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Conference Abstract

GAPeDNA: Assessing and mapping global species gaps in genetic databases for metabarcoding studies

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Abstract

Environmental DNA metabarcoding has recently emerged as a non-invasive tool for aquatic biodiversity inventories, frequently surpassing traditional methods for detecting a wide range of taxa in most habitats. One of the major limitations currently impairing the large-scale application of DNA-based inventories, such as eDNA or bulk-sample analysis is the lack of species sequences available in public genetic databases. These gaps are still largely unknown spatially and taxonomically for most regions of the world, which can hinder targeted future sequencing efforts. We propose GAPeDNA, a user-friendly web-interface (Fig. 1) that provides a global overview of genetic database completeness for a given taxon across space and conservation status. As an initial application, we synthetized data from regional checklists for marine and freshwater fishes along with their IUCN conservation status to provide global maps of species coverage using the European Nucleotide Archive public reference database for 19 metabarcoding primers. This tool automatizes the scanning of gaps in these databases to guide future sequencing efforts and support the deployment of DNA-based inventories at larger scale. It is flexible and can

be expanded to other taxa and primers upon data availability. Using our global fish case study, we show that gaps increase toward the tropics where species diversity and the number of threatened species were the highest. It highlights priority areas for fish sequencing like the Congo, the Mekong and the Mississippi freshwater basins which host more than 60 non-sequenced threatened fish species. For marine fishes, the Caribbean and East Africa host up to 42 non-sequenced threatened species. As an open-acces, updatable and flexible tool, GAPeDNA can be used to evaluate the completeness of sequence reference libraries of various markers and for any taxonomic group.

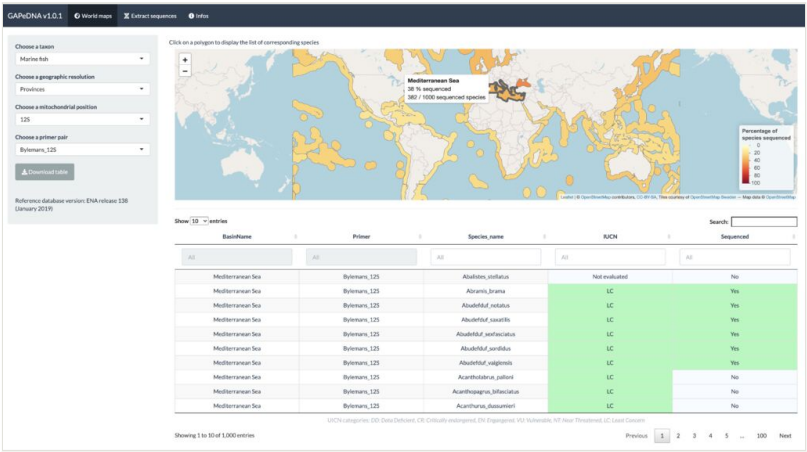

Figure 1. doi

Screenshot of the GAPeDNA web-application, developped with R shiny

Keywords

genetic markers, shiny, marine and freshwater fish, threatened species, IUCN, non-indigenous species, environmental DNA, reference database

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