The Ecosystem and Landscape Evolution Lab is looking for
MASTER STUDENTS

for the development of a new capture-based eDNA method to improve monitoring of marine fishes

Environmental DNA (eDNA) metabarcoding is increasingly used in marine habitats to monitor biodiversity. It relies on the isolation of DNA released from organisms in the environment and subsequent sequencing to detect the presence of species in an ecosystem of interest. Multiple applications of eDNA metabarcoding in marine ecosystems validate its effectiveness in apprehending useful ecological information about taxa, notably teleost fishes. So far, metabarcoding involves polymerase chain reaction (PCR) amplification of a single specific gene region. However, the taxonomic resolution (i.e., how good the region is in distinguishing species) can be limited and hinder species-level identification. Furthermore, the degraded nature of eDNA and the significant amount of microbial DNA can hamper PCR amplification and subsequent sequencing.

Target capture – or hybridization capture – can overcome those limitations related to single gene metabarcoding and circumvent the issues related to PCR amplification. Hybrid-capture uses RNA or DNA baits designed to bind to specific DNA regions of interest. This technique enables retrieving the sequences of very short DNA fragments and reduces the overall sequencing cost by increasing the amount of DNA of the targeted species group. It can also target multiple gene regions, which could highly improve the taxonomic resolution of eDNA analysis.

This master project is part of a broader project aiming to improve the monitoring of marine fish species across the globe to predict better the potential impact of climate change on their distribution. You will collaborate in developing and testing a new multi-gene target capture lab protocol. Such a protocol should significantly improve the detection of fish species in eDNA marine samples, notably endangered or rare fish species. During this project, you will learn innovative lab protocols, gain some knowledge related to bioinformatic analysis of genetic data, and ultimately learn how to use such data to monitor species' biodiversity.

Useful references

Foster et al. 2021 https://www.frontiersin.org/articles/10.3389/fevo.2021.735744/full
Lemmon & Lemmon 2013 https://www.annualreviews.org/doi/10.1146/annurev-ecolsys-110512-135822
Stat et al. 2017 https://www.nature.com/articles/s41598-017-12501-5
Garlapati et al. 2019 http://link.springer.com/10.1007/s11157-019-09501-4

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