My research experience has revolved around understanding how biological and environmental processes within and among populations or species have produced biodiversity and adaptations, and how to preserve them.

From nucleotides to satellite imagery: approaches to identify and manage the invasive pathogen *Xylella fastidiosa* and its insect vectors in Europe

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Biological invasions represent some of the most severe threats to local communities and ecosystems. Among invasive species, the vector-borne pathogen *Xylella fastidiosa* is responsible for a wide variety of plant diseases and has profound environmental, social and economic impacts. Once restricted to the Americas, it has recently invaded Europe, where multiple dramatic outbreaks have highlighted critical challenges for its management. Here, we review the most recent advances on the identification, distribution and management of *X. fastidiosa* and its insect vectors in Europe through genetic and spatial ecology methodologies. We underline the most important theoretical and technological gaps that remain to be bridged. Challenges and future research directions are discussed in the light of improving our understanding of this invasive species, its vectors and host–pathogen interactions. We highlight the need of including different, complimentary outlooks in integrated frameworks to substantially improve our knowledge on invasive processes and optimize resources allocation. We provide an overview of genetic, spatial ecology and integrated approaches that will aid successful and sustainable management of one of the most dangerous threats to European agriculture and ecosystems.

Diving into divergence: differentiation in swimming performances, physiology and gene expression between locally adapted sympatric cichlid fishes

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Sympatric speciation occurs without geographical barriers and is thought to often be driven by ecological specialization of individuals that eventually diverge genetically and phenotypically. Distinct morphologies between sympatric populations occupying different niches have been interpreted as such differentiating adaptive phenotypes, yet differences in performance and thus likely adaptiveness between them were rarely tested. Here, we investigated if divergent body shapes of two sympatric crater lake cichlid species from Nicaragua, one being a shore-associated (benthic) species while the other prefers the open water zones (limnetic), affect cruising (U$_{crit}$) and sprinting (U$_{sprint}$) swimming abilities – performances particularly relevant to their respective lifestyles. Furthermore, we investigated species differences in oxygen consumption (MO$_2$) across different swimming speeds and compare gene expression in gills and white muscle at rest and during exercise. We found a superior cruising swimming ability in the limnetic *Amphilophus zaliosus* compared to the benthic *Amphilophus astorquii*, while sprinting was not different, suggesting that their distinct morphologies affect swimming performance. Increased cruising swimming ability in *A. zaliosus* was linked to a higher oxygen demand during activity (but not rest), indicating different metabolic rates during exercise - a hypothesis supported by coinciding gene expression patterns of gill transcriptomes. We identified differentially
expressed genes linked to swimming physiology, regulation of swimming behaviour and oxygen intake. A combination of physiological and morphological differences may thus underlie adaptations to these species' distinct niches. This complex ecological specialization probably resulted in morphological and physiological trade-offs that contributed to the rapid establishment and maintenance of divergence with gene flow.

A comprehensive overview of the developmental basis and adaptive significance of a textbook polymorphism: head asymmetry in the cichlid fish Perissodus microlepis
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Identifying the evolutionary and developmental basis of adaptive phenotypes is a central interest in evolutionary biology. Cichlid fishes have been a useful research model due to their extraordinary phenotypic diversity reflecting adaptations to often very narrow niches. Among them, the scale-eating *Perissodus microlepis* is considered to be a textbook example for balanced polymorphism: its asymmetric head and handed behavior is thought to be maintained by negative frequency-dependent selection via prey-predator interactions. However, several contradictory findings and open questions have emerged in recent years, challenging our understanding of this model. Here, we review existing evidence for both genetic and non-genetic effects influencing head asymmetry, the association between morphological asymmetry and behavioral laterality, and the identification of signatures of balancing selection. Recent technological and theoretical developments have opened new exciting research avenues that can help identifying the drivers of adaptive traits in *P. microlepis* and other non-model organisms, and we discuss promising directions worth exploring. We highlight the importance of using integrative approaches that analyze genetic, environmental and epigenetic variation in natural populations to aid a comprehensive understanding of why cichlids are so diverse and how evolution has produced and continues to generate such a vibrant and often complex phenotypic diversity.

Gene(s) and individual feeding behavior: exploring eco-evolutionary dynamics underlying left-right asymmetry in the scale-eating cichlid fish *Perissodus microlepis*
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The scale-eating cichlid fish *Perissodus microlepis* is a textbook example for bilateral asymmetry due to its left or right-bending heads and of negative frequency-dependent selection that is proposed to maintain this stable polymorphism. The mechanisms that underlie this asymmetry remain elusive. Several studies had initially postulated a simple genetic basis for this trait, but this explanation has been questioned, particularly by reports observing a unimodal distribution of mouth shapes. We hypothesize that this unimodal distribution might be due to a combination of genetic and phenotypically plastic components. Here we expanded on previous work by investigating a formerly identified candidate SNP associated to mouth laterality, documenting inter-individual variation in feeding preference using stable isotope analyses, and testing their association with mouth asymmetry. Our results suggest that this polymorphism is influenced by both a polygenic basis and inter-individual non-genetic variation, possibly due to feeding experience, individual specialization and intra-specific competition. We introduce a hypothesis potentially explaining the simultaneous maintenance of left, right, asymmetric and symmetric mouth phenotypes due to the interaction between diverse eco-evolutionary dynamics including niche specialization or construction. Future studies will have to further tease apart the relative
Morphological and genetic correlates in the left-right asymmetric scale-eating cichlid fish of Lake Tanganyika
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The stable polymorphism in mouth asymmetry in the cichlid fish *Perissodus microlepis* is a textbook example of adaptive evolution accomplished by functionally-relevant morphological changes, ecological specialization and negative frequency-dependent selection. Knowledge about the morphological and developmental basis of this stable polymorphism, as well as the mechanisms driving intra-specific variation in this fish remain largely incomplete. Here, we focus on often neglected – but potentially important – aspects of the biology of this fish. In particular, we explored patterns of body shape variation, neutral genome-wide genetic diversity across its geographic distribution, and the presence of asymmetry in eyes centroid size in relation to mouth bending angle. Geographic space (or a factor associated to geography) has a significant effect on both morphological and genetic diversity suggesting restricted gene flow across the range of this species. We discuss potential implications of these observed patterns, including the possibility that the genetic basis of asymmetry could vary among locations. A significant association between eye and mouth laterality suggests that the entire head might be involved in the asymmetry. These findings highlight that head asymmetry in *P. microlepis* is a complex polymorphism involving the interaction of the genetic basis of multiple potentially independent traits and the environment.

Towards understanding the genetic basis of mouth asymmetry in the scale-eating cichlid *Perissodus microlepis*

How polymorphisms consisting in left–right asymmetries are produced and maintained in natural populations is a tantalizing question, which remains largely unanswered. The scale-eating cichlid fish *Perissodus microlepis* is a remarkable example of extreme ecological specialization achieved by morphological and behavioural laterality. Its asymmetric mouth is accompanied by a pronounced lateralized foraging behaviour, where a left-bending morph preferentially feeds on the scales of the right side of its prey, while the opposite is true for the right morph. This striking asymmetry made this fish a textbook example of the astounding degree of ecological specialization and negative frequency-dependent selection. Yet, the genetic basis underlying this spectacular laterality remains unknown. We addressed this question through analyses of wild-caught fish using high-throughput DNA sequencing data. A novel array of SNP markers was developed by ddRAD sequencing (ddRADseq) and the use of pooled DNA samples (PoolSeq). We obtained more than 155 000 SNPs using ddRADseq and 3 900 000 SNPs with PoolSeq. Among these, we identified one (ddRAD) SNP, and 38 or 378 (PoolSeq) windows that are differentiated between the left and right morphs accounting for spurious associations due to geographic structuring. This allowed us to uncover candidate genomic regions that potentially contain genes for this trait. Then, this interesting trait has a genetic basis that is likely to be influenced by multiple loci. This result contributes to a greater understanding of the genetic bases of left–right asymmetry and, ultimately, the evolutionary processes governing the maintenance of this striking case of laterality.
Established empirical cases of sympatric speciation are scarce, although there is an increasing consensus that sympatric speciation might be more common than previously thought. Midas cichlid fish are one of the few substantiated cases of sympatric speciation, and they formed repeated radiations in crater lakes. In contrast, in the same environment, such radiation patterns have not been observed in other species of cichlids and other families of fish. We analyze morphological and genetic variation in a cichlid species (*Archocentrus centrarchus*) that co-inhabits several crater lakes with the Midas species complex. In particular, we analyze variation in body and pharyngeal jaw shape (two ecologically important traits in sympatrically divergent Midas cichlids) and relate that to genetic variation in mitochondrial control region and microsatellites. Using these four datasets, we analyze variation between and within two Nicaraguan lakes: a crater lake where multiple Midas cichlids have been described and a lake where the source population lives. We do not observe any within-lake clustering consistent across morphological traits and genetic markers, suggesting the absence of sympatric divergence in *A. centrarchus*. Genetic differentiation between lakes was low and morphological divergence absent. Such morphological similarity between lakes is found not only in average morphology, but also when analyzing covariation between traits and degree of morphospace occupation. A combined analysis of the mitochondrial control region in *A. centrarchus* and Midas cichlids suggests that a difference between lineages in the timing of crater lake colonization cannot be invoked as an explanation for the difference in their levels of diversification. In light of our results, *A. centrarchus* represents the ideal candidate to study the genomic differences between these two lineages that might explain why some lineages are more likely to speciate and diverge in sympathy than others.

Biogeography investigates spatial patterns of species distribution. Discontinuities in species distribution are identified as boundaries between biogeographic areas. Do these boundaries affect genetic connectivity? To address this question of primary importance for conservation efforts, for the first time we applied a multi-species and multi-factorial hierarchical sampling design to explore phylogeography and historical demography of five marine benthic invertebrates across two of the major marine biogeographic boundaries in the central Mediterranean Sea (Ligurian-Tyrrhenian and Ionian-Adriatic). Our comparative approach did not support the presence of barriers to gene flow across these two biogeographic boundaries; however, we observed genetic differentiation between these two regions. Our findings suggest that the combined effects of past and present biological, demographic, oceanographic and geological processes influenced genetic structuring in these five species. These results highlight the importance of explicitly considering spatial scale and biological features when evaluating genetic patterns, and contribute to our understanding of the biogeography of the benthic
fauna along the Italian rocky shores. This information is crucial for proper coastal management and for the implementation of marine protected areas (MPAs) networks, and constitute the baseline for a future “Ecosystem-Based” management of the Italian biodiversity.

**Genetic diversity and differentiation in bluefin tuna (*Thunnus thynnus*): analysis of variation in space and time in the Mediterranean populations with neutral mitochondrial and microsatellites loci.**

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Fishery genetics have greatly changed our understanding of population dynamics and structuring in marine fish. In this study, we focused on the Mediterranean Bluefin tuna (*Thunnus thynnus*), a top-predator exhibiting highly migratory behaviour, large population size, and high potential for dispersal during early life stages. This fish is an ecologically and economically important species but has been severely impacted by overfishing. Information on population dynamics, genetic structuring and levels of genetic diversity in this species is still scarce yet it is crucial for both stock management and conservation of marine ecosystems dominated by these apex predators. To fill this gap, we compared genetic and demographic variation across the Mediterranean Sea using seven microsatellite loci and the mitochondrial *D-loop* sequence. We showed that this fish displays significant genetic differences over space and time, both at the fine and large scales of variation. Thus, this fish does not present a single panmictic population in the Mediterranean Sea, with important implications for stock management. We observed a significant demographic decline, although these populations are still not severely reduced in their evolutionary potential. However, it can increase the vulnerability of this economically important species to overexploitation or ecosystem changes. This study increases our understanding of spatial and temporal genetic diversity in this important marine species and suggests strategies for stock management and conservation of evolutionary potential in a severely exploited fishery resource.

*equal contribution*