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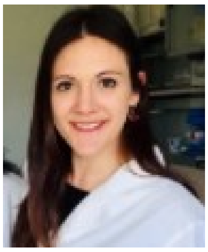

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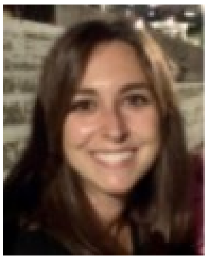

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Enhance

The symposium is organized in two sessions “**conservation biology**” and “**transposable elements**” in organisms. The former aims to understand how genetic biodiversity is crucial for species resilience; the latter focuses on the role of “**transposable elements**” in shaping genomes and regulatory networks to allow species adaptation.

Environmental changes are strongly impacting on our Planet causing loss of biological diversity. Many species have reduced population size and are at risk of extinction. It is now recognized the need to manage and conserve biodiversity resources and geneticists are playing an increasingly important role in this field identifying and monitoring the genetic variability. Indeed, genetic diversity is central to the long-term survival of any species since high levels of genetic variability are determinants of future population/species evolution, adaptation, and resilience. Several molecular markers have been adopted for DNA analyses and recently there is an increasing use of whole-genome sequence given its powerful potential of assessment. All these issues will be part of the session on “conservation biology”.

The Transposable elements session will be dedicated to one of the most fascinating components of eukaryotic genome. These are repetitive elements able to move throughout genome by transposition mechanisms. For a long time, they were considered junk DNA. Nowadays, it is recognized their pivotal role in shaping genomes and regulatory networks allowing species adaptation. Moreover, they create genetic biodiversity that is also crucial for species resilience.

Keynote Speakers

Marco Gerdol, University of Trieste, Department of Life Sciences

Valentina Peona, Swiss Ornithological Institute, Switzerland

CONSERVATION BIOLOGY

Oral presentation,

Chairs: Massimo Milan and Emiliano Trucchi

Using thermal priming to mitigate the lethal effects of marine heatwaves on the Manila clam *Ruditapes philippinarum*

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Abstract

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

Evaluating the risks of interpopulation translocations in critically endangered European mink *Mustela lutreola* L., 1761

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Abstract

The critically endangered European mink *Mustela lutreola* was studied to reassess its genetic diversity using complete mitogenome sequences from 52 individuals across four geographical populations: Russia, Romania, Germany, and France-Spain. Contrary to prior studies indicating genetic homogeneity, the French-Spanish population exhibited significant mitogenomic diversity. High nucleotide and haplotype diversity were found in Russian and captive German populations, suggesting a complex demographic history and potential gene flow. The French-Spanish population displayed high haplotype but low nucleotide diversity, indicative of historical bottlenecks and recent expansion. Limited gene flow and distinct genetic structuring were confirmed through AMOVA, Bayesian clustering, and UPGMA analysis. Two primary haplogroups were identified: Central-Eastern European and Aquitaine-Navarre, suggesting their classification as separate Management Units. Conservation recommendations emphasize the need for active gene pool protection, especially for the genetically diverse Central-Eastern European cluster, while questioning the necessity of supplementing the French-Spanish population given its unexpected genetic diversity.

Ancient DNA reveals historical demographic decline and genetic erosion in the Atlantic bluefin tuna

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Abstract

Overexploitation has depleted fish stocks during the past century, nonetheless its genomic consequences remain poorly understood. Characterising the spatiotemporal patterns of these consequences may provide baseline estimates of past diversity and productivity to aid management targets, help predict future dynamics, and facilitate the identification of evolutionary factors limiting fish population recovery. Here, we evaluate human impacts on the evolution of the iconic Atlantic bluefin tuna (Thunnus thynnus), one of the longest and most intensely exploited marine fishes, with a tremendous cultural and economic importance. We sequenced whole genomes from modern (n=49) and ancient (n=41) specimens dating up to 5000 years ago, uncovering several novel findings. First, we identify temporally stable patterns of population admixture, as bluefin tuna caught off Norway and in the eastern Mediterranean share a greater degree of ancestry with Gulf of Mexico bluefin tuna than western and central Mediterranean bluefin tuna. This suggests that Atlantic spawning areas are important mixing grounds for the genetic diversity of Mediterranean bluefin tuna and that spawning patterns may be more complex than previously understood. We model effective population size to show that Mediterranean bluefin tuna began to undergo a demographic decline by the year 1900 to an extent not observed across the previous millennia. Coinciding with this, we found that heterozygosity and nucleotide diversity was significantly lower in modern (2013-2020), than ancient (pre-1941) Mediterranean bluefin tuna, suggesting bluefin tuna underwent a genetic bottleneck. With this work we show how ancient DNA provides novel perspectives on ecological complexity with the potential to inform the management and conservation of fishes. Our work highlights the importance of incorporating long data-series to understand fish ecology and inform restoration targets, implying that human impacts on the diversity, demography, and dynamics of marine fishes are likely to have begun earlier and be more complex than previously thought.

Genetic characterization of *Staphylococcus aureus* isolates from hedgehogs: understanding wildlife microbial ecology

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Abstract

Hedgehogs are mammals facing various threats, including habitat loss and emerging diseases. *S. aureus* is a bacterium that can be found in hedgehogs, and some strains can cause infections. This study aims to investigate the genetic variability of *S. aureus* isolates from hedgehogs, contributing to the understanding of genetic diversity and species adaptation in wild environments.

A total of 110 swab samples were collected from hedgehogs admitted to a hedgehog rehabilitation center. Swabs were inoculated into Brain Heart Infusion broth supplemented with 6.5% NaCl and incubated. For the isolation of MRSA and *S. aureus*, the inoculum was streaked onto ChromAgar MRSA and Baird-Parker agar. *S. aureus* isolates were subjected to Whole Genome Sequencing, and the antibiotic resistance profile, virulence genes, plasmids, Mobile Genetic Elements (MGEs), and clonal lineages (including MLST, *spa*-typing, *agr*-typing, and SCC*mec* typing) were analyzed.

Out of the 110 samples, 22 *S. aureus* isolates were obtained, including 5 MRSA strains. Among the 5 MRSA isolates, 3 carried the *mec*C gene, while 2 carried the *mec*A gene conferring methicillin resistance. Most strains showed no resistance to any antibiotics but exhibited various antibiotic efflux pumps and a wide range of virulence genes. Regarding MGEs, 16 out of 22 isolates harbored MGEs, which were classified into 4 different types. All isolates, except for 3, carried plasmids. Concerning clonal lineages, a significant diversity of Sequence Types (STs) and *spa*-types was observed. Two *mec*C-MRSA strains belonged to ST130-t842-XI, while one belonged to ST49 and to a new *spa*-type described for the first time in this study. Both *mec*A-MRSA strains belonged to ST8-t711-IVc.

The study found a high prevalence of *S. aureus* in hedgehogs, with some harboring antibiotic-resistant genes and virulence factors. This suggests adaptation to the wild environment and highlights the importance of wildlife health surveillance for understanding the spread of antibiotic-resistant bacteria.

First steps towards the conservation of endemic Italian *Salvia* species through population genomics

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Abstract

Salvia is a common taxon in the collections of botanical gardens due to its long history of medicinal and culinary use across the world. Twenty-five species can be found in the wild in Italy; *S. pratensis* is one of the most common and is closely related to some endemic taxa with debated species rank, defined by some authors as the *S. pratensis* species complex (*S. ceratophylloides, S. saccardiana, S. pratensis* subsp. *haematodes, S. pratensis* subsp. *bertolonii*). We are interested in studying the distribution of genetic diversity in wild populations of *Salvia pratensis* and related taxa to inform species delimitation and define a conservation strategy that can be applied by botanical gardens to conserve genetic variation and resources of, potentially, any *ex-situ* collection. We are characterizing a collection of samples from wild populations of *Salvia* in Italy with Genotyping-By-Sequencing (GBS) to obtain genome-wide genetic variation data. Thanks to a network of collaborators, this collection spans a large portion of the Italian territory and 15 *Salvia* taxa. Preliminary population structure and phylogenomic analyses of 57 samples belonging to 6 different taxa showed some level of divergence between populations of *S. pratensis* and the related taxa, supporting the presence of different endemic species. Moreover, we have sequenced and assembled the genome of *S. pratensis* to use as reference for GBS. In the future, we are going to analyse more than 200 samples to complete the study and integrate the collection with a wider sampling range, potentially including samples from outside of Italy. As a final goal, we would like to identify markers from GBS to barcode species and phylogeographic variation that can be easily produced with Sanger sequencing to facilitate the creation of *ex situ* collections by botanists without genomic expertise.

THE ROLE OF TRANSPOSABLE ELEMENTS

Oral presentation,

Chairs: Irina Arkhipova and Andrea Luchetti

The endogenous promoter of Transposable Elements: a facilitator of horizontal transposon transfer (and beyond)

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Abstract

The importance of transposable elements (TEs) in shaping genomes is widely acknowledged, owing to their ubiquitous presence in nature. The lifecycle of TEs extends beyond the borders of a single species' genome, thanks to their ability to be horizontally transferred into the genome of a new host, even across unrelated species. This mechanism, known as Horizontal Transposon Transfer (HTT), prevents TEs extinction and has been theoretically and experimentally described for many types of TEs. An important and still unanswered question related to HTT concerns how transposition-related genes can be expressed by TEs upon HTT. TE genes are normally expressed by an endogenous promoter that responds to species-specific host transcription factors. However, the species-specificity of the transcriptional machinery represents a major hindrance for TE expansion upon HTT. We have recently characterized a set of TE promoters that we named "blurry promoters". Such promoters provide TEs with the ability to drive transcription when relocated to evolutionarily distant genomic backgrounds. In this context, this emerges as a potential evolutionary adaptation, ensuring at least basal transcriptional levels after horizontal transfer. In the effort to characterize the presence of blurry promoters in the TE realm, we tested the functionality of the promoters in four experimental expression systems using the luciferase-promoter assay. Our results show that the blurry promoters are overrepresented in a few superfamilies of DNA transposons. We have also applied blurry promoters in specific gene expression applications with the aim of developing new gene expression vectors that potentially allow for the expression of selected genes in multiple expression platforms using a single vector. In conclusion, the characterization of blurry promoters significantly advances our understanding of TE biology and enables the development of new gene expression tools with potential biotechnological applications.

Comparing the transposon landscapes of a putative ancient asexual and a sexual non-marine ostracod (Crustacea, Arthropoda)

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Abstract

Ostracods are microscopic, bi-valved crustaceans with the best fossil record of all living arthropods. Their fossil record, starting 400 million years ago, together with a high prevalence of parthenogenetic reproduction and putative ancient asexuality, make non-marine ostracods fascinating evolutionary model organisms. In the absence of high quality ostracod reference genomes, we here compare transposon landscapes between two Illumina genome assemblies from the putative ancient asexual *Darwinula stevensoni* and the fully sexual ostracod *Notodromas monacha*. Both assemblies have around 60,000 contigs, sizes of 360-380 Mb, more than 100X coverage and BUSCO scores of 93 and 94%, respectively. Because homology-based programs are not sensitive enough to detect families of transposable elements (TEs) in species missing from Repbase or Dfam, we used three different pipelines for de novo analyses: REPET, RepeatMasker2 (RM2) and EarlGrey (RM2-based, with automated curation).

TE diversity between the two genomes differs substantially regardless which pipeline was used. The Illumina assembly of *N. monacha* is dominated by LTR retrotransposons (6.5%) with some DNA transposons (3.7%), whereas DNA (15.5%), LINE-like (5.9%) and rolling circle Helitron elements (1.5%) were most abundant in the assembly of *D. stevensoni*. Our results on the dominance of DNA (Tc/mar, hAT) and LINE-like (CR1, RTE) TEs in *D. stevensoni* parallel earlier findings from a partial genomic library, and differ from those of other asexuals. TE copies with a low number of nucleotide substitutions are only observed with REPET ("L" shape landscape) in both genomes.

Although the presented results may underestimate TE abundance, they indicate pronounced differences of the transposon landscapes and diversity between these two ostracod species. Analysis of related species should determine whether the differences are correlated with the reproductive mode or are lineage specific. We are currently curating TEs in an Oxford Nanopore draft assembly of *D. stevensoni* to further confirm our initial results.

Transposable elements: architects of novel satellite DNA organization and origins of numerous satellite DNA sequences

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Abstract

Repetitive DNA sequences, such as transposable elements (TEs) and satellite DNAs (satDNAs), constitute significant parts of eukaryotic genomes. These sequences are acknowledged as important factors in genome architecture, and drivers of its evolution. By employing different experimental and bioinformatic methods, we have determined that oysters have unique traits that promote them as useful organisms in studying repetitive DNA sequences. We found that the heterochromatin of the Pacific oyster *Crassostrea gigas* is extremely scarce and predominantly constituted of DNA transposons. In *C. gigas* we have also observed novel organizational form of satDNA arrays, which are interspersed genome-wide, and lack association with heterochromatin, differing from the conventional concepts. This novel organizational pattern was shown to be caused by strong connection of satDNAs with TEs, especially Helitrons. In continuation, we have characterized the satellitomes of five additional oysters from the Ostreidae family, revealing not only a substantial number of satDNAs per genome (33 - 61), but also peculiarities in their composition. Numerous satDNAs were either associated to or derived from TEs, displaying a scarcity of TE-unrelated satDNAs in these genomes. Due to the non-conventional satellitome constitution and dominance of Helitron-associated satDNAs, comparative satellitomics demanded more in-depth analyses than standardly employed. Importantly, evaluating the satDNA “library model” highlighted the necessity to adjust this term when studying tandem repeat evolution in organisms with such constitution of the satellitomes. Therefore, when repetitive sequences with potential variation in the organizational form and repeat-type affiliation are examined across related species, we proposed the introduction of the term “repetitive DNA library”, encompassing both “satDNA library” and “TE library”.

Statistical patterns in the distribution of transposable elements in teleost genomes

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Abstract

Transposons or transposable elements (TEs) are selfish genetic elements, which can jump from one genomic locus to another and increase their copy number by exploiting host resources. Because the chromosome is a limited resource and occupying transcriptionally active genetic regions benefits the TEs to increase their copy number, there could be a conflict of interest among various types of TEs and the functional genes of the host to occupy same genomic loci. This conflict and the multilevel selection acting on the organism can lead to interesting patterns in distribution of TEs in the intra and intergenic regions of the chromosome. In the current study we explore the statistical patterns in the distribution of TEs, with respect to each other and with respect to the various genic regions of the host, to understand how the potential conflict of interests are resolved. We annotated complete genomes of representative fish species of the infraclass Teleostei using Extensive de-novo TE Annotator pipeline. Only structurally intact active TEs were extracted from the annotations and newly developed scripts were used to understand their distribution in the chromosomes of the fishes. Structurally active TEs occupied about 2 to 10% of the fish genomes. There was a significant positive linear relationship between the chromosome size and the number of transposons as well as cumulative size of the transposons. However, the slope of the lines was significantly different for different species, suggesting variation in the nature of conflict and its resolution in different species. Distribution of more than half of TEs overlapped with various genomic regions. Although more than half of the TEs occupied mRNA regions, most were found in introns, while only a very few overlapped with CDS. Our study provides interesting new insights on the maintenance of genomic integrity in the presence of selfish genetic elements.

Search for dispersed repeats in bacterial genomes

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Abstract

We have developed a de novo method for the identification of dispersed repeats based on the use of random position-weight matrices (PWMs) and an iterative procedure (IP) [1]. The created algorithm (IP method) allows detection of dispersed repeats for which the average number of substitutions between any two repeats per nucleotide (x) is less than or equal to 1.5. IP method made it possible to detect families of dispersed repeats in bacterial genomes which have not been previously reported. We applied this method to find dispersed repeats in the genomes of E. coli and 39 other bacterial phyla and could identify some repeat families comprising over 103 repeats with lengths between 400 and 600 bases. Moreover, each bacteria contains only one family of dispersed repeats. In E. coli, the identified repeat family occupy more than 50% of the genome. The number of copies is over 5x103 copies and the average repeat length is approximately 540 base pairs. Such extensive repeat family could not be detected in the E. coli genome by using the RED, RECON, or Repeat_masker programs but only by the IP method, which could find de novo repeat families with $x \le 1.5$, whereas all other programs could do it with $x \le 1.0$. The identified family of repeats is weakly similar and rather represents a specific motif that is superimposed on the coding sequences. Since family of dispersed repeats we found not only in the genome of E. coli but also in 39 bacteria from different phyla, it is also possible that the detected families of repeats could be involved in the creation of the liquid crystal structure within bacterial DNA through interactions between repeats within a family.

[1] Korotkov, E.; Suvorova, Y.; Kostenko, D.; Korotkova, M. Int. J. Mol. Sci. 2023, 24, 10964. https://doi.org/10.3390/ijms241310964

Transposable elements in the genome of Triatominae (Hemiptera: Reduviidae), Chagas disease vectors.

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Abstract

Chagas disease is a neglected disease from Latin America, affecting 6-7 million people worldwide and transmitted by haematophagous insects of the subfamily Triatominae. In the absence of vaccines, the reduction of disease incidence depends mainly on vector control. An accurate taxonomic identification and knowledge about the genome biology of these insects are keys to ensuring successful vector control campaigns. Triatominae comprise more than 150 species, being the Triatoma genus the most numerous with about 90 species. Repeated DNA sequences analysis are scarce in Triatominae. Hitherto, only mobile DNA of the first assembled genome species, Rhodnius prolixus is properly described. Hence a descriptive approach about transposable element landscape is mandatory within this subfamily, as well as their relative species. Nowadays, the rising of bioinformatic tools designed to characterize repetitive sequences, and the democratization of Next Generation Sequencing platforms, combine for a propitious scenario. Here, several species from different lineages from the early splitting tribes Triatomini and Rhodniini, were analyzed, showing that Triatominae genomes are extremely different. Proportions within genomes and variability regarding superfamilies revealed the diverse pathways suffered by Triatominae species genomes. However, the extended study on the unexplored Triatomini tribe reveled the importance of class II elements in the whole Triatominae subfamily.

POSTERS
Conservation biology

Integrated taxonomic approach for the study of endangered chondrichthyans species in the Mediterranean Sea

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Abstract

Sharks and rays are ecologically important taxa influencing community and ecosystem processes. Nevertheless, elasmobranchs suffer the ongoing and rapid declines in their populations being a susceptible resource to overfishing, for their biological characteristic (k-selected strategy). Indeed, to date about 40 species of Mediterranean chondrichthyans are included in the International Union for Conservation of Nature (IUCN) Red List due to their endangered status. The correct species identification of rare elasmobranchs is crucial to the management of their conservation status, mainly in consideration of the morphological similarity existing between congeneric species that makes difficult to discriminate specific diagnostic characters. The aim of the present investigation is to implement an integrated taxonomic approach (morphological and molecular) to verify the species identity of two rare and vulnerable specimen recently caught by local fishermen along the Italian coasts of the Mediterranean: the angel shark and the butterfly ray. The morphological identification was coupled and then validated by DNA barcoding based on Cytochrome Oxidase I sequences (COI). Both the morphological and molecular approaches confirmed the presence of the sawback angel shark, *Squatina aculeata* Cuvier, 1829 (critically endangered) in the Ionian Sea and of the spiny butterfly ray*, Gymnura altavela* (Linnaeus, 1758) (endangered) in the Sardinian waters. The sawback angel shark is locally extinct within the Mediterranean basin and need international cooperation for advancing in their conservation. The spiny butterfly ray has been affected by a dramatic reduction in population size due to overexploitation and bycatch fishing (in the Mediterranean Sea it is considered critically endangered). The new records of these species shed light on their local distribution promoting more effective conservation efforts in the basin. Furthermore, the new COI sequences obtained in our study highlight the importance of the integrated approach for species identification and increase the molecular dataset useful for future phylogenetic molecular studies.

New molecular insights on Mediterranean blue crab *Callinectes sapidus* Rathbun, 1896

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Abstract

The blue crab (*Callinectes sapidus* Rathbun, 1896) is an ecologically significant portunid crab native to the western Atlantic Ocean. In recent decades, and especially in last years, it has emerged as a highly invasive species in European coastal waters. This species is omnivorous, aggressive, large-bodied (carapace width can exceed 18 cm), highly mobile, shows high fecundity (egg mass can contain up to 8 milion eggs), and, moreover, is eurythermal and euryhaline. It, therefore, poses considerable ecological and economic threats to new colonized marine ecosystems. Our study presents a comprehensive population genetics analysis of blue crab populations across its range, spanning from its native waters to the recently colonized European territories of Italy and Turkey. Using a combination of mitochondrial DNA sequencing, molecular phylogenetics, and Darwinian selection analyses, we investigated population genetics among invasive blue crab populations in the Mediterranean Sea. Our aim is to reconstruct colonization history, current trends, and genetic structure of this invasive species, as well as highlighting patterns of positive selection across the OXPHOS mitochondrial gene complex.

Results from Maximum Likelihood and Bayesian inferences agree on the presence of a distinct cluster featuring solely Italian blue crabs, with the exception of two specimens found to be paired to a Turkish sample. Further analyses investigating evolutionary patterns at both site and branch level (MEME and FUBAR) revealed one codon out of the 207 analysed (position 191) to be under pervasive positive selection, while three were found to be under episodic Darwinian selection (71, 191, 207). These results add to the few existing data on the genetic structure on the blue crab in the Mediterranean basin and confirm a low connectivity between the Sicilian population and the other ones. Understanding the dispersal pattern of the blue crab populations is necessary to develop effective management strategies to mitigate the impacts of blue crab invasions on invaded ecosystems and associated fishing and aquaculture activities.

Wildlife monitoring in a coastal site of Natura 2000 network: a tool for habitat and species conservation

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Abstract

SAC IT7228221 Foce Trigno-Marina di Petacciato is a N2K site situated in Molise (Italy), along the central Adriatic coast. It hosts the pilot study site of the LIFEPLAN project, which aims to improve knowledge on biodiversity using big-data from approximately 200 monitoring sites around the world. To analyze the faunistic biodiversity in the site, we used an image dataset from the camera traps. The camera traps were installed in a square plot (100x100 m) with five sampling points, and were active for 233 days from February to December 2021, producing a total of 2953 wildlife pictures.

We calculated the Relative Abundance Index (RAI) for the total observations for each recorded species, each season, daily phase, and for two habitats found in the pilot site (EU habitat 2270* Coastal Pinewood and EU habitats 2230/2260 mosaic of maquis and annual grassland).

We identified 21 animal species belonging to 2 taxonomic classes, 8 orders, and 16 families, with 780 individuals observed.

The most abundant species observed was the wild boar *Sus scrofa*, followed by the common red fox *Vulpes vulpes*, the domestic cat *Felis catus*, the common wood pigeon *Columba palumbus*, the Eurasian magpie *Pica pica*, and the Eurasian jay *Garrulus glandarus*. We also recorded two species of EU conservation importance, the gray wolf (*Canis lupus lupus*) and the crested porcupine (*Hystrix cristata*). Abundance for the season peaked in spring, then gradually decreased in summer and autumn, and then dropped in winter. The analysis of the daily phases showed a high abundance during the day, and lower values for sunrise, sunset, and night. As for the analysis of RAI values per EU habitat for all species, we recorded the highest values statistically significant for the habitat mosaic 2230/2260, showing that the open environments of back dune areas were more frequented than wooded areas.

POSTERS
The role of Transposable Elements

Evaluation of transposable elements activity in *Xenopus laevis* focusing on subgenomes in six developmental stages

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Abstract

Transposable elements (TEs) play a key role as genome remodelers (e.g. contributing to genome size and influencing chromosomal rearrangements). Moreover, TEs are known to generate new coding genes and regulatory elements increasing genetic and epigenetic variability. These changes represent a substrate on which natural selection acts upon leading to advantageous functions that might help organisms to respond to stressful environmental conditions. Amphibians, especially *Xenopus* species, are valuable models in different fields such as developmental, cell biology, ecology, environmental health, and biological diversity. Interestingly, the African clawed frog *X. laevis* exhibits an uncommon polyploidy condition, rare in vertebrates, that consists in a tetraploid karyotype. This kind of chromosome set originated from two diploid progenitor species approximately 17-18 million years ago, causing the formation of the L (long chromosome) and the S (short chromosome) subgenomes. In the *X. laevis* TEs constitute a significant portion with about 30% of the genome. In accordance with these premises, we investigated the TE repertoire in *X. laevis* subgenomes in transcriptomes of six different developmental stages (zygote, blastula, gastrula, neurula, tailbud, and early tailbud). In particular, the highest TE transcriptional levels were recorded in blastula and DNA transposons represented the major impact followed by LINE and LTR retroelements. Analyzing the subgenome-specific TE elements, we identified 368 and 109 TEs in the L and S subgenomes, respectively. Regarding the total TE transcriptional contribution, higher values of these specific elements were identified in the L subgenome compared to the S subgenome. Moreover, in the former, the analyses showed a prevalence of DNA transposons and LINE retroelements in zygote and early tailbud while DNA transposons and LTR retroelements dominated the developmental stages from blastula to tailbud. Regarding the transcriptional impact of TEs specific of the S subgenome, DNA transposons dominated zygote, neurula, and early tailbud stages, LINE retroelements blastula and tailbud stages, and LTR retroelements gastrula stage. Finally, the Kimura landscapes showed differences in the age of these TEs. Overall, investigating TE activity at both genome and transcriptome levels might deepen our knowledge on the role played by the repetitive fraction in adaptive and evolutionary processes.

Tissue-specific response of transposable elements to temperature stress in the Antarctic fish *Trematomus bernacchii*

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Abstract

Genome architecture is deeply influenced by Transposable elements (TEs) activity. Through their ability to migrate from one location to another, TEs are one of the main responsible of genomic plasticity. This distinctive feature contributes to biological evolution and adaptation to environmental changes. Climate changes affect the whole world, as in Antarctica, where the suborder Notothenioidei dominate the fish fauna in terms of number of species and biomass. *Trematomus,* due to its peculiar characteristics, is one of the most studied genera belonging to Notothenioidei. It was very interesting to investigate the effects that the increase in temperature can cause in this species. We analyzed the available RNA-Seq data obtained from specimens exposed at two different temperatures, -0.9 °C and 0.6 °C, for three different period of exposition (six hours, seven days, and twenty days). The aim was to investigate the transcriptional activity of TEs and genes encoding for proteins involved in their silencing mechanisms in two different tissues (gill and brain). Our findings highlighted a variation in TE transcriptional activity in the two analysed tissues as consequence of the temperature stress. A remarkable upregulation of TEs in the six hours and seven days periods was observed. On the contrary, a stabilization of the TE transcriptional values was observed for the twenty days of exposition. Moreover, the transcriptional analysis of genes encoding proteins involved in TE silencing such as heterochromatin formation, the NuRD complex, and *argonaute* family highlighted their activity in both tissues with a prompter response in the brain. Overall, our findings suggested that *T. bernacchii* can adapt to temperature changes in less than twenty days corroborating the idea that TEs represent a promising molecular tool for species adaptation.

A comprehensive study of transposable elements transcriptional contribution across six zebrafish developmental stages

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Abstract

Transposable elements (TEs), well known as “jumping genes”, are essential in shaping genomic evolution and regulating gene expression. They represent a noteworthy portion of the eukaryotic genome. They can migrate within genomes influencing their size, generating new genes, and contributing to chromosome rearrangements. TE activity changes during different developmental stages, in relation to epigenetic modifications. *Danio rerio*, commonly known as zebrafish, has been extensively studied owing to its importance as a model organism across diverse fields of biology such as developmental biology, genetics, neuroscience, and toxicology. TEs in zebrafish represent a significant portion of its genome of about 55%. In the present study, the transcriptional TE contribution was evaluated during zebrafish development, analyzing six different developmental stages (zygote, blastula, gastrula, somitogenesis, pharyngula, and larvae), focusing on the different types of TE classes. In particular, an intriguing behaviour of LTR retroelements characterized the TE repertoire from gastrula to larvae stages and among them, a significant considerable impact was due to *DIRS* elements and ERVs. These results might help us to get a holistic view of the impact of TEs during animal development.