

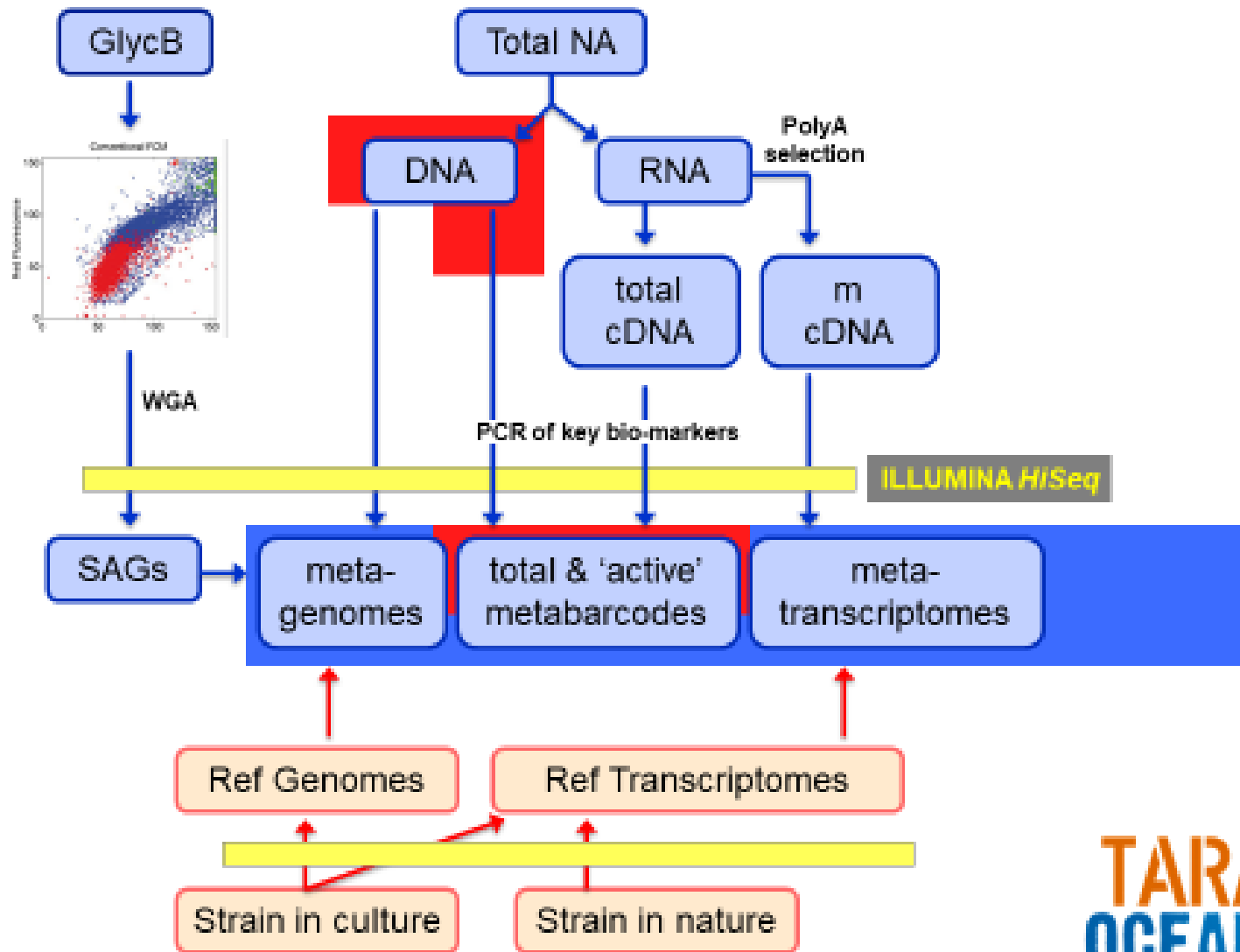
ADN et ARN environnementaux : découverte et fonctions

Patrick Wincker, Genoscope, CEA



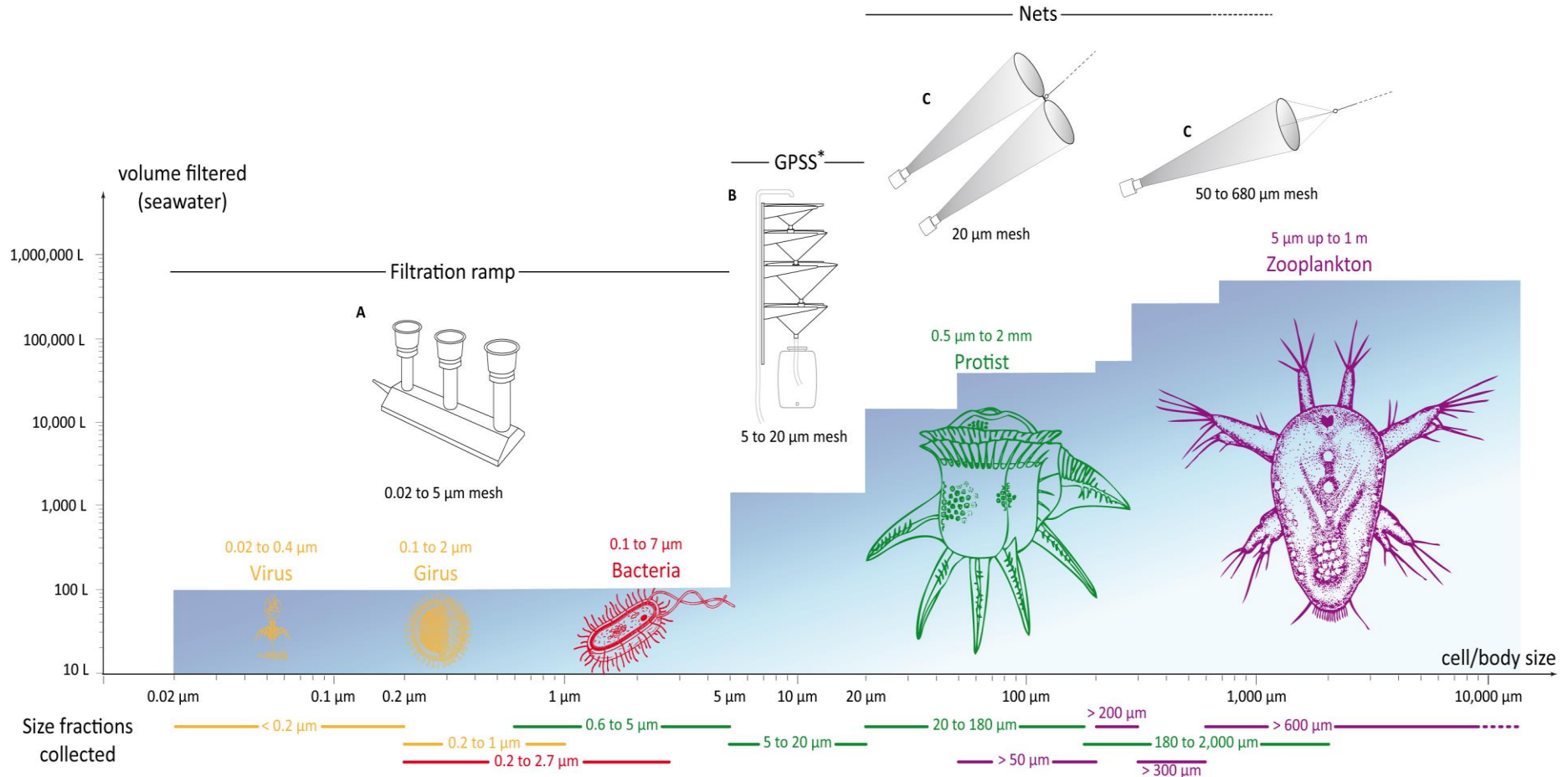
L'ADN (ADNe) et l'ARN (ARNe) environnementaux :
marqueurs du vivant dans les écosystèmes, 28/09/2023

Principles



TARA
OCEANS

Collection and Processing of Seawater

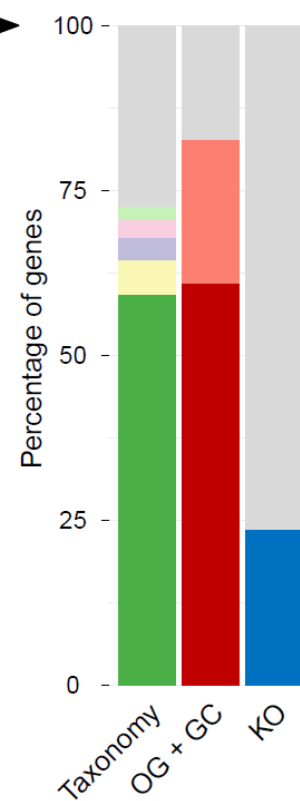
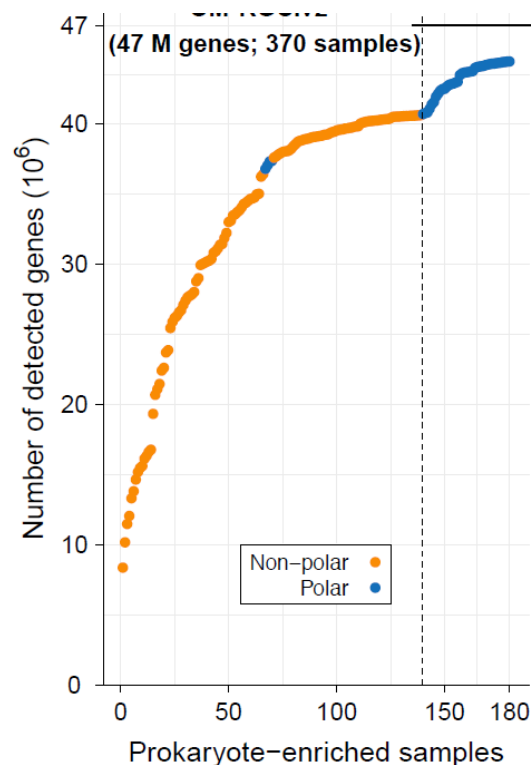
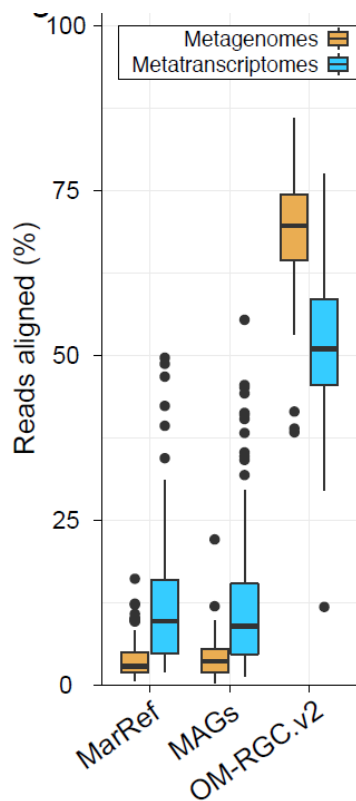


Méthodes

DNA : Gene collections and MAGs



Prokaryote-centered gene collection OM-RGC.v2



Taxonomy

- No annotation (27.48%)
- Archaea (2.03%)
- Eukaryota (2.61%)
- LUCA (3.36%)
- Viruses (5.26%)
- Bacteria (59.26%)

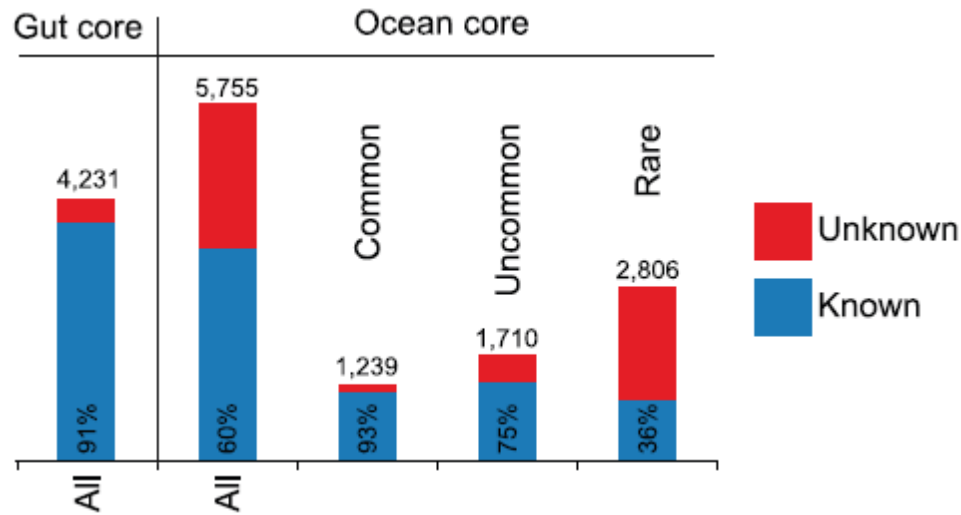
OG + GC

- No annotation (17.26%)
- GC (Gene Clusters, 21.8%)
- OG (eggNOG, 60.94%)

KO

- No annotation (76.41%)
- KO (KEGG 23.59%)

A large proportion of new genes

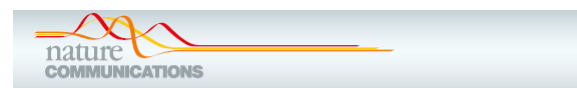


Prokaryote gene set

OCEAN PLANKTON

Structure and function of the global ocean microbiome

Shinichi Sunagawa,^{1,4,†} Luis Pedro Coelho,^{1*} Samuel Chaffron,^{2,3,4*} Jens Roat Kultima,¹ Karine Labadie,⁵ Guillem Salazar,⁶ Bardya Djahanshiri,¹ Georg Zeller,¹ Daniel R. Mende,¹ Adriana Alberti,⁵ Francisco M. Cornejo-Castillo,⁶ Paul I. Costea,¹ Corinne Cruand,⁵ Francesco d'Ovidio,⁷ Stefan Engelen,⁸ Isabel Ferrera,⁶ Josep M. Gasol,⁶ Lionel Guidi,^{8,9} Falk Hildebrand,¹ Florian Kokoszka,^{10,11} Cyrille Lepoint,¹² Gipsi Lima-Mendez,^{2,3,4} Julie Poulain,² Bonnie T. Poulos,¹³ Marta Royo-Llonch,⁶ Hugo Sarmiento,^{4,14} Sara Vieira-Silva,^{2,3,4} Céline Dimier,^{10,15,16} Marc Picheral,^{8,9} Sarah Seaton,^{8,9} Stefanie Kandel-Lewis,^{1,17} Tara Oceans coordinators; Chris Bowler,¹⁰ Colomán de Vargas,^{15,16} Gabriel Gorsky,^{8,9} Nigel Grimsley,^{18,19} Pascal Hingamp,¹² Daniele Iudicone,²⁰ Olivier Jaillon,^{5,21,22} Fabrice Not,^{15,16} Hiroyuki Ogata,²³ Stéphane Pesant,^{24,25} Sabrina Speich,^{26,27} Lars Stemann,^{8,9} Matthew B. Sullivan,^{10*} Jean Weissenbach,^{5,21,22} Patrick Wincker,^{5,21,22} Eric Karsenti,^{10,17,†} Jeroen Raes,^{2,3,4,†} Sílvia G. Acinas,^{6,†} Peer Bork,^{1,28,†}



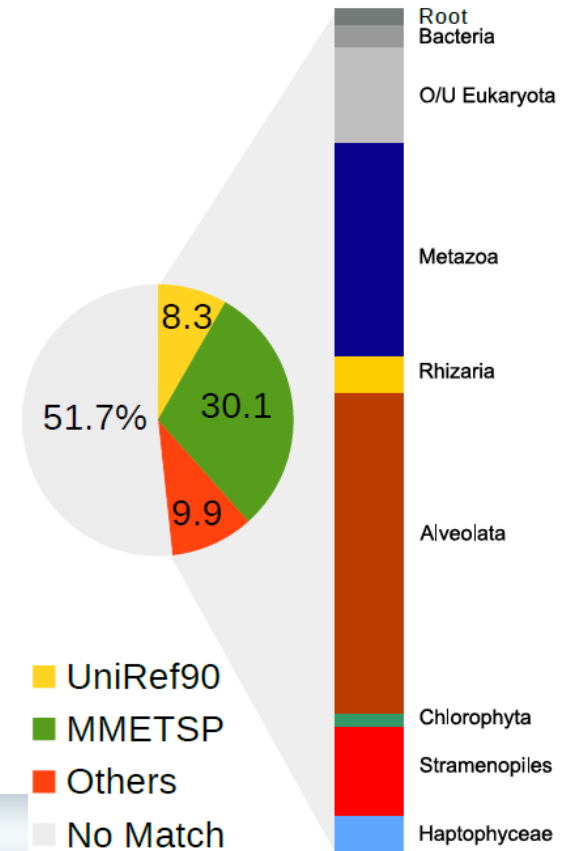
ARTICLE

DOI: 10.1038/s41467-017-02342-4

OPEN

A global ocean atlas of eukaryotic genes

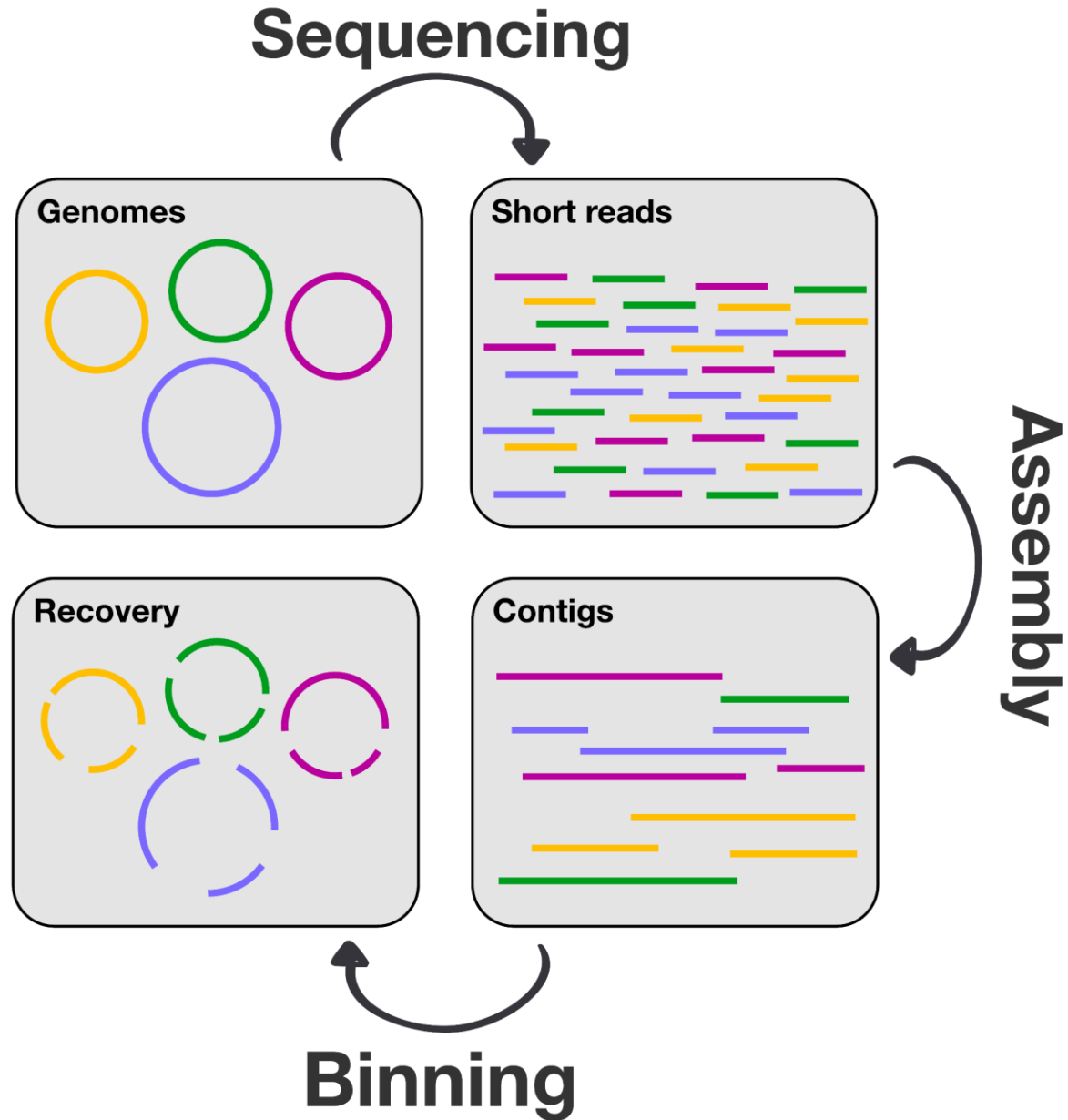
Quentin Carradec et al.[†]



Eukaryote gene set



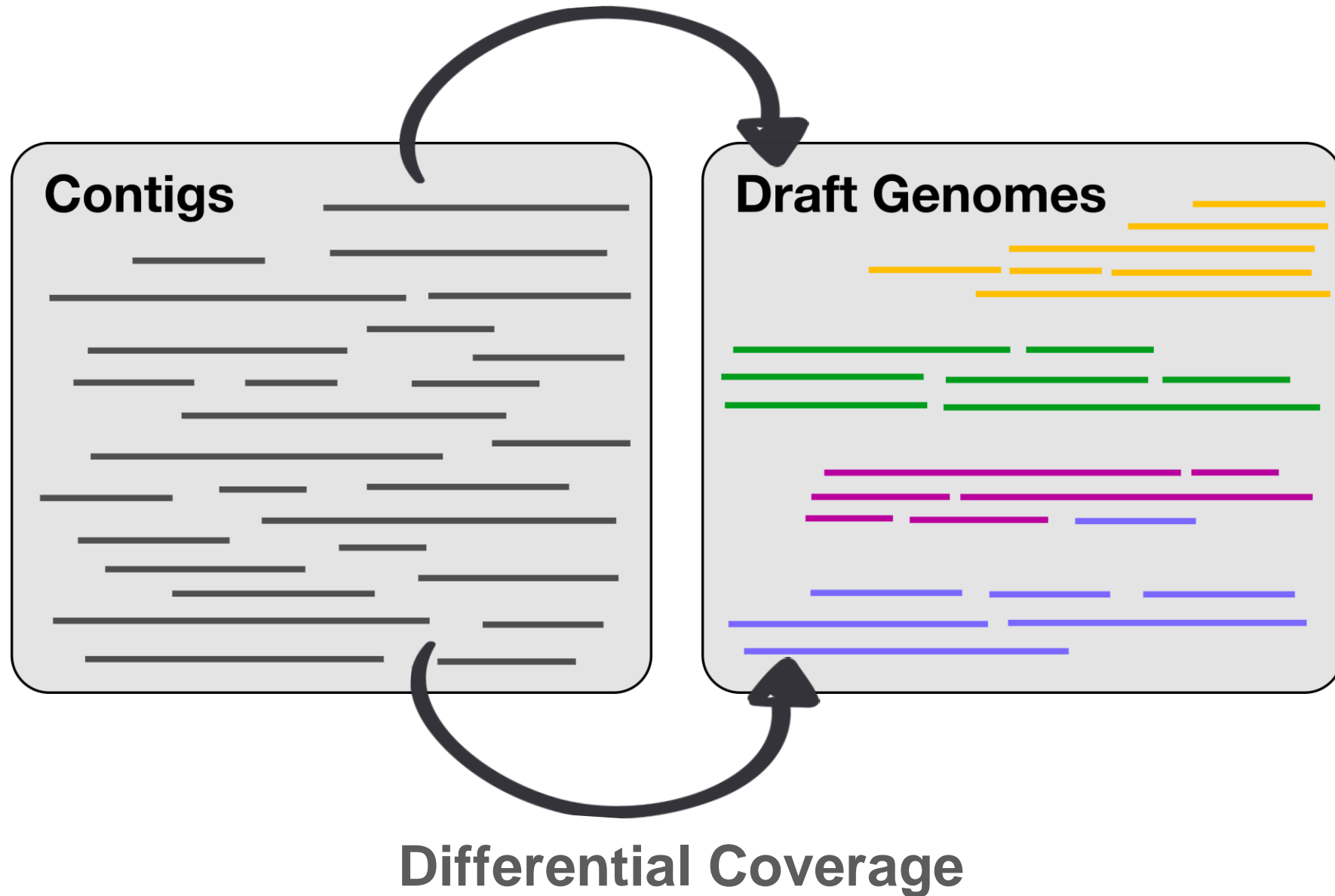
Genome-resolved metagenomics

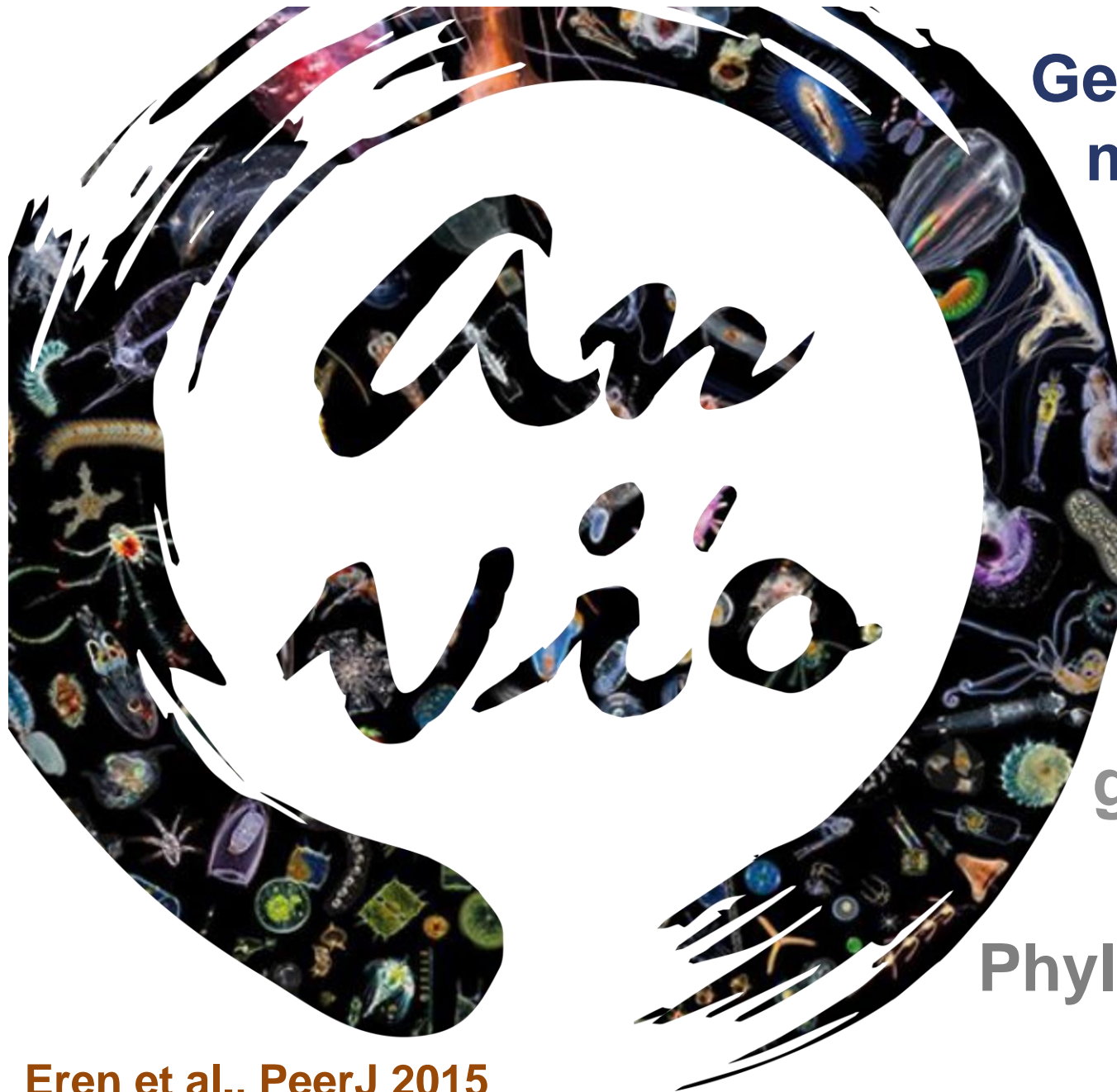


Genome-resolved metagenomics



Genomic signatures





**Genome-resolved
metagenomics**

**Population
genetics**

**Comparative
genomics**

Phylogenomics

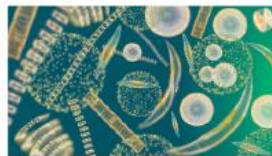
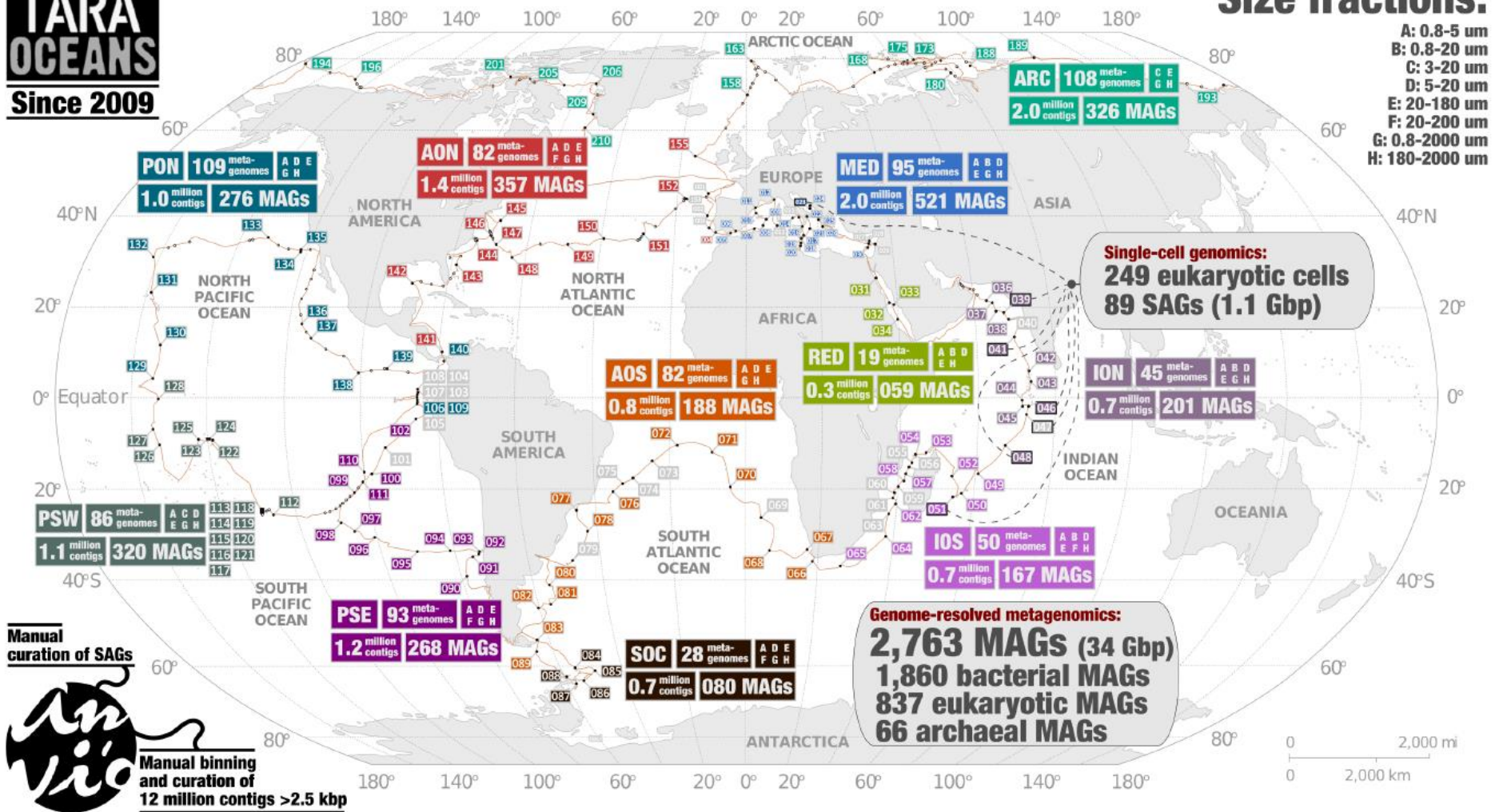
Eren et al., PeerJ 2015

Eren et al., Nature Microbiology 2021

Nearly one thousand eukaryotic MAGs and SAGs



TARA OCEANS
Since 2009

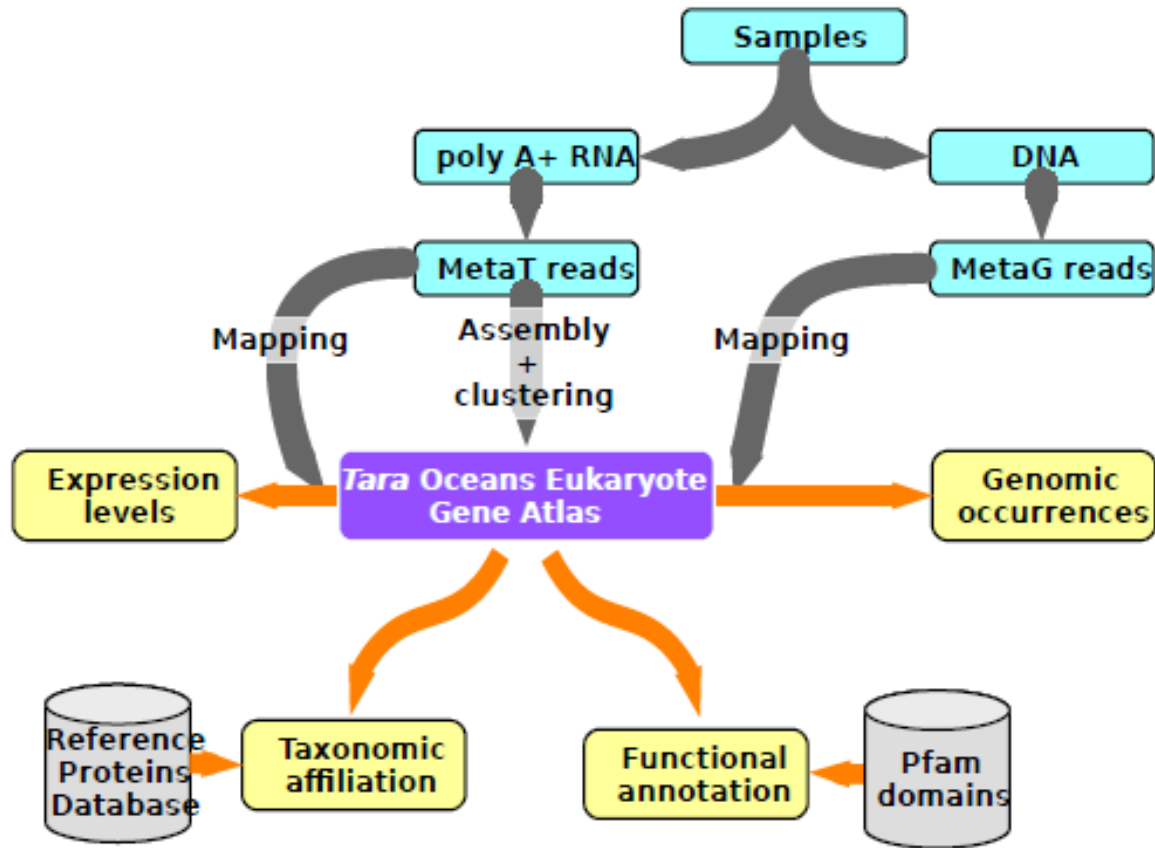


Méthodes

RNA : Transcript collections, RNA genomes and
Metagenome-assembled Transcriptomes



Building a gene catalog for ocean eukaryotes through metatranscriptomics



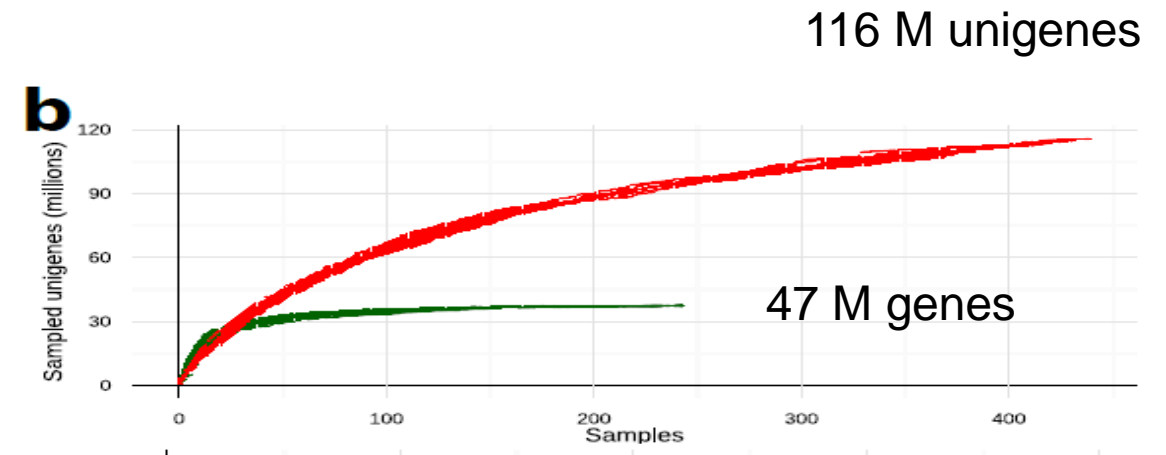
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DOI: 10.1038/s41467-017-02342-1

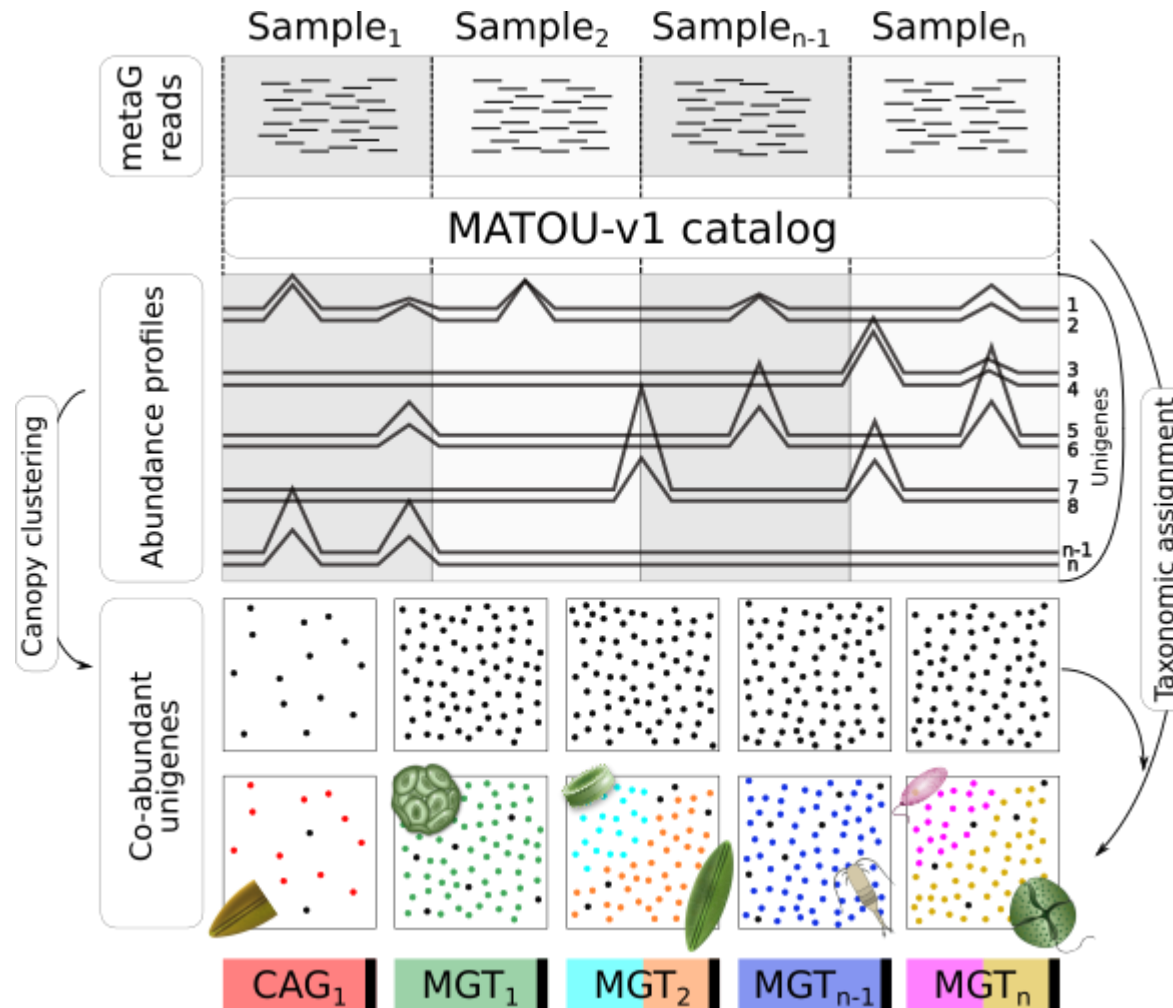
OPEN

A global ocean atlas of eukaryotic genes

Quentin Carradec et al.[#]



Reconstructing transcriptome from metagenomics and metatranscriptomics





Applications



Genomes eucaryotes reconstruits

Virus environnementaux inconnus



Article

Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean

Tom O. Delmont^{1, 2, 9}  , Morgan Gaia^{1, 2}, Damien D. Hinsinger^{1, 2}, Paul Frémont^{1, 2}, Chiara Vanni³, Antonio Fernandez-Guerra⁴, A. Murat Eren⁵, Artem Kourlaiev^{1, 2}, Leo d'Agata^{1, 2}, Quentin Clayssen^{1, 2}, Emilie Villar¹, Karine Labadie^{1, 2}, Corinne Cruaud^{1, 2}, Julie Poulain^{1, 2}, Corinne Da Silva^{1, 2}, Marc Wessner^{1, 2}, Benjamin Noel^{1, 2}, Jean-Marc Aury^{1, 2}

Tara Oceans Coordinators

New lineages of marine eukaryotes

Opisthokonta: 299 MAGs

Mostly copepods (Arthropoda) and *Oikopleura* related



Stramenopiles: 149 MAGs

Mostly diatoms, other Ochrophyta and MAST

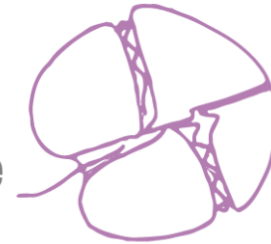


Hacrobia: 134 MAGs

Mostly Haptophyta and a new sister clade

Archaeplastida: 64 MAGs

Mostly Mamiellales, Chloropicales and new clade



Alveolata: 44 MAGs

Mostly Ciliophora, MALV, and new clade

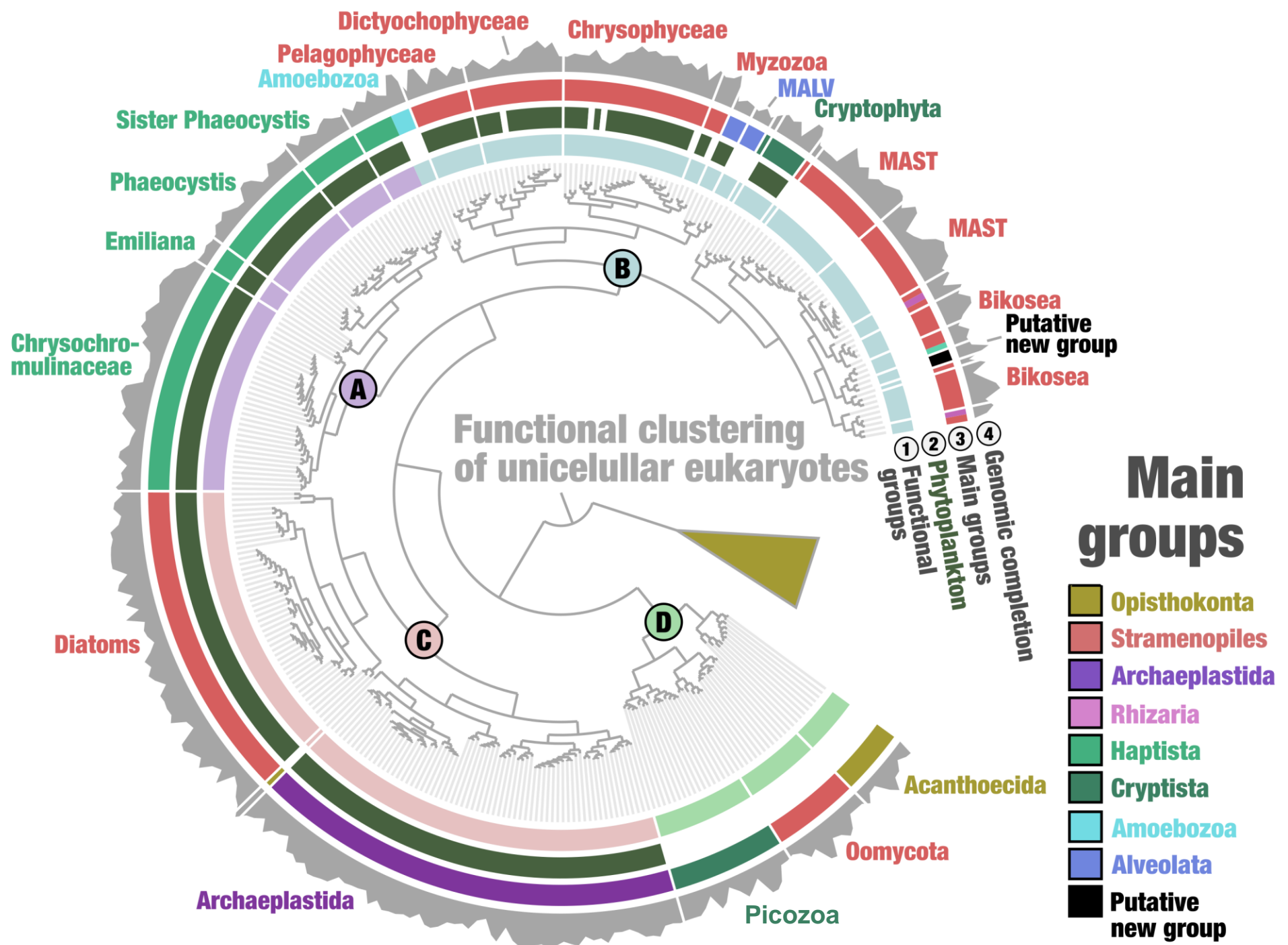


Rhizaria: 1 MAG

Cercozoa related

**Transcriptomes
from isolates
(mostly MMETSP)**

Only 24 MAGs match to METDB



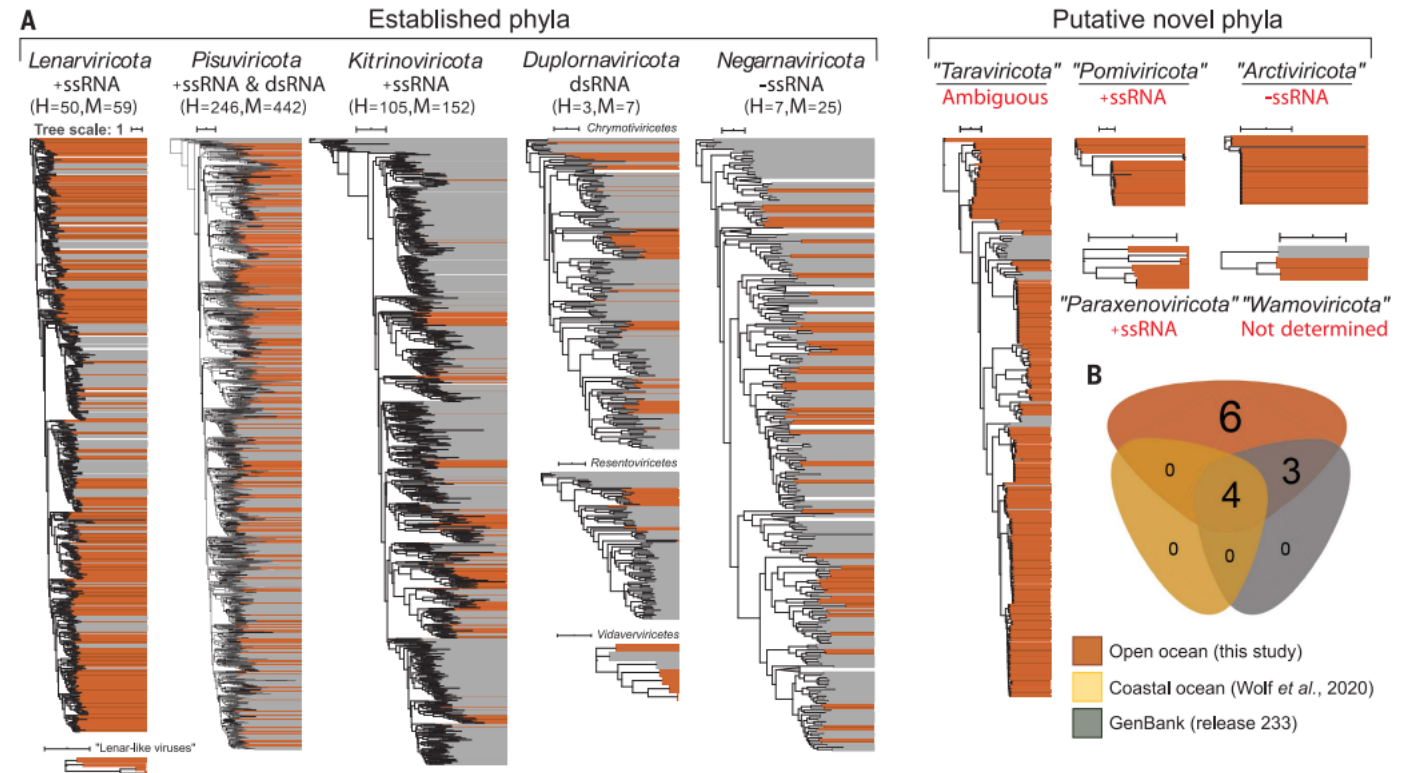
Detecting marine RNA viruses in metatranscriptomics data

RESEARCH ARTICLE

VIROME

Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome

Ahmed A. Zayed^{1,2,3,†}, James M. Wainaina^{1,3,†}, Guillermo Dominguez-Huerta^{1,2,3,†}, Eric Pelletier^{4,5}, Jiarong Guo^{1,2,3}, Mohamed Mohssen^{1,3,6}, Funing Tian^{1,3}, Akbar Adjie Pratama^{1,2}, Benjamin Bolduc^{1,2,3}, Olivier Zablocki^{1,2,3}, Dylan Cronin^{1,2,3}, Lindsey Solden¹, Erwan Delage^{5,7}, Adriana Alberti^{4,5,§}, Jean-Marc Aury^{4,5}, Quentin Carradec^{4,5}, Corinne da Silva^{4,5}, Karine Labadie^{4,5}, Julie Poulain^{4,5}, Hans-Joachim Ruscheweyh⁸, Guillem Salazar⁸, Elan Shatoff⁹, Tara Oceans Coordinators[†], Ralf Bundschuh^{6,9,10,11}, Kurt Fredrick¹, Laura S. Kubatko^{12,13}, Samuel Chaffron^{5,7}, Alexander I. Culley¹⁴, Shinichi Sunagawa⁸, Jens H. Kuhn¹⁵, Patrick Wincker^{4,5}, Matthew B. Sullivan^{1,2,3,6,12,16,*}



A new virus group with hybrid features

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Mirusviruses link herpesviruses to giant viruses

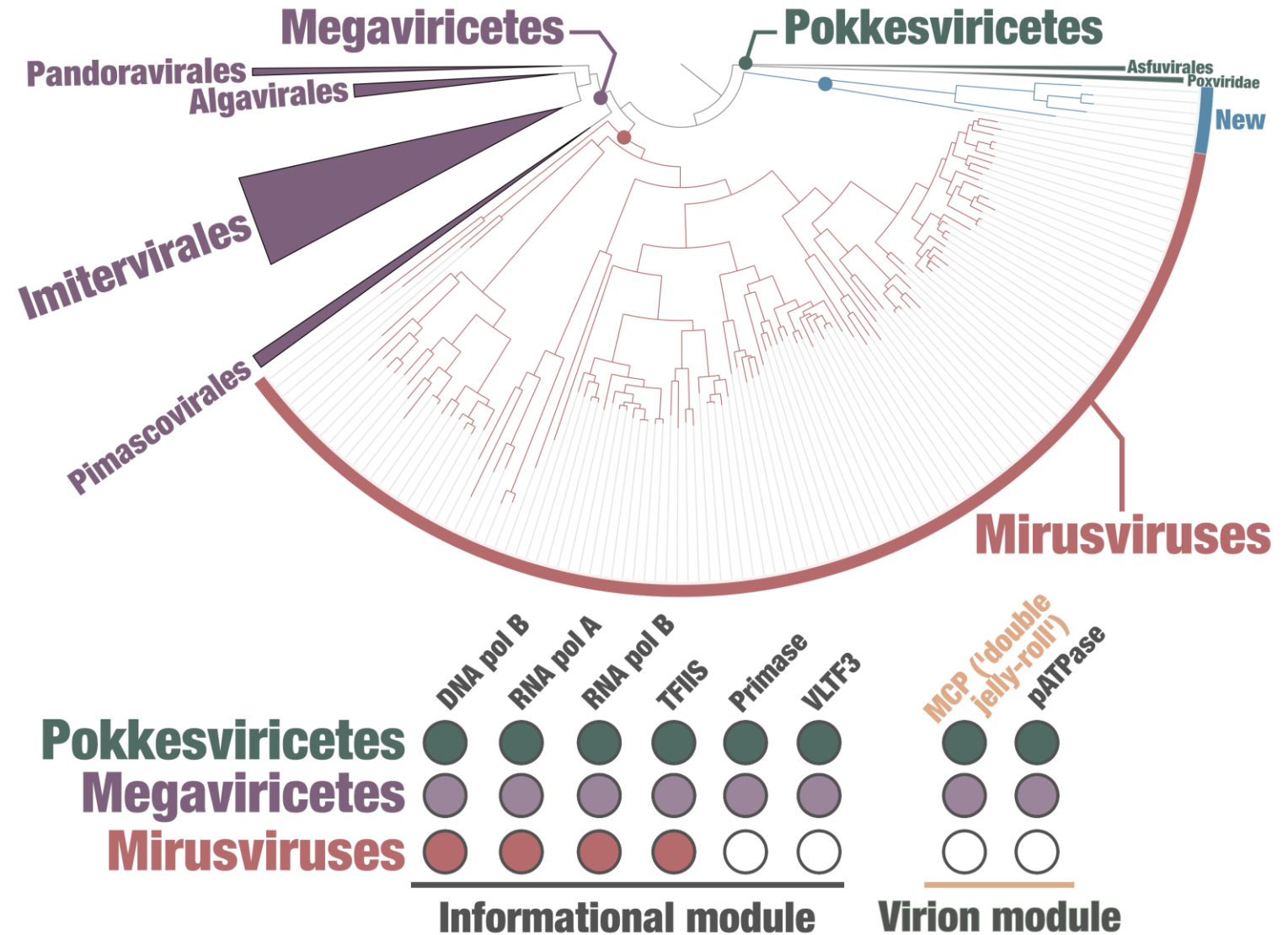
[Morgan Gaia](#), [Lingjie Meng](#), [Eric Pelletier](#), [Patrick Forterre](#), [Chiara Vanni](#), [Antonio Fernandez-Guerra](#), [Olivier Jaillon](#), [Patrick Wincker](#), [Hiroyuki Ogata](#), [Mart Krupovic](#) & [Tom O. Delmont](#) 

Nature **616**, 783–789 (2023) | [Cite this article](#)

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Abstract

DNA viruses have a major influence on the ecology and evolution of cellular organisms^{1,2,3,4}, but their overall diversity and evolutionary trajectories remain elusive⁵. Here we carried out a phylogeny-guided genome-resolved metagenomic survey of the sunlit oceans and discovered plankton-infecting relatives of herpesviruses that form a putative new phylum dubbed *Mirusviricota*. The virion morphogenesis module of this large monophyletic clade is typical of viruses from the realm *Duplodnaviria*⁶, with multiple components strongly indicating a common ancestry with animal-infecting *Herpesvirales*. Yet, a substantial fraction of mirusvirus genes, including hallmark transcription machinery genes missing in herpesviruses, are closely related homologues of giant eukaryotic DNA viruses from another viral realm, *Varidnaviria*. These remarkable chimaeric attributes connecting *Mirusviricota* to herpesviruses and giant eukaryotic viruses are supported by more than 100 environmental mirusvirus genomes, including a near-complete contiguous genome of 432 kilobases. Moreover, mirusviruses are among the most abundant and active eukaryotic viruses characterized in the sunlit oceans, encoding a diverse array of functions used during the infection of microbial eukaryotes from pole to pole. The prevalence, functional activity, diversification and atypical chimaeric attributes of mirusviruses point to a lasting role of *Mirusviricota* in the ecology of marine ecosystems and in the evolution of eukaryotic DNA viruses.



Interpréter l'ADNe : les génomes de référence pour les organismes non-modèles



EARTH BIOGENOME PROJECT

ABOUT EBP GOVERNANCE COMMITTEES REPORTS MEDIA CONTACT

A MOONSHOT FOR BIOLOGY

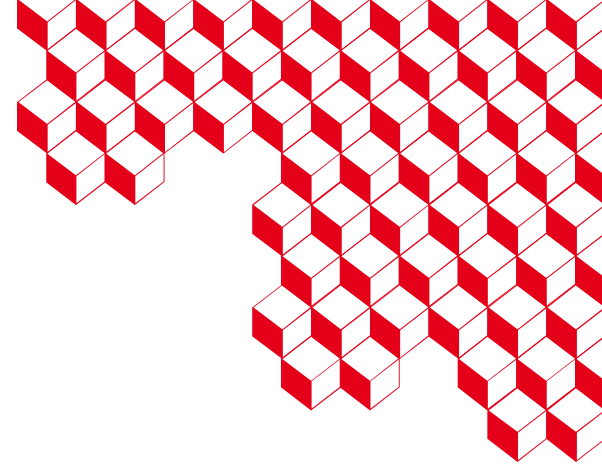
Sequence the DNA of all life on Earth in 10 years



ATLASea

Atlas des génomes marins





Merci

Tom Delmont
Julie Poulain
Olivier Jaillon
Eric Pelletier
Quentin Carradec
Morgan Gaia

Pedro Oliveira
Karine Labadie
Corinne Cruaud

Tara Oceans Consortium
Tara Pacific Consortium

