Sessione
La vita negli ambienti estremi

Comunicazioni

Riding the tide: where land meets sea and risk meets opportunity

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What makes intertidal zones a truly exceptional adaptive challenge is the dramatic variability of their chemical, physical, and biotic parameters, across both spatial and temporal dimensions and at a wide range of scales. These environments represent dynamic land-sea ecotones, shaped by the oscillations of the sea surface caused by gravitational forces exerted by the moon and the sun on the ocean's water mass. The already complex astronomical origins of tidal phenomena are further influenced by the configuration of ocean basins and the local geometry of coastlines. The result is a series of oscillations at the land-sea interface, characterized by multiple harmonic components that can reach levels of local complexity nearly beyond the predictive capacity of even sophisticated computational systems.

The animal organisms inhabiting intertidal systems develop intricate morphological and physiological adaptations—from the molecular to the macroanatomical level—that enable them to achieve significant fitness in such conditions. These are almost invariably complemented by complex behavioral strategies that allow organisms to cope with environmental fluctuations and exploit the unique resources that arise from them.

Thus, spatio-temporal complexity often translates into opportunity, both at the species and community level, with high degrees of species packing. Over the long term, this generates extraordinary evolutionary potential. In this sense, tidal systems have played a pivotal role in biological evolution—from the origin of life itself to the colonization of terrestrial environments, and even the return of terrestrial organisms to the sea. Human demographic expansion, particularly that of *Homo sapiens*, has likewise been closely tied to the capacity to exploit the resources of tidal environments while avoiding their associated risks.

Characterization of free-living nematode assemblages in Mediterranean ports: implications for benthic monitoring

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Ports are maritime zones of high economic importance, hosting a range of activities such as industrial operations, container terminals, petrochemical handling, and tourism. These activities make port areas both sources and recipients of environmental stressors that can significantly impact marine fauna. Effective management of port environments is therefore essential for marine conservation, with environmental assessment and monitoring representing key steps—particularly through the use of bioindicators such as free-living benthic nematodes.

However, a major limitation remains the lack of baseline data for this phylum. To address this gap, we characterized free-living nematode assemblages in seven Mediterranean ports, spanning from the Adriatic to the Ligurian Sea. We analyzed their abundance, taxonomic composition, diversity, and functional traits.

Our results suggest that nematodes may exhibit adaptation to long-term contamination, likely in synergy with other benthic components such as diatoms and prokaryotes. Canonical analysis of principal coordinates allowed us to distinguish faunal assemblages across port basins, while routine distance-based linear modeling identified key environmental drivers shaping nematode communities, including sediment mud/silt content, water depth, and polycyclic aromatic hydrocarbon (PAH) concentrations. These findings highlight the importance of site-specific environmental conditions in structuring nematode assemblages, which limits the identification of a universal set of stress-indicator genera. At present, synthetic indices such as the Maturity Index and Shannon diversity remain the most effective tools for assessing ecological quality in marine ecosystems using nematodes.

Unraveling the impact of urbanization on pollinator insects through a metabolomic approach

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Pollinators play a crucial role in maintaining ecosystem functionality and food security. However, rapid urban expansion is altering their habitats, phenology, and behaviour, favouring species more adaptable to urban settings. In this study, we investigated the effects of urbanization on wild pollinators widely distributed in Italian cities. Using targeted and untargeted metabolomic approaches, we aimed to assess the impact of urban stressors on pollinator populations and explore potential adaptive responses to urban environments, leveraging the capacity of metabolomics to detect subtle physiological and biochemical changes that serve as early indicators of stress and reveal potential metabolic adaptations to urban conditions. In the initial phase, we collected 82 of *B. terrestris* individuals from 12 semi-natural and urban sites in the Milan metropolitan area. Metabolites were extracted from the entire body and first analysed using a targeted approach to quantify malondialdehyde (MDA), a biomarker of oxidative damage. A subset of 30 samples was then analysed through untargeted metabolomics (LC-MS) to investigate broader metabolic responses. Afterwards we expanded the study to a national scale, sampling across four major Italian cities: Milan, Rome, Turin, and Florence, and also including samples of *B. pascuorum* and *Osmia cornuta*. Around 120 *B. terrestris*, 120 *B. pascuorum*, and 60 *O. cornuta* were collected from 28 sites along an urbanization gradient. As before, whole-body metabolites were analysed using LC-MS untargeted metabolomics to assess metabolic changes across varying land use scenarios. Results from the first experimental phase on *B. terrestris* showed clear differences between urban and semi-natural individuals. MDA levels were higher in urban habitats, suggesting greater oxidative stress. We also found consistent changes in stress-related and adaptive metabolites: for instance, urban bumblebees had higher levels of unsaturated phospholipids, possibly reflecting adaptation to higher urban temperatures. Results from the nationwide sampling revealed significant differences in the metabolic profiles of all species along the urbanization gradient. Ongoing analyses will identify key compounds varying with urban intensity. These findings will advance our understanding of how urbanization affects pollinators and inform conservation and urban planning strategies.

Under anthropogenic pressure: honeybees may amplify the effects of retreating glaciers on wild bee diversity and bee-plant networks

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Human impacts on the planet span several scales, from local management activities to global change. Wild bees (Hymenoptera: Apoidea) are important pollinators whose diversity is increasingly undermined by anthropic pressures. While the effects of managed honeybees on wild bee diversity and foraging patterns have been largely demonstrated, studies have rarely been conducted in extreme and fragile environments such as high mountain plains affected by glacier retreat. Here, wild bee biodiversity and bee-plant networks were studied across a 170-year gradient of glacier retreat in Valais, Switzerland. This provides a unique case study, linking global change effects (glacier retreat) and local management activities (beekeeping) with wild bee communities, whose diversity and the robustness of bee-plant networks should be maximised at intermediate stages of glacier retreat and with lower honeybee abundance. A total of 231 wild bees and 105 honeybees were sampled at four stages of glacier retreat, and the plant they were feeding on was recorded. Wild bee abundance and Hill's numbers were strongly influenced by both glacier retreat and the proportion of honeybees over the total number of bees sampled per stage. The most recent areas of glacier retreat were characterised by richer communities (*N, q0*), while *N, q0*, and *q1* were negatively correlated with increasing honeybee proportion. *H2'* (network-level specialisation), bee niche overlap, and connectance increased, and modularity decreased, with increasing honeybee proportion. This suggests that honeybees may monopolise floral resources in poorer environments (i.e. next to and furthest from the glacier front), whereas in habitats with lower proportions of honeybees resources are more evenly distributed among bee species. Glacial retreat stage had weaker effects on network metrics, although older stages were characterised by lower modularity and higher niche overlap. These results have strong conservation implications, since glacier loss is likely to reduce wild bee abundance and support poorer bee communities as succession progresses towards more closed (i.e. forest) habitats. Furthermore, glacier retreat may be changing the floral resources available to wild bees, with honeybees possibly displacing them through competition. Hence, conserving wild bee communities in such delicate environments would benefit from maintaining beekeeping at low levels, especially at most recent and oldest glacier retreat stages.

Beneath Borders: tracing hidden waters and subterranean life in the Reka-Timavo system through environmental DNA

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The Reka-Timavo hydrological system, with an underground course extending approximately 90 km, represents a still partially unexplored environment in the transboundary area between Italy and Slovenia. The environmental DNA (eDNA) approach has significantly enhanced the ability to collect data on species distribution across a wide range of ecosystems.

In this study, we investigated the metazoan community present in the waters of the Reka-Timavo system through eDNA analysis. Sampling was conducted at two sites within the Škocjan Caves Park (Slovenia) and one site in the Luftloch Cave (Italy) between late July and the first week of August 2024. Environmental DNA was extracted, amplified and purified using commercial kits, and sequenced with Illumina technology (NovaSeq6000 SP) at a depth of 2×250 bp.

The three analysed sites displayed distinct biological assemblages. In the Slovenian locations, most of the zooplanktonic community belonged to the phylum Rotifera, particularly the genus Ploima. In contrast, the dominant taxa in the Italian site (Luftloch Cave) were from the phylum Arthropoda, primarily the class Copepoda (*Acanthocyclops spp.*) and class Insecta (order Diptera). Hydrozoan detections in subterranean environments are rare; thus, we highlight findings related to this taxonomic group. DNA from *Craspedacusta sowerbii*, a freshwater jellyfish native to East Asia, was identified in all sampled caves. Although considered common in Western European freshwater systems, this species is often underreported due to its inconspicuous polyp stage. Its detection in the Reka-Timavo system supports a recent report by the Natural History Museum, confirming its presence as an alien species in the upper Timavo (Slovenia).

Additionally, DNA from *Hydra vulgaris*, a species already known in the region, was found in the Slovenian samples. Of particular interest was the detection of *Velkovrhia enigmatica* (Matjašič & Sket, 1971), the only known stygobiotic freshwater hydrozoan, endemic to the Dinaric Karst. This finding is especially noteworthy and warrants further investigation due to its ecological significance.

These preliminary results lay a solid and promising foundation for the application of eDNA methodologies in the study of subterranean environments. The data collected so far suggest that this approach could become a powerful and innovative tool for biodiversity assessment in underground ecosystems, paving the way for more detailed and targeted future research.

Light pollution, global warming, and behavior: an overview from fish models.

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The impact of anthropogenic action on aquatic and terrestrial ecosystem is increasingly recognized as the major driver of ecological disruption, altering both biotic and abiotic environmental conditions. In particular, the global warming is accelarating and will likely continue to increase in the coming decades, leading to biodiversity and ecosystems services loss. Although less considered as a stressor, light pollution has become a serious threat by altering physiology and behaviour of both vertebrates and invertebrates. Understanding how the cumulative impacts of global warming and light pollution alter animal behavior is essential for developing effective conservation strategies for natural populations. To date, we have performed a series of experiments in which larvae and adult zebrafish (*Danio rerio*) were exposed in mesocosms simulating these anthropogenic stressors (i.e., heat stress and Artificial light at night-ALAN) to investigate their effects on behavior at different developmental stages. Exposure to ALAN altered total activity, brain lateralization and learning in zebrafish larvae, while more complex cognitive functions were affected in adults. ALAN-exposed adult zebrafish also showed a disrupted daily pattern of behavioral activity, losing their photic entrainment. Moreover, brain transcriptome analysis revealed significant alterations in the expression of core clock (*per1* and *cry1*) and clock-related genes (*aanat2*), and genes associated with immunity, stress response, responses to sensory stimuli, energy production and reproductive processes. When experiencing heat stress during development, zebrafish larvae showed reduced total activity and impaired cognitive performance. Alterations on swimming activity and lateralization were also observed in adult zebrafish exposed to simulated heatwaves. Overall, our findings confirm that global warming and light pollution significantly affects several aspects of zebrafish behavior and cognition at different life stages, with potential consequences for individual fitness. By taking advantages from these results, we have extended our approach to the Mediterranean killifish *Aphanius fasciatus*, a good target species for studying the ecological and evolutionary effects of anthropogenic stressors on Mediterranean coastal ecosystems.

Unveiling the resilience of the blackmouth catshark *Galeus melastomus*: growth, maturity, and habitat use in the Western Mediterranean Sea

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Deep-sea elasmobranchs are particularly susceptible to overexploitation due to their slow growth, delayed maturity, and low reproductive output. Among them, the blackmouth catshark (*Galeus melastomus*) is one of the most frequently captured species in the Mediterranean Sea, acting as a generalist and opportunistic predator across a wide bathymetric range (˜300–1873 m). Despite its broad distribution and significant presence as bycatch in deep-water trawl fisheries, critical aspects of its life history, particularly growth, remain insufficiently understood. Given their relevance for fisheries management, this study aims to advance current knowledge on the species' reproductive cycle, growth dynamics, and bathymetric segregation.

Specimens were collected between 2012 and 2023 from both fishery-dependent and independent surveys in FAO Geographic Subareas (GSAs) 9 (Ligurian and Northern Tyrrhenian Seas) and 11 (Sardinia). Individuals were measured and macroscopically assigned to sex and maturity stages. A subset of 1,201 individuals (788 from GSA9, 413 from GSA11) ranging from 6.5 to 53.0 cm in total length was selected for age estimation via sectioned and crystal violet-stained vertebral centra. Age–length data were analysed through a multi-model inference analysis.

Results indicate a continuous reproductive cycle throughout the year, with a seasonal peak in winter. Females reached sexual maturity at slightly larger sizes than males in both areas (L50: 41.3 vs. 39.2 cm in GSA9; 44.4 vs. 41.2 cm in GSA11). Among the tested growth models, the von Bertalanffy function provided the best fit, as indicated by Akaike's Information Criterion. No significant differences in growth patterns between sexes were observed. Estimated growth parameters for combined sexes were L=60.76 cm, k=0.20, t =–1.30 in GSA9, and L=52.34 cm, k=0.26, t=–0.94 in GSA11. These values were consistent with parameters derived from length–frequency distribution analyses on the whole dataset, thus corroborating the direct ageing protocol.

A marked bathymetric segregation was observed, with immature individuals nearly absent below 1000 m and a female-biased sex ratio beyond 1200 m. These deeper zones may serve as partial refugia from fishing pressure. Together with an extended reproductive cycle and relatively rapid growth compared to other elasmobranchs, these traits may help explain the continued abundance of *G. melastomus* in the Mediterranean despite ongoing exploitation.

Trace elements accumulation and parasitic charge in 4 species of deep-sea chondrichthyes from the Sicilian Channel: results from DEEP-MED project

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Trace element contamination in deep-sea ecosystems is a topic of growing scientific interest, as these environments, although remote, are not free from direct and indirect anthropogenic pressures. In this context, the present study aims to evaluate the bioaccumulation levels in four deep-sea benthic and benthopelagic fish species: *Raja clavata*, *Scyliorhinus canicula*, *Galeus melastomus* and *Chimaera monstrosa*, with the aim of exploring any species-specific differences attributable to ecological and trophic characteristics and correlating the results obtained with the structure and composition of parasitic helminth communities. The concentrations of 17 elements (Al, As, Cd, Co, Cu, Mn, Mo, Ni, Zn, Se, Sr, V, Pb, Cr, Fe, Bi and U) were determined by inductively coupled plasma mass spectrometry (ICP-MS, PerkinElmer ElanDRCe). The results allowed to elaborate specific abundance profiles for each species, where arsenic was the dominant element in all the examined taxa, followed, in variable order, by zinc, iron and aluminum. Higher mean bioaccumulation values emerged in *R. clavata* and *S. canicula* compared to *G. melastomus* and *C. monstrosa.* This pattern seems consistent with the different ecological strategies: the first two species show a greater affinity for the substrate and demersal sediments, which can act as reservoirs for trace elements, compared to the other two species more frequently associated with the water column and characterized by greater vertical mobility.

As regards parasites, the species *C. monstrosa* was found to be parasitized only by *Chimaericola leptogaster*, *R. clavata* with 10 species of parasites and a prevalence of 48.15% was the species with the highest parasitological diversity; *G. melastomus* and *S. canicula* showed a very high prevalence that was equal to 98% for both species, with an average intensity between 46.3 and 48.3 but with communities represented by three and four species of parasites: among these, *Grillotia sp.* was the one with the highest intensity, with peaks of over 300 individuals per host, located almost exclusively in the muscle tissue. The work contributes to improving the understanding of bioaccumulation processes and their relationships with parasite loads in deep-sea fish and lays the basis for future ecotoxicological and food risk assessments in bathyal contexts of the Central Mediterranean.

New data on the inter- and intra-population variability of the eco-morphology and trophic ecology of the longspine snipefish, *Macroramphosus scolopax*, linnaeus, 1758

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Despite the great ecological and social relevance of deep-sea ecosystems, and the growing anthropogenic impacts affecting them, the knowledge base on the biodiversity and trophic dynamics of deep-sea communities remains relatively poor. In this context, it is important to provide valuable data on both the eco-morphology of deep fauna and the ecological dynamics regulating deep-sea communities. In the Mediterranean Sea, the long spine snipefish, *Macroramphosus scolopax*, is one of the most widely distributed and abundant teleost species, ranging between 25 and 600 m of depth. It is a fast-growing short-living cosmopolitan species, essential in the energy transferring between different depth strata and domains. Present research aims to examine the intra and inter population variability in feeding habits and eco-morphology of two *M. scolopax* populations inhabiting the Italian waters.

A total of 340 specimens were collected from trawl fishery operating in the central-western Mediterranean Sea around Sardinia (220 Ind.), and in the southern and central Tyrrhenian Sea (120 Ind.). Once transported in laboratory, they were measured, weighted, and divided in two size classes (Class I $\leq$ 110 mm; Class II $\geq$ 110 mm). Once sampled otoliths and stomachs, sagittae were analysed for age estimation and photographed for morphometrical and shape analyses, while stomachs contents were examined to reconstruct the feeding habits. The prey-specific index of relative importance was calculated for each prey, also assessing, in both populations, the niche breadth, trophic niche overlap and trophic level of each identified age and size class.

Results confirmed the capability of the species to feed on both planktonic and benthic organisms in the two studied areas, partitioning the trophic resources, at intra-population level, between the different size and age classes. Smaller and younger individuals of both populations showed more pronounced planktivorous habits than the larger and older ones, with otoliths morphology and shape reflecting the benthopelagic habits of the species in both the studied areas. At inter-population level, the *M. scolopax* specimens showed slightly differences in otoliths' features and diet composition. This highlighted the capability of the species to adapt to the variability in resources availability and environmental features between different geographical areas, an essential features to thrive in the deep oligotrophic Mediterranean ecosystems.

Reproduction in deep sea cephalopods: adaptations and mating errors in *Rossia macrosoma* (Delle Chiaje, 1830)

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Cephalopods are an important component of marine ecosystems around the world, and most species (coleoids) are considered semelparous, short-lived and fast-growing. Reproduction in coleoids has long been studied in coastal species and schematised as a internal fertilisation of small and numerosus eggs within a single reproductive event followed by death. More recent studies on some deep-sea cephalopods have revealed how they have a great flexibility in adapting to the environment, showing, peculiarities in morphological and/or ethological reproductive aspects. This is in response to some limitations such as difficulties in meeting the mate due to the absence of light.

To upgrade this issue on the stout bobtail squid *Rossia macrosoma*, 88 males and 156 females at different maturity stages were sampled by trawl net in Sardinian waters (western Mediterranean Sea) at an average depth of 500 m. *R. macrosoma* doesn't exceeding 84 mm (females) and 60 mm (males) in mantle length and reaches the mature stage starting from about 30 mm. Both sexes produce a relatively low number of sexual products with large dimensions. In females, mature ovaries contained about 500 oocytes at various developmental stages, although only a small percentage was smooth and located in the oviduct, ready to be laid—suggesting a multiple spawning strategy. In the Needham's sac of mature males were counted up to 146 spermatophores (35 ± 24) with an average length of 17.9 mm and large sperm mass.To ensure reproductive success in rapid and fleeting matings and in absence of a seminal receptacle, intradermal spermatangia (SPG, inverted spermatophores) implantation represents an efficient way to allow sperm storage in the body of females, even not mature yet. Moreover to this is associated the ability of the SPG to move and pass from the external of the mantle to the inner cavity to fertilisate the oocytes. Mated females analysed carried up to 90 SPG, predominantly (76%) located in the anterior ventral area above the oviduct—an optimal site for fertilization. However, spermatangia were also found on the head, funnel, and arms, likely due to errors during rapid mating. Given the presence of spg implanted in males, we can hypothesize that a mating error may concern also a mating between males.

Living in marinas and ports: underwater noise pollution effects on the behavior and physiology of the ascidian *Botryllus schlosseri*

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Marinas and ports represent extreme environments for sessile animals, which cannot escape the variety of anthropogenic pressures characterizing them, including underwater noise generated by maritime traffic. The latter is considered a pollutant of concern in the European Marine Strategy Framework Directive, being pervasive in our basins. However, the marine invertebrate ability to cope with it is mostly unknown. Here, we present our results on the effects of anthropogenic underwater noise on the colonial ascidian *Botryllus schlosseri*, a species commonly found in shallow waters of marinas and ports. We exposed colonies, sampled in the Venetian Lagoon close to Chioggia (Italy) to continuous and discontinuous noise (peak bands 63-125 Hz), mimicking the low frequency maritime traffic noise. After measurements of the lagoon soundscape, we tested noise levels (138.36-163 dB) comparable to those produced by boats passing close to Chioggia. Colonies underwent both short-term (30 min, continuous noise) and long-term (3 days, discontinuous noise) exposures. Some were also primed by noise, exposing them to a noise pulse before the noise exposure, to verify if priming could enable them to subsequently tolerate noise treatment better. To verify the effects induced by the treatments, we used behavioral assays (verifying the animal ability to detect mechanical stimuli), and physiological assays (verifying the heartbeat frequency, also over time, and the filtration rate). The expression of stress related genes, such as *sod*, *c3*, *rbl*, *catalase* (quantified by qPCR), and the immune system functionality (phagocytosis activity assays at FACS) were evaluated. After long-term exposures, we also verified the effects at developmental level, considering the asexual cycle progression and the ability to regenerate excised portions of the colonial tunic and its circulatory system. Moreover, we analyzed the possible noise transgenerational effects by exposing colonies to a long-term treatment and evaluating at behavioral and physiological level its effects on two generations of buds, once become adults. Results show that noise has negative effects on behavioral, physiological, immunological and developmental levels, inducing stress-related responses. The study evidences the necessity to monitor this pollutant for reaching the Good Environmental Status of European basins.

Transfer and physiological effects of microplastics in soil invertebrates

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The presence of microplastics (MPs) and nanoplastics (NPs) in terrestrial and aquatic ecosystems has become a significant concern, as they are a novel and pervasive form of pollution. The generation of plastic waste is a consequence of a number of human activities, including agricultural practices (e.g. plastic mulching, sewage sludge). In terrestrial ecosystems, MPs/NPs enter the food web through the root and leaf systems of plants and then reach primary and secondary consumers. However, the dynamics of microplastic transfer trough the soil trophic web remains poorly understood, as well as their sublethal effects on the ecological functions of terrestrial invertebrates. To investigate the trophic transfer of polystyrene (PS-MPs), a simplified prey-predator system was studied using *Cantareus aspersus* (Müller, 1774) snails as primary consumers and the helicophagous larvae of *Carabus lefebvrei* (Dejean, 1826) (Coleoptera, Carabidae) as predators. Second and third instar larvae were fed snails previously exposed to either 0.01% or 0.1% PS-MPs, which had been labelled with europium to be detected in tissue by ICP-MS (Inductively Coupled Plasma Mass Spectrometry). The results showed a dose-dependent accumulation of microplastics in both snails and the beetle larvae. No statistically significant differences were observed between larval stages in terms of total MP accumulation (p ¿ 0.05), suggesting that developmental stage did not influence uptake. However, the detection of MPs in exuviae collected during the moult from the second to the third larval stage suggests the existence of an efficient detoxification mechanism in the preimaginal stages of this carabid species, enabling partial elimination of ingested particles. In addition, larvae fed on contaminated snails exhibited significant increases in phenoxidase enzyme activity compared to the control group (p¡0.05 for the 0.01% and 0.10% PS-MP groups, respectively), indicating a sublethal exposure effect on immune system function involved in melanisation processes. In conclusion, this study provides new insights into the trophic transfer of microplastics in soil food webs, demonstrating both physiological effects and potential detoxification strategies in a ground predator species. These findings highlight the need for further ecotoxicological assessment of plastic pollution in terrestrial ecosystems, particularly regarding its impact on invertebrate immune function and sublethal effects on wildlife.

Reproductive strategies of the bamboo coral *Isidella elongata*: crucial data for the conservation of deep-sea corals

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The bamboo coral *Isidella elongata* (Esper, 1788) is an octocoral crucial to deep-sea ecosystems. Nearly endemic to the Mediterranean, it typically resides at depths of 500–1656 m, forming communities on soft bathyal seabeds. Classified as Critically Endangered on the IUCN Red List in both the Mediterranean and Italian waters, it is also an indicator species for Vulnerable Marine Ecosystems according to the General Fisheries Commission for the Mediterranean Sea. Despite its ecological importance, no reproductive information existed for *I. elongata.* This study aimed to investigate its reproductive biology, including reproductive mode, gametogenesis trends, polyp fecundity, sexual product (SP) development, and size at first reproduction.

Between June and September 2024, 68 colonies of *I. elongata* were collected off the southwestern coast of Sardinia at unusual depths of 160–187 m during trammel net fishing for the spiny lobster (*Palinurus elephas*). The basal diameter (BD) and height (H) of each colony were measured, and histological analyses were performed on randomly selected polyps to determine sex and maturation stages of male and female SP. A total of 2175 polyps were dissected to estimate relative fecundity, calculated as the number of SP per polyp.

All colonies were gonochoric, at both the colony and polyp levels. Sex-ratio was biased toward females, with no significant differences. On average, female polyps contained 2.58 SP, with a maximum of 24 in one polyp, while male polyps contained 7.61 SP, with up to 28 SP in one polyp. All female colonies (BD: 1.9–3.7 mm; H: 25.6–63.2 cm) were sexually mature, with SP at late vitellogenic stages. Most male colonies (BD: 2.0–4.6 mm) were in maturing or mature stages. The smallest female colony (BD 1.9 mm) had mostly empty polyps, with a few containing 3–4 mature SP, while the smallest male colony (BD 2 mm) had polyps filled with mature SP.

This study provides the first reproductive data on this species. The gonochorism observed is typical for octocorals. The absence of planula larvae suggests *I. elongata* reproduces via broadcast spawning, with large female SP indicating a lecithotrophic larval type. The findings show early sexual maturity and a potentially high reproductive output. Gaining deeper insight into the reproductive strategies and cycles of deep-sea corals like *I. elongata* is essential to improve our understanding of these key habitats and to guide future research and conservation efforts.

Growth of bamboo coral *Isidella elongata* (Esper, 1788): an example of the adaptation to the deep environment in Mediterranean

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The General Fisheries Commission for the Mediterranean (GFCM) recognises bamboo coral forests as Vulnerable Marine Ecosystems due to their high ecological importance (e.g. habitat-forming, hot-spot biodiversity). The major cause of bamboo coral vulnerability lies in their slow growth rate, which limits their ability to recover from fisheries-related damage. Despite the need to take action to ensure the conservation of the *I. elongata* forests, crucial information regarding life-history traits such as age, growth rate, and life span is still limited. This study takes advantage of the incidental catch of 751 *I. elongata* colonies (basal diameter 0.36-7.3 mm) through experimental trawl fishing surveys (2012-2023) in South-Adriatic Sea. We modelled the species' growth through thin sections (basal diameter ¡2 mm) and radiocarbon dating (basal diameter ¿4 mm). The estimated ages, considering both methods, ranged between 1 and 59 years, while the species' lifespan in the area was predicted to be from 57.5 to 59 years. Age data were fitted to seven different growth models, with the exponetial model proving to be the most accurate in describing the species' growth with significant difference between two groups of age data (¡12 and¿48.8 years). This difference could be linked to the branching growth pattern of *I. elongata*, since young colonies are unbranched, while both the number and the size of ramifications increase with the colony age. A higher number of branches means a greater number of polyps and implies a greater feeding capacity, supporting the higher growth rate that we observed in older colonies. Fan-shaped branching might also impose biomechanical demands to resist current-induced stress, potentially limiting axial growth but, at the same time, needing a larger and more robust stem to support the colony, thus stimulating BD growth. On the contrary, it is expected that sexual maturity would lead to a decrease in growth rate, as energy is diverted from growth to reproduction. The observed exponential growth pattern may result from a trade-off adaptation among increased feeding capacity (positive effect), structural constraints (both positive and negative effects) and sexual maturity (negative effect). Our findings are the first providing direct ageing of *I. elongata* in the Mediterranean Sea, which is a critical aspect in determining the species' long-term population dynamics and recovery capacity from an ecosystem-based fishery management perspective.

The desiccome of the tardigrade *Bertolanius volubilis*

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Anhydrobiosis, a reversible metabolic state enabling survival without water, is a key adaptation in tardigrades, involving a molecular toolkit that includes Tardigrade Disordered Proteins (TDPs). Three TDP families, Cytosolic (CAHS), Secretory (SAHS), and Mitochondrial (MAHS) Abundant Heat Soluble proteins, contribute to structural stabilization, oxidative stress resistance, and biomolecule protection. Despite their role, TDPs show considerable diversification and remain poorly studied in rare clades like Eohypsibioidea, which includes few species mainly found in polar and alpine regions. Within this group, *Bertolanius volubilis* is known to survive extreme conditions through multiple dormancy strategies. However, due to its limited distribution, molecular data on anhydrobiosis are lacking. To address this gap, the transcriptomic response to desiccation in *B. volubilis* was investigated, providing novel insights into this clade.

A population of *B. volubilis*, collected from the Apennines in 2007 and stored dry for 18 years, was used. Desiccation tolerance was assessed by a rehydration survival assay. RNA was extracted from four groups of specimens in hydrated and desiccated states. The transcriptome was *de novo* assembled and analysed to identify the repertoire activated during desiccation, focusing on TDPs expression and diversity.

B. volubilis showed high survival upon rehydration. Transcriptomic analyses revealed differentially expressed genes, many lacking homologs in other tardigrades, suggesting they may be unique to this clade. Several CAHS genes were highly and constitutively expressed, with moderate upregulation during desiccation, while one SAHS gene showed stable high expression in both states. Evolutionary comparisons revealed sequences similar to known TDPs and novel variants, highlighting lineage-specific adaptations.

Results confirm *B. volubilis* as a desiccation-tolerant species and provide the first omics data for Eohypsibioidea. Its transcriptomic profile, marked by high baseline CAHS expression and limited desiccation-induced modulation, suggests a constitutive strategy for coping with rapid dehydration, as observed in other desiccation-tolerant tardigrades.

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New insights into the adaptive molecular evolution of a bipolar ciliate, *Euplotes nobilii.*

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The biological concept of “metapopulation” (i.e, a group of populations of the same species separated by space but linked by dispersal and migration) applies properly also to protists’ biogeography, as originally fostered by Finlay and Fenchel (2004) with particular reference to ciliates. By sampling ciliates over many years from coastal marine waters of Antarctic, Patagonian and Arctic sites, we realized a wide collection of strains representing heterospecific psychrotrophic and psychrophilic populations of *Euplotes*, an extremely diversified genus that stands at the forefront of experimental ciliatology. Among these strains, those representing *E. nobilii* have more profitably been used to improve our knowledge of the molecular adaptation of single-celled organisms to the extreme environmental conditions of polar waters. Following evidence from genetic and breeding analysis that they effectively represent geographically separated populations of the same panmictic metapopulation, a dozen of them (growing better at 4 °C at a stable rate of one fission every other day) were chosen to determine the structures of their water-borne pheromones (cell type-specific proteins that preside self/not-self cell-cell interactions) and get insights on the molecular basis of the cell defense against UV radiation and protein oxidation. In comparison with its sister species, *E. raikovi*, that is widespread in temperate sea waters, *E. nobilii* (i) synthesizes less thermostable pheromones characterized by a marked reduction of regular helical structures and a consequent extension of random coil regions (functional to improve structural flexibility), and (ii) reinforces its enzymatic barriers to UV and oxidative damages also utilizing chaperons and antioxidant enzymes (including methionine sulfoxide reductases responsible for reducing methionine sulfoxide back to methionine) which are continuously released into the cytoplasm by endosymbiotic *Parafrancisella* bacteria that appear to be pervasive colonizers of *E. nobilii* cells.