiko’ in conservation front lines: Unifying approaches to manage anthropogenic threats

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Short summary: Anthropogenic threats impacting on ecological targets should be mitigated and solved using fast and schematic tools applied in conservation strategies. Here, using an example, I suggest a mixed approach implementing the coarse-grained (and expert-based) threat analysis with the fine-grained (analytical) DPSIR indicators, all included in a single causal chain.

Keywords: IUCN Project cycle, Threat analysis, DPSIR indicators, halo-psammophilous plants, *Charadrius alexandrinus*, Academic student’s training

I. BACKGROUND

Anthropogenic threats are human activities or processes that are currently causing or may lead to the degradation of biodiversity and natural processes [1]. Recently, Threat Analysis (TA) has been proposed as an invaluable coarse-grained framework to identify, characterize, quantify, and rank threats impacting on ecological targets in conservation front lines [1].

DPSIR is an analytical framework useful to analyze and assess environmental problems through sets of indicators along the threat-target causal chain (i.e., D: indirect drivers, P: threat pressures, S: state of the system, I: impacts on ecological targets, R: responses through projects and actions) [2].

These two approaches may be unified in a conceptual framework, so allowing to clarify the causal relationships among drivers, threats, and targets and, therefore, define strategies and monitor expected outcomes. Following this schematic approach, it may be possible to quantify threats both at a coarse-grained (1° step, expert-based evaluation) and a fine-grained level (2° step, analytical measurements).

II. AN INTEGRATED CONCEPTUAL FRAMEWORK

TA conceptual framework is composed by components (drivers, threats, and targets) and cause-effect relationships (causal chains). Using expert-based evaluations may be possible to obtain values of threat regimes that, once summed, may express a score of threat magnitude, as a coarse-grained proxy of the threat pressure [1]. Therefore, comparing multiple threats acting on ecological targets in sites of conservation concern, experts may rank them in a decreasing order of priority [1]. Once obtained the priority threats (Fig. 1, in red), it is possible apply a set of DPSIR indicators (Fig. 2). An example for halo-psammophilous dune plants is here provided (details in [3]).

III. APPLICATIONS AND CONCLUSIONS

TA has seen still limited use in Italy. Moreover, although these approaches (TA or DPSIR) have been used independently in nature reserve’s management plans and conservation measures (Natura 2000 sites), they are never adopted in a unified way.

Due to its schematic format, this ‘Risiko’ of conservation, can also be used to communicate to academic students the complexities of socio-ecological systems in the conservation front lines.

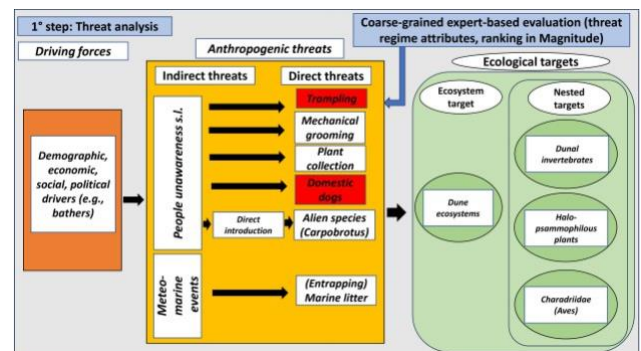


Fig. 1. Simplified conceptual framework for TA (case study on dune ecosystems; details in [4]). The first step includes the coarse-grained expert-based evaluation (procedure in [1]) of threat regime attributes; ranking in Magnitude (the priority threats are in red).

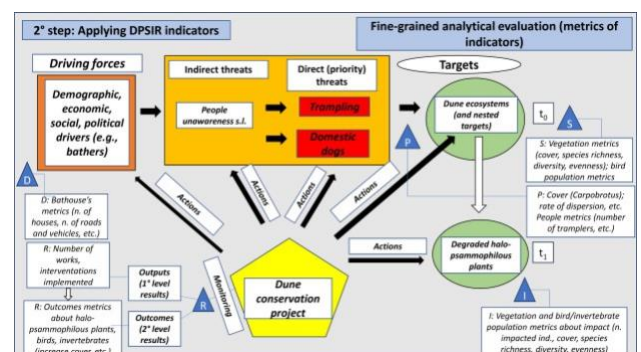


Fig. 2. Unified conceptual framework for TA including the DPSIR indicators applied only to priority threats (in red; case study on dune ecosystems). The second step includes a fine-grained analytical selection of indicators (using specific metrics) focused on priority threats.

ACKNOWLEDGMENTS

I am grateful to students, colleagues and ‘citizen managers’ meet in conservation front lines.

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AI-based solutions for autonomous underwater observing systems and science discovery

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Short summary: Artificial intelligence solutions stimulate new ways for observing the underwater ecosystems and at the same time can be used to formulate new hypothesis on the ecosystem functioning and the biodiversity dynamics.

Keywords: Artificial Intelligence, Intelligent Observing Systems, Edge Computing, Science Discovery, Biodiversity

I. BACKGROUND

The recent advances in Artificial Intelligence (AI) support the scientific discoveries not only by providing new advanced data analysis tools, rather supporting scientists generating new hypotheses, designing new experiments, allowing the acquisition of large datasets, providing new insights on their interpretation [1]. As AI needs a vast amount of data to be developed, data-rich environments provide for more opportunities to advance their domain of knowledge, allowing AI-based approaches to perform autonomous intelligent actions. The underwater domain is a remarkable case of data-rich environment, where AI approaches have a relevant impact on the scope and scale of ocean observations and smart sensors lead to a continuous flood of data. This work presents a research perspective on the continuum between two novel topics relevant for the biodiversity research: the study of underwater intelligent multi-parameter observing systems and the study of novel methodologies for multi-varied data analysis based on explainable AI approaches.

II. AI FOR AUTONOMOUS UNDERWATER OBSERVING SYSTEMS

The investigation of the temporal and spatial biodiversity dynamics needs observations extended in time and space. Underwater observing technologies equipped with onboard AI capabilities extend the autonomy and the effectiveness of data acquisition systems. The smart observatories under development within the PNRR-RAISE and PNRR- ITINERIS projects have the capability to process the acquired data directly on board (Edge Computing), dynamically adapting their behavior according to the observed environmental parameters and to user-defined applications. The dynamic adaptation consists of activating/deactivating and changing the configuration of the hosted sensors and extracting and transferring relevant information from the acquired data (e.g. early warning). For example, an observatory equipped with an imaging device can be configured to automatically track the change of species assemblage, with high frequency time-lapse images, especially during triggering events like heat waves, storms or algal blooms, through the use of appropriate sensor packages, for long periods across seasons.

III. AI FOR SCIENCE DISCOVERY

Autonomous and intelligent observatories, spatially distributed into networks, acquire heterogeneous data for

extended periods in time. Although the acquired datasets might be scientifically relevant, its underlying knowledge is not directly accessible without the use of appropriate analysis methodologies. AI tools for modeling species abundance or distribution, larval dispersion or harmful algal blooms occurrence, can be used to support marine stakeholders in making decisions with high social impact. Nevertheless decision-makers can take decisions only if they fully understand and assess the motivations behind decisions. Although AI methodologies, like for example those based on deep neural networks, have either achieved or overcome human-like performance in many tasks, they largely remain “black boxes” which cannot be considered fully reliable as they do not allow for a complete understanding of the phenomena they analyze. This limit can be overcome through the use of eXplainable and interpretable AI-based approaches (XAI). XAI methodologies learn knowledge from data and produce models that are human-understandable, capable to explain the mechanisms underlying the observed phenomena. Solutions based on XAI, as for example symbolic regression approaches [2,3], can shed new light on biodiversity dynamics difficult to understand otherwise.

IV. DISCUSSION AND MAIN CONCLUSIONS

An end-to-end solution based on the “compute continuum” paradigm combining AI-based intelligent observatories and XAI-based approaches for data analysis is proposed. The use of AI solutions for acquiring data stimulate new ways for observing the underwater ecosystems and at the same time XAI methodologies fosters the “science discovery” paradigm where new hypothesis on the ecosystem functioning might be extracted from the acquired data.

ACKNOWLEDGMENT

This work was carried out in collaboration with the projects “RAISE - Robotics and AI for Socio-economic Empowerment” and “ITINERIS - Italian Integrated Environmental Research Infrastructures System” both supported by European Union - NextGenerationEU.

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Earth Observation Tools for Invasive Species Management in Italy and Portugal

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Short summary: Two Italian and Portuguese SMEs showcase advanced earth-observation tools used in three distinct projects focused on alien invasive species detection, monitoring, and biomass estimation in forest and riparian ecosystems, using artificial intelligence.

Keywords: Invasive species, Earth observation, Artificial intelligence, Forest monitoring, Riparian ecosystem, Ecological restoration

I. BACKGROUND

Leveraging different technologies, an Italian and a Portuguese SME propose robust approaches – with drone and satellite imagery, spectral analysis, artificial intelligence – for earth observation of aquatic and forests ecosystems, monitoring invasive species and protecting biodiversity. They will showcase three end-to-end use-cases, one already developed, one in an advanced developing phase, and one planned for 2024.

The two enterprises will demonstrate the transfer of knowledge from the industrial sector. Optimal cooperation has emerged through collaboration with five Italian and Portuguese research centers, along with two environmental associations operating in the Iberian Peninsula.

MATERIALS AND METHODS

In the three projects different technologies were used, depending on the scope and expected results, using drones with multispectral cameras, high-resolution and low resolution multi-spectral satellite images from Copernicus and Planet archives.

These datasets were pre-processed using SOTA and industry standard techniques, and analyzed through advanced artificial intelligence models (leveraging both classical and deep learning algorithms), which serve as the backbone of the analytical framework, to achieve the desired objectives with precision and efficiency.

II. RESULTS

LudVISION – tool focused on a specific invasive aquatic species, *Ludwigia peploides*, arrived in Portugal in the last decade. Present in only 6 locations, the invasive plant was well known for its high impacts on river ecosystems, its threats to biodiversity, and the clogging of waterways clogging. The project delivered an AI-powered detection and mapping tool able to detect and geo-reference the presence of the target species. The tool was used as a support for the 2022 removal operations and the following assessment of the removal efficacy. It helped to understand and verify the containment of the spread of the invasive species, as well as allowing it to detect its presence in other nearby locations [1],[2].

The model used in this project is an adaptation of an existing context aware model, using connected high-to-low resolution convolution streams. Custom adaptations of the model allowed high effectiveness in dealing with multispectral data, as well as the specificities of the data and problem. The proposed method was able to achieve a

user's accuracy of 95.5% in detecting the targeted species on drone-captured images.

ForestVISION – online platform to support forest management, using satellite high and low-resolution multispectral images to provide insights about anomalies in a forestry ecosystem. The 2023 development focused on detection of invasive plants, like *Acacia dealbata*, and illegal deforestation, while in 2024 will be focusing on drought and diseases visible from multispectral cameras. The platform leverages AI by employing multiple algorithms, such as more traditional Random Forests to aid in the pre-processing and labeling process, as well as deep learning models to get more comprehensive insights. The gathered results are then converted into visual form and presented to the user via an online interface, including species classification, detection of deforestation and conditions such as tree health, surface temperature and water content.

RiparianEye Biomass – project to 1. evaluate the potential, 2. prototype a digital platform to support decision-making processes, 3. conduct a quantitative analysis on the use of plant biomass for energy, pharmaceutical, cosmetic and nutraceutical purposes. The AI component of the project will deliver a platform prototype to quantify the resource's abundance through the creation of a dataset, artificial intelligence models, and biomass distribution modeling.

The results from these projects are establishing the foundation for future cooperation, including the development of projects for 1. invasive species early detection in natural reserves, 2. comprehensive invasive alien plants analysis, using data from both satellite data and citizen-science projects, and 3. forests management to detect undesired events such as illegal deforestation or specific diseases that can be detected through multispectral images analysis.

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Ecological restoration of vegetated habitats: a path towards the recovery of coastal biodiversity

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Short summary: Restoration interventions on vegetated habitats, such as the seagrass *Cymodocea nodosa* and the brown macroalga *Gongolaria barbata*, provide evidence of the efficacy of available protocols for these habitat-forming species.

Keywords: Ecological restoration, Habitat-forming species, *Cymodocea nodosa*, *Gongolaria barbata*, Adriatic Sea, UN Decade Ecosystem Restoration

I. BACKGROUND

Seagrass meadows and macroalgal (Fucales) forests are hot spots of biodiversity in coastal areas and play a key role in the provisioning of ecosystem goods and services. These habitats often show a regression due to a combination of multiple anthropogenic and climate-induced impacts. The ecological restoration of these habitat-forming species is a priority to reverse biodiversity loss and for the recovery of their ecosystem functions. Here, we report successful case studies of ecological restoration of seagrass (*Cymodocea nodosa*) [1] and Fucales (*Gongolaria barbata*) along the coasts of the Marche region [2,3].

MATERIALS AND METHODS

Benthic biodiversity (using meiofauna as a proxy) was analyzed in terms of abundance, richness of taxa and taxonomic/species (nematode) composition. Three interventions were carried out: 1) transplanting of the seagrass *Cymodocea nodosa* at Gabicce [1] and the restoration of the brown alga *Gongolaria barbata* in the Conero Riviera [2] and in Site of National Interest (SNI) of Falconara Marittima [3] (Fig. 1). In the site "Falconara" we investigated both active and passive restoration interventions, as this site has been interdicted for years.

II. RESULTS

Seagrass transplant at Gabicce. One year after the transplant, the abundance and biodiversity of meiofaunal (higher taxa) assemblages in the restored seagrasses were still lower than in donor seagrass meadows. Conversely, nematode (at species level) biodiversity in restored seagrasses was more similar to that in the donor site than in unvegetated sediments.

Fucales transplant at Conero Riviera. One year after the intervention, the canopy extended to ca. 15 m² with a significant increase in meiofaunal abundance and biodiversity compared with reference areas. However, the assemblage structure in the restored site was still significantly different from that of reference pristine areas.

Fucales transplant at Falconara Marittima SNI. The use of cages on artificial reefs, over a relatively short period (6 months), represented a useful tool to let the macroalgae grow enough without the threats of herbivory. The biodiversity of the fauna in the restored site was different from that of the controls (reefs without the macroalgae).

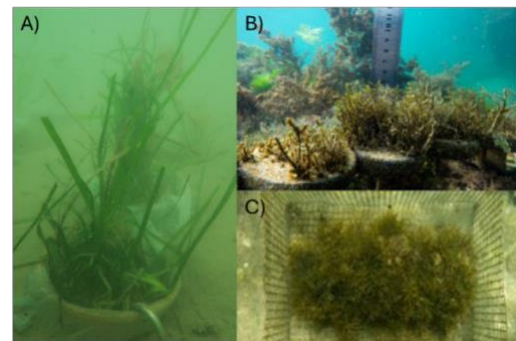


Fig. 1. Seagrass (*C. nodosa*) transplant at Gabicce (A), Fucales (*G. barbata*) transplant at Conero Riviera (B) and F. Marittima SNI (C).

III. DISCUSSION AND CONCLUSIONS

All the applied approaches were successful in restoring the damaged habitats and recovering natural populations. Active and active/passive restoration interventions, however, 6/12 months after the interventions, showed both biodiversity and assemblage structure different from the controls. Nematodes resulted useful indicators of restoration success. In conclusion, macrophytes' restoration can be successful and has positive effects on benthic local biodiversity, however, is a relatively long process that can take years to reach a complete recovery. A multilevel approach and habitat inter-connected approach could be useful to increase restoration success and resilience of damaged vegetated habitats.

ACKNOWLEDGMENT

This study was conducted within the EU MERCES, CLIMAREST and AFRIMED and NFBC and Cariverona projects.

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Law, art and science: plurality of languages, for the preservation of biodiversity

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Short summary: Since 2019, we have been dealing with ancient conservation plant varieties with an innovative and multidisciplinary approach. Our focus is on agricultural biodiversity, not only from a biological, organoleptic and nutritional point of view, but also from a cultural point of view, and we address the issue of biodiversity preservation in a syncretic way.

Keywords: *Heritage seeds, Arts, law, Mamaseeds, Parco dell'Anima, education*

We pursue our goals, through a nonprofit model and a for-profit model, believing both to be indispensable, for the survival of biodiversity.

NON-PROFIT: "Parco dell'Anima" and AVASIM Consortium

The "Parco dell'Anima" represents an innovative fusion of art, science, and biodiversity. Works by artists, such as Michelangelo Pistoletto, Sebastiao Salgado and many others make the scientific message immediately accessible and deeply engaging, serving as a bridge between the world of research and the public. An open-air museum, a "seed bank of the world," grown in situ, with popularization purposes, where collections of traditional plant varieties dialogue with contemporary art collections.

Collaboration with research centers and public and private institutions, such as the Georgofili Academy, the Caltagirone Graniculture Station and IILA (Italo-Latin American Institute), are necessary, to provide the Parco dell'Anima with knowledge and expertise, ranging from the conservation of plant varieties to new technologies. Just as the universal language of art and its ability to evoke emotions and stimulate reflection is necessary for science, to make research results understandable.

The AVASIM Consortium (Alliance for the Enhancement of Ancient Italian and Mediterranean Seeds) carries out activities to communicate and disseminate the results of scientific research through easily understandable languages in order to make biodiversity information accessible to a wider audience.

In addition, on the assumption that clear and protective legislation is essential for the preservation of biodiversity, and that without adequate regulations conservation efforts risk being ineffective, AVASIM, in line with Article 9, has prepared a bill. This bill proposal calls for the recognition and distinction of Italian seeds, born and historically present in Italian territory, from seeds only grown in Italy, but originating from other countries. In fact, today the *ius soli* is in force, which does not allow immediate recognition and protection to our cultural heritage. In addition, we urge the inclusion of heritage seeds in the "Testo Unico of Italian Cultural Heritage": our crops represent an intangible heritage consisting of history, traditions, customs, memories, flavors, landscapes. They represent the identity of peoples and should be protected, just like our cultural heritage.

Finally, AVASIM is engaged in the drafting of texts, aimed at the UNESCO candidacy of native Italian and Mediterranean seeds as Intangible Heritage of Humanity.



FOR-PROFIT: MAMA-SEEDS the first agri-food chain of heritage Italian seeds

In order to act concretely, for the sake of the survival of ancient crops and biodiversity, it is necessary to create new sustainable production systems and new agri-food supply chains, which incentivize farmers and "contadini custodi" to use heritage seeds - and thus agricultural biodiversity - with a certain outlet in the market.

Hence, the creation of a brand-stamp "MAMA.SEEDS" affixed to all agri-food products derived from the processing of heritage seeds, to create a new business model of biodiversity. There are more and more producers, who use heritage seeds, but in isolation, without the formation of a real agribusiness chain. The golden dandelion MAMA.SEEDS aims to stand as a symbol that makes the consumer immediately perceive the added value, given by the use of traditional heritage seeds, for the processing of products, as for the green leaf stand to the bio-organic supply chain.

The MAMA.SEEDS food chain is made up not only of products and producers, but also of restaurants, hotels, stores in Italy and the Mediterranean area, which use ancient seeds, thus reintroducing, as an immediate effect, biodiversity.

We have also created a portal www.mama-seeds.com, for e-commerce, to support "heroic" producers, who cannot, in isolation, penetrate the market.

CONCLUSIONS

Thanks to scientific research, today we hold a plant heritage of immense value, because it is not only organic, but also cultural - representing our history, our roots - and a potential economic driver, not yet exploited. An unknown heritage, which must be preserved, enhanced and, above all, made known, with a plurality of languages.

The change in species distribution and species distribution studies: *HIC SUNT LUPI*, an innovative project on wolf monitoring in a recolonized habitat

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Short summary: *HIC SUNT LUPI* is a newly launched project on the management of the wolf in Salento, which uses innovative approaches to monitoring, data management, and interaction with social components.

Keywords: *Canis lupus*, Salento, Monitoring, Management, Citizen Science, FAIRNESS

I. BACKGROUND

Increasing evidence shows how the Italian wolf (*Canis lupus*) is re-colonizing the lower Salento (Apulia, Italy), from where it had been absent for over a century due to eradication and habitat loss. The expansion of the range of some large carnivores is a phenomenon that is characterizing the contemporary Anthropocene and on which research efforts on a global scale are focusing. The study of the dynamics of diffusion and behavior of wolves in Salento constitutes an important frontier on this topic, particularly relevant considering that the recolonization of the Salento by the wolf occurs in an unprecedented context of contraction of agricultural activities and spontaneous rewilding of the countryside following the *Xylella fastidiosa* olive trees epidemic.

MATERIALS AND METHODS

The tools available to understand, manage and share data on a novel phenomenon such as the rapid recolonization of Salento by the wolf have significantly innovated and diversified in recent years. The *HIC SUNT LUPI* project (start date: December 2023) aims to integrate traditional tools and innovative approaches to produce management guidelines developed ad hoc for the local eco-cultural context.

A. Traditional approaches

HIC SUNT LUPI will be deeply based on the consolidated ecological knowledge accumulated over the years on the behavior and monitoring of the Italian wolf. This knowledge, combined with active collaboration with experts in the rural and natural environments of Salento, allow us to set up monitoring plans aimed at the local context. The use of a molecular dog unit will allow the collection of fecal samples for spatially explicit dietary analyses. The installation of a camera trap array will allow estimating the minimum number of packs and individuals present in the area.

B. Innovative approaches

HIC SUNT LUPI will make use of recent developments in the field of genetics and metabarcoding to support the analysis of diet starting from feces and to determine origin,

relationship and level of hybridization with the domestic dog of wolves in Salento.

LifeWatch Italy will support the project by providing a web application for sampling records and ensuring that the project data and other products adhere to FAIR principles, promoting reproducibility, transparency, and knowledge discovery.

C. Social involvement

HIC SUNT LUPI will produce guidelines on wolf management specific not only for the natural context, but also for the socio-economic and cultural context of Salento. To this end, both health sector operators and trade and naturalistic associations interested in the wolf phenomenon will be consulted and effective collaboration will be established. A Citizen Science web application developed by LifeWatch Italy will allow us to create an extensive monitoring network and will have an important dissemination and education role. <https://citizenscience.lifewatchitaly.eu/webapp/#/home/hic-sunt-lupi>



Fig. 1. The *HIC SUNT LUPI* project logo

ACKNOWLEDGMENT

The *HIC SUNT LUPI* project is the result of the collaboration between Assessorato Ambiente of the Regione Puglia, CNR-Istituto di Ricerca sugli Ecosistemi Terrestri (IRET), NBFC, University of Rome La Sapienza, LifeWatch Italy and is mainly funded by the Assessorato Ambiente of the Regione Puglia.

New Technologies to Complement Underwater Visual Census Protocols

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Short summary: Improved, depth-gauge video cameras can be used to complement underwater citizen science monitoring protocols, especially when they deal with large conspicuous species.

Keywords: Underwater visual census, New technologies, Marine citizen science, Mediterranean Sea, Underwater camera

I. BACKGROUND

The advancement of underwater scientific research heavily relies on the continual development of new technologies, an aspect that extends to community engagement through citizen science [1]. In this context, our study evaluates the effectiveness of the Paralenz Vaquita camera in applying of the Reef Check Med Underwater Coastal Environment Monitoring Protocol (RCMed U-CEM) [2].

MATERIALS AND METHODS

Paralenz Vaquita is an innovative underwater video camera, issued in 2020, capable of recording GPS position at the surface, depth, temperature, and salinity during dive, and featuring a depth-based white balance enabling bright lifelike colours underwater without headlights.

Field tests were conducted from June 2021 to October 2021 at two distinct Tyrrhenian Sea locations (Marina di Camerota, Campania, and the Elba Island, Tuscan Archipelago), including a total of 11 randomly selected sites and applying the RCMed U-CEM protocol to a subset of 30 out of 43 target species. At each site, three data acquisition methods were applied:

- 1) traditional RCMed U-CEM on-site visual census;
- 2) RCMed U-CEM visual census applied to videos recorded with Paralenz Vaquita;
- 3) combined integration of two previous methods.

The three methods were compared in terms of estimated individual taxa abundance and assemblage structures.

II. RESULTS

Overall, 33 surveys were conducted, 11 per method. On-site visual census alone and complemented by post-processing of the simultaneously recorded videos provided slightly higher abundances of smaller species compared to using videos alone. All three methods provide similar abundance estimates for large conspicuous species. Although the three methods provide slightly different assemblage structures site-by-site, all three consistently distinguish the assemblages of the two Tyrrhenian Sea locations (Fig. 1).

III. DISCUSSION AND MAIN CONCLUSIONS

Since the RCMed U-CEM protocol is intended for volunteer divers, although previously trained, and is mainly based on large conspicuous species, it should not be surprising that post-processed videos can provide results comparable to the traditional on-site visual census method.

However, visual census alone or augmented with videos tends to be more effective in identifying and quantifying smaller species.

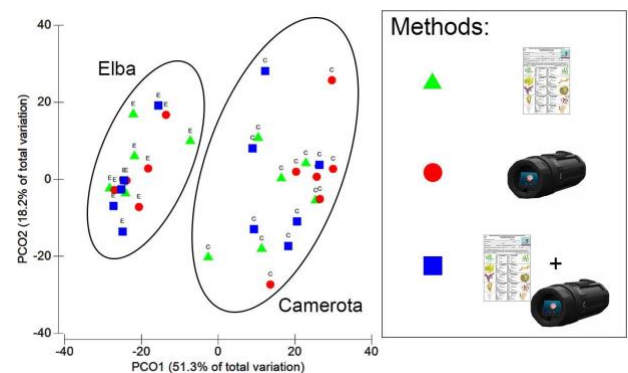


Fig. 1. Principal Coordinates Analysis (PCoA) ordination plot of assemblage structures based on Bray-Curtis dissimilarity on data obtained from the three methods at each randomly selected site in two locations.

This kind of underwater camera can stimulate the involvement of volunteer divers and provide a huge amount of high-quality georeferenced footage accompanied by information on the water's depth, temperature and salinity. If disseminated online, they can contribute to Web Ecological Knowledge [3]. However, their use in and comparability with biodiversity monitoring protocols must be assessed case-by-case.

ACKNOWLEDGMENT

We are grateful to the staff of Biodivers Diving and Continente Blu Diving, especially Dr. Chiara Luciani and Dr. Rosalia Calicchio, for their valuable support and expertise in facilitating the underwater surveys.

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“A fast and accurate pipeline to sequence fresh- and preserved soft-bodied meiofaunal specimens”

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Short summary: Meiofauna plays a vital role in all aquatic ecosystems. Unfortunately, it can be challenging to identify soft-bodied species, particularly in preserved specimens. We employed an innovative pipeline based on WGA to obtain high-quality genomic data from gastrotrich samples that date back to 2009. This approach can provide a means of comparing old and new faunas.

Keywords: Meiofauna, Whole Genome Amplification, Next-Generation Sequencing, Gastrotricha, Bioinformatics, Biodiversity

I. BACKGROUND

Molecular approaches are becoming prevalent in the study of biodiversity. However, meiofauna (benthic animals <1mm in body length) provide a limited quantity of genetic material per specimen, which can present a significant obstacle. Additionally, preserved soft-bodied animals lose many morphological diagnostic traits over time. Accurate identification of these samples becomes thus possible only through molecular analysis. The Whole Genome Amplification (WGA) approach makes it possible to amplify a great quantity of DNA from small amounts of biological tissue. This can overcome some limitations when working on these minute, but ecologically important, animals. We studied gastrotrichs, soft-bodied animals with a body length of 0.1-3.0 mm [1]. We focused on the sequences of the ribosomal operon and the mitochondrial cytochrome oxidase I (COI) gene as they are reliable markers for barcoding and phylogenetic studies.

MATERIALS AND METHODS

The gastrotrichs were obtained during several sampling campaigns (2009-2023). Some specimens were used fresh but most were fixed in 95% ethanol and conserved at -20°C inside 2 ml criovials at the Unimore MeioLab BioBank. We used both whole specimens and previously extracted and frozen purified DNA as WGA templates. WGA was carried out through the REPLI-g Single Cell Kit (QIAGEN, Hilden, Germany). After a validation step through Sanger sequencing, the WGA product was processed with a TrueSeq DNA PCR Free Library kit and whole genome de novo sequencing at NoveSeq 6000 Illumina Platform to generate a total of 40 million reads per sample (paired-ends 2 ×150 bp). The bioinformatics pipeline for genome assembling was optimized from Serra et al. 2020 [2]. The assembled contigs matching ribosomal and mitochondrial genes (COI) were identified with blastn and tblastn analysis using published gastrotrich sequences as queries. The reads mapped to these contigs were subsequently extracted and assembled with SPAdes software [3] to obtain the whole ribosomal operon and the mitochondrial genes in single separate contigs. Prediction of the ribosomal operon structure was performed using the StructRNAFinder web tool.

II. RESULTS

Starting from 13 single specimens, we obtained novel complete sequences of the whole ribosomal operon (containing the gene regions 18S, ITS1, 5.8S, ITS2, 28S)

of 11 species and the COI sequences of 10 species, retrieved from complete or partial assembled mitogenomes.

Using either DNA extracts or whole fresh or alcohol fixed specimens showed no appreciable difference or decrease in sequence quality. This was assessed by comparing the novel sequences to sequences obtained through Sanger sequencing.

III. DISCUSSION AND MAIN CONCLUSIONS

The pipeline developed in our study proved to be a fast, reliable, and accurate tool to obtain multiple sequences several kbps long from a single small-bodied animal, with a high success rate (e.g., 11 genomes from 13 sequenced samples). By contrast, traditional Sanger sequencing produces 100-1000 bps sequences with a lower success rate. This is especially important when dealing with rare specimens with low amounts of genomic material. This approach can be applied to encourage and facilitate molecular research on meiofaunal organisms with similar limitations that are yet to be properly studied. Additionally, the whole genome amplification (WGA) approach can be useful for the accurate identification of well-preserved small-sized specimens. This is supported by the fact that no decrease in the quality of the obtained sequences was observed in fresh, older samples, or in extracted DNA. Thus, this approach can facilitate comparison between old and new faunas.

ACKNOWLEDGMENT

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A virtuous alliance between ecologists, taxonomists and citizens

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Short summary: The results of the study of lacewings collected in an ecological study project of urban forestation are interpreted in light of a perspective of multi-disciplinary collaboration with the involvement of citizens.

Keywords: Green lacewings, Urban biodiversity, Bioindicator, Tree canopy, Citizen science, Multidisciplinary approach

I. BACKGROUND

The celerity with which environmental changes due to anthropic causes are occurring requires an equally rapid activation of an interdisciplinarity between scientific skills and the ability to communicate and involve the community, in order to significantly impact on a common sensitivity for environmental and human well-being.

MATERIALS AND METHODS

The research project “Habitat Trees: home for biodiversity”, coordinated by Claudia Canedoli (Univ. Milano Bicocca) and Davide Corengia (VerticalVerde, Brianza, IT), is oriented towards four main objectives:

1. How many species of living organisms can be found on a tree?
2. Test different sampling methods and verify their suitability, costs and reliability.
3. Disseminating principles of conservative arboriculture among tree workers and technicians and develop protocols to evaluate ecological value;
4. and Increasing awareness of people about the role of old trees in sustain biodiversity in urban areas

This study, conducted by forest ecologists with the involvement of citizens from Milan (IT) (Fig. 1), takes advantage of the collaboration of specialists from various living groups.

II. RESULTS

Results focus on Chrysopidae (Insecta Neuroptera) as it is known how green lacewings diversity in urban green spaces is connected with the structure and composition of vegetation [1]; they are summarized in Tab I.

TABLE I. GREEN LACEWING DISTRIBUTION BY TREES AND TRAPS

N.	Tree species and traps*								
	species	P	T	Q	N	M	C	B	W
52	Ape_pra	46	6	19	15	13	0	94	2
14	Ape_pic	29	14	7	14	22	14	79	0
9	Chr_luc	10	10	70	0	10	0	70	0
68	Chr_pal	18	13	18	15	25	12	75	13
11	Cun_sp.	9	18	36	18	9	9	82	18
1	Nin fla	0	99	0	0	0	0	99	0

*N. total number of specimens; P *Platanus acerifolia*; T *Tilia cordata*; Q *Quercus robur*; N *Pterocarya fraxinifolia*; M *Magnolia gradiflora*; C *Cedrus deodara*; B bottle trap; W window trap; Ape_pra *Apertochrysa gr. prasina*; Ape_pic *Apertochrysa sp. pr. picteti*; Chr_luc *Chrysoperla lucasina*; Chr_pal *Chrysoperla pallida*; Cun_sp. *Cunctochrysa sp.*; Nin fla *Nineta flava*. Numbers in tree species and traps are %

Two arboreal species (*Apertochrysa gr. prasina* and *Chrysoperla pallida*) are dominant and bottle traps have proven to be the most suitable tool for monitoring green lacewings. The vertical distribution of this group of insects has also been analyzed.



Fig. 1. Communication actions and citizen involvement in the “Habitat Trees: home for biodiversity” project.

III. DISCUSSION AND MAIN CONCLUSIONS

Many of the challenges for a paradigm shift with which humanity will face climate change related to the environmental changes of the Anthropocene will take place in city areas. Human well-being connected to the presence of city trees [3] may represent an important element of this mental process. The use of systematic groups of insects such as the Neuroptera have already demonstrated the possibility of being an indicator of peculiar habitat changes [2]: the analysis of the presence of these insects on the tree canopy shows promising repercussions on the objectives of projects such as “Urban Trees”.

ACKNOWLEDGMENT

I am grateful to the project coordinators for giving me the opportunity to deepen my ecological knowledge of this group of insects in this particular habitat.

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Monitoring marine benthic biodiversity through innovative, integrative, and standardized methods

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Short summary: Here we presented the effectiveness of Autonomous Reef Monitoring Structures (ARMS) together with integrative taxonomic approaches to assess and monitor spatial-temporal changes in marine benthic biodiversity in the Adriatic Sea.

Keywords: Mediterranean Sea, Artificial structures, Long-Term Ecological Research site, Cryptobenthic diversity, Alien species, port

I. BACKGROUND

Monitoring changes in marine biodiversity over time and space is crucial for establishing and implementing effective measures for habitat conservation and preservation. Autonomous Reef Monitoring Structures (ARMS) have been developed as standardized sampling tools to study hard-bottom marine communities (Obst et al. 2020), and to generate findable, accessible, interoperable, and reusable data (FAIR data). Here, we present how ARMS are used to 1) assess changes in benthic communities in a Long-Term Ecological Research site (LTER) and 2) monitor Non-Indigenous Species (NIS) in port environments.

MATERIALS AND METHODS

Following standardized ARMS protocol (<https://data.arms-mbon.org/>), since 2021 we deployed three ARMS for one year at the LTER “Acqua Alta” oceanographic platform (Venice). While in Ravenna port, we deployed three ARMS in a touristic marina and three in the inner part of the harbor, for three months during the spring season to maximize larval recruitment, to assess the presence and abundance of NIS. Benthic communities structure was assessed using an integrative taxonomic approach based on photo analysis, morphological identification, and COI and 18S metabarcoding data (Fig. 1). These last data are still in progress and not presented here.

II. RESULTS

A. Temporal monitoring on LTER site

In two Years (2022-2023), 99 taxa were identified, of which 30 taxa belonged to Annelida, 27 to Arthropoda, 23 to Mollusca, 9 to Bryozoa, 3 to Echinodermata, 2 to Porifera, Cnidaria and Chordata each, and 1 to Platyhelminthes. Statistical test performed by PERMANOVA highlighted no statistical differences between Years for all univariate indexes considered (taxa richness (S), Pielou's index (J') and Shannon's index (H')), while community structure of sessile assemblages changed in the two Years ($p(\text{MC}) < 0.05$).

B. Spatio-temporal monitoring of NIS

Between two Years of sampling and across the two Sites, 69 taxa were identified, with 16 of them being NIS: 5 Arthropoda, 4 Annelida, 3 Mollusca, 2 Ascidiacea, 1 Bryozoa and 1 Porifera. Considering the NIS assemblages, the structures significantly changed between the two Sites ($p < 0.001$), marina and harbor, and Years d ($p < 0.001$) and in the interaction between Sites and Years ($p < 0.01$).

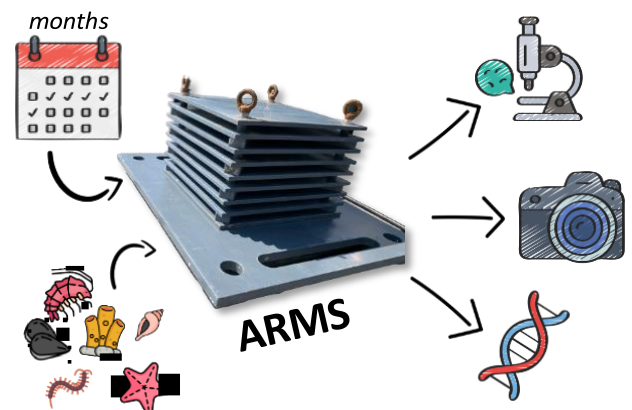


Fig. 1. Graphical summary of how ARMS protocol work.

III. DISCUSSION AND MAIN CONCLUSIONS

Overall, the use of ARMS combined with an integrative approach, which consider both photo and morphological analyses, has proven to be good tools for monitoring temporal changes and detecting NIS. Our results stressed the need to extend ARMS protocols in other marine LTER sites. Moreover, the number of detected NIS in Ravenna port is higher than that found in other Italian port with traditional methods and with SERC standard protocol (Tamburini et al., 2021). Our results, integrated with the future results on metabarcoding data, can enhances the ARMS power to assess benthic biodiversity changes, revealing also interspecific variation both within and between ARMS units (Thomasdottir et al. 2023).

ACKNOWLEDGMENT

The project is part of the European ARMS program within the European Marine Omics Biodiversity Observation Network (EMO BON). This study was carried out within the RETURN Extended Partnership and received funding from the European Union Next- GenerationEU (National Recovery and Resilience Plan – NRRP, Mission 4, Component 2, Investment 1.3 – D.D. 1243 2/8/2022, PE0000005).

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Blueat – A possible way to manage Alien Species.

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Short summary: Mariscadoras srl benefit created the project Blueat- The sustainable fisheries with the aim of implement human consumption of alien blue crab *Callinectes sapidus*. The project is a bottom up solution to manage alien species, to reduce their expansion caused by human maritime traffic and implemented by climate change.

Keywords: Blue Crab, Circular Economy, Climate Change, Alien Species, Supply Chain

I. BACKGROUND

Mariscadoras Srl is a Benefit Company and innovative startup founded by 5 young women to create supply chains for the exploitation of Invasive Alien Species (IAS). *Blueat – The sustainable fisheries* is the first project of Mariscadoras for the exploitation of blue crab *Callinectes sapidus*.

MATERIALS AND METHODS

In the summer of 2021, we used the methods of bibliographic research [1], citizen science and local ecological knowledge through questionnaires provided by UNIVPM [2] to investigate the presence of Invasive Alien Species and their expansion caused by climate change in Adriatic and Ionian Seas [3]. After our initial analysis, we decided to establish our benefit company to create a supply chain of blue crabs *Callinectes sapidus* with the aim of:

- contain his proliferation and reducing the problems caused to the environment and the marine ecosystem.
- minimize the damage to traditional fishing equipment by mitigating the negative socio-economic consequences for the small-scale coastal fishing sector.
- reduce the invasion of blue crabs in seaside areas along the Italian coast, and the damage to the tourism sector and personal injuries.

II. RESULTS

a. Blue crab supply chain

A blue crab food processing line has been created by producing a supply chain, in agreements with fishing cooperatives, fish market operators, and local processing and processing companies. The products (Frozen Raw Crab, Pulp, Sauces, Crab Meatballs and Crab Mayonnaise) are distributed in the catering sector, and supermarkets and exported to the US market.

The fishermen involved in the project (in the Po Delta of Emilia-Romagna and Veneto Regions) catch crabs using target traps that only catch blue crabs and the whole process is controlled by the Company Mariscadoras. The Blueat brand is responsible for guaranteeing the sustainability of the supply chain.

b. Circular economy spin-off.

In order to exploit the crabs in a circular economy perspective, we are developing solutions to use crab waste to produce compostable bioplastics by extracting chitin and

chitosan from our industrial waste produced during the crab pulp extraction.

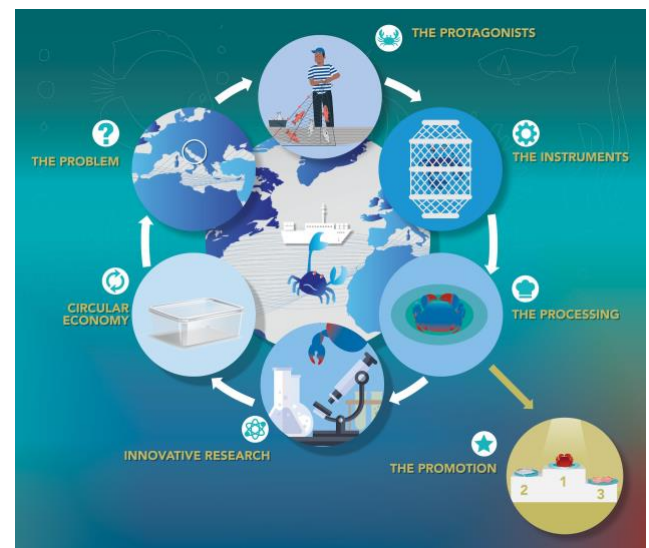


Fig. 1. This figure represents the circular approach of the Blueat project.

III. DISCUSSION AND MAIN CONCLUSIONS

Blueat – The sustainable fisheries is the Mariscadoras project dedicated to searching for new scenarios for managing Alien Species that are spreading in the Mediterranean due to the transformation of the Marine Environment. Their proliferation has been endangering the survival of native resources and, consequently, the work of thousands of families who live thanks to small-scale artisanal coastal fishing.

Building new scenarios to manage the Alien Species means protecting the environment and generating a positive economic impact.

Our experience is a bottom-up solution to the changes in the marine environment caused by human intervention and a form of human resilience to the mutations of our ecosystems.

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The approach of LifeWatch Italy for an open and FAIR research lifecycle

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Short summary: LifeWatch Italy built a national digital infrastructure to ensure open and FAIR management of digital research products from the biodiversity and ecosystem research, enhancing accessibility and addressing societal challenges.

Keywords: LifeWatch, FAIR principles, digital, Metadata, Data life cycle, Digital object

I. BACKGROUND

In recent years, there has been a growing awareness among researchers about the immense value of sharing all the products of their research with the wider scientific community by adopting open science practices. With the universal acceptance of the FAIR principles [1], the requirements and standards of research products publications have changed substantially. Researchers are encouraged to manage the digital research products as per the FAIR principles, by ensuring that the raw and processed data, semantic artefacts, research codes, software, policy documents, training materials, metadata records, etc. are securely stored and made available with the completion of the research. However, the FAIR principles do not specify technological implementation methods to meet their criteria. Rather, the discussion on what standards or best practices adopt to structure, describe, store, and share research products often depends on the reference research community [2]. Here, we present the approach that we developed in LifeWatch Italy for an open and FAIR management of digital research products produced by the biodiversity and ecosystem scientific community.

II. THE LIFEWATCH ITALY DIGITAL INFRASTRUCTURE

LifeWatch Italy is the Italian node of the European Research Infrastructure Consortium, LifeWatch ERIC [3], the distributed e-Science Infrastructure for biodiversity and ecosystem research. The main aim is to develop and maintain digital solutions for FAIR and open management of digital research products. Thanks to the PON-IR “LifeWatchPLUS”, LifeWatch Italy has enhanced its infrastructure to offer a set of digital solutions that support scientist along the full cycle of their research (Fig. 1). The first step of curation involves the review and validation of (meta)data, verifying syntax and taxonomy, assured by the alignment against curated taxonomic backbones (Italian checklists, Catalogue of Life, WoRMS, GBIF). The Semantic Platform allows annotating metadata, variables, and datasets. Additionally, it employs semantic technologies for information discover and re-use. The Data Portal and Metadata Catalogue provide access to data and associated resources. Moreover, the integration with DataLabs allows the collaborative code creation for biodiversity and ecosystem data analysis. A dedicated platform has been created to store and give access to citizen science projects and their products. The integration with the helpdesk and e-training platforms ensures user support and

training, enhancing the accessibility and usability of LifeWatch Italy's digital tools and services.

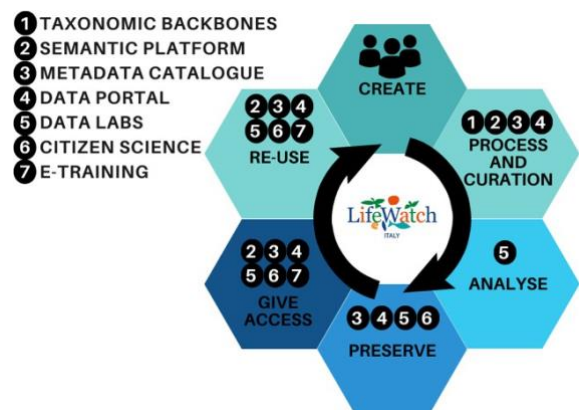


Fig. 1. Exemplification of how the components of the LifeWatch Italy infrastructure fulfil the data lifecycle management steps.

III. DISCUSSION AND MAIN CONCLUSIONS

The improvement made by LifeWatch Italy represent a model for organizing and facilitating FAIR research products management and long-term reuse. Our aim is to increase the volume of FAIRified digital objects in the biodiversity and ecosystem research field, contributing to addressing significant societal challenges associated with climate change, resource efficiency, food security, agriculture, sustainable development, energy, and health.

ACKNOWLEDGMENT

The infrastructure development has been funded the Italian project “LifeWatchPLUS” - PIR01_00028.

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The BRAIN database: a long-term perspective on plant biodiversity in Italy

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Short summary: BRAIN - Botanical Records of Archaeobotany Italian Network is the first database listing sites from which plant micro- and macro-remains are available in Italy. The study of plant records from human-modified settlements (on-sites) and Holocene sedimentary sequences (off-sites) is essential to understand current biodiversity and the extent of human impact on a long-term scale.

Keywords: Archaeobotany, Palynology, Human impact, Landscape, Archaeological sites, Holocene

I. BACKGROUND

In Italy, a huge number of studies of plant records from archaeological contexts has been conducted so far, which have improved our knowledge on the complex bio-cultural diversity of this nation [1]. Since 2014, palynologists and archaeobotanists started the recognition of all existing palaeo/archaeobotanical studies in Italian sites. The main output of the cooperative recognition was the scientific network and database 'BRAIN - Botanical Records of Archaeobotany Italian Network', proposed as an inventory of all existing plant data from archaeological sites in Italy.

MATERIALS AND METHODS

BRAIN is organised as a large collection of sites classified as 'on-sites', 'off-sites' or 'spot records', and provided with ID. The dataset includes metadata, collected by compiling geographical, archaeological, chronological, and scientific reference data of each site [2]. The inventory of the sites was achieved through a combination of consulting the specialist literature (both peer-reviewed and grey literature) and checking the accuracy of sources with archaeobotanists involved in the research. Each site providing data on plant remains, both microscopical (pollen, phytoliths, spores, cysts, other non-pollen remains, and starch) and macroscopical records (seeds, fruits, woods/charcoals, basketry, and artifacts) has been entered into a dataset under the same ID number.

II. RESULTS

BRAIN is free online. Currently, it includes 800 sites and 980 references on archaeobotanical studies. The database (<https://brainplants.successoterra.net/>; Fig. 1) consists of 19 columns reporting data of each site. The database mask shows the meta-data of the sites and allows to browse and select by a filter search the items. In the page 'Easy card and search', a map search allows the rapid identification of sites in each region. A Leaflet map shows the distribution of sites included in BRAIN, and three real-time graphs show the number of sites per geographical district, type of record or cultural chronology, both updated with each new entry (Fig. 1). Data can be exported in Excel. The dataset is prepared to be interactive and can be linked to other datasets or repositories (e.g., IRIS UNIMORE).

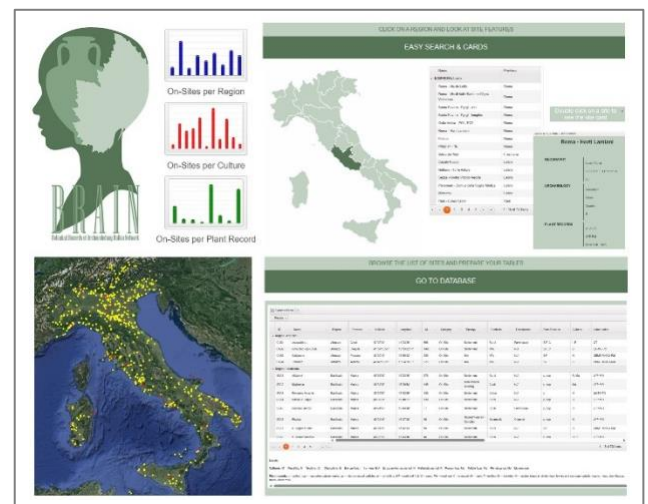


Fig. 1. The interactive BRAIN database: real-time statistics of the sites, easy search for region and cards of sites, distribution map (Leafletjs.com) of archaeobotanically studied sites, list of sites to download as Excel tables.

III. DISCUSSION AND MAIN CONCLUSIONS

BRAIN improves our knowledge on plant-human interaction during pre-historical and historical times, and increases the impact of archaeobotanical research on recent issues such as biodiversity and nature conservation under global change. To improve BRAIN regarding FAIR principles and open science, support will be sought from existing research units (e.g., LifeWatch).

ACKNOWLEDGMENT

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Testing a SAR-based ship classifier with different loss functions

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Short summary: This study investigated the influence of six different loss functions on Synthetic Aperture Radar (SAR) ship classification accuracy across two datasets. Kullback-Leibler Divergence Loss emerged with the highest average accuracy (69.5%), followed by L1 Loss (69.12%) and Focal Loss (68.4%). Interestingly, L1 and Focal Loss exhibited contrasting performance across datasets, suggesting potential data-specific suitability for certain functions. These findings highlight the importance of considering data characteristics and task requirements when selecting loss functions to optimize SAR ship classification performance.

Keywords: Loss Functions, Deep Learning, Ship Classification, SAR

BACKGROUND

Selecting the optimal loss function is crucial for effective image classification, particularly in challenging tasks, like SAR-based object classification. This study aims at investigating the repercussions deriving from different choices of the loss function on the classification of ship targets observed in SAR imagery, across two public SAR datasets (Fusar [1] and Opensarship [2]). Our aim is to assess the influence of loss function choice and explore potential dependencies on data characteristics.

MATERIALS AND METHODS

Both datasets exhibited class imbalance, necessitating an analysis focus on the three prevailing ship categories: Cargo, Fishing and Tanker.

To address imbalances between the considered categories and augment data diversity, random resizing, cropping and flipping were implemented during preprocessing. Six different loss functions were evaluated: KLDivergence (KLDiv), FocalLoss, Mean Squared Error (MSE) loss, L1 Loss, Cross-Entropy Loss (CEL), and Binary Cross-Entropy with Logits Loss (BCEL, one vs all).

A convolutional neural network (CNN) architecture implemented in PyTorch (code available**) was employed for image classification. The hyper-parameters consisted of a learning rate of 0.001, batch size of 64, and 10 epochs. Datasets were divided into training and testing using Random splitting. Classification accuracy was utilized as the primary performance metric to assess the effectiveness of each loss function.

**github.com/cm-awais/loss_fun_SAR

I. RESULTS

The evaluation of loss functions for SAR ship classification revealed distinct performance patterns (Fig. 1). KLDiv Loss achieved the highest average accuracy 69.5%, followed closely by L1 Loss 69.12%, Focal Loss 68.4% and BCEL 67.3%, while CEL and MSE Loss demonstrated moderate performance.

Interestingly, while L1 Loss and Focal Loss achieved similar average accuracy, they exhibited contrasting performance across datasets. L1 Loss excelled on Fusar but underperformed on Opensarship, whereas Focal Loss displayed the opposite trend. This suggests potential dataset-specific suitability for certain loss functions.

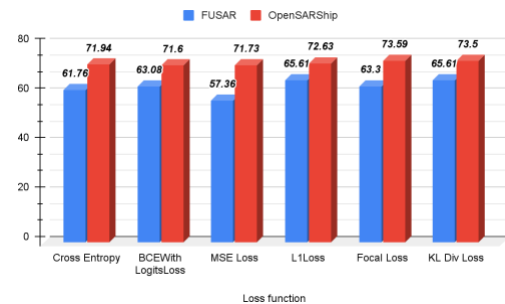


Fig. 1. This figure shows the accuracy of loss functions for each dataset .

III. DISCUSSION AND MAIN CONCLUSIONS

The findings suggest that the choice of loss function can significantly impact performance in SAR ship classification tasks. Notably, L1 and Focal Loss, despite similar average accuracy, exhibited opposing performance trends across datasets, suggesting potential data-specific suitability for certain loss functions. This underscores the need for task-specific evaluation of loss functions to optimize classification accuracy, particularly in scenarios involving diverse datasets or specific performance requirements for certain categories. Further research could explore the underlying factors contributing to the observed performance differences and investigate additional loss functions tailored to the nuances of SAR ship classification.

ACKNOWLEDGMENT

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Facing global changes: adaptive genetic variation in Chestnut populations

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Short summary: We explored the relationship between genetic variability and environmental variables in natural *Castanea sativa* population, unveiling how the different climatic scenarios drove local adaptation processes.

Keywords: Local adaptation Genetic diversity, Sweet Chestnut, nSSRs, EST-SSRs

I. BACKGROUND

Trees are generally long-lived sedentary organisms and their ability to adapt to changing climate depends on genetic variation within and among populations (Aitken et al 2008). This work aims to highlight the potentiality of genetic diversity studies to identify species/germplasm adapted to different environmental conditions, to be preserved and used in conservation and management.

MATERIALS AND METHODS

Using five genomic nSSRs and eight functional EST-SSRs markers, 268 individuals belonging to ten different natural European chestnut populations distributed in contrasting climatic sites were genotyped. In addition, associations between allelic variation and climatic variables (environmental association analyses approach) were performed. To compare present and future scenarios of tree populations in view of climate change, twenty-one climatic variables for each population were used (Fig. 1) Through the “Ecocrop” function implemented in DIVA-GIS, it was possible to determine the areas in which chestnut performs best in present and future climatic conditions (Hijmans et al. 2004).

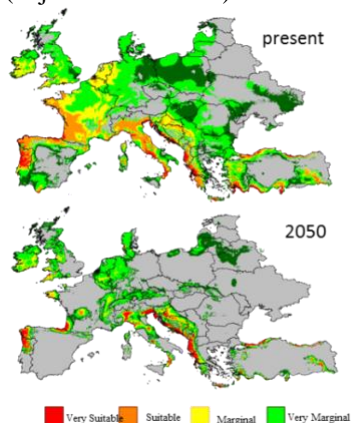


Fig. 1 Representation of the areas with best suitability for chestnut development in reference to present and 2050.

II. RESULTS

Results highlighted a strong inter-relationship between climate variables and evolutionary processes

resulting in adaptive variation. STRUCTURE analysis based on functional markers split the populations in three separate gene pools ($K = 3$), mostly in agreement with the different climatic conditions existing in the studied areas (Fig. 2) Divergent spatial patterns of genetic variation between rainy and arid areas were found. We detected a total of 202 associations with climate among 22 different alleles, 9% of which related with the outlier locus FIR059, known to be implicated in regulatory mechanisms

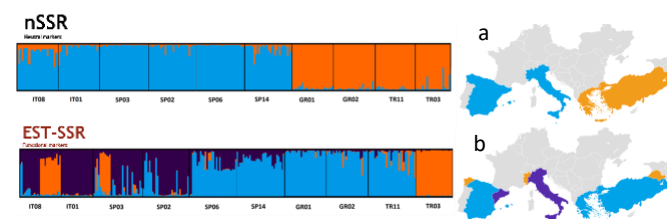


Fig.2. Population genetic structure of ten sweet chestnut populations grouped into clusters I (blue color) and II (orange) according to gSSRs markers ($K = 2$) (a) and grouped into clusters I (blue), II (purple) and III (orange) according to EST-SSR markers ($K = 3$) (b).

III. DISCUSSION AND MAIN CONCLUSIONS

Past and current climate changes have affected the pattern of genetic diversity and genetic structure of extant species. Landscape genomics analyses revealed a pattern of adaptive variation, where specific climatic variables influenced the frequencies distribution and fixation of several alleles, resulting in local adaptation processes of the populations in the investigated areas. Our findings underline the close inter-relationship existing between climate and genetic variability and indicate how this approach could provide valuable information for management of forest species in rapidly changing environment.

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The Italian Omics Observatory Network of Marine Biodiversity

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Short summary: The establishment of the Italian Omics Observatory Network of the NBFC is presented as a preservation strategy in response to the increasing threats to marine biodiversity.

Keywords: Marine biodiversity, Marine omics data, Marine observatory

I. BACKGROUND AND AIMS

Marine biodiversity is severely affected by multiple threats from human activities and climate change. Deterioration of natural populations, invasion by exotic species, extinction of native species, reduction of genetic diversity, loss/alteration of ecosystem dynamics and disease outbreaks are increasingly being linked to the introduction of pathogens and antibiotic resistant bacteria. To address these challenges, within the NBFC, the Activity 5 (A5) will implement last-generation technologies for the collection of Marine Omics data, their analysis and interpretation to implement Scalable, Fast and Cost-effective (SFC) response actions to Emergent Biodiversity threats. In collaboration with the National Marine Biodiversity Observatory System (Spoke 1), A5 will establish the Italian Omics Observatory Network fostering the development and application of last generation molecular technologies for present and future Marine Biodiversity studies in the Mediterranean Sea.

II. METHODOLOGICAL STRATEGY

Four marine (LTER) stations will be monitored: Golfo di Napoli, Promontorio di Portofino, Golfo di Trieste and Meda Senigallia (**Fig. 1**). Standard Operating Procedures for omics analysis of marine samples (sample collection, preservation, nucleic acid extraction and analytical workflows) have been defined. For protists/phytoplankton molecular data will be validated with microscopy-based and high throughput imaging devices. Last generation sampling methods will be employed to conduct size-fractionated filtrations (**Fig. 2**) of large seawater volumes at different depths on a monthly basis. DNA extraction and biobanking protocols, implementation of sequencing technologies in compliance with international standards for metabarcoding and shotgun metagenomics of marine communities will be performed. Environmental data (e.g T°C, salinity, nutrients, Chl-a, DOM) will be linked to biodiversity. Activities will be carried out following established protocols and international initiatives such as TARA-Oceans¹, EMOBON² and AtlantEco³.



FIG. 1. ITALIAN OMICS OBSERVATORY NETWORK SITES.



FIG. 2. SIZE-FRACTIONATED FILTRATIONS SCHEME REFERENCE

¹<https://fondatio3ntaraocean.org/en/expedition/tara-oceans/#results>;

²<https://www.embrc.eu/services/emo-bon>; ³<https://zenodo.org/records/6956974>

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Alien and neonative biodiversity: What is going on in Sardinia?

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Short summary: In the framework of an incoming European project on alien species a comprehensive review on existing literature on alien and neonative species in Sardinia is performed in order to set a baseline for incoming assessment.

Keywords: NIS, Alien species, Sardinia, Review, Non-native biodiversity

I. BACKGROUND

The assessment of marine alien species distribution, the areas at high risk of introduction, the main pathways and vectors of introduction are essential elements in designing effective management and conservation programs. Sardinia in the second biggest island of the entire Mediterranean Sea, with a coastline of about 1,850 Km, located in the center of the Western basin. In the framework of an Interreg Marittimo Italy-France project devoted to limit, manage and survey actions related to the introduction of invasive alien species in this area, a review on existing data on alien and neonative species in Sardinia was performed.

MATERIALS AND METHODS

A query to Scopus Database was investigated with the following keywords: (alien AND Sardinia/Sardegna) OR (NIS AND Sardinia/Sardegna) OR (non indigenous AND Sardinia/Sardegna) OR (IAS AND Sardinia/Sardegna). Additionally, ORMEF database (<https://www.ormef.eu/>) for fishes was consulted. Scientific publications and data collected were sorted and checked including data until 2023, regarding marine and brackish records.

II. RESULTS

Bibliographic search revealed that in 2008 only 2 manuscripts were published while in 2023 a total of 37 resulted. Sardinia could be apparently an historically understudied area compared to mainland, at least for some sectors, but also potentially an under-invaded region with an average of alien species per 100 km of coastline slightly below to the average Italian trends. Main research (number of recorded species) was performed by Pavia University [1, and references therein] on alien fouling communities of marina harbors or brackish environments (lagoons, enclosed bays) while other studies (especially for marine environment) were mainly reporting species opportunistically and rarely devoted to a specific project on alien species inventory. Findings were mostly from regional source (Sardinia Region or Sardinian Universities). An Italian review reported for Sardinia 13 species in 2010 (all groups) [2], moving to 19 in 2017 [1, only fouling communities were investigated]. After that, overall other species have been reported for Sardinian non-native biodiversity, raising the account to a total of 51 introduced species at 2023. Regarding alien fishes, they were reported as the oldest reports for an alien species in Sardinia, with *Psenes pellucidus* as the first reported (1955) and *Abudefduf* cf. *saxatilis* the last one (2020) [3]. *Fistularia commersonii* was the most frequent report with

more than 20 record in the region. Moreover, despite the lack of unambiguous photographic proof documentation, recently at least 3 different unconfirmed records of *Pterois miles* have been sighted respectively from a bather, a scuba diver and two fishermen all along the island in the last years (2020-2023; unpublished data).

III. DISCUSSION AND MAIN CONCLUSIONS

This review allowed to depict a preliminary baseline of alien species in the Sardinia region as a starting point for research implementation. Widest geographical records come from ORMEF database, while the fouling community studies were only located in North Sardinia (only 4 harbors investigated vs the 82 currently existing). These few sites concentrate most of the reported alien records (invertebrates), eliding harbors as a good proxy for the interception of the incoming alien species, despite the need of strong specific taxonomic skills. To fill the lack of knowledge it should be desirable in the next future to increase the fouling communities' studies also in other geographical areas of the island. Another important point is to involve society (LEK, Citizen Science) in the context of alien species driving their attention to the most charismatic Phyla (fish and other striking colorful invaders) by applying already existing protocol settled and tuned in the framework of international projects.

ACKNOWLEDGMENT

I am grateful to Aquatic Ecology Lab - Pavia University for the organization of the "Assessment of fouling alien species in ports with the SERC protocol and experimental applications" and the IMC Trainee Margot Burton in the framework of ECOGESTOCK FEAMP (EMFF).

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Characterization of soft-bottom macrozoobenthic community: a case study from Sirolo (Adriatic Sea)

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Short summary: This work focuses on the characterization of mobile bottom biocenoses found in the area in front of Sirolo to gain an understanding of the macrozoobenthic assemblages and ecological status. The results will inform targeted initiatives for risk analysis and the protection or restoration of the region biodiversity.

Keywords: Monitoring, Macrozoobenthic community, Soft bottom, Adriatic Sea

I. BACKGROUND

The soft-bottom macrozoobenthic community plays a key role in sedimentary processes and is highly responsive to variations in environmental quality, regarding the physico-chemical characteristics of sediments [1]. Therefore, benthic communities are a valuable tool for assessing environmental quality, as they provide insight into biodiversity changes occurring in response to fluctuations in different factors. This study is part of a multidisciplinary investigation carried out for a feasibility study aimed to a future protection of the Sirolo's beaches. The results will constitute a reference for the elaboration of site-specific projects such as risk analyses and protection or restoration actions.

MATERIALS AND METHODS

In the present study, five sampling sites (SN_1, SN_2, SN_3, U_1, and U_2) were selected along two transects placed orthogonally to the coast in an area located in front of Sirolo (AN), at about 5, 8 and 12 m depth (Fig. 1).

At each site three replicates of sediment were collected using a Van-Veen grab (capacity: 18 L; surface: 0.1 m²). The samples were sieved on board through a 0.5 mm mesh and preserved in 5% buffered formalin. In the laboratory, macrofauna was sorted using a stereomicroscope and a binocular microscope, identified to the species level, when possible, counted and weighted (fresh weight). For each site abundance, biomass, and other biotic indices were calculated. Considering the abundance data, to identify possible similarities among sampling sites, a MultiDimensional Scaling (MDS) analysis was conducted using PRIMER software [2]. Furthermore, the main biocenosis was identified for each station. Finally, to evaluate the ecological status of the area, the M-AMBI (Multivariate-Azti Marine Biotic Index) was calculated [3].

II. RESULTS

In the overall sampling period, a total of 86 taxa was found, mainly polychaetes (29), molluscs (28), crustaceans (21), and echinoderms (5). The faunal composition showed that the communities found at all sites belonged to the Well-Calibrated Fine Sand biocenosis, according to the grain size analysis. The most abundant species were the bivalve *Chamelea gallina*, the polychaetes *Owenia fusiformis* and *Micronephtys stammeri*, and the amphipod *Pariambus typicus*.

The results of the M-AMBI index showed a homogeneity among the sampling sites, as the ecological status was found to be high in all of them.

With a similarity of 60%, MDS showed three clusters: one containing the site at lower depth (SN_1), the other one the sites at intermediate depth (SN_2 and U_1), and the last one the sites at greater depth (SN_3 and U_2; Fig. 1). This separation can be explained by the different abundance of the main species, e.g. *C. gallina*, *O. fusiformis*, and *P. typicus*.



Fig. 1. Left: study area. Right: MDS applied to the abundance data of macrozoobenthic species.

III. DISCUSSION AND MAIN CONCLUSIONS

The study results contribute to the comprehension of the ecological dynamics in the area and highlight the importance of monitoring to understand the biodiversity of macrozoobenthic assemblages. These data are fundamental to assessing the ecological status through the information given by a variety of biotic indices. Moreover, due to the great responsiveness and sensitivity, the benthic communities' variations, both in terms of abundance and composition, can be a signal of natural and/or anthropogenic changes. Statistical analyses carried out on data available from monitoring surveys can help identify possible causes of such variations.

Considering that the latest study conducted in the area date back to the early 2000s, further studies are necessary to continuously monitor the biodiversity status.

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Five case studies in the Mediterranean Sea to evaluate a different and faster approach to detect changes in nematode community structure

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Short summary: The combination of four morpho-functional traits (i.e., buccal cavity, amphid, cuticle, tail) has been suggested as an alternative to the taxonomic identification of marine nematodes. This is in order to develop alternative approaches as proxies applicable in biomonitoring assessment.

Keywords: Free living marine nematodes, Biological indicators, Marine environment, Human pressure, Faster prevention actions

I. BACKGROUND

Human pressure on marine ecosystems often compromises their proper functioning. In order to prevent irrecoverable damage, it is important to quickly identify environmental critical issues and nematodes are recognized good bioindicators of anthropogenic disturbance.

However, a general limitation in their use is related to their difficult and time-consuming taxonomic identification. Therefore, nematologists are investing many efforts to develop alternative approaches as proxies applicable in biomonitoring assessment.

MATERIALS AND METHODS

An alternative method that combines morpho-functional traits was proposed for detecting assemblage changes of marine nematodes. To assess this new approach, we considered five study cases carried out in several Mediterranean areas: two ports (Voltri and Marina degli Aregai), a coastal area influenced by riverine inputs (Adriatic Sea), a fish farm (Olbia) and a tuna farming (Vibo Marina).

Meiofaunal samples were treated as described by Danovaro et al. (1). Nematodes were first identified at the genus level and after defining of the various categories of each morpho- functional trait, each genus was assigned to the most suitable category based on its morphological appearance according and each taxon obtained its own number code (see Fig. 1 and 2 for details).

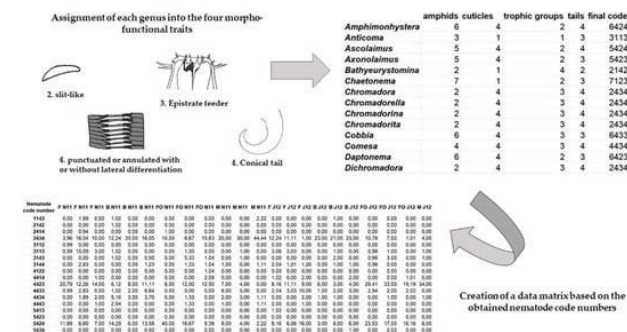


Fig. 1. Data matrix created on the combination of morpho-functional traits assigned to each genus.

II. RESULTS

Multivariate analyses (nMDS and ANOSIM) revealed similar pattern distributions of the sampling stations in all the study cases (Tab. I).

TABLE I. Results of ANOSIM performed to detect the presence of significant differences among the stations and sampling periods of each study case (n.s. indicates when significant differences were not found).

Study Case	Structure at Genus Level		Structure at Morpho-Functional Level	
	Sample Statistic	Pairwise Tests	Sample Statistic	Pairwise Tests
Genoa Voltri port	Stations R = 0.80; p = 0.001	St. I vs. St. O: R = 0.99; p = 0.03 St. I vs. St. M: R = 0.65; p = 0.03 St. O vs. St. M: R = 0.75; p = 0.03	Stations R = 0.78; p = 0.001	St. I vs. St. O: R = 0.99; p = 0.03 St. I vs. St. M: R = 0.60; p = 0.03 St. O vs. St. M: R = 0.70; p = 0.03
Aregai marina	Stations: p = n.s. Periods R = 0.81; p = 0.029		Stations: p = n.s. Periods: p = n.s.	
Riverine outfall areas	Stations R = 0.38; p = 0.001	F vs. B: R = 0.26; p = 0.05 F vs. FO: R = 0.60; p = 0.002 F vs. M: R = 0.48; p = 0.002 B vs. FO: R = 0.67; p = 0.002 B vs. M: R = 0.30; p = 0.017 FO vs. M: n.s.	Stations R = 0.35; p = 0.001	F vs. B: R = 0.25; p = 0.05 F vs. FO: R = 0.59; p = 0.004 F vs. M: R = 0.34; p = 0.004 B vs. FO: R = 0.70; p = 0.002 B vs. M: R = 0.28; p = 0.017 FO vs. M: n.s.
Olbia Fish-farm	Stations: p = n.s. Periods: p = n.s.		Stations: p = n.s. Periods: p = n.s.	
Vibo Fish-farm	Stations: p = n.s. Periods: p = n.s.		Stations: p = n.s. Periods: p = n.s.	

III. DISCUSSION AND MAIN CONCLUSIONS

The results showed that functional trait codes perfectly reflect the taxonomic structure of nematode communities at the genus level in all cases studied. This approach makes it possible to suggest that its implementation, associated with advances in machine learning, could transform nematode ecological surveys.

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Including Climate within MSP and MPA

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Short summary: We propose a guidance to include Climate Change (CC) in MSP processes, MPA and MPA network identification, implementation and design to better preserve marine biodiversity as key element of adaptation and resilience. The guidance need was partly tested by analyzing management questions from test-sites. CC-related criteria could be relevant for 68.6% of them.

Keywords: Biodiversity Conservation, Global Change, Vulnerability Assessment, Guidelines, Adaptivity, Sensitivity

I. BACKGROUND

Marine Spatial Planning (MSP) is emerging as a vital tool for sustainable ocean management and conservation [1]. MSP significance in the designation, establishment and design of Marine Protected Areas (MPAs) is becoming increasingly apparent [2], especially considering the goal of safeguarding 30% of EU sea by 2030 [3] and conserving biodiversity. However, the increasing impact of Climate Change (CC) is barely considered in MSP. The project MSP4BIO, financed by Horizon Europe, intends to address this gap by proposing a guidance aiming to better evaluate and include CC in European MSP processes to improve biodiversity conservation. We present here the guidance flowchart including a climate-revised criteria list. To test the guidance relevance, we propose a first evaluation of the current state of CC inclusion in the European management framing in the light of guidance.

MATERIALS AND METHODS

The guidance was established based on an up-to-date bibliography screening including 424 articles. The literature review covered the key aspects of CC, ranging from CC incidence on marine biota and ecological traits to MSP and MPA management. It was supported by complementary systematic review and expert interviews for some key aspects such as the identification of criteria for climate smart MPA networks implementation (78 papers identified). The evaluation of CC inclusion in European MPA framing was performed using a textual and cluster analysis of the 156 management questions arising from the 6 test-sites of the project: Baltic Sea, North Sea, Atlantic (Cadiz and Azores), Mediterranean and Black Sea.

II. RESULTS

a. The MSP4BIO guidance

The guidance proposes a methodology for integrating climate into each component of MPA and MPA network creation and adaptation. It is structured around 5 main steps (Fig. 1) related to a list of criteria and methodologies. The analysis core merges velocities analysis and trait-based vulnerability assessment at different scales from species to ecosystem. The vulnerability assessment is based on a ranked list of traits of sensitivity, adaptability and exposure under climate change previously identified. The analysis of vulnerability assessment leads to the creation of a climate-portfolio related to management objectives and linked to decision trees guiding managers into the workflow from the identification of the purpose of the network to the decision process.

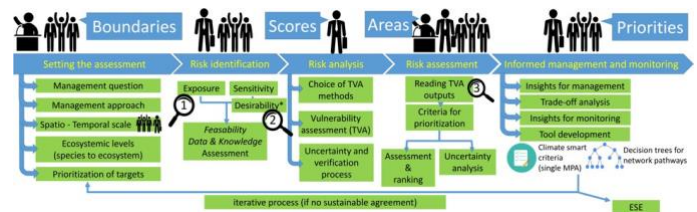


Fig. 1. Guidance Flowchart

b. Guidance example: evaluating CC in MSP framing

To evaluate the inclusiveness of CC into management issues, the first step “Setting the assessment” list of criteria was tested on management questions arising from the 6 test-sites. Among the 156 questions, 12.8% are directly related to CC by managers, 55.8% more could benefit from CC criteria inclusion (pointed as related to CC following the guidance) and 31.4% are not climate related. Only 7.8% of all the management questions are considered sufficiently precise to allow optimum selection of criteria, the others could benefit from the guidance.

III. DISCUSSION AND MAIN CONCLUSIONS

The analysis of management questions highlights a need of CC-related guidelines in MSP. Indeed, 68.6% of management questions could benefit from CC-criteria whereas CC inclusion is pointed out as a key component to assure adaptation and conservation. Nevertheless, CC is still not a priority for most of the test sites as only three of them mentioned climate objectives and only 12.8% of questions are related by managers to climate in their clarification-process. We also highlight that most of the management objectives are not yet clearly formalized, revealing a dichotomy between bottom-up and top-down questions and the necessity to better connect management scales. The guidance is currently feeding an ESE model.

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“Make Kin Don’t Kill”: a transdisciplinary study on the Blue Crab in the Northern Adriatic

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Short summary: We investigated the complex and different narratives at play in shaping attitudes, mass media communication, and policies around the management of biodiversity and allochthonous species. The Blue Crab (*Callinectes Sapidus*) in the Northern Adriatic was taken as a case study.

Keywords: Blue Crab, Biodiversity, Allochthonous Species, Environmental Humanities, Narratives, Transdisciplinarity

I. BACKGROUND

This research is grounded on the importance of working with citizens and a wide variety of stakeholders, to explore the ecological, social, cultural, and economic impacts of allochthonous species on local communities and on biodiversity, adopting the perspectives of multispecies studies¹. Through an extensive and transdisciplinary study in the field, we wish to unveil the main narratives on a specific case study - the Blue Crab (BC; *Callinectes Sapidus*) in the Northern Adriatic - and how they may shape public approaches and policies. Inspired by the word “kinship” as used by Donna Haraway [1], this research points at the need for new connections between human and non-human communities.

MATERIALS AND METHODS

Public narratives of different actors on the case study were firstly gathered and examined using text-analysis of academic articles, newspapers, videos, and books. The literature was collected from different disciplines, in particular marine ecology and biology, anthropology, critical animal studies, sociology, and communication studies. The most important actors (entrepreneurs, associations, scientists, fishermen and clams’ farmers) dealing with the *Callinectes sapidus* in the Northern Adriatic were selected through a wide mapping of the territory. The research on the field was performed using qualitative methods (i.e. semi-structured interviews and non-participant observation) and compared with quantitative data (questionnaires).

II. RESULTS

The preliminary results of this study found complex and polarized positions (some of them shortly reported in Tab. I), exemplifying the diversity of interests that play a role in shaping and informing eradication and/or commercialization strategies of the Blue Crab. The outcomes highlight the importance of a transdisciplinary approach when dealing with the increasing presence of allochthonous species [2].

TABLE I - POLARIZATION OF THE NARRATIVES

<i>The BC as an opportunity</i>	<i>The BC as an emergency</i>
Fishermen who quickly adapted their fishing tools and strategies to make them suitable for capturing the BC and clams’ farmers who rapidly protected their crops profited economically from the BC arrival.	The species was an emergency for most clams’ farmers who used intensive, monospecific aquaculture. Politicians fought the emergency providing financial subsidies to counteract the damages caused by the species.
<i>The BC as an individual</i>	<i>The BC as a species</i>
Animal rights activists advocated for the right-to-life of each individual of BC. This position coexists and is inevitably in contrast with their own interests for biodiversity and ecosystem conservation in the affected areas.	Ecologists and biologists studied the species <i>Callinectes Sapidus</i> , overlooking its individual subjectivity. The research activities were mainly driven by the emergency and thus prioritized the study of the species’ reproductive strategies and life cycles. So far, the impact on ecosystems and biodiversity has not been analysed extensively.

III. DISCUSSION AND MAIN CONCLUSIONS

A crucial facet of the research lies in the incorporation of anthropological methods, which have proven pivotal in amplifying the voices of marginalized communities. By engaging with traditional fishermen, citizens, and local communities, the research contributes to a more equitable representation of their perspectives. Although our results are still in the initial phase, they already show their potential to grounding policymaking in the authentic experiences and needs of citizens, for more effective and socially responsible strategies [3] on allochthonous species and biodiversity.

ACKNOWLEDGMENT

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LIFE PROMETHEUS

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Short summary: The Life PROMETHEUS project will involve 25 partners from 5 countries to enhance elasmobranchs' conservation at Mediterranean scale and beyond, and at the same time will contribute to mitigate the spread of invasive species.

Keywords: Elasmobranchs conservation, By-catch, Ecotourism, Sustainable fisheries, Invasive alien species, Blue economy

I. BACKGROUND

The Mediterranean Sea is a hotspot of biodiversity for chondrichthyan species hosting over 80 species, but it is also one of the world's regions facing the highest risk of extinction. Here, between 1980 and 2015, the percentage of shark and ray species listed as threatened increased by 18% in the Mediterranean Sea [1]. Furthermore, this basin is considered the most heavily invaded region of the world [2], with ca. 100 introduced marine alien species categorized as IAS – Invasive Alien Species.

II. PROJECT ACTIONS

The LIFE23-NAT-IT-LIFE-PROMETHEUS is a transnational project focusing into 12 different Project Areas (Fig. 1) in Italy, Spain, France, Cyprus, and Greece, and aiming at the conservation of elasmobranch populations while mitigating the spread of IAS. The main aims of the project are i) the reduction of by-catch of 8 elasmobranch species included in the IUCN-Mediterranean Red List by using electro-magnetic deterrents and alternative fishing practices, ii) the promotion of sustainable fisheries targeting IAS instead of elasmobranchs, and iii) the protection of elasmobranchs aggregation areas.



Fig. 1. Project areas in which LIFE-PROMETHEUS consortium will carry out its concrete actions for elasmobranch conservation in the Mediterranean Sea.

Specifically, LIFE PROMETHEUS wants to: 1. apply cutting-edge deterring technology (both electric and magnetic devices) to reduce the bycatch of threatened elasmobranch species; 2. promote alternative sustainable fisheries in specific areas/periods critical for the selected elasmobranch species, supporting the shift to IAS fishery; 3. promote sustainable ecotourism in areas of

elasmobranchs aggregation; 4. provide guidance for financial incentives for fishers who decide to implement conservation-aimed mitigation measures; 5. increase public awareness involving both the public and coastal users in the adoption of a shark-free ecolabel, but also through the consumption of IAS.

III. EXPECTED RESULTS

LIFE PROMETHEUS consortium foresees of saving: 1200 specimens of *Rostroraja alba* (EN), 9200 *Raja radula* (EN), 9 *Isurus oxyrinchus* (EN), 400 *Prionace glauca* (CR), 3200 *Carcharinus plumbeus* (EN), 300 *Gymnura altavela* (EN), 300 *Aetomylaeus bovinus* (CR), 150 *Glaucostegus cemiculus* (DD).

The other expected results are:

- the involvement of ca. 800 fishers that will apply the use of the proposed electric and magnetic deterrents;
- the adoption of the “Shark Free” ecolabel by at least 30 fish markets/fish shops;
- the promotion of the use of alternative and more sustainable fishery gears in IAS fishery and their adoption by at least the 30% of participants;
- the involvement of ca. 15 restaurateurs or fish shops that will sell or offer in their menu IAS species (specifically, *Pterois miles* and *Callinectes sapidus*);
- the development of a Code of Conduct for diving activities carried out in areas in which elasmobranchs aggregate and its adoption by at least 10 diving centers, 800 divers, and 2 Marine Protected Areas;
- the identification of essential fish habitats for elasmobranchs and fine definition of their aggregations.

ACKNOWLEDGMENT

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Recreational fishing, the hidden value of fisheries: an environmental-economic assessment

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Short summary: The paper contributes to the debate on the management of the recreational fishing sector, analyzing its economic potential and highlighting the critical issues linked to environmental management and socio-economic evaluation of regulatory aspects. Focus is on the trade-off between the economic benefits derived from expenses and social benefits and how to manage the sustainability of marine resources using appropriate policy instruments (access and control, quotas, etc.).

Keywords: Biodiversity, Marine resources exploitation, Recreational fishing, Economic valuation, Surveys and monitoring

I. BACKGROUND

Marine ecosystems provides multiple benefits (and resources) to nature and humans and fisheries is a relevant sector for local communities and regional economic perspective. While benefits from commercial fishing are readily observable from national accounts and statistics, those of recreational fishing are poorly analyzed (e.g. our own literature review, and Hyder et al., 2018). The contribution of recreational fishing to well-being can be evaluated under two key approaches (Scheufele & Pascoe, 2022): an expenditure based approach, which is captured by national accounts, referring to the income generated by fishing related activities (license if any, boat and durable equipment expenditures etc.) and a welfare based approach resulting from the benefits perceived by anglers (outdoor sports, aggregation, competitiveness etc.) which is measured with the aggregated willingness to pay (consumer surplus). On the other hand, as fish provision is a renewable resource and competitive uses can diminish the stock and compromise the sustainability of the marine environment, the efficient access to the resource is crucial and the central regulator should consider societal long run net benefits for supporting/designing policy instruments.

MATERIALS AND METHODS

To understand the scope of recreational fishing valuation we conducted a worldwide literature review on ecosystem accounting case studies including the fishery sector. 88 publications from Scopus and Web of Science database were considered, of which 12 clearly adopted a recognized accounting approach (SEEA-consistent). This is accompanied by more generic research on the economic benefits and environmental impacts of recreational fishing, with particular attention to the European context. Finally, a questionnaire interview was conducted with 202 Italian fishermen participating in tuna fishing competitions, who were asked for information on their habits regarding fishing trips, catches, expenses and their attitude towards questions on recreational fishing management.

II. RESULTS

a. The state of recreational fishing valuation

Nine of the twelve publications included in the review assess the fishing sector, but only three consider recreational fishing accounting. This confirms lack of

estimates of catch effort and socio-economic benefits, especially for the Mediterranean sea.

b. Economic benefits and environmental impact

The review of benefits confirmed that recreational fishing is a widespread activity, capable of generating considerable income e.g. 6 billion euro just in Europe, with an average of 680€/year expenditure per capita (Hyder et al., 2018). However, the authors report a lack of evidence from Mediterranean regions (the Balkan countries, Spain, Italy etc.) which impact the capacity to properly assess the fish stock and design appropriate management strategies (Lewin et al., 2019).

c. Bluefin tuna survey results

The survey highlights an average expenditure per fishing trip of 372€, with an incidence of durable equipment of 11%, port expenses and boat maintenance 42% and expenses for non-durable materials (bait, hooks, fuel etc.) 47%. On average the number of annual trips are 21 with a total annual per capita expenditure of 7,820€. From the attitudinal questions, it emerges that over 63% of respondents think that sustainability is hindered by excessive fishing level but majority of respondents (71%) disagree that bluefin tuna is subjected to excessive harvesting, and ask for a higher recreational quota.

III. DISCUSSION AND MAIN CONCLUSIONS

The study reveals the necessity to assess and value the recreational fisheries due to their contribution to societal wellbeing but to monitor their non-rivalry access to critical marine resources. Management challenges exist in order to trade-off anglers' preferences and conservation issues. This signals the importance to adopt a multidisciplinary approach where scientific knowledge pairs the economic analysis.

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The invasive *Mnemiopsis leidyi* & the Venice Lagoon

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Short summary: In the last decade the invasive sea walnut, *M. leidyi*, arrived in the Venice Lagoon (Italy). The aims of this work are to investigate how *M. leidyi* affects the lagoon ecosystem and its artisanal fisheries using an interdisciplinary approach. This work assesses the short- and long-term impacts of this invasive ctenophore in the Venice Lagoon.

Keywords: Invasive species, Local ecological knowledge, field samplings, temperature, fishery landings

I. BACKGROUND

The Venice Lagoon is valued as a productive ecosystem and a biodiversity hotspot but is also heavily impacted due to multiple anthropogenic pressures and climate change [1], making it an ideal place for the spread of invasive species, as *Mnemiopsis leidyi*. The massive *M. leidyi* blooms in lagoons may have strong negative impacts on artisanal fisheries and ecosystem [2]. To clarify this complex issue, we use an interdisciplinary approach.

MATERIALS AND METHODS

Local Ecological Knowledge: a structured interview was conducted with 10 lagoon artisanal fishers, that use traditional fyke nets as fishing gear, about the arrival and spread of *M. leidyi* and their perceptions of its impact on their own fishing activities.

Lagoon fisheries records: to evaluate changes on lagoon fishers' target species, official time series of landings at the Chioggia' fish market from 1997 to 2019 were analyzed.

Water temperature data: to observe if the spreading of *M. leidyi* was favored by an increasing of lagoon waters, daily lagoon SST records from 1997 to 2019 were analyzed.

Field sampling: to understand if *M. leidyi* can mechanically affect fishing activities, we performed 6 field sampling campaigns on board with local fishers during peak months of the bloom period in the Venice Lagoon (summer 2019). To evaluate its spatial distribution, field sampling in 2022 and 2023 using a bongo-net was made.

II. RESULTS

All fishers reported no blooms before 2014 and agreed that ctenophore biomass increased year after year with a related decrease in target species catch. The clusters identified by a nMDS on lagoon landings corresponds almost perfectly to the periods of *M. leidyi* occurrence observed by the fishers (Fig. 1).

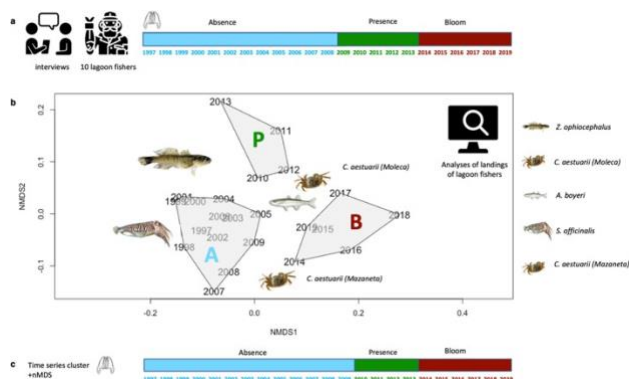


Fig. 1. nMDS of the Lagoon landings and the construction of the time series of occurrence of *M. leidyi*.

Multinomial Logistic Regression showed a statistically significant relationship between warming water (+1.75°C over the studied period) and the appearance and blooms of *M. leidyi*. We also built a linear model showing a significant negative effect of the occurrence of *M. leidyi* on the total lagoon landings, which decreased by 40% from its absence to its bloom period.

From the field sampling campaign on board with local fishers, we observed that the percentage of weight in fyke nets made up by *M. leidyi* was typically more than 50% of the net weight, and in many cases the net was completely filled by ctenophores, causing its mechanical obstruction.

From the field samplings between 2022 and 2023 using a bongo-net, we observe that *M. leidyi* is widely spread throughout the whole Venice Lagoon, finding it also near rivers outlet. Moreover, the total number of ctenophores was higher in 2023 while the animal size was significantly lower with respect to 2022.

III. DISCUSSION AND MAIN CONCLUSIONS

The traditional small-scale fishery considered in this study is an important and still lively component of the long-term human-nature relationship in the Venice Lagoon and an example of cultural heritage. The strong negative impacts by *M. leidyi* on local artisanal fishery, taking place since 2014-2016, could bring to the total loss of this traditional type of fishing in this lagoon, thus impacting both the local economy and lagoon ecosystem. The bloom of the invasive ctenophore, probably favored by the warming temperatures of the Lagoon waters, appears as one of the key reasons for the landing reduction of some main fishing target species, such as *Zosterisessor ophiocephalus* and *Sepia officinalis*. The sampling activities demonstrated high densities and a complete adaptation of the animal to the lagoon environment, surviving also in low salinity areas. This study demonstrates the usefulness of an interdisciplinary approach to study marine invasive species and their impacts.

ACKNOWLEDGMENT

We thank the fishers who made their time and knowledge available to contribute to this research.

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Assessing the biodiversity in the air: First approaches in an alpine environment

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Short summary: The pollen in the bioaerosol of Rifugio Larcher al Cevedale reflects the local flora, and estimates quite accurately the main plant cover constituted by Poaceae.

Keywords: Bioaerosol, Pollen-plant relationship, Pollen representativity, Biodiversity, Alps

I. BACKGROUND

Many plants use the air as a vector for reproduction, releasing pollen with species-specific morphological traits. We explore the intriguing potential of air as a means for biodiversity assessment in an alpine environment, known to be especially sensitive to impacts of global change. As a first approach, we look at the representativity of the pollen sample for the vegetation on site.

MATERIALS AND METHODS

The bioaerosol at Rifugio Larcher al Cevedale was collected for microscopical and molecular analysis by deposition sampling. Concomitantly, flora and vegetation were assessed: i) in a circle of 10 m radius from the sampler; ii) in 5 randomized plots of 2 x 2 m within the radius of 100 m from the sampler; iii) in a 1000 m x 2 m transect.

The pollen (P) - plant (V) representativeness was calculated as follows [1]:

$$P/V = \text{SPIn} (\%) / \text{plant cover} (\%)$$

where SPIn is the Seasonal Pollen Integral (p/cm²d).

II. RESULTS

A. Pollen taxa

Between 26/7 and 20/9/2023, 21 pollen taxa, 84% of herbal, 16% of woody plants, were detected. Out of 21 pollen taxa, 9 constituted > 1% of the SPIn in the bioaerosol (Fig. 1). The protocol of environmental DNA (eDNA) extraction and amplification, a tailored reference database on ITS1 and ITS2 regions for pollen and fungal taxa identification, and an efficient bioinformatics pipeline have been concurrently developed.

B. Pollen-vegetation relationship

The study site mainly features open acidophilous alpine grassland. A total of 46 vascular plant taxa were recorded in five plots (total area 20 m²). For nine taxa the P/V ratio could be calculated; when P/V = 1, the plant family was equi-represented; if P/V > 1, the family was over-represented by pollen analysis; if P/V < 1 it was under-represented:

Apiaceae = 1; Asteraceae = 0,02; Cyperaceae = 0,11; Fabaceae = 0,13; Juncaceae = 3,28; Poaceae = 1,76; Polygonaceae = 0,18; Salix = 0,08

Ten taxa recorded in the vegetation analysis were not represented as pollen in the air samples. The air sample, on the other hand, featured 13 taxa from non-local sources.

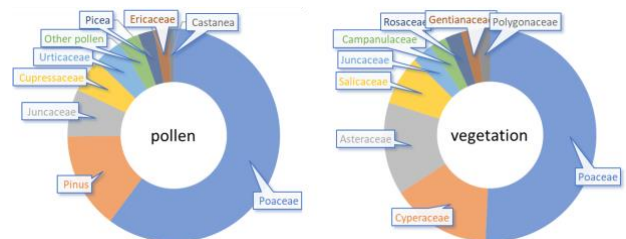


Fig. 1. The main pollen taxa (p/cm²d) in % (left) versus plant cover in % in vegetation plots at Rifugio Larcher al Cevedale (right).

III. DISCUSSION AND MAIN CONCLUSIONS

Besides the known role of airborne pollen on human health, we show that pollen in the air can be a means to assess plant biodiversity. The local flora of the open alpine environment dominated by grasses is well represented in the airborne pollen spectrum. However, there is a fraction of remote biodiversity transported by winds from lower elevations and/or longer distances to the receptor site. In addition, results of the ongoing molecular analysis of eDNA are expected to provide a higher taxonomic detail of airborne pollen. Long-term aerobiological monitoring at high altitudes would provide insight on changes in terms of plant composition, reflecting for example, the upward movement of invasive species, and on flowering phenology. To our knowledge, this is the first study that investigates the potential of the air as a matrix for plant biodiversity monitoring at high altitudes using both eDNA and microscopy.

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Molecular monitoring of *Dinophysis* spp. in mussel farms of the Northwestern Adriatic Sea

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Short summary: In a changing environment, a rapid, sensitive, and effective qPCR assay was developed and tested for the time-series monitoring of *Dinophysis* spp. abundances along the NW-Adriatic coasts.

Keywords: Monitoring, *Dinophysis*, qPCR

I. BACKGROUND

Emilia-Romagna and Marche regions are subjected to mussels DST contamination [1], even at low *Dinophysis* spp. cell concentrations with human health and socio-economic impacts. This study proposes the application of a qPCR assay for the monitoring of *Dinophysis* spp. abundances over time.

MATERIALS AND METHODS

Dinophysis spp. site-specific single cells were isolated and analyzed by qPCR to obtain the mean rDNA copy number per cell.

157 environmental samples collected from May 2022 to June 2023 were fixed with Lugol and counted by light microscopy. They also underwent DNA extraction and qPCR analysis. Toxins were quantified in mollusk flesh.

A qPCR standard curve using a previously developed genus-specific primers pair targeting the 28S region [2] of the rDNA was generated using 10-fold scalar dilutions of PCR product.

II. RESULTS

a. Standard curve

The standard curve has a sensitivity of 10 copies per reaction and an efficiency of 98%.

b. Estimation of rDNA copy number

The mean copy number per cell was obtained for *D. sacculus*, *D. acumianta* and *D. caudata*, with no difference in means observed (one-way ANOVA test for equal means, $F(2, 24) = 0.06$, $p > 0.05$). The mean number for the *Dinophysis* genus was calculated as $1.21 \times 10^4 \pm 1.81 \times 10^3$.

c. Evaluation of the assay for *Dinophysis* spp. monitoring

Light microscopy estimates were generally lower than qPCR ones, and a 2.24 ratio (qPCR/LM ratio) was obtained. Light microscopy and qPCR estimations in environmental samples showed a similar seasonal trend for *Dinophysis* spp., with higher abundances in May 2022, a decrease in autumn, a slight increase in winter and a new

increase in late spring. No exceeding of the toxin limit was recorded in mussels during the study period (Fig. 1). qPCR was able to count *Dinophysis* spp. in 48 samples in which light microscopy was unable to quantify it.

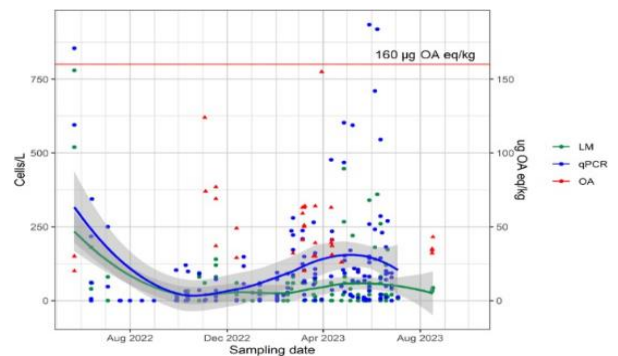


Fig. 1. Data points represent measurements of *Dinophysis* abundance obtained by LM and qPCR at all the sites between May 2022 and June 2023. The points fitted with smooth lines of best fit, with grey areas representing 95% confidence intervals. Red line: legal limit value of 160 µg OA eq/kg according to Reg. EC 853/2004

III. DISCUSSION AND MAIN CONCLUSIONS

The recent changes of the Adriatic Sea state towards reduced eutrophic conditions (Ricci et al., 2022) could influence *Dinophysis* spp. occurrence with limited predictability due to its mixotrophic nature. Therefore, this assay provides the ability to quickly monitor this genus in a changing environment in a sensitive and efficient way, with a less time-consuming approach than traditional light microscopy-based methods.

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The experience of the CNR-Istituto di Scienze Marine (ISMAR) to enhance the Natural Science Collections in the RI DiSSCo

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Short summary: ISMAR Natural Science Collections (NSCs) will be part of a national repository for digital collections, data and metadata, shared with FAIR principles in the frame of the DiSSCo Research Infrastructure. This action highlights the relevant role of NSCs in detecting biodiversity changes and developing appropriate conservation measures.

Keywords: DiSSCo, Natural science collections, Digitization, Digital twin, Biodiversity data

I. BACKGROUND

Two and a half centuries of natural history are preserved in museums. However, research activities produce collections of physical objects (i.e. minerals, plants, animals, and fossils) which are not always available to different stakeholders. The aim of DiSSCo Research Infrastructure is to virtually bring together natural science collections (NSCs) and related information in a single Findable, Accessible, Interoperable and Reusable (FAIR) portal at European level [1].

MATERIALS AND METHODS

Working protocols are been defined for the cataloguing, metadating and digitization of the NSCs hosted in CNR-ISMAR, and in line with international standards [2, 3]. The protocols support defining the NSC, the types of samples it comprises, the selection of vouchers, and the organization of associated information. The digital records will be deposited in GBIF platform (Fig. 1).

II. RESULTS

In the three ISMAR institutes currently involved in DiSSCo, a total of 11 NSCs are being digitized (Tab. I), by collecting and organizing the metadata according to the identified MIDS.

TABLE I. NSCs OF CNR-ISMAR SELECTED IN THIS STUDY

NSCs type	CNR-ISMAR NSCs		
	NSCs location	Number of NSCs	Numerical consistency
BOTANICAL	Venice	4	1600
ZOOLOGICAL	Venice	5	12000
PALEONTOLOGICAL	Bologna, Naples	2	~ 6000

NSCs present some critical issues (objects with many specimens of the same species, multi-species samples, matrices), resolved by structuring the acquisition of data and meta-data appropriately. These ancillary files will be associated to each voucher in the NSCs, and we have chosen to use the GBIF platform to make the NSCs available externally, guaranteeing access to users of different levels (researchers, teachers, museums, and public). We are also developing protocols to standardize the procedures. NSCs resulting from research activities are

different from these produced in museums, we will publish and make the protocols available to share the solutions we are adopting.

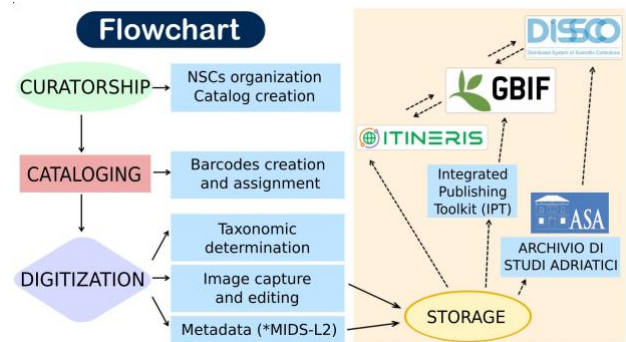


Fig. 1. Workflow conceptualization.

III. DISCUSSION AND MAIN CONCLUSIONS

Documenting the present and the past biodiversity status provides solid foundations for observing the changes taking place. The creation of digital twins of NSC objects originating from research activities, together with those deposited in museums, will offer fast and efficient information sharing, encouraging collaboration, communication, and dissemination.

ACKNOWLEDGMENT

We thank the PNRR Project IR0000032 – ITINERIS - Italian Integrated Environmental Research Infrastructures System.

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Monitoring the evolution of biodiversity for management planning. The example of Verona

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MShort summary: An example is reported on how scientific research, citizen involvement, and the utilization of museum collections can be used in territorial planning by the management authorities.

Keywords: Flora, Fauna, Citizen Science, Hotspots, Veneto

I. BACKGROUND

The city of Verona has a long tradition of natural science studies. One of the first natural history museums was founded here 16th century and the first surveys aimed at checking the presence and distribution of flora and fauna were carried out in the 19th century. Recent surveys on the flora and studies on specific animal taxa [1] make it possible to estimate the current biodiversity, compare it with data collected in the past and implement actions to maintain it.

In order to apply these data to the management of urban areas, two projects, funded by the Cariverona Foundation and coordinated by the Municipality of Verona (NaturAzioni and éVRgreen), are currently ongoing. The projects focus on the identification of areas with greater biodiversity and areas where renaturation is necessary and possible [2, 3].

MATERIALS AND METHODS

The data were obtained by consulting historical (e.g. Goiran herbarium, Cartolari entomological collection, Dal Nero collection) and current collections, consulting the bibliography and carrying out targeted research in the field, also by the means of Citizen Science actions (Bioblitz) in the frame of some re-naturation projects.

The data obtained were then recorded in a database and a GIS was created.

II. RESULTS

Comparison of historical and current data revealed a decrease in plant species, the disappearance of 369 species no longer found and the appearance of 313 previously unreported species, including 108 alien species. With regard to animal species, the data are much less precise and more fragmented, as there are a large number of species belonging to the various groups; unfortunately, we do not have a complete list of the species present. The most abundant data concern Lepidoptera, for which we know of the disappearance of 15 species in the second half of the last century and the arrival of 9 alien species.

By plotting the data collected on the distribution of fauna and flora, it was possible to highlight areas with a higher concentration of biodiversity and areas where there was a

lack of data. In the latter areas, research was concentrated, and urban bioblitzes organized.

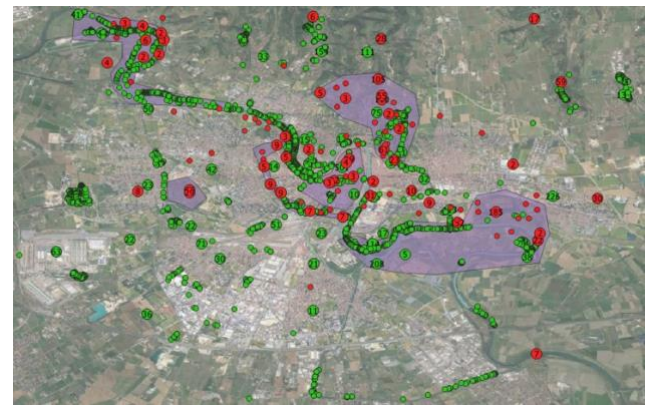


Fig. 1. Sites with the highest concentration of plants (green dots), animals (red dots) and diversity hotspots (purple areas) in the urban area of Verona.

III. DISCUSSION AND MAIN CONCLUSIONS

Bibliography analysis and data mining in museum collections, together with research carried out in the field, have made it possible to identify areas of the highest biological diversity and urban ecological corridors. Two main ecological corridors run through the city from North East to South West, these are the banks and waters of the Adige River for aquatic and riparian fauna and flora and the city walls and the ramparts for terrestrial fauna and flora. Hotspots are also the areas of the urban hills, in continuity with the surrounding mountain areas and the wetlands to the north and south of the city (Fig. 1).

The data were obtained also thanks to the participation of citizens within the NaturActions Citizen Sciences project. They will then be used for identifying urban areas to be reforested and for identifying indicators for future biodiversity monitoring within the éVRgreen project.

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Omniscient Mind and Biodiversity

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From the book "From Knowing to Understanding - Did Evolution Produce an Omniscient Mind?"
(L. Contoli Amante, by La Ruota Edizioni)

Hyperthelia (a concept, nowadays, no longer very "fashionable", indeed) refers to those traits that, once were useful in an adaptive sense, assuming e.g. a "social" value in intraspecific relationships, and that tend to be favored beyond the functional limit, e.g., by sexual selection (deers with large antlers, saber-toothed tigers, etc.), to the point of being detrimental for the species. **Hyperconceptualization**: a hypertelic pathway of the human mind...?

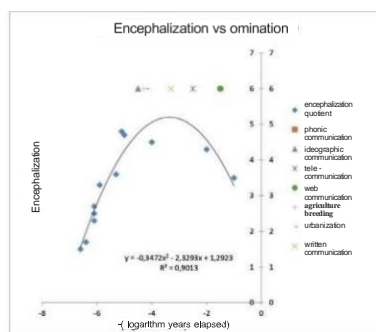
I. BACKGROUNDS

The human seasons: - animality > unawareness (cf. Ungaretti!) - inevitable death > terror - natural deities > fatalism - one God > illusion - God - man > hope - churches > disappointment - enlightenment > awareness - technology > shortsightedness - God - Man > conceit - widespread warfare > resignation - human helplessness > despair - delegation to computer > mind renunciation - virtual reality > world renunciation

It has been observed that the tumultuous increase in cranial and, therefore, cerebral size, observable in the course of our evolution seems to stop, starting perhaps 10^4 - 10^5 years ago, and then even tending to a slight decline (Tab. 1; Fig. 1).

Note: the trend line, drawn in a purely suggestive way, although very significant, is certainly inadequate, because it is simplistic, to describe the phenomenon. In the course of our evolution, therefore, the "brain/body weight" ratio (Encephalization Ratio, cf. Vrba; Martin 83; Smith; Aiello & Bean '90.) increased continuously until shortly after the appearance of H. sapiens,

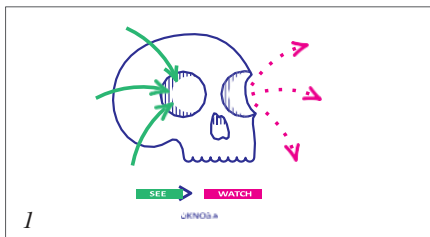
Tab. I; Fig. 1



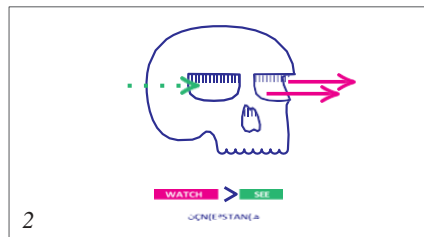
and then stopped \approx at 10^5 years ago; since then, a slow descent is observed, until today... Can, the above, be related to the unfolding of the various stages of cultural evolution, which tends to replace the strictly genetic evolution?

Who knows if the halt in brain growth, perhaps due to limitations related to the dilation of the birth canal in relation to the infant's head, did not almost entail a choice, between which parts of the brain could or should continue to grow, resulting in a gradual prevalence of the "modern," i.e., rational (and conceptual) parts over the still rather instinctual ones?

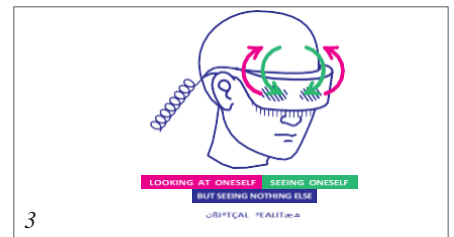
II. RESULTS



1. **Pre-anthropoid hominids:** large eyes open to the surrounding reality seem to symbolize maximum openness to external cognitive messages (green arrows) and pre-conceptual scrutiny toward ever new knowledge (red dashed arrows).



2. **Homo sapiens, until the recent past:** the low, reduced orbits (cf. the "Cro-magnon" features) symbolize a conceptual gaze, aimed at some result, directed to an interpreted reality and to some extent assimilated through understanding, less ever less open for profound insights.



3. **Homo sapiens from the present to the foreseeable future:** the eyes are now closed to the outside world and fully engaged by the viewer of a virtual "internal" reality far more fulfilling and functional than external reality (dis. by Susanna Contoli, on schematics by the A.).

Comparing two skulls of Hominina: from large eyes and low forehead to small eyes and high forehead...from more sight to more mind...the eyes and sight yielded towards the forehead and brain...from seeing to looking, during conceptual evolution...from looking at what we see to seeing what we look at...more brain, more concepts and more understanding; less sight, less knowledge...is this perhaps the symbolic fate of Homer? ...from seeing what we don't know... to looking at what we already understand...more and more self-referential...first, the image of reality; then, that of the window; next step: not windows, but screens...perhaps, it is the future of Man, imprisoned and almost condemned to virtual reality (not virtuous!), illusion, dream and increasingly isolated from the real world that, for us, is already "ending"...

III. DISCUSSION & MAIN CONCLUSIONS

Understanding encloses us into ourselves, while on the other hand Knowing opens us to the world?

Our understanding of reality is still linked to the evolutionary adaptation of a species, ours that covers (like others) a very specific eco-ethological role; even if with clear differences between the various human cultures. Ever more we have been seeing the affirmation of self referential human power, expressed by the increasing understanding and enslavement of nature.

In the absence of a direct selective reward, the structure of the mind could, perhaps, reduce its evolution to the gradual quantitative dominance of the neocortical component over the others, without acquiring qualitatively new structural potential while gradually beginning to show more and more of its limitations.

Over time, two possibilities have shown up: binding reality to ourselves (idealism), or ourselves to reality (materialism, objectivism)...? These seem to be two divergent paths but, both, steps towards anthropic complexification.

Is Biodiversity useful to an Omniscient Mind now closed in its own Digital Universe?

Artificial intelligence may become a possible solution, for the evolutionary leap of a new "chimeric" mind, amongst the anthropic and the artificial, towards a future approach to reality, with the risk of transferring, to the machine, our own mental limitations; e.g., the binary logic "all or nothing" may be a symbol of it; thus we would deny a true originality to the automated "thinking" and their evolutionary role with respect to our intelligence... For now and sic stantibus rebus, Man seems to me to be getting ever more closer to the limits of the evolutionary maladjustment of his own mind.

A price to be paid (perhaps, the price to be paid!) would seem to be the loss of the "real," external world in exchange for a coruscating, consoling and deceptive virtual reality that, for that matter, we are already being fed. Could we end up locked up in an "inner environment" of the new superorganismic level that we ourselves have created and to which we would entrust the practice and knowledge of a new world, for us, inaccessible and unintelligible?

Forest management and monitoring after a catastrophic climate event: the case of *Salamandra atra aurorae* and the VAIA storm.

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Short summary: The VAIA storm in 2018 had a strong impact on *S.a.aurorae* habitat, causing the disappearance of the subspecies from several areas. The need to carry out forest management after the storm has led to the establishment of guidelines, resulting from dialogue among all stakeholders. Considering that catastrophic climate event will be more frequent due to the climate change, information on the consequences on the species and strong relationship with all stakeholders will be crucial for conservation.

Keywords: Habitat alteration, Climate change, Monitoring, Forest management, Stakeholders, *Salamandra atra aurorae*

I. BACKGROUND

Salamandra atra aurorae is a rare and endangered subspecies of alpine salamander that inhabits a very restricted area (26 km²) between Veneto and Trentino. In 2018 the VAIA storm caused the fall of millions of trees in North-East Italy, with a strong impact on *S.a.aurorae* habitat. We monitored the subspecies before and after the storm in order to understand the consequences over time. In collaboration with local stakeholders and institutions of public administration we established and applied guidelines for forest management after the storm, in order to minimize the negative impact on the subspecies.

MATERIALS AND METHODS

We monitored the population of *S.a.aurorae* in Trentino in the same 50 plots before (2017) and after the storm (2019- 2021) with a Capture-Mark-Recapture approach. In addition, we collected some environmental variables related to the forest structure in order to assess the impact of the storm on the study area. Guidelines for forest management were established by specialist in herpetology conservation after several meetings with local stakeholders and institutions of public administration.

II. RESULTS

The storm VAIA had a strong impact on the study area. We registered the mean fall of 31.5% of the trees (range 0-69.2%) with a significant difference in number of trees between 2017 and 2019 (before and after the storm). The percentage of deadwood brushwood piles increased from a mean of 4.4% in 2017 (range 0-27.5%) to 18.6% in 2019 (range 0-70%), with an average increase of 14.2% (range 0-38.75%) and a significant difference before and after the storm. The increased exposure to sunlight due to tree falls led to a decrease in surface occupied by mosses with an average negative difference of - 8.5% (range -70 - +30%). Demographic estimates in the two years after the storm (2019/2020) were not considerably different from estimates obtained before the storm (2017). However, we weren't able to obtain estimates in 2021 due to the limited number of salamanders sampled (5 individuals). The study area occupied by *S.a.aurorae* has changed considerably over the years (Tab. I).

TABLE I.

	Presence of <i>S.a.aurorae</i> before and after storm VAIA			
	2017 (before)	2019 (after)	2020 (after)	2021 (after)
Nr and % of plots	13 (26%)	17 (34%)	9 (18%)	2 (4%)

Guidelines for forest management after the storm included several indications like: specific timeframe for the works execution (only in winter), use of less invasive vehicles (more compact and efficient) or cableway system, if possible, increase of deadwood on the ground using forestry work processing waste. In addition, 500 deciduous trees were planted in forest lands destroyed by the storm, in order to restore the suitable habitat for *S.a.aurorae* and facilitate the establishment of new suitable areas.

III. DISCUSSION AND MAIN CONCLUSIONS

Attributing a specific weather event like VAIA to the climate change is very difficult. Nevertheless, in the framework of climate change is reasonable to assume that catastrophic climate events will be more frequent in the future. Therefore, the understanding of the possible consequences on species both in spatial and temporal terms will have a pivotal role in planning future conservation actions. Further research on habitat condition and ecology are needed to gain a deeper understanding of the dynamics and causes of these consequences. Furthermore, establishing a dialogue among experts, stakeholders, and public administrations is crucial for implementing mitigation and conservation measures, in order to draft guidelines that consider different needs and enable the best possible management of unforeseen situations.

ACKNOWLEDGMENT

We want to thank the director of "Ufficio distrettuale forestale di Pergine Valsugana" Giorgio Zattoni, the municipality of Levico Terme, Nicola Gozzer and Fabrizio Iori (forest wardens of the municipality of Levico Terme), Elisabetta Romagnoni and Matteo Sartori (Autonomus Province of Trento).

Assessing and preventing human-bear conflicts through spatial ecology in the northern Pakistan

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Short summary: *Ursus arctos isabellinus* and *Ursus thibetanus* are listed by IUCN as critically endangered and vulnerable in Pakistan. Here, we use spatial ecology to assess and prevent human-bear conflicts for both the species in the northern Pakistan, providing precise indications on where these two bears live and how to protect them.

Keywords: Camera trapping, Ecological modelling, Human-bear conflict, Pakistan, Spatial ecology, Wildlife management

I. BACKGROUND

Ursus arctos isabellinus and *Ursus thibetanus* (Fig. 1) are listed by IUCN as critically endangered and vulnerable in Pakistan, respectively [1]. Their main threats are represented by anthropogenic habitat loss and fragmentation, leading to frequent human-bear conflicts. We used spatial ecology applications to assess and prevent human-bear conflicts in Pakistan analyzing the bears' distributions and activities.



Fig. 1. Adult specimens of *Ursus arctos isabellinus* (left) and *Ursus thibetanus* (right). Photo courtesy of Wildlife Ecology Lab| FWM, The University of Haripur.

MATERIALS AND METHODS

We installed several camera traps in multiple areas of the northern Pakistan to collect *U. arctos isabellinus* and *U. thibetanus*' occurrences. We integrated these presence records and the most important bears' environmental predictors and built species distribution models. We combined camera trap pictures and GIS analyses to estimate bears' activities. To understand interactions between humans and bears, we conducted an interview-based questionnaire surveys in several villages frequented by bears in the last two decades.

II. RESULTS

Our observations indicated that *U. arctos isabellinus* and *U. thibetanus* occurred in several areas of the northern Pakistan, especially between 1,600 and 4,500 m above sea level. We recorded bimodal activities for both bears with movement peaks during mid-day and sunset for *U. arctos isabellinus*, and after sunset and during the night for *U.*

thibetanus. Livestock depredation and crop damage emerged as the main reasons of human-bear conflicts. Our questionnaire survey indicated that the majority of survey participants were not in favor of coexistence with these bears. Our models showed that there were several potential suitable areas for both bears in the northern Pakistan. However, these areas are often located in close proximity to human settlements.

III. DISCUSSION AND MAIN CONCLUSIONS

Our spatial analysis revealed that many suitable areas for *U. arctos isabellinus* and *U. thibetanus* are placed both in protected areas and close to human settlements. Conflicts between humans and the two bear species are a growing problem for wildlife managers. People's negative perception of bears and large carnivores in general is quite common in Pakistan, e.g., [2, 3]. Although both bears are legally protected, growing human population in the area is most likely going to lead to an increase in human-bear conflicts, with the consequent increase in numbers of bears killed, thus making implementation of effective mitigation actions an immediate conservation priority. Effective management plans are needed to guarantee the conservation of *U. arctos isabellinus* and *U. thibetanus* in Pakistan, as well as in neighboring countries. Our results provide indications for effective conservation strategies to protect this species.

ACKNOWLEDGMENT

We are thankful to Gilgit Baltistan & Khyber Pakhtunkhwa Wildlife Department for their support during data collection process.

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Comparing two types of Convolutional Neural Network to maximize Seahorse image recognition

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Short summary: The goal of the Project is to go to increase the biological, ecological, and distribution knowledge of the seahorse through the use of machine learning, implementing photo identification software.

Keywords: Seahorses, Foto ID, YOLOv5, VGG16

I. BACKGROUND

Effectiveness of species and individual identification is an essential tool for reliable information on behaviour, ecology and physiology of many animal species. Marine biologists and conservationists are very keen on using non-destructive and automatic ways for fish sampling to cut down labor costs and delays in achieving the outcomes as a result of manual sampling. Seahorses and their relatives (family Syngnathidae) are charismatic fishes that are a focus of marine conservation efforts. Individual identification is particularly important for ethological studies and sampling design [1]. Previous studies have developed various types of marking by tags and chemical marks, but these methods involve significant manipulation of the individuals. Our study aims to evaluate the effectiveness of machine learning algorithms on the identification of two morphologically similar European seahorse species: *Hippocampus hippocampus* and *Hippocampus guttulatus* which inhabit sympatrically in the Mar Piccolo di Taranto (MPT)

MATERIALS AND METHODS

The long-snouted (*Hippocampus guttulatus*) and the short-snouted (*H. hippocampus*) seahorse are notable residents of European coastal waters [2]. Individuals were characterized by peculiar characteristics that could allow us to identify it through machine learning and Artificial Intelligence (AI) tools to detect, count and re-identify seahorses. Here we illustrate the ability of our neural network to recognise the two species. For the validation, we trained a YOLOv5 neural network on our dataset (4000 photos all taken in our Study Area) with manually annotated frames containing Seahorse images to obtain an automatic detector, evaluating it with

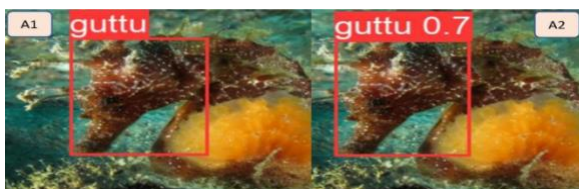


Fig. 1. A1 represent the image with the bounding box for the training; A2 represents the AI prediction with the percentage of Precision

k-fold cross-validation to estimate the average precision of our model. In parallel, we will train another CNN with VGG16 and we will compare it with the YOLO one according to define pros and cons.

II. RESULTS

A. YOLO Results

Results in species recognition showed an average precision of 86% (sd 0,05%), suggesting this approach is a valuable tool for monitoring natural populations and developing specific conservation actions to preserve them.

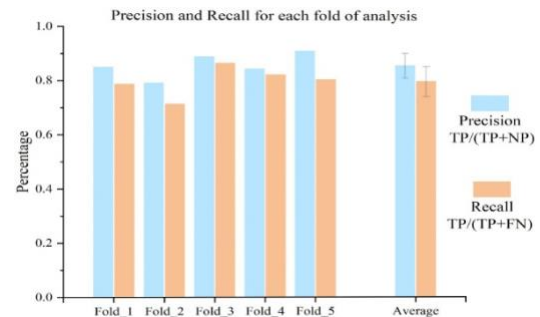


Fig. 2. Precision is the ratio of the number of True Positives (TP) to the total number of positive predictions (TP + False Positive (FP)). Recall is the ratio between the number of TP and the total number of actual (relevant) objects (TP + False Negative (FN))

B. VGG16 Expected results

After these excellent results we are now working on the same data but with a different neural network to then be able to compare and define the most suitable tool for our research.

III. DISCUSSION AND MAIN CONCLUSIONS

Nevertheless, our results showed that the technique is reliable and can serve as a starting point for further studies such as the last step of our project the identification and reidentification of individuals so that the true distribution of seahorses within the MPT can be traced according to the fact that each seahorse is characterized by peculiar characteristics that could allow us to identify them at an individual level.

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Pathogenic microorganisms from the marine environment: friends or foe for the biodiversity?

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Keywords: Parasites, Marine environment, Cetaceans Zoonosis Biodiversity One health

I. BACKGROUND

Over the past three decades, it has become increasingly clear that the emerging and/or re-emerging pathogenic microorganisms originate in animals, especially wild ones. Moreover, the main drivers of their occurrence are associated with human activities, including changes in ecosystems and land use, agricultural intensification, urbanisation, travel, and climate changes. Understanding the ecology of each emerging/re-emerging pathogenic microorganism requires a collaborative, multidisciplinary approach, crossing the boundaries of animal, human and environmental health, in order to better understand the role that these microorganisms may have into global biodiversity and ecosystems conservation [1]. Among wildlife, marine mammals, due to their long lifespans, global distribution in both coastal and offshore waters, migratory patterns and their ecological role in the marine food web, may serve as flag species for potential pathogenic microorganisms [2].

MATERIALS AND METHODS

In order to investigate the presence of potential pathogenic microorganisms from marine environment, a total of n. 34 faecal samples from free-ranging individuals of fin whale (*Balaenoptera physalus*; n. 11), sperm whale (*Physeter macrocephalus*; n. 18) and long-finned pilot whale (*Globicephala melas*; n. 5) were collected between 2000 and 2022, as part of a long-term research project on cetacean ecology, conducted in the “Pelagos Sanctuary” area (North-Western Mediterranean Sea) (Fig. 1). Faecal samples were then subjected to coprological examination, in order to identify eggs/cysts/oocysts of potential pathogenic microorganisms and to DNA extraction and molecular analysis to genetically characterise the detected microorganisms.

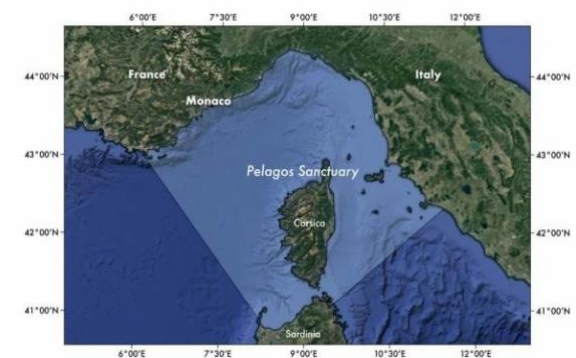
II. RESULTS

Microscopic examination identified cyst/oocysts of enteric protozoan parasites in the cetaceans' samples. Molecular analysis identified the presence of *Giardia duodenalis* in five and three samples of fin and sperm whales, respectively. *Cryptosporidium* was identified in four and two samples of sperm and long-finned pilot whale, respectively and *Blastocystis* in five and two samples of sperm and pilot whale, respectively. After sequencing, zoonotic species of *C. parvum*, *G. duodenalis* Assemblage A and *Blastocystis* ST3 were genetically characterized (Tab. I).

TABLE I: Protozoan parasites found in cetacean species

Tot. dataset (n: 34)	<i>Balaenoptera physalus</i> (n:11)	<i>Physeter macrocephalus</i> (n:18)	<i>Globicephala melas</i> (n:5)
<i>Giardia duodenalis</i> (Assemblage A)	5	3	
<i>Cryptosporidium parvum</i>		4	2
<i>Blastocystis</i> ST3		5	2

Fig. 1: Pelagos Sanctuary



III. DISCUSSION AND MAIN CONCLUSIONS

This is the first study in which zoonotic enteric protozoan parasites were detected in three different species of free-ranging cetaceans and the first record of *C. parvum* and *Blastocystis* ST3 in long-finned pilot whales. This survey also provides a baseline investigation into the possible implications of anthropogenic activities, possibly due to the spread of these microorganisms in coastal waters contaminated by sewage, agricultural and urban discharges shared between humans and wildlife. These results provide an overview of potential zoonotic microorganisms circulating in Mediterranean marine megafauna, indicating the need for more integrated research to understand the associated risk and to prevent the exposure of humans and the marine ecosystems to these invasive anthropogenic pathogenic microorganisms in term of biodiversity conservation effort.

ACKNOWLEDGMENT

We are grateful to all the researchers of Tethys Research Institute for their cooperation and collaboration.

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An example of the role of Virtual Research Environments in biodiversity data management and analysis: the Phytoplankton VRE

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Short summary: Efficient data discovery, integration and analysis is fundamental to address research questions and tackle global societal and environmental challenges. The LifeWatch Italy Phytoplankton VRE is an example of collaborative computing platform that fosters the open and integrative research in biodiversity and ecosystem sciences.

Keywords: Virtual Research Environment, Phytoplankton, Data harmonisation, Computational services

I. BACKGROUND

Studying ecological processes, making forecasts and giving support to decision making increasingly relies on the capability to process and analyse large collections of data held electronically. Virtual Research Environments (VREs) are web-based platforms providing user-centric support for discovering and selecting data and software services from different sources, and composing and executing application workflows. The availability of reliable networks, storage facilities, and associated services is necessary to enable efficient and collaborative research. Research support environments, such as Research Infrastructures, enable the analytical components to be run on powerful distributed computing systems, putting at scientists' disposal a high computational power. Here we describe the Phytoplankton VRE, a Virtual Research Environment designed by LifeWatch Italy, the Italian node of LifeWatch ERIC, to address studies on phytoplankton ecology [1].

II. THE LIFEWATCH ITALY PHYTOPLANKTON VRE

The Phytoplankton VRE offers resources and tools to generate, access and analyse harmonized phytoplankton data on taxonomy, morphological and functional traits. Specifically, two atlases, a thesaurus on phytoplankton traits and six web services to perform calculations and data analysis were developed.

A. Atlas of Phytoplankton, Atlas of Shapes and Traits Thesaurus

The *Atlas of Phytoplankton* provides a reference guide for the identification of marine, transitional and freshwater species. Additionally, it provides formulas to calculate phytoplankton biomass, based on the geometrical shape that best approximates the actual cell shape. The *Atlas of Shapes* contains schematic drawings of geometrical models for the cells, showing the relevant linear dimensions and the formulas for biovolume and surface area. The two atlases are integrated and can be easily joint switching from taxonomic identification to morphological characterization. The *Phytoplankton Traits Thesaurus* provides unequivocal and standardized definitions and semantic properties of morpho-functional traits, resulting from the interdisciplinary collaboration of a scientific expert community within LifeWatch Italy [2]. The thesaurus was developed following Semantic Web

methodologies to address data harmonization, integration and discovery, and to enhance interoperability and effectiveness of phytoplankton data exchange among different sources.

B. Computational Services

The Phytoplankton VRE provides six web services, based on scripts written in the R programming language, that allow automating a set of calculations and analyses at different spatial and temporal levels, using standardised procedures and algorithms. The *Traits Computation*, *Data Filtering*, *Size Class Distribution*, *Size Density Relationship*, *Community Indices* and *Community Matrix and Analyses* services support scientists in the calculation of morpho-functional traits, body mass, diversity indices, filtration of rare species, and analyses of the community structure, abundance and size spectra.

III. DISCUSSION AND MAIN CONCLUSIONS

Phytoplankton plays an important role in the biodiversity architecture of aquatic ecosystems and is considered a useful biological element for water quality monitoring assessment. Currently, biodiversity and ecosystems data are often very heterogeneous and better management is fundamental to improve the actual scientific knowledge extracted, support monitoring activities, and inform decision making. The Phytoplankton VRE is an example of how LifeWatch Italy promotes the use of FAIR principles and open science practices in biodiversity data and metadata management, within a working environment similar to what scientists would normally use, but with better performance in terms of computational capabilities and storage space.

ACKNOWLEDGMENT

MLM has been supported by LifeWatch Italy through the project "LifeWatchPLUS" - CIR01_00028. The update and new implementation of the Phytoplankton VRE has been funded by the Italian project "LifeWatchPLUS" - PIR01_00028.

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Knitting information about Italian biodiversity: the Italian Taxonomic Backbone

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Short summary: The LifeWatch Italy Taxonomic Backbone aims to aggregate, standardize and make accessible authoritative checklists provided by Italian taxonomists. The backbone can be exploited by the scientific community to harmonize taxonomic information promoting their interoperability and integration.

Keywords: Biodiversity, Taxonomic backbone, Interoperability, Harmonization

I. BACKGROUND

Scientific names have historically served as the globally recognized standard for comprehending biodiversity and facilitating access to accumulated knowledge about all life forms on Earth [1].

In recent years, the conceptualization of FAIR principles [2] has shed light on the deficiency in resource interoperability, leading to the emergence of numerous initiatives aimed at addressing this issue [3]. LifeWatch Italy, in the framework of the PON-IR "LifeWatchPLUS", is actively working toward enhancing information interoperability by undertaking the aggregation and standardization of taxonomic information at the national level.

This effort has led to the establishment of an access point for nomenclature and distributional data, known as the Italian Taxonomic Backbone (<https://taxonomicbackbone.lifewatchitaly.eu>) with the active contributions of the scientific community.

II. THE ARCHITECTURE

Checklists comprising accepted scientific names and associated synonyms of the Italian fauna, vascular plants, and lichens, holding approximately 70,000, were provided by Italian taxonomists (Tab. I). These checklists were harmonized in accordance with the Darwin Core Standard (<https://dwc.tdwg.org/>).

Checklists	No. of taxa
Italian fauna	27,642
Vascular plants	26,113
Lichens	15,233

Table I. Number of scientific names of taxa for the shared checklists

The contents were reshaped into a relational database, to be integrated into the new Global Names Architecture.

The Italian Taxonomic Backbone features a user-friendly interface designed for: *i.* searching for one or more taxa, *ii.* accessing information and downloading the results, *iii.* sending requests for modification of an existing taxon or the addition of a new one.

Requests' management follows a workflow in which information are going to be checked and validated by taxonomist.

Information alignment is fundamental for interoperability, therefore, the backbone can be exploited by scientific community to harmonize taxonomic information. Furthermore, the backbone has been integrated into the data curation workflow within the national HUB, enabling researchers to cross-reference taxonomic information of their datasets against the national nomenclature.

III. DISCUSSION AND MAIN CONCLUSIONS

LifeWatch Italy has established a centralized system for Italian biodiversity, marking a crucial initial stride in providing a solid and reliable center for aggregation and dissemination of biodiversity data in Italy.

For long-term viability, taxonomic data necessitate sustained expert involvement, necessitating engagement from the expert community, succession planning, and technological support. However, like any other initiative, its success hinges upon the availability of information to facilitate and prioritize experts' engagement.

ACKNOWLEDGMENT

The infrastructure development has been funded the Italian project "LifeWatchPLUS" - PIR01_00028

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Engaging fishers in marine protected species conservation

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Short summary: Fishers engagement is a priority in marine species conservation. This study provided successful indications on how to achieve largescale species conservation, which could be replicated in other areas.

Keywords: Biodiversity Conservation; Fishers' Engagement; Protected, Endangered, and Threatened species (PETs); Sustainable Fishery

I. BACKGROUND

In the Mediterranean Sea, high bycatch rates for Protected, Endangered, and Threatened species (PETs) are reported. Defining how to engage the fishers who are directly involved in incidental catches is critical to raise their interest, increase awareness and foster their collaboration with the scientific community and authorities.

MATERIALS AND METHODS

We developed a conceptual model to define the objectives of sea turtle conservation (Final Targets, FTs) at a management, technical, educational, and social level. The achievement of FTs was assessed through four Indicators (*i1* - interest, *i2* - scepticism, *i3* - awareness, *i4* - cooperation) based on the perception and behaviour of fishers. A 3-phase roadmap was set to engage fishers: *Phase 1*, it is the initial contact between the scientific community and the fishers to create baseline information on where, when, and how bycatch occurs; *Phase 2*, it mainly consists on trainings to increase fishers' awareness of good practices and sustainable fisheries; *Phase 3*, where scientists and fishers test innovative bycatch reduction devices (BRDs) aboard on commercial fishing vessel to comprehend the perspective of fishers in terms of the technical solutions proposed by scientists.

II. RESULTS

Main outcomes and indicators performance varied from phase to phase (Fig. 1). In general, there were no particular critical issues in *Phase 1*, other than "getting to know" the fishers in order to gather their feedback. Almost all the indicators were at low levels, with the exception of *i2*, reflecting the fishers' initial reticence and suspicion of this form of "passive" interaction with scientists.

In *Phase 2*, the issues relating to logistics, organization, and timing became increasingly critical. Gathering a substantial number of fishers in training courses, despite increasing difficulties, assured a step forward in breaking down the barriers of scepticism (*i2*) on the part of fishers and an infusion of trust in cooperation activities (*i4*).

Phase 3 was the most critical phase. It was the stage that facilitates the removal of obstacles in the form of the fishers' scepticism (*i2*), the advancement of collaboration (*i4*), and was a step closer to the concepts of sustainable fishing (*i3*). The lesson learnt was that certain perks such as payment for on-board hospitality and the free use of the BRDs once the collaboration is over may help mitigate obstacles to allow activities to progress.

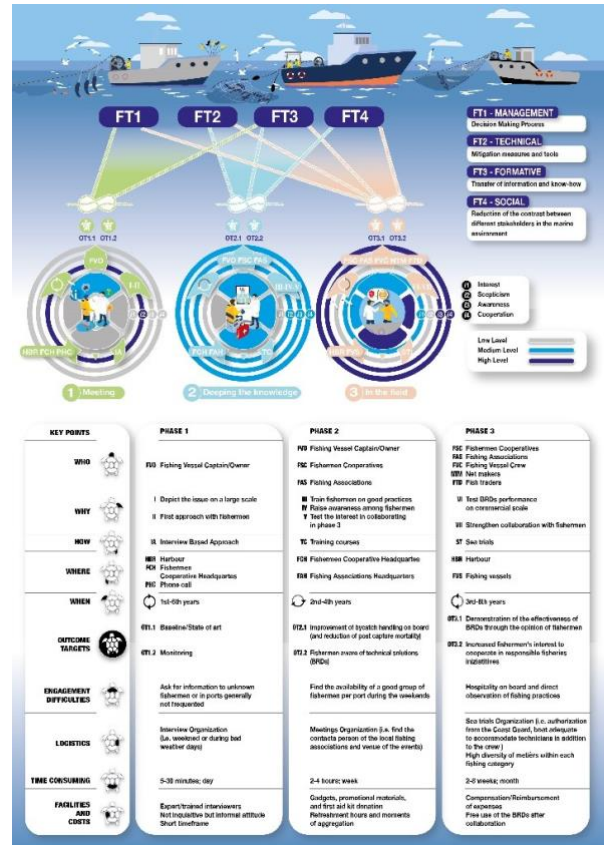


Fig. 1. Road map depicting the three phases and level of indicators and criticalities for each phase.

III. DISCUSSION AND MAIN CONCLUSIONS

Combining a theoretical and an empirical approach, this study provides successful indications (bycatch hot-spots, technological innovation of fishing gear, communication strategies, eco-labelling, improved sea turtle survivability) on how to achieve largescale species conservation, which could be replicated in other areas.

ACKNOWLEDGMENT

This study was conducted with the contribution of the LIFE financial instrument of the European Community, DELFI Project-Dolphin Experience: Lowering Fishing Interactions (LIFE18NAT/IT/000942).

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Tell me what you like to eat: Predation of *Callinectes sapidus*, *Hexaplex trunculus* and *Echinaster sepositus* on the native keystone species *Paracentrotus lividus* and *Ostrea edulis*

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Short summary: The predation rate of three invertebrate species on the European flat oyster *Ostrea edulis* and the purple sea urchin *Paracentrotus lividus* were evaluated. *Callinectes sapidus* resulted in a high predation rate on *O. edulis* recruits, suggesting that *C. sapidus* could represent a serious threat for the success of *O. edulis* restoration projects.

Keywords: Invasive species, Blue crab, Biodiversity loss, Oyster restoration, Active restocking

I. BACKGROUND

In recent years, active restocking projects have been developed aiming to restore overexploited populations of commercially important marine species, such as the European flat oyster *Ostrea edulis* (Pogoda, 2019) and the purple sea urchin *Paracentrotus lividus* (Couvray, 2019) in Mediterranean Sea. However, the success of restoration projects depends by the survival rate of the animals after release, which suffers mainly due to natural predation (Poh, 2018). The aim of this study is to evaluate the potential predation of three benthic invertebrate species commonly distributed in the Mediterranean Sea.

MATERIALS AND METHODS

We evaluated the predation rate of four predators on two prey species at different size (Fig. 1). For each experiment, 5 individuals (replicates) of each predator were offered 10 prey items and consumption monitored at 24 h after deployment. All experiments were conducted in five 150 L gently aerated tanks (one tank per predator) at 37 ppt, 25 °C and 14 h light photoperiod.

II. RESULTS

No predation of *H. trunculus* and *E. sepositus* was recorded. Contrarily, *C. sapidus* resulted in high predation rate on *O. edulis* recruits, and low predation on *P. lividus* recruits. No predation was observed on other sizes (Tab I).

PREDATION RATE (MEAN±SE) AT 24H

PREDATOR	PREY	Recruits	Juveniles	Adults
<i>C. sapidus</i> male	<i>O. edulis</i>	62±19%	0%	0%
	<i>P. lividus</i>	0%	0%	0%
<i>C. sapidus</i> female	<i>O. edulis</i>	94±4%	0%	0%
	<i>P. lividus</i>	14±7%	0%	0%
<i>H. trunculus</i>	<i>O. edulis</i>	0%	0%	0%
	<i>P. lividus</i>	0%	0%	0%
<i>E. sepositus</i>	<i>O. edulis</i>	0%	0%	0%
	<i>P. lividus</i>	0%	0%	0%

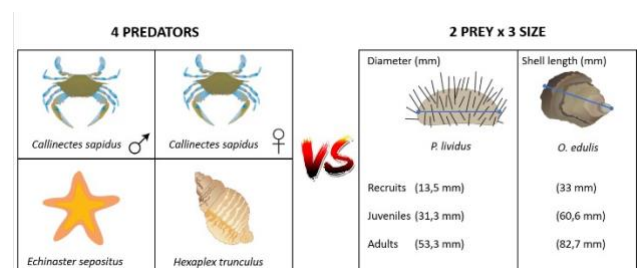


Fig. 1. Experimental design: predators (*C. sapidus* male and female, *E. sepositus* and *H. trunculus*) and prey (*P. lividus* and *O. edulis*) species and size.

III. DISCUSSION AND MAIN CONCLUSIONS

The results obtained in our study suggest that *C. sapidus* could represent a serious threat for the success of *O. edulis* restocking projects. This suggests considering the presence of *C. sapidus* in selected restocking sites. When the presence is verified, it becomes fundamental to employ suitable methodologies useful to limit the *C. sapidus* predation.

ACKNOWLEDGMENT

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Mediterranean Sea: *Caretta caretta* nesting at high latitudes, minimally-invasive approach to promote their survival

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Short summary: Here we present a new approach to promote hatching success of *C. caretta* at high latitudes.

Keywords: *Caretta caretta*, Adriatic Sea, Nesting temperature, Innovative solution to temperature control

I. BACKGROUND

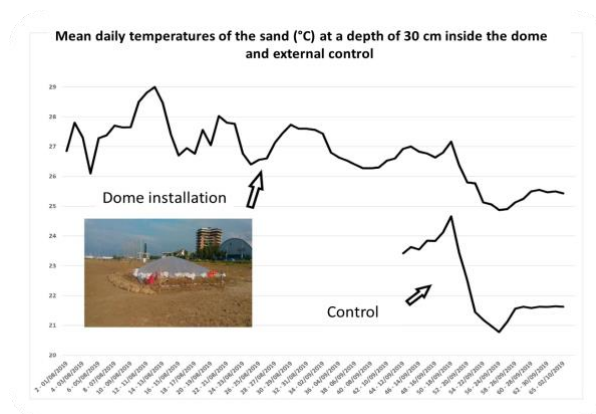
In the Mediterranean Sea, the growing occurrence of sporadic nesting sites of *Caretta caretta* sea turtles at elevated latitudes, resulting from climate change, increasingly implies the need to seek adequate strategies to promote hatching success.

MATERIALS AND METHODS

The nesting which occurred on July 30, 2019, in Pesaro (PU), Italy, by the central Adriatic Sea and located at a latitude of 43°55'21" N, was the northernmost nesting site in the Mediterranean Sea. It offered the optimal conditions to experiment with an innovative, minimally-invasive and sustainable strategy to promote incubation, the so-called "dome", consisting in an igloo-shaped waterproof sheet covering the nest and aimed at protecting it against climatic adversities, in order to ensure more suitable incubation times", installed on the 28th day of incubation and consisting in an igloo-shaped waterproof PVC sheet covering the nest and aimed at protecting it against climatic adversities, in order to ensure more suitable incubation times. Specifically, it permitted to limit temperature drops of the nest due to rainfall; in fact, we noted a mitigation of the temperature curve variations. Starting from the 46th day of incubation, a control thermometer was applied in the sand outside the dome: the mean temperature of the sand inside the dome, measured at a depth of 30 cm was 25.9 ± 0.78 °C, 3.53 °C higher than the temperature measured outside the dome, that is 22.37 ± 1.23 °C.

II. RESULTS

The application of the "dome" allowed to: 1) avoid sudden temperature decreases of the nest during rainy phenomena; 2) reduce the thermal dispersion of the nest during the night; 3) heat the surface of the sand during the daytime especially with the beginning of autumn; 4) it demonstrated to be an economic, minimally invasive, and sustainable method. The survival rate of the embryonated eggs and hatchlings was 76%.



III. DISCUSSION AND MAIN CONCLUSIONS

The success of nest hatching at high latitudes depends primarily on the date of deposition. Late nests suffer from the reduction of the hours of light and the temperature drops due to rainy phenomena, postponing the date of hatching towards colder periods, increasing the chances of nest failure. The dome strategy could be a possible solution to address this problem.

ACKNOWLEDGMENT

We are grateful to the Gaudenzi Veterinarian clinic for its support.

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Contribution of roadless areas to nature protection

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Short summary: This study provides an assessment of the distribution, environmental representativeness, and current protection of the remaining roadless areas in the EU, with a focus on Italy. The findings underscore the critical role of safeguarding roadless areas, emphasizing the need for targeted nature protection efforts in the face of ongoing global changes.

Keywords: Conservation, R, Representativeness, Rewilding, Roadless areas, Spatial analysis

I. BACKGROUND

The identification of remote and unfragmented areas has emerged as a crucial tool for spatial planning in the context of international commitments to nature protection. Evaluating the extent and environmental characteristics of roadless, infrastructure-free areas is key to planning effective nature protection actions in face of current biodiversity changes. This research aims to provide an EU wide assessment of roadless areas as a tool for conservation planning.

MATERIALS AND METHODS

We developed a reproducible R workflow using data from OpenStreetMap to identify roadless, infrastructure-free areas at large spatial scales. Roadless areas were evaluated for their environmental representativeness (e.g., across biogeographic regions, habitats, abiotic envelopes) and current protection status. The latter was assessed by overlaying consolidated spatial data from the World Database of Protected Areas (WDPA). Within the framework of the National Biodiversity Future Center, we further investigate the potential of Italian roadless areas to achieving biodiversity protection targets.

II. RESULTS

Roadless areas encompass about 15% of the EU land territory (Fig. 1). Almost 75% of them are smaller than 10 km², and less than 3% are larger than 100 km². Italy exhibits an even lower amount of roadless areas - about 10% - mainly composed by small patches.

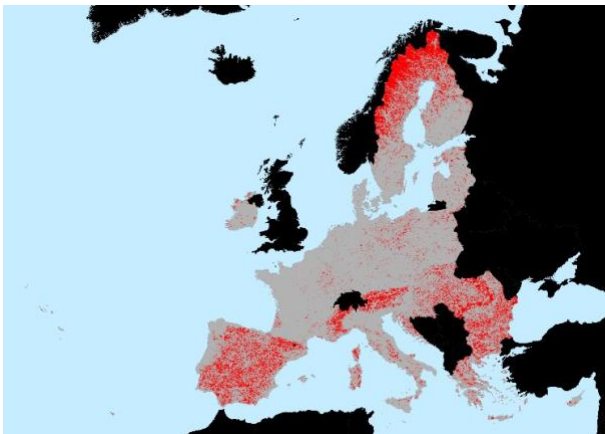


Fig. 1. Distribution of roadless areas (in red) across 27 EU countries.

Italian roadless areas are mainly located in mountains (>90%) and largely encompass vegetated areas (e.g., forests, shrublands and grasslands). Over 50% of Italian roadless areas fall inside protected areas (PA). The protection of roadless areas adjacent to PA would increase the PA coverage to 25% of Italian land surface.

III. DISCUSSION AND MAIN CONCLUSIONS

Roadless areas are key to fulfilling international nature protection objectives. Identifying and protecting roadless areas in the EU, particularly in densely populated countries like Italy with high landscape fragmentation, represents an opportunity to strengthen conservation efforts and achieve biodiversity protection targets. Further analyses should evaluate the ecological value of roadless areas by, e.g., including fine-scale data on species and habitat distribution. Such information could inform decisions on the allocation of roadless areas to distinct nature protection strategies (e.g., conservation vs rewilding).

ACKNOWLEDGMENT

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Ecological role and faunal associations of the calcareous sponge *Paraleucilla magna* alien in the Mediterranean

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Short summary: *Paraleucilla magna* represents an alien and invasive calcareous sponge in the Mediterranean Sea. Is widely distributed in the benthic communities of the Taranto seas and the present preliminary study suggested that this species could act as an ecosystem engineer.

Keywords: *Paraleucilla magna*, Sponges, Associated macrofauna, Ecosystem engineer, Alien species

I. BACKGROUND

Paraleucilla magna is a calcareous sponge originally from the coasts of Brazil [1], but it's becoming more prevalent in the continuously warming Mediterranean Sea. In the marine communities of Taranto, its biomasses, due to size and morphology, provide shelter and a suitable habitat for various communities of epi- and/or endobionts. In this work, the fauna associated with this alien sponge was studied to evaluate its ecological role as an autogenous ecosystem engineer.

MATERIALS AND METHODS

Ten specimens of *P. magna* were collected monthly from the Gulf of Taranto (NW Ionian Sea) for one year. From each sample, macrofauna (body length >1 mm) living inside the sponge or on its outer surface was extracted under a stereomicroscope. The selected organisms were sorted into taxonomic groups to calculate the frequency, abundance and density [2].



Fig. 1. One of the sponge samples during the sorting phase in the laboratory.

II. RESULTS

All the specimens of *Paraleucilla magna* were characterized by the presence of associated macrobenthic invertebrates. Overall, the study led to the identification of 4791 individuals, divided into 6 phyla, on a total sponge volume of 3863 mL.

Most sorted individuals belonged to the phylum Crustacea, followed by Mollusca and Annelida, while a minority belonged to Bryozoa, Chordata and Echinodermata (Tab. I).

TABLE I. BREAKDOWN OF INDIVIDUALS BY TAXONOMIC GROUP

Phyla	Total number of individuals
Annelida	344
Bryozoa	3
Chordata	1
Crustacea	3642
Echinodermata	1
Mollusca	800

III. DISCUSSION AND MAIN CONCLUSIONS

The results of the present study agree with literature data, reporting Crustaceans as the best represented group of associated organisms [3]. After Crustaceans, the second most abundant taxon is that of Molluscs, probably due to the recruitment of the bivalve *Mytilus galloprovincialis*, actively bred in the Mar Grande of Taranto. Molluscs were also found to be the second most abundant group of *Paraleucilla magna* from Brazil. However, despite Annelida it has been described in the literature as the second best represented taxon in calcareous sponges [3], in the present study it was found to be conspicuous but less abundant than Molluscs.

Information on taxa associated with *P. magna* could be useful in the future to produce rapid assessments of environmental conditions in the Mar Grande di Taranto and other semi-confined basins subject to significant fluctuations in ecological parameters.

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Use of AIS Data for Fisheries Monitoring

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Short summary: Leveraging AIS data analysis for fisheries monitoring empowers researchers and authorities to better understand and manage fishing activities, ultimately contributing to the conservation of marine resources and ecosystems.

Keywords: AIS Data, Fishing effort, Fishing grounds, Adriatic Sea, Big data

I. BACKGROUND

AIS data analysis has emerged as a valuable tool for monitoring fisheries activities and assessing their impact on biodiversity. AIS is a tracking system used on ships and vessels to exchange information, including vessel identity, position, course, and speed. By analyzing AIS data, it is possible to gain insights into vessel movements, fishing patterns, and their effects on marine ecosystems. Assessment of fishing pressure and monitoring of Marine Protected Areas (MPAs) are only two of the several contributes that AIS data analysis could give to safeguarding biodiversity. Data analysis was performed for the entire Adriatic Sea and covers the period from 2019 to now.

MATERIALS AND METHODS

Each vessel's activity was determined based on the relationship between its speed and course, with a 4-step process. Steps involve grouping data into polylines, discriminating between navigation and fishing and finally identifying fishing gear using a series of Logistic regression models. Models were built using nine different parameters identified as crucial to determine the fishing gear. The method integrates statistical analysis and machine learning techniques to infer vessel activities and gear usage from AIS data, enabling effective monitoring of fishing activities.

II. RESULTS

Validation of AIS information

Reliability of AIS-based identification of trawl type and activity (fishing and navigating) was assessed by comparing it with data from boat surveys to estimate bias. The study aimed to validate the accuracy of algorithmic interpretation in identifying fishing activities through AIS data against direct observations at sea [1].

TABLE I. VALIDATION OF VESSELS WITH TRAWLING GEARS

Year	Fishing			Navigating		
	Observed	AIS-based	% Correct	Observed	AIS-based	% Correct
2018	104	104	100	13	12	92.3
2019	139	139	100	13	13	100
2020	81	81	100	14	14	100
2021	111	111	100	17	17	100
Tot	435					

*Only vessels with trawling gears are considered for validation

Spatial distribution of fishing effort

The spatial distribution of fishing effort, derived from AIS data analysis, reveals patterns of fishing activities with very great details. By tracking vessel movements and identifying fishing behavior, AIS data allows for precise mapping of fishing hotspots and distribution trends over time. This information aids in understanding the spatial dynamics of fishing activity, including areas of high intensity fishing and potential overexploitation zones. Analyzing AIS data provides valuable insights into the spatial behavior of fishing fleets, supporting sustainable fisheries management strategies and conservation efforts aimed at preserving marine ecosystems.

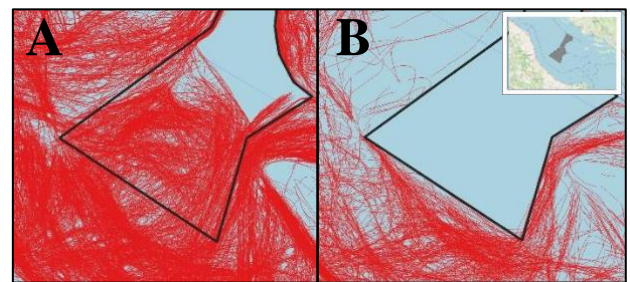


Fig. 1. Fishing tracks in the area of Pomo pit. A: May and June 2023; B: September and October 2023

III. DISCUSSION AND MAIN CONCLUSIONS

AIS data analysis could provide a detailed description of fishing activities at sea. Understanding the intricacies of where, when, and how fishing occurs offers crucial insights into its impact on marine ecosystems. By comprehensively documenting fishing practices, we can quantify their impact in areas of high biodiversity and vulnerability, enabling targeted conservation efforts. Moreover, such descriptions aid in assessing the effectiveness of fisheries management measures. This detailed understanding serves as fundamental information to guide researchers in identifying the best measures to avoid habitat destruction and biodiversity loss.

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Some reflections on how humans can relate to marine ecosystems in the Anthropocene

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Short summary: As ecosystems are threatened and deeply transformed in the Anthropocene, there is an urgent need to reflect on how humans can satisfy both their well-being and that of other living beings.

Keywords: Anthropocentrism, Biocentrism, Satisfaction of human needs, Recognition of intrinsic value of nature

Although awareness of environmental degradation had existed since Plato's time (428-348 BC), it has taken more than 2000 years to become aware of man's capacity to alter and sometimes destroy nature and thus himself. *Homo sapiens* have neglected the limits of ecological resilience of natural ecosystems and underestimated the risk of reaching a "point of no return". Over the past two centuries, urbanisation has exponentially increased and the human impact on the natural ecosystems has grown rapidly all over the world. The exploitation of earth's resources has been impressive. The fossil fuels, generated over several hundred million years, are being quickly depleted. Nitrogen is more synthetically fixed and applied as fertilizers in agriculture than naturally fixed in all terrestrial ecosystems. In the oceans, fishery resources are often in overfishing and overexploited, and several non-commercial taxa are in critical or endangered conditions. The human impacts have been recorded also in glacial ice cores, showing the growth in the atmospheric concentrations of several greenhouse gases, in particular CO₂ and CH₄. A rise in global temperature has been recorded as a direct result of anthropogenic greenhouse gas emissions. Climate change has become the most recognized human-induced impact that affects everyone in their lifestyles and affairs. In this context, a new geological era called the Anthropocene, has been proposed by scientists, in which humans are now one of the primary forces shaping the planet, modifying climatic, geological, and biological systems at an unprecedented rate. This raises several questions. What should a wise relationship be between humans and nature? Should it be based exclusively on the satisfaction of human needs, considering the natural ecosystem as an

instrumental good? Are we really entitled to "fundamentally alter" natural ecosystems? To answer these and other similar questions, humans should agree on their role as masters of the earth or living beings among others. Thinking in terms of fishing resources, for instance, humans should decide if fish must live so that humans can enjoy it, or if fish have the right to live regardless of their humans' use. These different approach to the "value" of natural resource distinguishes the vision of anthropocentrism from that of biocentrism. An anthropocentric vision places importance on what humans as main use want while a biocentric vision places importance on nature which exists independently of humans. Being fully aware that marine ecosystems are threatened and transformed by man and that to ensure human well-being they must be urgently managed, a "wise" way to relate humans to ecosystems should focus mainly on these two aspects: (1) decision-making actions on natural resources cannot be based solely on the most advantageous financial statement, as was often done, considering "fair" what costs less to produce/provide; (2) by managing meta-ecosystems through areas of harvest and protection, under a temporal rotational scale, continuous evaluation of their health status, and a real-time compliance framework, it is possible to ensure sustainable quotas for both "fish to be left for human consumption" and "fish to be left to enjoy their own lives". To address both aspects, it is necessary to improve the understanding, description, and modelling of ecosystem dynamics under the influence of anthropogenic and natural drivers, moving towards a more holistic and ecocentric vision that allows the integration of anthropocentrism and biocentrism.

Microbial diversity in deadwood: the role of varying microhabitat conditions and forest management

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Short summary: Shifts in deadwood microbial communities' composition and functions respond to micro-environmental conditions determined by changing abiotic/biotic factors and forest management.

Keywords: Deadwood biodiversity, Microbial communities, Forest management, Environmental conditions, Nutrients cycling

I. BACKGROUND

Deadwood is a key resource in forest ecosystems supporting biodiversity and a variety of ecosystem services. The availability, distribution and quality of deadwood is determined by climatic conditions and forest management. Therefore, understanding the effect of environmental changes determined by both climatic fluctuations and silvicultural practices, may reveal important patterns of wood creation/removal. As decomposition of wood is mainly driven by microbial communities, our research aimed at:

- i) Determining how microbial communities respond to changing microhabitat conditions related to substrate physio-chemical traits and local environmental variables.
- ii) Investigating the effect of forest management on selecting specialized microbial taxa.

MATERIALS AND METHODS

We have investigated the structural and functional diversity of microbial communities in deadwood using shotgun metagenomics. Microbial DNA was extracted and amplified from wood sawdust in two different forests in northern Italy (Bolzano, sessile oak stand) and Slovenia (Jelendol, beech stand), to address the i) and ii) aim, respectively. DNA extracts were quantified and then shipped to the facilities of the sequencing company. Taxonomic classification was performed using Kraken software with default settings and the standard RefSeq database. Functional annotation of bacteria, fungi, and archaea was performed using both MG-RAST server v4.0.3 and Humann3 pipeline. Alpha and beta diversity and all statistics were run on R software using specific packages.

II. RESULTS

A. Wood traits

Bacterial alpha diversity was significantly affected by decay stage and wood characteristics. Bacterial communities in well-decayed wood had higher Shannon and Evenness. Similarly, Carbon to Nitrogen (C/N) ratio positively affected Shannon diversity and Evenness. In contrast, diversity indices of fungi and archaea did not respond to variation in wood physical and chemical characteristics. The overall community structure of bacteria was mainly determined by deadwood diameter. Carbon content, log length and diameter were significantly related to the structure of fungal communities, although, decay class resulted the main driver. Also archaea were influenced by the diameter of log, but no significant effect

of decay class was observed. Genes encoding for plant cell wall degradation were proportionally different between bacteria and fungi and most of them differ between decay classes. For archaea, several genes involved in the methanogenesis pathway were significantly different between decay classes. Ultimately, species co-occurrences patterns also changed according to decay stage.

B. Forest management

The effect of forest management at different intensity did not affect the diversity indices of bacteria, fungi and archaea. However, relative abundance of some taxonomic groups changed across management type. By contrast, beta diversity was significantly different according to stand management for all kingdoms.

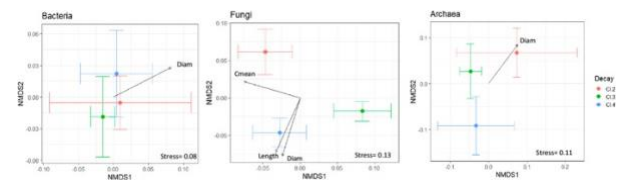


Fig. 1. Nonmetric multidimensional scaling (NMDS) ordination of Bacteria, Fungi, and Archaea. Different colours indicate a different decay class. Cmean, average wood C content; Nmean, average wood N content; Mean_CN, average C/N ratio; Diam, average log diameter; Length, log length.

III. DISCUSSION AND MAIN CONCLUSIONS

Understanding the drivers of microbial diversity in wood may be useful to predict the response of key ecosystem processes such as carbon and nutrients cycling under changing climatic conditions in forests. On the other hand, the study of species interactions, functional pathways and diversity at different spatial scales under varying management may provide important indications for implementing sustainable forest practices that enhance deadwood biodiversity, thus supporting forest ecosystems' resilience to global changes. Our research highlighted the importance of deadwood availability and variety in terms of size and decay stage for supporting taxonomically and functionally diverse microbial communities, therefore, management practices aiming at increasing deadwood heterogeneity and abundance should be preferred. However, future research should investigate functional diversity and inter- and intra-species interactions to better understand the effect of natural and human-induced environmental changes on the whole ecosystem.

Environmental DNA for the census of non-indigenous species

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Short summary: Non-indigenous species (NIS) are increasingly threatening marine biodiversity and ecosystem functioning. The multi-marker eDNA metabarcoding allowed the identification of 31 alien species already detected in the Mediterranean Sea. This study highlighted that the combination of molecular and morphological approaches is essential for timely detecting a broad number of NIS.

Keywords: Environmental DNA, Alien species, Morphological approaches, Mediterranean Sea

I. BACKGROUND

The global expansion of maritime transportation and international trade prompts the spread of non-native species (NIS). Certain NIS can settle in a new area and become invasive, leading to negative consequences for local biodiversity and ecosystem functioning [1]. The introduction and establishment of NIS, further facilitated by the effects of global climate change, worsens human-induced pressures, ultimately resulting in the gradual loss of biodiversity and the destruction of habitats. Most of NIS are likely introduced through shipping, making commercial and tourist ports crucial checkpoints for their entry into new marine environments and subsequent spread in surrounding areas [2]. There is a growing recognition of the importance of promptly detecting and identifying early developmental stages of NIS [3]. These stages can be challenging for expert taxonomists to recognize, and once established, the chances of eradicating them are minimal.

MATERIALS AND METHODS

We have developed new protocols for species detection including NIS by employing environmental-DNA (eDNA) metabarcoding analyses, using multiple genetic markers (i.e., *18S rRNA*, *COI* and *rbcL*) and different databases (i.e. NCBI, PR2, SILVA, MIDORI2, MGZDB, BOLD) in seawater and sediment samples collected in different Mediterranean coastal ecosystems on a seasonal basis. We conducted a comparison between eDNA methodology and traditional morphological methods to evaluate the efficacy of both techniques in detecting species with a focus on NIS.

II. RESULTS

eDNA metabarcoding identified double the number of species compared to morphological analyses, yet only a small fraction (ca 5%) was recognized by both methods (Fig. 1). Comparing results obtained by molecular and morphological approaches for NIS identification, the percentage of commonly detected species rises only to 8%.

Over 50% of non-indigenous species (NIS) were only detected via eDNA metabarcoding, unveiling several previously unidentified taxa in Italian coastal environments, including some never observed in the Mediterranean basin. This method proved to be highly sensitive in detecting genetic signatures of various organisms in seawater of both hard and soft substrates.

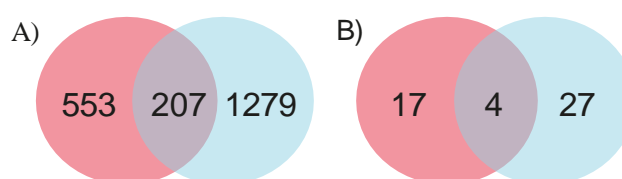


Fig. 1. Venn Diagrams showing the total numbers of shared and exclusive species (A), along with non-indigenous species (B) found with eDNA metabarcoding (light blue circles) and traditional approaches (red circles).

III. DISCUSSION AND MAIN CONCLUSIONS

The combination of molecular and traditional approaches is essential for depicting the local biodiversity and promptly detecting and mapping NIS on a large scale. This integration can be crucial within Marine Strategy Framework Directive 2008/56/EC, as it facilitates the implementation of more effective prevention strategies for minimizing ecological impacts.

ACKNOWLEDGMENT

This study was funded by the Italian Ministry of Environment and Energy Security (MASE) under the Operating Agreement with the Italian Institute for Environmental Protection and Research (ISPRA), implementing art. 11 "Monitoring Programs" of Legislative Decree n. 190/2010 transposing Marine Strategy Framework Directive 2008/56/EC.

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Session #4 – Ph.D. Spot

Moderator: Stefano Goffredo & Emiliano Mori

Summary of the thematic session

Ph.D. Students and early career scientists feel the need of promoting collaboration and open science, by encouraging the sharing of data, resources, and knowledge among researchers, even at the international level, to accelerate scientific progress. Improving communications and bureaucracy amongst European universities would simplify the processes of exchanging information and recognizing qualifications, creating a more homogeneous and transparent system at least within the European Union. Therefore, communication should also be increased with businesses and the private sector, by establishing effective dialogue channels to facilitate collaboration. Dialogue should also be improved between science and politics fostering a clear and timely communication to facilitate the use of scientific evidence in decision-making.

Another important issue to be solved to improve the future of national science is to raise public awareness, by promoting a widespread scientific culture through information campaigns and dissemination initiatives, bringing the general public closer to research topics. Regaining trust in science could be carried out by counteracting the spread of false news and scientific disinformation through awareness campaigns and education in critical analysis of information. Recognizing the fundamental role of scientists in society and promote them as credible and authoritative reference points would also valorize the social role of scientists.

Furthermore, it has been highlighted the need to simplify the procedures for requesting and obtaining funding and resources for research, reducing time and bureaucratic burdens.

Ensuring stable and dignified employment contracts for researchers, valuing their skills and protecting their rights would improve engagement in science, together with increasing research funding, reducing bureaucracy and promoting an evaluation system based on merit and the real impact of research, rather than on the mere quantity of publications.

These aims could be achieved by encouraging interdisciplinary collaboration, creating strong support network for researchers, such as the Association “Successione Ecologica” and improving scientific communication also to the general public, in a clear and accessible way.

As to future perspectives, Ph.D. students acknowledged the difficulties of a direct dialogue between scientists and politicians/policy makers. Therefore, to build a solid future for research, it has been proposed to create a citizen delegation for dialogue with politics and the media, by establishing a group of citizens representative of civil society who may interface with institutions, promoting public debate on science and its social relevance.

Furhermore, it would be important also to organize events and initiatives for the public, in order to promote scientific dissemination events, science festivals, and edutainment initiatives, in turn to bring the public closer to research topics in an engaging and interactive way. The main ingredient, however, would be to trigger coalition and collaboration among doctoral students, for instance supporting the creation of networks and associations of doctoral students who can promote their rights, protect their interests, and represent their needs.

The microbiome of calanoid copepods in the Mediterranean Sea

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Short summary: We investigated the microbiome of planktonic copepods in two coastal areas of the Mediterranean Sea to assess changes in copepod-microbe associations and to have a broader comprehension of marine ecosystem changes.

Keywords: Calanoids, Copepods, Microbiome, Microbiota, Symbiosis

I. BACKGROUND

The associations between marine invertebrates and microbes are widespread throughout the oceans. Microbiota can indeed play crucial roles in the digestion, nutrient uptake, reproduction, immune response, and defense mechanisms of almost all marine animals, thus influencing their health and well-being [1]. So far, information about the copepod microbiome is limited, although copepods represent key components in the functioning of marine ecosystems. There is strong evidence that copepods have associations with microbes, and the microbiome's diversity can change in response to environmental conditions and different copepod genera [2,3]. The scientific aim of this study is to examine the microbiome diversity of different calanoid copepod species in Mediterranean coastal ecosystems and to assess its potential changes under different anthropogenic impact conditions.

MATERIALS AND METHODS

Planktonic copepods were collected using a WP2 net (200- μ m mesh) in two coastal sites, characterized by different anthropogenic impact conditions, of the Adriatic Sea and the Tyrrhenian Sea (see Fig. 1 for details). Two copepod species (*Temora stylifera* and *Acartia clausi*) present in both areas were selected. DNA was extracted from the specimens and purified to analyze the diversity of the microbiomes in terms of Bacteria. Metabarcoding analyses for assessing bacterial diversity were carried out on 40 samples by amplifying 16S rRNA genes on a high-throughput sequencing platform (Illumina MiSeq). Bioinformatic analyses based on the Qiime 2 software were used to obtain ASVs (Amplicon Sequence Variants) and diversity indexes.

II. RESULTS

The taxonomic composition of copepod microbiomes was significantly different between the species. In particular, Vibrionaceae, Rhodobacteraceae, and Flavobacteriaceae largely contribute to the microbiome in both copepod species. However, each copepod species showed a specific

core microbiome. In addition, changes in ASV diversity and a microbiome composition shift were observed considering different anthropogenic impact conditions.

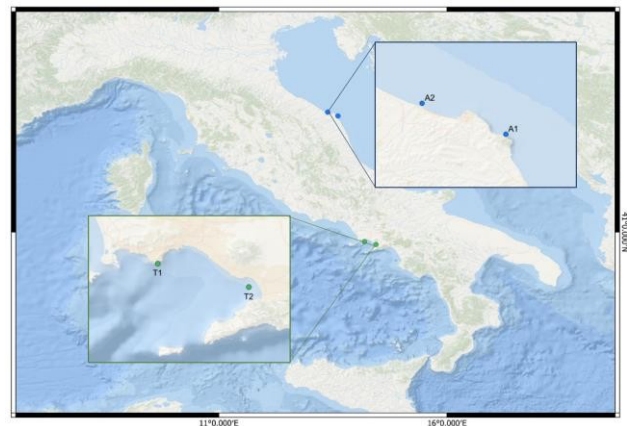


Fig. 1. Sampling area: A: Adriatic coast (A1: Portonovo bay; A2: mouth of Esino river); T: Tyrrhenian coast (T1: LTER- Mare Chiara; T2: mouth of Sarno river).

III. DISCUSSION AND MAIN CONCLUSIONS

Each copepod species exhibited a distinct core microbiome suggesting that it is species-specific. However, the presence of bacterial families shared among different hosts allows us to hypothesize their key role in the functions of all copepods. Interestingly, the contribution of different bacterial families increased based on the impact level of the sampling sites. These results expand the knowledge of the close relationships between copepods and their associated microbiota, opening new research perspectives on the crucial role of symbiosis in the oceans.

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Updated checklist of alien marine animal species along the Apulian coast

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Short summary: The list of alien marine faunal species reported along the Apulian coasts until 2010 is updated with data resulting from numerous ad hoc samplings adding several new findings. 70 new species were added, especially among Polychaeta, Mollusca, Crustacea, Ascidiacea, while alien Bryozoa are recorded for the first time. Among the recorded species, some are new to the Mediterranean Sea and the Italian Peninsula. Commercial harbors represent hotspots of alien invasion in the studied area.

Keywords: Biodiversity changes, Non-indigenous species (NIS), Mediterranean Sea

I. BACKGROUND

Apulia, for its geographical position, represents the border between the Eastern and the Western Mediterranean basins. The coastlines of Apulian have been extensively studied especially in the last 40 years since they were the subject of several in-depth faunal studies. Recently, several new surveys were carried out in the area, giving the opportunity to record new arrives especially established in commercial harbor.

MATERIALS AND METHODS

Most of the past data come from a paper dating back to 2010 [1]. At that date the number of introduced species was 37. Since then, and especially in recent years, the coasts of Apulia (about 940 km) have been the subject of many ad hoc extensive samplings for faunistic purpose [2].

II. RESULTS

The inventory of non-indigenous species in Apulia totals to 107, With the arrival of 70 new species since 2010 (Table1).

TABLE I. COMPARISON IN NUMBER OF ALIEN SPECIES

Taxa	until 2010 data	added species	Today
Porifera	1	0	1
Cnidaria	4	3	7
Ctenophora	0	1	1
Polychaeta	12	17	29
Mollusca	3	14	17
Crustacea	11	15	26
Bryozoa	0	7	7
Ascidiacea	3	8	11
Pisces	3	5	8

Taxa	until 2010 data	added species	Today
	Total	37	70

III. DISCUSSION AND MAIN CONCLUSIONS

Most of the alien species recorded in 2010 came from studies conducted in enclosed areas especially from fouling of the Taranto Sea which is a hot spot of alien biodiversity [3]. Successive investigations reported non-indigenous species from additional habitats. The intense faunal studies are witnessed by the description of 21 species new for science in the same period. While some NIS were documented as a singular occurrence with a few specimens, others, particularly Polychaeta, Mollusca, and Crustacea, exhibited established populations around Apulia, becoming a component of the local communities. The prevalence of recent arrivals is from tropical regions and only recently these NIS expanded their distribution towards the western Mediterranean Sea. Their successful establishment may be due to the ongoing increase of the seawater temperature that constantly remain above the average limits. Among the species new for Apulia coast, *Syllis similisunzima* (Polychaeta) represents the first record for the Mediterranean Sea, while *Lepidonotus tenuisetosus* (Polychaeta), *Temora turbinata*, and *Macandrewella* sp. (Copepoda) are reported for the first time for Italian waters.

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What factors contribute to the spread of the invasive bivalve *Anadara spp.* in the Adriatic Sea?

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Short summary: This work reveals the correlation between the abundance of two bivalve invasive species and environmental variables, allowing the prediction of their future spread while providing useful information for future stock assessment analysis.

Keywords: Alien species, Adriatic Sea, Invasive species, Time series analysis, Spatial distribution model

I. BACKGROUND

Predictive studies of biological invasions are of utmost importance as they provide key information on the spatio-temporal variability of one of the main threats to biodiversity that in turn impacts the environment, economy and human well-being [1]. The present study focuses on two alien species present in the Adriatic Sea since the 1970s, *Anadara kagoshimensis* (Tokunaga, 1906) and *Anadara transversa* (Say, 1822), which have been reported as some of the worst invasive species in the Mediterranean Sea [2].

MATERIALS AND METHODS

Processed data originate from a scientific beam trawl-survey consisting of 67 sampling stations located in Northern and Central Adriatic Sea carried out each year since 2007. Abundance indices of both species were estimated for each station from 2008 to 2023. Indices were used to perform a time series analysis aimed to evaluate fluctuations in each species over time and understand the dynamics of potential sub-populations inhabiting the Adriatic basin. Besides, environmental parameters identified as drivers of the population dynamics were used to perform a species distribution model (SDM) to predict the potential future distribution of both species.

II. RESULTS

a. Time series analysis

Both population species showed continuous fluctuations over time with mean values per station ranging from 52.9 to 528,544 N/km² for *A. kagoshimensis* and 47.4 to 4,454,771 N/km² per station for *A. transversa*. Bathymetry, grain-size and salinity were found as the main drivers of the population dynamics. Both species revealed a preference for silt bottoms in depths above 20 m.

b. Spatial distribution model

The main area of distribution of both species was out of the Po river at depths above 20 m, although both were also present out of Ancona (Fig. 1). *A. transversa* abundance was also consistent in the Gulf of Trieste where no *A. kagoshimensis* was found. A displacement towards southern areas over the years was observed for *A. transversa* while *A. kagoshimensis* displacement was less evident even if its abundance increased in northern areas specially out of the Po river.

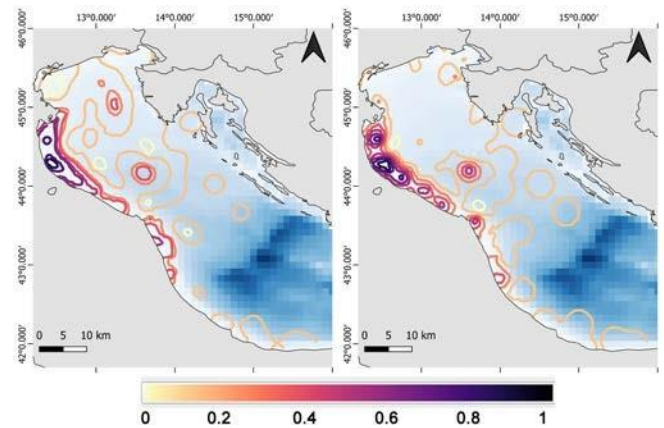


Fig. 1. Actual probability of occurrence of *A. kagoshimensis* (left) and *A. transversa* (right).

III. DISCUSSION AND MAIN CONCLUSIONS

The study gathers scientific data of two invasive non-native bivalves within Northern and Central Adriatic Sea flagged as high-impact by the European Alien Species Information Network (EASIN) [1]. Results are of major importance for a potential management plan in order to sustainable exploitation of both species which in the future could replace other commercial bivalves.

ACKNOWLEDGMENT

We are grateful to the SoleMon survey. The survey is supported by the Italian Ministry of Agriculture, Food and Forestry Policies (MASAF, ex MIPAAF) under EU Regulation 2017/1004, and contributes vital data for marine resource management. Its findings are instrumental for fostering sustainable fisheries within the EU MAP framework.

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First survey of rodenticide resistance in house mice in inhabited island systems of the Mediterranean

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Short summary: Invasive rodents represent a major threat for island ecosystems worldwide and their eradication through anticoagulant rodenticides is often one of the most direct ways to protect native wildlife. We found widespread rodenticides resistance in house mice in multiple inhabited island systems in the Mediterranean, suggesting the need for a more conscious use of rodenticides.

Keywords: Rodenticides resistance, *vkorc1*, House mouse, *Mus*, Invasive rodents, Island conservation

I. BACKGROUND

The Mediterranean basin is one of the oldest continuously inhabited areas in the world as well as a very important biodiversity hotspot. Due to intense anthropic activity, human commensal rodents are a constant presence on the Mediterranean islands causing damage to native biodiversity. To protect native wildlife, more than 100 rodent eradications have been attempted until now by using anticoagulant rodenticides (ARs). Despite their high efficiency, resistance to ARs has been observed in many countries and it is mostly related to missense mutations (SNPs) in the VKORC1 gene [1]. The presence of resistant individuals reduces the efficiency of rodent control and increase the risk of poisoning in non-target species. In this study, we performed the first survey of ARs resistance in the house mouse *Mus domesticus* in multiple human-inhabited island systems in the Mediterranean.

MATERIALS AND METHODS

We collected 83 mice from the islands of Ventotene, Pantelleria, San Domino, San Nicola, Lipari, Vulcano, Panarea, Salina, Stromboli, Alicudi and Filicudi. All these islands are inhabited and have ARs use history. DNA was extracted from tissue samples and the VKORC1 gene was amplified through PCR. Sequences were aligned and visually checked for the presence of SNPs.

II. RESULTS

We found seven missense SNPs in six of the eleven islands we sampled (Fig. 1). Pantelleria is the island with the highest frequency and variety of SNPs with five different mutations (Tyr139Cys, Ser149Ile, Gln151His, Gln155Lys, Lys157Asn). Three missense SNPs were found in Ventotene Island (Tyr139Cys, Ser149Asn, Gln155Lys). We found Tyr139Cys also in San Domino Island and Gln155Lys both in San Domino and in the neighboring island of San Nicola. Mice from Filicudi, Salina, Stromboli, Vulcano and Panarea all showed wild type sequences. The only missense mutations we found in the Aeolian Archipelago are Tyr139Cys in Lipari and Val114Phe in Alicudi.

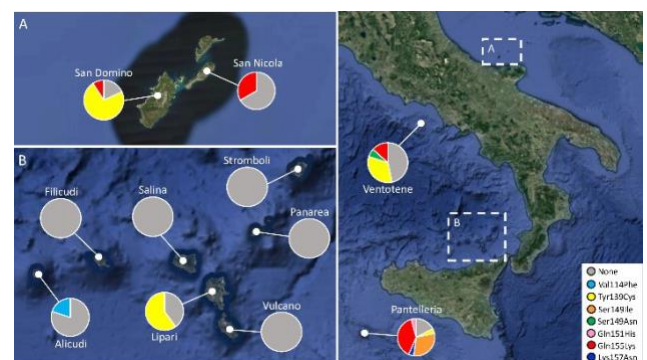


Fig. 1. Distribution of missense VKORC1 mutations in the study area.

NB: several SNPs co-occurred in the same individual.

III. DISCUSSION AND MAIN CONCLUSIONS

Tyr139Cys, Ser149Ile, Ser149Asn and Gln155Lys have already been detected in rodents in previous studies [2], while Val114Phe, Gln151His, Lys157Asn are newly described ones. Specifically, Tyr139Cys is known to confer resistance to different ARs also in heterozygous condition and it was already found in Ventotene with an allelic frequency of 2.6% [3]. We found the same SNP at a significantly higher frequency (17.9%) after a 4-year long ARs-mediated rat eradication. This could be due to the selective pressure of ARs that allowed the mice carrying the mutation to survive. Resistance to ARs is a crucial issue that must be carefully addressed before undertaking rodent eradications. Furthermore, more data are necessary to fully evaluate the permeability of island ecosystems to ARs and the effect on non-target species.

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A global meta-analysis on the impact of climate change on subterranean ecosystems

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Short summary: Through a systematic literature survey, we assembled a dataset covering 347 measurements of climate change impact on subterranean ecosystems. Using meta-analytical models, we demonstrated that climate change effects act at gene to community levels with varying strength and direction depending on habitat, taxa, and degree of subterranean specialisation.

Keywords: Meta-Analysis, Climate Change, Subterranean Ecosystems, Conservation

I. BACKGROUND

Subterranean ecosystems are largely overlooked in global climate change agendas [1]. This is problematic insofar as there is growing evidence of widespread impacts of climate change on subterranean ecosystems. Yet, quantification of the magnitude of these impacts across scales and ecosystem components is still lacking. Therefore, we conducted a meta-analysis to explore the relative strength and importance of different impacts of climate change on subterranean ecosystems [2]

MATERIALS AND METHODS

Following a systematic literature search, we selected 75 articles, and extracted all statistical tests used to measure the impact of climate change on subterranean ecosystems. We categorised effect size measures into four main groups: Organismal physiology, Behaviour, Population/Community, and Habitat. For each measure of impact, we constructed a meta-analytical model using R package 'metafor' v.3.0.2.

II. RESULTS

All physiology variables showed significant effects, with notable changes in stress response, mortality, and metabolism. Behavioural responses, including seasonality, locomotor activity and burrowing, were significant, while habitat selection was not. Population/community ecology variables did not yield any significant result. Climate change substantially reduced habitat availability with minimal effect on habitat shift (Fig. 1).

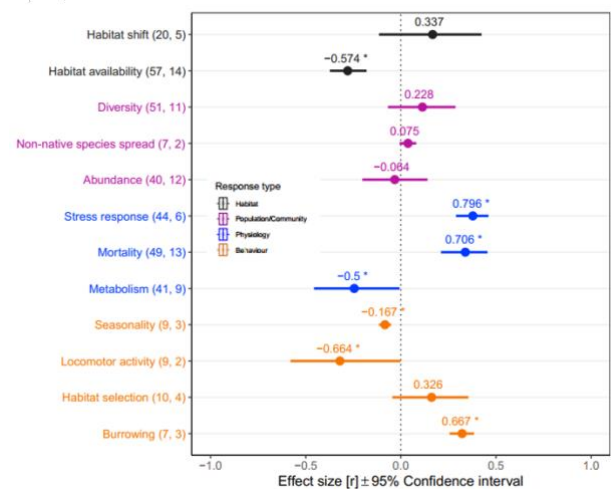


Fig. 1 - Effect sizes for the measures of climate change impact. The numbers in brackets report sample sizes (number of estimates, number of studies), and asterisks (*) mark significant effects.

III. DISCUSSION AND MAIN CONCLUSIONS

Our meta-analysis provides a starting point for understanding the biological impacts of climate change in subterranean ecosystems, but also emphasizes how considerable knowledge gaps still linger. We observed how long-term data series are lacking, multidisciplinary studies are limited, and tropical systems are significantly understudied. Furthermore, quantitative research primarily focuses on metazoan species, neglecting subterranean microbial communities [3]. Bridging these gaps is essential to integrate subterranean ecosystems into climate change targets and design effective conservation actions.

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Invasion processes and food web effects explored with ecosystem models

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Short summary: This work explores marine invasions using food web models and how they are aided by ecosystem traits and ecological interactions. The approach establishes a framework for representing processes facilitating the invasion and enables prediction of invasion's cascading effects. Invasion success was found to depend on both invasion drivers and prey-predator behaviours.

Keywords: Invasion, Marine ecosystem, Ecosystem model, Food web

I. BACKGROUND

Marine invasions are one of the biggest threats to marine biodiversity worldwide, causing serious global ecological and socio-economic impacts. Recognized as a threat, invasive alien species (IAS) and their effects on ecosystems have been studied increasingly also through modelling tools. In this context, food web models offer significant research opportunities, as they can be used as tools for carrying out synthetic experiments to test how ecosystem structure, interactions, and stressors influence and/or are influenced by invasion.

Better understanding of factors that promote or hamper invasion process and the invasion impacts on ecosystems may help us characterise past and occurring invasions, potentially producing helpful information for IAS management. Here, we used as a test case the invasion of the Adriatic Sea by an allochthonous species, *Fistularia commersonii*, simulating different processes that drive invasion such as: potential IAS native predators' and competitors' declines, behavioural traits of predator and vulnerabilities of prey to predator. Other than assessing the success of invasion we analysed how the recipient ecosystem and ecological interactions were modified by the invasion and in general the effects on the food web.

MATERIALS AND METHODS

We used Ecopath with Ecosim (EwE) ecosystem model, which simulates food web dynamics of biomasses and flows over time considering consumption rates, predation changes, fishing pressure and environmental forcings. To explore the invasion processes and impacts on an ecosystem modelled with two taxonomic resolutions, we used two existing Ecopath models of the Adriatic Sea [1, 2]. The simulated IAS, *F. commersoni*, is a famous Lessepsian migrant with available life history and diet information needed for the model input.

II. RESULTS

The invasion success was measured by the rate of biomass increase and the final biomass achieved by invader. The biggest established invader biomasses were achieved in scenarios with long-term decline of its potential predators, and in scenarios where IAS was spending less time feeding lowering its predation risk. But the fastest invasions were achieved in scenarios in which IAS was not avoiding predators. Models with different taxonomic resolutions showed similar patterns of invasion process. Some ecosystem functional groups were impacted by invasion regardless the invasion scenario, e.g. IAS prey, red mullets and demersal fish declined in all scenarios of invasion. Although all scenarios of invasion showed similar general effects on the food web, the different

invasion drivers produced secondary effects that were specific to the scenarios of invasion used (Fig. 1).

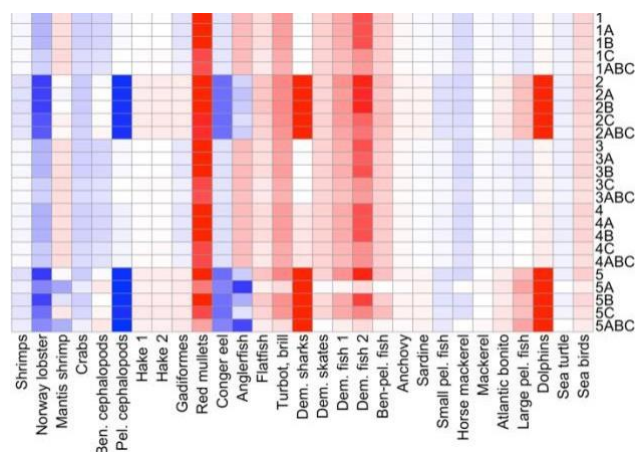


Fig. 1. Relative biomass changes for some functional groups in the lower taxonomic resolution Adriatic ecosystem model after IAS establishment for different invasion scenarios. Red colour – decreases in biomasses, blue colour – increases. Rows: scenario groups (1-5) represent different invasion drivers, while subgroups (A,B,C) - behavioral parameters.

III. DISCUSSION AND MAIN CONCLUSIONS

We modelled marine invasions in EwE using only recipient ecosystem traits and ecological interactions. This enabled us to connect the invasion rate, biomass and food web effects to the main ecological factors involved in the invasion process, regardless of taxonomic resolution of the model used.

Although limited data on IAS and non-fishery-target species is a challenge, the next step would be to test the modelling techniques presented against real invasion data.

ACKNOWLEDGMENT

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Award Number: Project code CN_00000033, Concession Decree No. 1034 of 17 June 2022 adopted by the Italian Ministry of University and Research, CUP D33C22000960007, Project title “National Biodiversity Future Center – NBFC”.

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Can we convert a biological invasion into a commercial opportunity? The case of *Anadara* spp. in the Adriatic Sea

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Short summary: A scientific support to the adaptive management of the invasive *Anadara* spp. was carried out considering a wide range of aspects that characterise its status in the Adriatic Sea.

Keywords: Biological invasion, Management of invasive species, *Anadara* spp., Bivalvia, Adriatic Sea

I. BACKGROUND

The ark clams *Anadara kagoshimensis* (Tokunaga, 1906) and *Anadara transversa* (Say, 1822) invaded the Adriatic Sea. They were reported on the list of the 100 worst invasive species in the Mediterranean Sea [1] and were included in the “proposed inventory of alien and cryptogenic marine species with reported moderate to high impacts on biodiversity, ecosystem services or human health” [2].

MATERIALS AND METHODS

The data collection and the sampling were realised within the framework of the SoleMon project (an experimental trawl survey carried out with a modified beam trawl called “rapido”). The data, collected from 2008 to 2022, allowed a study on their abundance, distribution and on their stock- assessment, carried out through the model AMSY [3], which can estimate the status of a stock using CPUE indexes without catch data. Sub-samples were subjected to nutraceutical analyses.

II. RESULTS

A. Abundance and distribution

Both species display the highest density in Italian waters, from the Northern to the Central Adriatic (Fig. 1). The mean abundance related to the whole sampling period of *A. transversa* and of *A. kagoshimensis* have values ranging respectively between 47.4 and 4454771 individuals/km² and between 52.9 and 528544 individuals/km². The highest abundance of both lies in the first 30 m of depth.

B. Status in relation to MSY reference points

The preliminary AMSY results indicate that both resources are in an under-exploitation status and their Maximum Sustainable Yields are relatively high if compared with other bivalves exploited in the area.

C. Nutraceutical Analysis

A. kagoshimensis contains a higher quantity of protein (P value = 0.0032) and iron (P value = 0.0007), while *A. transversa* shows a higher content in carbohydrate (P value = 0.0354) and energy value, in both kcal (P value = 0.0198) and kJ (P value = 0.0125). There is no significant difference in fat content (P value = 0.1102).

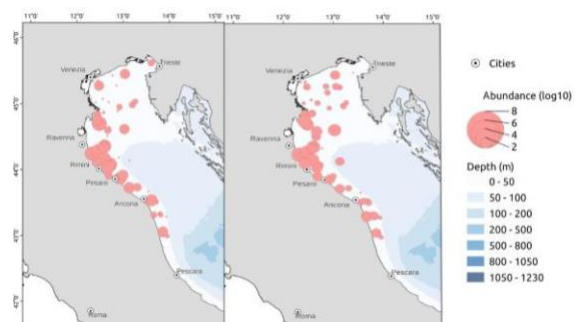


Fig. 1. Abundance and distribution of *A. transversa* (on the left) and *A. kagoshimensis* (on the right).

III. DISCUSSION AND MAIN CONCLUSIONS

“Tempora mutantur, nos et mutamur in illis”: it has now become a priority to manage biological invasions. Considering all these results, their potential commercial use (either for human or animal food or for a shell-based biomaterial) is one of the most effective strategies for their management from the ecological, economic, and social points of view. These initial findings provide a preliminary glimpse into the potential of *Anadara* spp. as a promising new commercial fishery resource in Italy.

ACKNOWLEDGMENT

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A low-cost tracking architecture for Small-Scale Fisheries Data Collection

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Short summary: Mandatory small-scale fisheries (SSF) data collection lacks legislative regulation, impeding comprehension of the fleet activity and its impact on biodiversity. In addressing this data-poor scenario, cost-effective technology coupled with artificial intelligence is key for providing highly resolved geospatial data and improving the spatial distribution of SSF activity knowledge towards an ecosystem-based approach to management.

Keywords: Monitoring, Small-scale fisheries, Database, Vessel positional data, Cloud computing, Fishery management

I. BACKGROUND

Today big data is available to track routes and behaviors of vessels belonging to large-scale fisheries (LSFs), generally with an overall length $\geq 12-15$ m), thanks to the development of various ship-reporting systems (e.g., VMS, AIS) and remote sensing technologies (e.g., SAR imagery). While plenty of information is available on LSFs, small-scale fisheries (SSFs, defined by CE Regulation N° 508/2014 as fishing with vessels under 12 m in length and not using towed gears) are characterized by a paucity of quantitative and spatial data. It results in scant possibilities for securing the compliance of the fisheries and in the insufficient reliability of spatial fishing pressure indicators, which, at best, now rely on local approaches that mainly include interviews/participatory mapping^{1,2}. Only some national initiatives have been implemented to obtain fine-scale SSF spatio-temporal data, but none in Italy even though mandatory tracking of SSF is under active consideration in the EU (EC Regulation No 1224/2009, 2018). Knowledge of the SSF fishing activity is key for its effective management and understanding of related interactions with habitats and species and between other users of marine space.

MATERIALS AND METHODS

A low-cost architecture was developed by Tassetti *et al.*³ to collect real-time positional data sent over LoRaWAN or 2G/3G/4G connections by small-scale fishing vessels. The architecture relies on Traccar, while the high-tech and cost-efficient Teltonika FMM640 worldwide tracker is proposed as Fleet Management System hardware. A sensor attached to the hauler is used in tandem to record when and where it is activated, indicating that the retrieval of the gear is occurring. The movements of the boats can be observed and downloaded from the Traccar server. Adequate methods were developed to partition GPS records into individual fishing trips, infer spatially explicit fishing events and quantify the spatial distribution of fishing effort.

II. RESULTS

The cost-effective prototype is currently installed on 40 small-scale fishing vessels, displaced along the northern-central Adriatic Sea coastline and within the Sicilian Aegadian Islands Marine Protected Area. An architecture collects and ingests data sent by the tracked vessels and feeds machine-learning automated analyses, allowing for

mapping and quantifying the spatial distribution of fishing effort and generating an informed baseline to address data-poor scenarios.

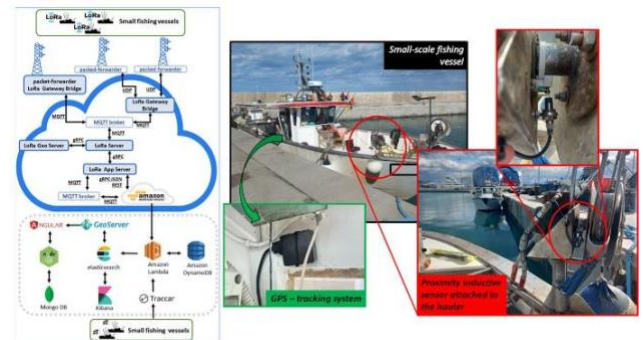


Fig. 1. The architecture that manages real-time data sent over LoRaWAN and 2G/3G/4G connections (left). One of the SSF vessels involved in the project, onboard which the tracking device was installed, together with the proximity sensor connected to the pots and traps hauler (right).

III. DISCUSSION AND MAIN CONCLUSIONS

Highly-resolved vessel tracking data provide reliable indicators of fishing effort. It is essential from the Marine Spatial Planning point of view, as it supports decision-making processes and the sustainable management of the fisheries and the marine ecosystem. For instance, the collected data could be exploited to assess the fishing pressure as a driver in fish population shifts over space and time.

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Biological control of *Halyomorpha halys* in Sardinia

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Short summary: *Trissolcus japonicus* was released in Sardinia against *Halyomorpha halys*. Pentatomid egg masses were sampled for 3- years (2021-23) in pre- and post-release. A total of 90 and 22 egg masses of *H. halys* and native pentatomids respectively were collected. *Tr. japonicus* emerged from *H. halys* eggs; native parasitoids belonging to the genus *Anastatus*, *Trissolcus* and *Ooencyrtus* emerged both from *H. halys* and native pentatomid egg masses. The genus *Telenomus* emerged only from native pentatomid egg masses.

Keywords: Parasitoids, Invasive species, Pentatomidae, *Trissolcus japonicus*, Hymenoptera

I. BACKGROUND

The brown marmorated stink bug *Halyomorpha halys* (Stål, 1855) (Heteroptera, Pentatomidae) is an invasive and highly polyphagous species [1]. Native to Asia, it was first detected in Italy in 2007 and is now widely established in the peninsula where has become a key pest of many crops. *H. halys* was detected in Sardinia in 2016 [2] and has slowly spread throughout the island without apparently causing damages yet. Classical biological control of *H. halys* using its natural egg parasitoid *Trissolcus japonicus* (Ashmead, 1904) (Hymenoptera, Scelionidae) is the most promising method to control this pest.

In 2020, a national network coordinated by CREA and named *H. halys* Technical Committee was established, within the frame of the action of the Ministry of Agriculture, with the aim to set up a national program of biological control.

Here, the results of 3-years (2021-23) of *Tr. japonicus* releases in Sardinia are reported.

MATERIALS AND METHODS

Tr. japonicus release sites were chosen considering both the presence and abundance of *H. halys* during the previous years and their geographic position. Each release of laboratory reared *Tr. japonicus* was repeated twice per year and consisted of 100 fecundated females.

Pre- and post-release egg masses samplings were performed following the national protocol. Both *H. halys* and native pentatomid egg masses were collected and reared in laboratory. Number of eggs, newly hatched bugs and emerged parasitoids per egg mass were recorded.

II. RESULTS

A total of 90 and 22 egg masses of *H. halys* and native pentatomids respectively were collected. *Tr. japonicus* emerged from three *H. halys* egg masses collected in two sites during post release samplings in 2022. The exotic parasitoid never emerged from non-target pentatomid egg masses. Native parasitoids belonging to the genus *Anastatus* (Eupelmidae), *Trissolcus* (Scelionidae) and *Ooencyrtus* (Encyrtidae) emerged both from *H. halys* and

native pentatomid egg masses. The genus *Telenomus* (Scelionidae) emerged only from native pentatomid egg masses.

III. DISCUSSION AND MAIN CONCLUSIONS

Typically, after the introduction into a new area, *H. halys* shows low population levels for a long period. Its slow and silent spread should not be underestimated. According to Tortorici et al. [3], Sardinia, particularly its western coast, appears to be a suitable area for *H. halys*. Important agricultural productions are potentially threatened by this invasive alien species.

In Sardinia before any serious damage from *H. halys* was recorded it was decided to introduce *Tr. japonicus*. The possible establishment of the exotic parasitoid would promote a long-lasting control of *H. halys* avoiding the massive use of insecticides.

ACKNOWLEDGMENT

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Ocean warming and acidification detrimentally affect coral tissue regeneration at a Mediterranean CO₂ vent

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Short summary: The regenerative response to ocean warming and acidification was investigated at a shallow CO₂ vent for three Mediterranean scleractinian coral species characterized by different trophic strategies and growth modes. Our results show a decrease in regenerative capacity, especially in the zooxanthellate species, with increasing seawater temperature and acidification.

Keywords: Climate change, Corals, Mediterranean Sea, Lesion recovery rate, Natural pH gradient, Field study

I. BACKGROUND

Climate change, driven by human activities, is rapidly affecting ocean waters and marine communities through warming and acidification, eliciting physiological responses in marine organisms, including corals. We investigated the effects of *in situ* exposure to different pH levels and seasonal temperatures on the tissue regeneration rate of the zooxanthellate solitary scleractinian coral *Balanophyllia europaea*, the solitary azooxanthellate stony coral *Leptopsammia pruvoti*, and the colonial azooxanthellate stony coral *Astroides calycularis* transplanted along a natural pH gradient off Panarea Island (Aeolian Islands, southern Italy).

MATERIALS AND METHODS

Sample of *B. europaea*, *L. pruvoti* and *A. calycularis* were transplanted, during a cold, intermediate, and warm period (range 16–24 °C), along a natural pH gradient (range pH_{TS} 7.4–8.1) generated by an underwater volcanic crater at Panarea Island. Coral tissue damage was caused by gently brushing the metal bristle on the lateral surface, exposing the axial skeleton. Tissue regeneration rates were quantified by subtracting the lesion area measured at the beginning of the experiment by the lesion area measured at the end of the experiment, divided by the former and expressed as percentage of injury regenerated as a function of time (per month; $((A_{i0} - A_{t1})/A_{i0} \times 100)/Dt_{\text{month}}$).

II. RESULTS

Tissue regeneration rates in *B. europaea* were significantly lower at low pH sites during both the coldest and warmest periods, with pH explaining approximately 30% and 50% of the variation, respectively. *L. pruvoti*, exhibited diminished tissue regeneration rates at low pH sites throughout all periods, with pH accounting for

approximately 15% and 24% of the variability in tissue regeneration during the coldest and warmest periods, respectively. *A. calycularis* exhibited lower regeneration rates at low pH sites in the intermediate and warmest periods, with pH explaining about 60% of the variation in tissue regeneration during the warmest period. Notably, the zooxanthellate species showed steeper slopes than non-zooxanthellate ones during both the coldest and warmest periods. Moreover, during the warmest period, the colonial species displayed markedly steeper slopes compared to the solitary coral *L. pruvoti*.

III. DISCUSSION AND MAIN CONCLUSIONS

All species exhibited decreased tissue regeneration with rising seawater temperature and acidification; however, the zooxanthellate corals experienced the most substantial decline. This might result from reallocating resources for reproduction and calcification, affecting tissue maintenance. These results contribute to the growing evidence of the harmful effects expected from future warming and acidifying conditions on critical aspects of shallow-water ecosystems, hindering the recovery of Mediterranean stony corals after physical damage.

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A gap in Italian media communication of human-bear conflicts management

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Short summary: In the Digital Anthropocene, the future of conservation highly depends on media communication of wildlife. We highlight gaps in Italian media communication regarding the management of both problematic and flagship brown bear individual (M49).

Keywords: Mass media, Conservation, Large carnivores, Human-wildlife coexistence, Stakeholders, Content analysis

I. BACKGROUND

In the 21st century, with urban areas rapidly encroaching on natural habitats, human-wildlife conflicts are becoming more frequent, significant, and widespread globally (Nyhus, 2016). With the advent of internet and online media, communication centrality in wildlife conservation has become more and more evident. Communication may strongly influence public perception and tolerance towards species. However, well-planned communication is often overlooked in conservation projects. Here, we study the media framing of both problematic and flagship brown bear individual (M49 or 'Papillon') which attract a lot of media attention, to highlight gaps in media communication and devise guidelines for journalists and conservationists for better communication around human-bear conflicts.

MATERIALS AND METHODS

We collected 311 online media reports regarding the brown bear M49 and performed a content analysis. Specifically, for each news we searched if it included: (a) sensationalistic components, i.e. strong negative emotional evoking words or pictures; (b) scientific explanations for management choices; (c) pro-conservation messages, (d) the bear nickname "Papillon"; and (e) stakeholders mentioned in the reports.

II. RESULTS

Only a few online reports discussed motivations behind management choices (1.7%, n=5). Pro-conservation contents were found in 62 reports (19.9%). The majority of reports named the bear "Papillon" (86.2%, n=268) and had no sensationalistic components (92.3%, n=287). However, sensationalism was higher before the bear was nicknamed "Papillon" ($\chi^2_1 = 4.5$, $P = 0.03$). Stakeholders were represented differently in the media, which mainly mentioned politicians, managers and NGOs (Fig. 1).

III. DISCUSSION AND MAIN CONCLUSIONS

The mass media is a key stakeholder in conservation (Nanni et al., 2022). Since human bear conflict is rising in Italy, newspaper news should include more balanced and useful information on how to behave in bear territories and prevent conflictual situations or report benefits for local communities brought by bear presence and motivate

management choices with ecological perspective explanations. We recommend conservationists to be more present on the most successful channels for public communication, e.g. social media, podcast and traditional media. They should use visual communication together with plain and simple language to make scientific content available to journalists and the public and maintain regular communication also in low conflict periods. A greater focus on positive messages is needed, conservationists should inform the media on successful conservation stories and positive interaction with problematic species. At a more local scale conservationists should invest time and money in building trustable and long-term relationships with stakeholders.



Fig. 1. The stakeholder representation in the media, from the larger to the smaller circle: politicians, managers, NGOs, scientists, farmers, tourists/recreationists, residents, and hunters. Percentage represents how frequently each stakeholder were mentioned in the newspaper news. However, each news often nominated more than one stakeholder at time, thus the sum of the percentage does not return 100%.

ACKNOWLEDGMENT

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Antibiotic resistance in mariculture settings: an emerging threat for marine biodiversity

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Short summary: This study is aimed to understand the occurrence and sources of antibiotic resistance to improve fish farm practices, ensure a safer food production, and tackle the antimicrobial resistance threat to human and animal health.

Keywords: Antibiotic resistance genes, Aquaculture, Bacterial community, Coastal Marine environment

I. BACKGROUND

The presence of antibiotics (AB) and antibiotic resistance (ABR) in marine ecosystems caused by human activities has global implications for marine life and human health. In particular, intensive mariculture practices, aimed to maximize fish growth and yields [1], has led to negative impacts on farmed fish resulting in pathogen outbreaks and the consequent (over)use of antibiotics (AB) [2]. The AB (over)use is likely to increase the selective pressure for antibiotic resistant bacteria (ARB) and is expected to impair biodiversity. In this study, sources and pathways of antibiotic resistance (ABR) in mariculture settings was explored.

MATERIALS AND METHODS

Field campaigns for the collection of environmental (water and sediment) and fish samples were performed in a mariculture plant (Fig. 1). The sediment microbial community was characterized in terms of cell abundance and functional properties (i.e., heterotrophic respiration, metabolic potential and functional diversity), along with ABR potential by BiologTM assays. The AB resistome and pathogenic signature was analyzed through shotgun metagenomic sequencing, as well as by qPCR applications on selected antibiotic resistance genes (*blaCTXM*, *sul2*, *ermB*, *int11*).



Fig. 1. Mariculture sampling site in Portovenere (Liguria).

II. RESULTS

Preliminary results show a higher heterotrophic microbial respiration in sediments below the fish cages, higher values of metabolic potential in sediments of “Castagne” site and higher values of microbial functional diversity in sediments of “Canale” site. The patterns of ABR revealed the presence of microbial communities likely resistant to a higher number of antibiotics passing from “Castagne” to “Cage 5” to “Canale”. Finally, analyses on the presence of ABR genes show that *sul2* and *int11* were more abundant in environmental samples (water and sediment) rather than in the gut of farmed fish, where *ermB* is more abundant.

III. DISCUSSION AND MAIN CONCLUSIONS

Results from functional properties analyses suggest the presence below the fish cages of a higher availability of sediment organic matter, a microbial community characterized by a prompt microbial degradative activity and suitable to express multiple metabolic pathways. qPCR data will be analyzed under the light of metagenomic sequencing data that are being produced, to provide a step forward to understand the resistome and the spread of pathogenic microbial species both in mariculture and RAS systems.

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Climate change impacts and anthropogenic pressures: integrated research and approaches to protect and preserve the biodiversity in coastal environments

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Short summary: This project aims to define the effects of chemical and microbiological pollutant discharges and the impact of climate change on the coastal ecosystem and its biodiversity in order to improve its protection and conservation, and ultimately mitigate their effects.

Keywords: Anthropogenic pressure; Climate change; Biodiversity; *Escherichia coli*

I. BACKGROUND

This project aims to define an innovative approach to allow for a more efficient, reliable, and integrated-based approach study of the coastal environment. In particular, the discharge of chemical and microbiological pollutants into the sea will be the focus of this project, as a consequence of both human activities and events linked to climate change (Fig. 1). Therefore microbiological, especially faecal and pesticide contamination will be assessed in both riverine and coastal marine environments. Faecal bacteria will be characterized at the genetic level to identify the host or environment from which they were derived, as indicators of contamination sources. The ultimate objective is to better define the effects of discharges on the coastal ecosystem and its biodiversity in order to improve its protection and conservation, ultimately mitigate their impacts.



Fig. 1. This figure has been reproduced from a published paper

MATERIALS AND METHODS

Five sampling stations were chosen along the Arzilla River (Fano, Italy) closed to contamination sources: 1) near a little town; 2) near an oil mill, industries and horse riding centre; 3) in proximity of a reservoir where the digestate is discharged; 4) above the sewer outflow; 5) near the mouth of the river, next to the bathing area

The hydro-meteorological station located near the mouth of the river allows for temporal monitoring of river flow and rainfall levels with a real-time visualization of the data.

Multiple Parameters Analysis:

- Trophic status: nutrient concentration of nitrogen and phosphorus, and dissolved oxygen;
- Microbial contamination: analysis of faecal contamination in river, seawater, and sediment samples analysed using culture-based methods for faecal indicator bacteria (*Escherichia coli* and intestinal enterococci) and through innovative molecular (qPCR) methods (using different types of primers to establish from which type of organism the contamination originates) [1];
- Pesticides: neonicotinoid and polar anionic classes;
- Biodiversity status: Indicator species found in the sediment (meiobenthic analysis).

II. EXPECTED RESULTS

This PhD project is at the beginning of the first year and does not yet allow for obtaining results, but the expected results will concern:

1. Identification of major sources of chemical and microbiological pollution in the coastal areas and overall assessment of water quality.
2. Evaluation of the biodiversity status through the analysis of the trophic status and the study of indicator organisms (i.e., meiofauna) in sediment samples. This evaluation will provide insights into the ecological condition and overall quality of the coastal ecosystem.
3. Enhanced understanding of the impacts of climate change on the health of coastal environments. This knowledge can help inform future research and policies addressing the combined effects of these factors.

ACKNOWLEDGMENT

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DNA Metabarcoding of Crangonid Shrimp Gut Contents as a Natural Tool for Biodiversity Evaluation

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Short summary: The Pomo/Jabuka Pits play a vital role in the ecology of the Adriatic Sea. Consequently, it is imperative to thoroughly analyse and assess changes in biodiversity within this region. As such, the unique biodiversity of the Pomo/Jabuka Pits is currently under evaluation using a “natural sampler DNA” approach, based on metabarcoding of shrimp gut contents.

Keywords: Biodiversity observatories, Monitoring, DNA, Trophic metabarcoding, Crangonidae

I. BACKGROUND

The Mediterranean Sea is experiencing a significant decline in marine biodiversity, with the Adriatic Sea appearing particularly affected. In recent years, molecular technologies like DNA metabarcoding have proven valuable for evaluating and monitoring biodiversity in cases where traditional methods may not deliver comprehensive results.

MATERIALS AND METHODS

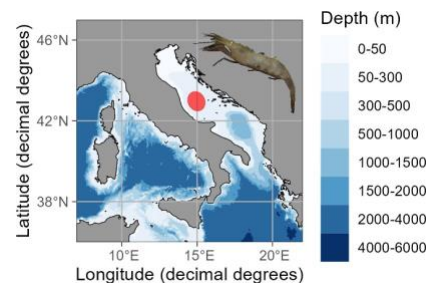
In the area of Pomo/Jabuka Pits, the oceanographic patterns of the North and South portions of the Adriatic Sea converge, creating a unique environment in which water exchange does not happen annually (Fig. 1). As one of the main nursery areas for hake, *Merluccius merluccius*, and Norway lobster, *Nephrops norvegicus*, this area is recognised as a Vulnerable Marine Ecosystem and an Essential Fish Habitat. A Fishery Restricted Area was implemented in 2017 to safeguard the distinctive biological and ecological characteristics of the area. During the surveys carried out in the area by CNR-IRBIM of Ancona, 300 individuals of Crangonidae were collected. Guts will be removed from each individual and pools comprising multiple sympatric specimens (e.g. N=4-8) will be formed to ensure an adequate amount of genetic material. Taxonomic diversity and composition will be assessed using DNA metabarcoding, through employment a primer for the whole community, targeting the mitochondrial cytochrome c. oxidase subunit I (COI) region [1]. Furthermore, water and sediment samples were collected in order to obtain a comparison with the results obtained from shrimps.

II. RESULTS

The results of this work are currently undergoing processing. At present, shrimp species identification and extraction processes are being conducted at the CNR-Istituto per le Risorse Biologiche e le Biotecnologie Marine (IRBIM) laboratories in Ancona, Italy. Subsequent amplification, sequencing, and bioinformatic analysis will be performed at Liverpool John Moores University in the UK. Currently, three species of Crangonidae have been identified across the samples: *Aegaeon cataphractus*,

Philocheras echinulatus and *Pontophilus spinosus*, respectively 2, 25, 73 % of the samples analysed.

Fig. 1. The Adriatic Sea, red polygon indicates the sampling site



III. DISCUSSION AND MAIN CONCLUSIONS

The Adriatic Sea's ecosystem faces significant environmental challenges, from large scale climatic changes, to more localised pollution and fishery induced perturbations. Monitoring and evaluating biodiversity levels over time are essential for effectively managing sensitive and productive areas such as the Pomo/Jabuka Pits [2]. Recently, there has been pronounced interest in combining the high resolution of novel DNA sequencing approaches with the natural sampling capabilities of ubiquitous generalist invertebrates, whose foraging habits can capture the main biodiversity features of a marine region. The study will test for differential capabilities among shrimp species in capturing biodiversity, and estimate the role of habitat type, bathymetry, and fishing pressure in determining changes in benthic biodiversity patterns.

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How a massive river flood event affects the microbial composition of surface marine sediments

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Short summary: In this study, we attempt to clarify the impact of one of the most important flooding events in recent years on the Adriatic coast on benthic microbial communities.

Keywords: Benthic microbial diversity, River flood, Microbial pollutants, Adriatic Sea

I. BACKGROUND

Extreme flooding events are becoming increasingly frequent as the consequence of climate change, driving modifications in coastal hydrology, hydrodynamics and ecosystem functioning. The transported contaminants and materials often form plumes that are clearly visible in the marine environment, determining long-lasting impacts on ecosystems and biodiversity [1]. Benthic microbial communities, which play an essential role in nutrient turnover and food webs, may also be potentially impacted by these events, but the impacts on the seafloor are still poorly studied. It is, therefore, necessary to clarify the response of marine microbial assemblages to flooding events. In this study, we explored the diversity of benthic microbial communities in relation to an extreme flooding event occurred in the Adriatic Sea in 2022, also focusing on pathogenic bacteria having a riverine origin.

MATERIALS AND METHODS

Sampling was performed on 23rd September 2022, a few days after a massive flooding event that affected the central Adriatic coast (16th September 2022). Surface sediment samples were collected from 9 coast-offshore transect in correspondence of 6 main river mouths involved by the flood (Fig. 1). Changes in diversity and microbial community composition was analyzed by 16S rRNA gene amplicon sequencing. The occurrence of indicators of microbial pollution was carried out focusing on detecting potential fecal contaminants (i.e., traditional faecal bacteria such as Enterobacteriaceae, including *Escherichia coli* and *Enterococcus* spp., as well as alternative feces- and sewage-associated taxa) [2,3]. In addition sedimentological analysis was conducted on the benthic samples.

II. RESULTS

Statistically lower richness and diversity values were observed in samples close to the coast, with a gradual increase towards the open sea. All samples displayed similar composition in the most abundant phyla and classes; nevertheless, a certain degree of variability was observed in their abundances, such as a higher value of Acidobacteriota in coastal samples than in seaward stations. Beta-diversity analyses showed that benthic prokaryotic communities displayed a clear gradient according to the distance from the coast, with the only exception of samples collected in front of the Musone River, where samples grouped together and showed a similar community

composition. Traditional, alternative, faeces- and sewage-associated bacteria were retrieved at all stations with a range between 0.006 to 0.78%, but no clear patterns observed according to the distance from river mouths.

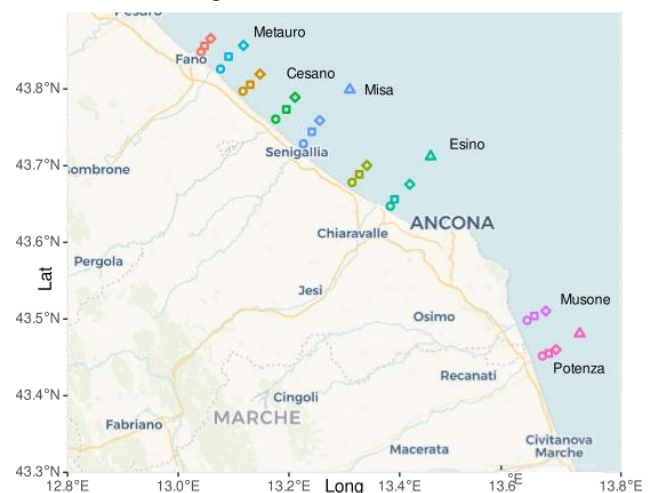


Fig. 1. Map showing the sampling sites with the coast-offshore transects in correspondence of 6 river mouths and the 3 additional transects.

III. DISCUSSION AND MAIN CONCLUSIONS

Our results suggest that severe river flooding events may affect benthic microbial communities and that their impact may vary in accordance to the distance from the coast, as opposed to what has been reported in previous works in the same area [1]. Further analyses, will be necessary to assess how such extreme events may influence both the Adriatic coastal ecosystem functioning and public health risks associated with the microbial pollution, e.g. on recreational water quality and seafood consumption.

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