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The Ocean Gene Atlas: exploring the biogeography of plankton genes online

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ABSTRACT

The Ocean Gene Atlas is a web service to explore the biogeography of genes from marine planktonic organisms. It allows users to query protein or nucleotide sequences against global ocean reference gene catalogs. With just one click, the abundance and location of target sequences are visualized on world maps as well as their taxonomic distribution. Interactive results panels allow for adjusting cutoffs for alignment quality and displaying the abundances of genes in the context of environmental features (temperature, nutrients, etc.) measured at the time of sampling. The ease of use enables non-bioinformaticians to explore quantitative and contextualized information on genes of interest in the global ocean ecosystem. Currently the Ocean Gene Atlas is deployed with (i) the Ocean Microbial Reference Gene Catalog (OM-RGC) comprising 40 million non-redundant mostly prokaryotic gene sequences associated with both Tara Oceans and Global Ocean Sampling (GOS) gene abundances and (ii) the Marine Atlas of Tara Ocean Unigenes (MATOU) composed of >116 million eukaryote unigenes. Additional datasets will be added upon availability of further marine environmental datasets that provide the required complement of sequence assemblies, raw reads and contextual environmental parameters. Ocean Gene Atlas is a freely-available web service at: http://tara-oceans.mio.osupytheas.fr/ocean-gene-atlas/.

INTRODUCTION

Marine plankton provide essential ecosystemic functions on the planet: at the basis of the ocean food web, they contribute about half of global primary production (1). Plankton are also key players of biogeochemical cycles in the ocean and drive the biological carbon pump (2). Due to their large distribution (oceans represent 71% of the Earth surface) and their substantial biogeochemical roles, plankton are considered to be main actors in the global climate regulation (3) and also constitute a potential source of innovations for blue biotechnology (4). Because of the difficulties associated with sampling plankton in the open and deep ocean, and because of the ultra high throughput required to sequence the genetic makeup of such complex communities, environmental genomics resources for these elusive organisms have only become available recently (reviewed by (5)). The first large scale sequencing of marine microorganisms led by the Global Ocean Sampling expedition (6) produced a 6.1 million gene catalog mostly from sunlit ocean prokaryotes.

More recently, the Tara Oceans pan-oceanic expedition deployed a holistic sampling of plankton ranging in size from viruses to fish larvae, coupled with comprehensive in situ biogeochemical measurements which provide the detailed environmental contexts necessary for ecological interpretation of marine microbiomes (7). Two complementary genescats have been released so far from the Tara Oceans sequencing effort: (i) the Ocean Microbial Reference Gene Catalog (OM-RGC) and (ii) the Marine Atlas of Tara Oceans Unigenes (MATOU). The OM-RGC is a comprehensive collection of 40 million genes from viruses, prokaryotes and picoeukaryotes with a size up to 3 μm (8) retrieved from public marine plankton metagenomes and reference genomes. The MATOU is a catalog of 116 million unigenes.

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obtained from poly-A+ cDNA sequencing of different filter size fractions ranging from 0.8 to 2000 µm (9). About half of the unigenes have a predicted taxonomic assignation representing genes from >8000 mostly eukaryotic organisms. Such environmental genomics datasets are increasingly used in marine biology, ecology and evolutionary studies to understand the mechanisms by which genes influence phenotype in the wild. In parallel to the holistic systems biology approaches that tackle these datasets as a whole, biologists also frequently apply reductionist approaches that target specific marker genes known or hypothesized to play a role in processes such as metabolic pathways, biotic and abiotic interactions. Testing such candidate marker gene hypotheses requires detailed analyses of voluminous genomic data in their precise environmental context, a task which requires extensive expertise in interrogating heterogeneous data types (i.e. sequencing reads, assemblies, genes together with their taxonomic and functional annotations, environmental variables) to provide integrated interpretations. In order to allow biologists to easily mine such large and complex datasets without the requirement for either significant hardware or programming skills, we make freely available a web service to visualize the geolocalized abundances of taxonomically annotated plankton genes in the context of environmental features.

**INTERFACE AND FUNCTIONALITY**

The Ocean Gene Atlas (OGA) web service provides a submission interface to collect a nucleic or protein sequence query, it then executes data mining procedures on dedicated high performance hardware, and returns interactive result panels for data exploration (Figure 1). A user manual and two case study example sequences are provided online.

**The query submission interface**

The user-provided query (Figure 1A) may be a nucleotide or amino acid sequence in FASTA format, or a hidden Markov model profile (HMM; 10). Users can search for sequences similar to their query in either one of two marine gene catalogues (Figure 1B): the OM-RGC (8) or the MATOU (9). Users can select different methods to identify sequence similarity (Figure 1C) depending on the type of query (nucleotide/amino acid sequence or HMM) and the user preferred trade-off between accuracy and speed of the
search (11). For protein sequence queries, similarity search tools are BLASTP (12) and Diamond (13). For nucleotide sequence queries, users can choose to carry out the similarity search against a nucleotide database (BLASTN), or to translate the nucleotide query to search against a protein database (BLASTX, DIAMOND BLASTX). For more sensitive sequence similarity searches, users can provide an HMM profile file instead of a FASTA sequence (either pre-built, e.g. by Pfam (14), or custom-built from protein alignments using the hmmer package, http://hmmer.org). Pre-built Pfam HMM profiles are also searchable from the OGA submission form by simply filling the corresponding field with the Pfam accession ID. For both sequence similarity and HMM searches, the e-value threshold may be customized (Figure 1D), as well as the number of interactive panels in the results page (Figure 1E). The email field (Figure 1F) is strictly optional since a bookmarkable URL for the results is immediately provided to the user upon submission. Results are usually returned to the user within 30 seconds, but for slower queries (e.g. HMM searches against the larger MATOU catalog which may take up to several minutes or longer in cases of high affluence), the user can choose to provide an email address in order to be notified when results are available (Figure 1F). Results will remain available for 15 days on the OGA web server.

The interactive result panels

The quantitative distribution of environmental sequences presenting similarities to the user query are displayed in three interactive panels: geographic distribution (Figure 2A), co-variation with environmental features (Figure 2B), and taxonomic distribution (Figure 2C). Furthermore, the underlying data necessary to build the figures can be downloaded as tab delimited flat files for further analysis outside of OGA (Figure 2D): list of similarity search hits and corresponding FASTA formatted sequences, gene per sample abundance matrix, as well as contextual environmental features for each sample. The set of similarity search hits that are included in the three interactive panels can be interactively filtered by click-and-drag adjustment of the E-value threshold directly over the provided E-value distribution histogram. The world maps of Figure 2A display quan-
Gene abundances

The abundance of each catalog gene in specific biosamples was estimated by evaluating the coverage of raw sequencing reads mapped to the gene's nucleotide sequence. Tara Oceans sequencing reads from 243 metagenomes corresponding to the smallest size fractions (0–0.22, 0.1–0.22, 0.22–0.45, 0.45–0.8, 0.22–1.6 and 0.22–3 μm) and GOS reads from 38 metagenomes (from two size fractions, 0.1–0.8 and 0.8–3 μm, 6) were mapped onto OM-RGC, whilst the reads from 441 metatranscriptomes corresponding to the largest size fractions (0.8–5, 5–20, 20–180 and 180–2000 μm) were mapped onto MATOU. When OM-RGC is queried, abundance estimates may be expressed in one of two available normalization schemes: (i) the gene’s read coverage is divided by the sum of the total gene coverages for the sample (‘percent of total genes per sample’), or (ii) the gene’s read coverage is divided by the median of the coverages of a set of 10 universal single copy marker genes (‘average copies per cell’) that were previously benchmarked for their suitability for metagenomics data analysis (17). MATOU gene abundance estimates are expressed as gene read coverage computed in RPKM (Reads Per Kilobase covered per Million of mapped reads) divided by the sum of the total gene coverages for the sample (‘percent of total genes per sample’).

Environmental context

For Tara oceans biosamples, contextual environmental parameters are linked to the sequence datasets via barcodes assigned to each Tara Oceans sample (18). These metadata serve to geo-localize the samples and provide biogeochemical characteristics of the sampled seawater. Environmental parameters used by the OGA web service are obtained from PANGAEA (https://doi.org/10.1594/PANGAEA.875582), the open access library which archives and distributes georeferenced data from earth system research. For GOS biosamples, environmental data was extracted manually from Table 1 of Rusch et al. (6). The environmental parameters provided by OGA (Figure 3) are either classical oceanographic measures obtained in situ (e.g. depth, salinity, temperature, oxygen, chlorophyll a, etc.) or mesoscales features estimated from oceanographic models and remote satellite observations (e.g. nutrient concentration at 5m depth or net primary production). Estimated values are indicated by a star in the drop-down menu of bubble plot panels (Figure 2C). Descriptions of the environmental parameters available in OGA as well as corresponding PANGAEA hyperlinks are provided in the ‘OGA user manual’ hyperlinked from the OGA results page.

IMPLEMENTATION

The Ocean Gene Atlas web server is implemented through a classical Model-View-Controller pattern architecture using the Laravel 5.4 PHP framework. Developed on the GNU/Linux, the application server communicates with the user through an Apache HTTP server using HTML5, CSS3, Javascript and AJAX to retrieve user requests and display results. The PHP application server queries abun-
Figure 3. *Tara* oceans data sources for the the Ocean Gene Atlas workflow. Field campaigns (blue) have collected plankton biosamples and measured *in situ* environmental parameters. The OGA web server (yellow) combines heterogeneous data published by distinct archives (pink): EBI ENA for sequencing reads, published articles companion websites for gene catalogs and taxonomic annotations, PANGAEA for contextual environmental data. For GOS, metadata was manually extracted from table 1 of Rusch *et al.* (6).

CASE STUDY

Upon phosphorus deficiency, bacterioplankton have established a widespread strategy of replacing membrane phospholipids with alternative non-phosphorus lipids. Sebastián *et al.* (19) have shown that this response is conserved among diverse marine heterotrophic bacteria. Several experiments of mutagenesis and complementation have then confirmed the roles of the phospholipase C (PlcP) and a glycosyltransferase in lipid modelling. Analyses of metagenome datasets such as GOS and *Tara* Oceans have confirmed that PlcP is abundant in low phosphate concentrations areas. We reproduced the analysis of Sebastián *et al.* (19) using OGA to verify that the web service conforms to the published results. We used the same phospholipase C (EAQ46983) as a BLASTP query sequence with the author’s e-value threshold of $10^{-40}$ to search for similar sequences in the OM-RGC catalog (the same metagenome dataset used by Sebastián *et al.*). The 952 PlcP hits identified showed higher abundances in Mediterranean subsurface samples (Figure 4A) related to low phosphorus concentration (Figure 4B) and mostly originated from Proteobacteria and Bacteroidetes (Figure 4C), which agrees with the previously published interpretations of Sebastián *et al.* that marine heterotrophic bacteria display reduced phosphorus requirements upon phosphorus deficiency by PlcP-mediated replacement of membrane phospholipids by alternative non-phosphorus lipids.
Figure 4. Phospholipase C (PlcP) biogeography produced by the Ocean Gene Atlas web service. (A) Abundance of PlcP hits in the OM-RGC subsurface samples. (B) Bubble plot of the PlcP abundance in relation to PO₄ concentrations; DCM: Deep Chlorophyll Maximum layer, SRF: subsurface and MES: mesopelagic zone. (C) Krona plot of the taxonomic distribution of the PlcP hits.

**CONCLUSION/PERSPECTIVES**

By hiding the complex and time consuming integration of heterogeneous data sources behind a user-friendly minimalist web form, the Ocean Gene Atlas web server has the potential to broaden the access to the rapidly accumulating environmental marine genomics datasets. Enabling marine biologists to mine such data—without specific high performance hardware or programming skills—is one of the keys to extract knowledge and understanding from these valuable but underexploited resources. With the current first release of OGA, users can search by sequence similarity genes and proteins in two of the largest marine gene catalogs representing all three eukaryotic, prokaryotic and viral lineages. These two first catalogs will be periodically updated as further marine environmental genomics databases are publicly released. The prerequisites for inclusion in OGA are the availability of the three core resources: gene sequence catalogs, gene abundance estimates in biosamples, and geolocalized environmental context of biosamples. Leveraging the total 2100 Tara Oceans biosamples sequenced so far (20), our short term roadmap is to (i) extend the Tara Oceans datasets by including further sampling sites from the Tara Polar Circle expedition, (ii) complement the eukaryotic MATOU metatranscriptome catalog with corresponding metagenomic abundances and (iii) complement the OM-RGC with prokaryotic metatranscriptomes.

In addition, we envisage adding the increasingly available pangenomes relevant to the marine biome, such as the large scale *Prochlorococcus* metapangenome (21). Such target OGA datasets would allow users with the powerful option to focus queries to their pangenome of interest, in order to track their species specific distribution across the world oceans.

We also plan to complement the current MATOU metatranscriptomes and OM-RGC metagenomes Ocean Gene Atlas results panels with corresponding barcoding based taxonomic profiles (e.g. Krona plots) available for 18S eukaryotic (22) and 16S prokaryotic rRNA genes (8,23). One limitation of the current OGA analyses is that pairwise sequence comparisons with uncultured fragmented microbial community genomes naturally impede fine grained taxonomic interpretations. Two alternatives may be considered to mitigate this shortcoming: (i) phylogenetic tree inference using the subset of full length environmental sequence hits aligned with known reference sequences and (ii) phylogenetic mapping on reference trees of all hits, including partial sequences. Both approaches are being actively pursued but compared to the well established and computationally efficient pairwise alignments, these still present conceptual and algorithmic challenges before being applicable to (semi) automatic online on-the-fly computation.
DATA AVAILABILITY

Ocean Gene Atlas is a freely-available web service at: http://tara-oceans.mio.osupytheas.fr/ocean-gene-atlas/
Source code is available at: https://github.com/hingamp/oga
Shotgun sequences are available at the European Nucleotide Archive (ENA, https://www.ebi.ac.uk/ena) under accession number PRJEB402 (OM-RGC), PRJEB6609 (MATOU) and PRJNA13694 (GOS). The predicted genes from the OM-RGC are available at ENA under the accession numbers ERZ096909 to ERZ097151, and the genes from the OM-RGC and MATOU are available at ENA under accession numbers PRJEB6609 to PRJEB6707 and the predicted genes from the MATOU are available at ENA under accession numbers ERZ096909 to ERZ097151. All MATOU resources are available at http://www.genoscope.cns.fr/tara/.

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