

The role of waterbirds in the functioning and services of the Venice Lagoon ecosystem.

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The Venice Lagoon is vital for waterbird biodiversity in Europe, hosting many breeding and wintering species. Yet, their ecological role in the Lagoon is unexplored, with rare studies on few species' feeding strategy or habitat use, despite the recent increase in total bird abundance and species, also including invasive ones. Clarifying the ecological role of waterbirds is crucial to understand the relationship between biodiversity, ecosystem functions and services, and to implement sustainable coastal management: birds not only depend on wetlands but impact them too. This project will quantify the ecological role of selected waterbird species in the Lagoon, by assessing their use of space (also including areas outside of the Lagoon such as agricultural fields, landfills, rivers, and other wetlands), diet (with direct observation and pellet analysis), as well as their impact on nutrient cycles (analyzing excreta) and saltmarsh soils and plants (through manipulative experiments, e.g. on trampling and bioturbation). The project will also analyze the impact of waterbirds on aquaculture and lagoon fisheries, and design and test measures to mitigate possible waterbird conflicts with these local economic activities.

Fighting extinction using genomic tools.

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Increasing anthropogenic pressures have substantially accelerated the decline of wild animal populations with possible severe consequences for long-term species survival due to environmental and demographic stochastic events, negative effects of reduced genetic diversity and adaptability to changing environments. Thus, maintaining genetic diversity is crucial for the preservation of species. However, because of limited empirical data, the genomic consequences of rapid population decline remain largely unexplored. The project aims to apply whole genome and transcriptome sequencing approaches to species of the Italian endemic ichthyofauna, at high risk of extinction and with high evolutionary interest. The genomic and transcriptomic information will integrate the classical population genetics approaches currently in progress with standard genetic markers.

Biological signals of anthropogenic environmental changes: integrating museums and dissemination into contemporary scientific research.

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In marine ecosystems, species interactions may modify the impact of environmental stressors, such as seawater acidification, warming and pollution. Potential beneficial effects of macrophytes on the associated fauna under multiple-stressor conditions will be investigated by the PhD student in both laboratory and field experiments. In this context, physiological, behavioural and reproductive performances of the studied species will be assessed. Data obtained during the research carried out by the PhD student in both the Department of Biology and in the Hydrobiological Station of the University of Padova will be disseminated at the Darwin Dohrn Museum (DaDoM) & Historic Archive of the Department of Marine Animal Conservation and Public Engagement (Stazione Zoologica Anton Dohrn of Naples), where the PhD student will spend a period of 6 months. Moreover, the PhD student will work for 6 more months in a foreign laboratory within established collaborations.

Fine-scale interpolation of Eurasian genetic components across time and space.

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The established field of human paleogenomics yielded thousands of ancient genomes worldwide. At least 10.000 are readily available today through the Allen Ancient DNA Resource, and thousands more are expected to be released. Recent analyses have unveiled several genetic signatures that characterized the major population movements across Eurasia with a coarse resolution in space and time, bundling together several events already known to the scientific community of archaeologists and historians. The current project proposes to dissect all available ancient human genomes into their key ancestry components and, along with their geographical and chronological coordinates, to produce a spatial and temporal interpolation of such components. This interpolation will constitute a crucial resource for at least two main purposes: 1) it will provide a prediction for the genetic makeup of any historical or prehistoric society of interest – with a measurable reliability dictated by the distance in the time and space from the nearest actually available genome; 2) it will offer a way to observe and dissect local deviations from the expected smooth transitioning from one ancestry component to another, hence inferring previously undetected

demic events which will then be interpreted in light of the available evidence from the material culture archaeological records.

Live cool, live long? Exploring longevity and ageing in Antarctic fish.

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The Southern Ocean is dominated by the in-situ radiation of highly specialized and geographically restricted Antarctic fish of the suborder Notothenioidei. In this project, we would like to focus on the large disparity in longevity (maximum age, tmax) within these Antarctic fish to begin understanding why some notothenioid species can live more than 60 years, yet others can live less than 7 years. This project has two objectives: 1) Phylogenetical reconstruction of the evolution of longevity in notothenioids to assess if increased longevity evolved just once or multiple times across their phylogeny. 2) Identification of candidate “longevity genes” that share convergent selection signals within long-lived notothenioids vs. short-lived notothenioids. These genes will represent prime candidates for future complementary studies investigating potentially causal associations with longevity and ageing via proteomics, transcriptomics and epigenetic analysis. The PhD student will collaborate with different research groups that work jointly with Prof. Chiara Papetti: Prof. Michael Matschiner (University of Oslo), Prof. Kevin Bilyk (Montclair State University) and Prof. Lisa Chakrabarti (University of Nottingham). The prospective PhD student should be fluent in English, able to work in team, with a MSc in the Biological field and with some knowledge of and interest in bioinformatics for genomics.

Mate choice, sexual selection, and chooser fitness in tropical livebearing fishes.

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What good is mate choice? The direct and indirect costs and benefits of mate choice remain poorly understood, as do the population-level effects of sexual selection. Which elements of mate choice and sexual competition enhance or harm individual survival, population persistence, and adaptation to a changing world? This project tests these questions on guppies in the laboratory in Padova and/or swordtails at the CICHAZ field station in central Mexico, using genomic and behavioral approaches.

Environmental DNA and RNA approaches to monitor biodiversity of the Adriatic Sea.

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Environmental DNA (eDNA) metabarcoding is an emerging tool for assessing biodiversity and understanding spatial and temporal community patterns and processes, directly from sequencing of DNA obtained by environmental samples such as air, water and sediments. Despite its attractiveness, the eDNA application is complex and involves multiple steps from field sampling design, lab work, and bioinformatics analyses with the robustness of results strictly linked to adequate experimental and modeling methods, accounting for spatiotemporal variation, uncertainty in eDNA collection, and imperfect detection. In addition, recent studies showed that environmental RNA (eRNA), which is only produced by living organisms, can also be collected from environmental samples, and it can be used for metabarcoding and characterization of metabolically active communities. This project will apply eDNA/eRNA to long term monitoring of the vertebrate and invertebrate communities at selected coastal sites in the Adriatic Sea. The project will involve field work, laboratory work and bioinformatic analysis and it will be performed in an existing collaboration network aimed at developing methodological advancements to monitor biodiversity changes at the ecosystem/seascape level. The ideal candidate should be interested both in the development/application of molecular tools than in bioinformatic/statistical analysis of data; previous experience with eDNA approaches will be appreciated. The PhD student will join an expanding group, dealing with eDNA tools, and will collaborate with other PhD students in Italy and abroad working on the same topic.