NEMO TOOLS

Next-generation monitoring
& mapping tools
to assess marine
ecosystems & biodiversity

Deliverable D2.3

An integrated atlas of OTU-based taxa of the different biocommunities

Greece 2.0
NATIONAL RECOVERY AND RESILIENCE PLAN

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	01/08/2025	1st Draft	S. Genitsaris	C. Gubili
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Executive Summary

Deliverable 2.3 is connected to Task 2.2 of WP2. This deliverable provides the taxa retrieved by the approaches described in D2.1 and D2.2. These taxa belong to a large diversity of higher taxonomic groups (Classes) spanning bacteria, protists, and metazoa, including invertebrates and fishes. The deliverable is based on the three fasta databases clustered at >97 % similarity levels into Operational Taxonomic Units (OTUs), submitted in Milestone M2.3, after bioinformatic curation to exclude errors and chimeras (see steps described in D2.2). The next deliverable of the WP2 includes ecological and statistical analyses of the eDNA datasets to understand best practices on sampling and analyses pipelines, and to retrieve spatial taxonomic and functional alpha and beta-biodiversity patterns.

Beyond the scope of the NEMO-Tools project, to further the impact of the project's outputs beyond the duration of the project a reference and classification eDNA database is published in the project's site (https://nemotools-project.com/the-nemo-tools-greek-coastal-database/) where all data are open and available for downloading. The NT (NEMO-Tools) Greek Coastal database aims to gather curated and taxonomically annotated eDNA sequences produced from several different genetic markets targeting marine biodiversity from bacteria and protists to metazoa. The curated eDNA reads produced within NEMO-Tools serves as a base to update the inventory of sequences from past projects that the NEMO-Tools partners were involved from Greek coastal areas into an exhaustive eDNA atlas of Greek marine biodiversity spanning from prokaryotes to larger fish. This way, marine biodiversity researchers can use a focused reference database to Greek marine ecosystems leading to more accurate taxonomic assessment of their datasets.

All data and files produced as outcomes for this deliverable are accompanying this document.

TABLE OF CONTENTS

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TABLE 1 NAMES AND ROLES OF CONTRIBUTORS TO THIS DELIVERABLE.

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D2.3 Approach

In D2.3, we analyzed raw read datasets produced from the high-throughput sequencing of 4 different genetic markers (16S rRNA gene, 18S rRNA gene, 12S rRNA gene and COI), targeting on retrieving the deep diversity of prokaryotic communities, unicellular eukaryotes and some metazoa, and fish and other metazoa, respectively (see D2.2) After bioinformatics, analytically described in D2.2, several fasta files were produced, from which three [M2.3_12S OTUs (Fishes), M2.3_16S OTUs (Prokaryotes), M2.3_18S OTUs (Eukaryotes)] constituted the basis (Milestones) to generate an integrated and thorough Atlas (Species list) of bacteria, protists, metazoa, and fishes, that were retrieved from the NEMO-Tools samplings and are part of the deep Greek coastal biodiversity.

Beyond the scope of the deliverable and the described objectives of the WP2, we used these datasets as a base to construct the first taxonomic database of microbes and fishes of Greek coasts and we made the V.1 of the database public through the project's website (https://nemotools-project.com/the-nemo-tools-greek-coastal-database/) These databases are curated be used with Mothur software (D2.2) for taxonomic comparisons of raw sequencing reads of other projects, under the same principles of widely used similar databases, such as NCBI, PR2 and SILVA. The V1 of the database will be enriched with more curated reads with taxonomic annotations from past and future projects. The overarvhing aim is to create the first comprehensive eDNA database of Greek marine biodiversity.

Attached file: D.2.3_An integrated atlas of OTU-based taxa of the different biocommunities.xlsx