

ORIGINAL ARTICLE

Exploring nucleocytoplasmic large DNA viruses in
Tara Oceans microbial metagenomes

Pascal Hingamp^{1,11}, Nigel Grimsley², Silvia G. Acinas³, Camille Clérissé², Lucie Subirana²,
Julie Poulant², Isabel Ferrera^{1,12}, Hugo Sarmiento², Emilie Villar², Gipsi Lima-Mendez²,
Karoline Faust², Shinichi Sunagawa¹, Jean-Michel Claverie², Hervé Moreau²,
Yves Desreux², Peer Bork², Jeroen Raes^{1,6}, Colomán de Vargas², Eric Karsenti²,
Stefanie Kandel-Lewis², Olivier Jallouin², Fabrice Not², Stéphane Pesant², Patrick Wincker²
and Hiroyuki Ogata^{1,10,11}

¹CNRS, Aix-Marseille Université, Laboratoire Information Génétique et Structurale (UMR 7256),
Méditerranée Institute of Microbiology (FR 3479), Marseille, France; ²CNRS and Université Pierre et Marie
(Paris 06), UMR 7222, Observatoire Océanologique, Banyuls-sur-Mer, France; ³Department of Marine Biology
and Oceanography, Institute of Marine Science (ICM), CSIC, Passeig Marítim de la Barceloneta, Barcelona,
Spain; ⁴CEA, Institut de Génétique, Evry, France; ⁵Department of Structural Biology, VIB,
Brussels, Belgium; ⁶Department of Applied Biological Sciences (DBIT), Vrije Universiteit Brussel, Brussels,
Belgium; ⁷European Molecular Biology Laboratory, Heidelberg, Germany; ⁸CNRS, Université Pierre et Marie
Curie (Paris 06), UMR 7144, Station Biologique de Roscoff, Roscoff, France; ⁹MARUM—Center for Marine
Environmental Sciences, Universität Bremen, Bremen, Germany and ¹⁰Education Academy of Computational
Life Sciences, Tokyo Institute of Technology, Tokyo, Japan

Nucleocytoplasmic large DNA viruses (NCLDVs) constitute a group of eukaryotic viruses that can have
crucial ecological roles in the sea by accelerating the turnover of their unicellular hosts or by causing
diseases in animals. To better characterize the diversity, abundance and biogeography of marine
NCLDVs, we analyzed 17 metagenomes derived from

The abundance of viruses (*Ostreococcus tauri* virus
(OIVs)) infecting the smallest free-living green alga
O. tauri could vary from undetectable levels to over
10⁶ viruses ml⁻¹ depending on the season and the
distance from the shore (Belloc et al., 2010). The
abundance of EhVs could reach over 10⁷ viruses ml⁻¹
in rapidly expanding host populations in mesocosm
experiments simulating host blooms (Schroeder
et al., 2003; Pagarete et al., 2011). A typical observa-
tion in these studies was an episodic sudden increase
(> several orders of magnitude) in virus concentra-
tion. These studies focused on specific viral species/
strains and depended on the availability of host
cultures for virus evaluation or on relatively simple
community compositions amenable to FC analysis.
Currently, no direct method is available to assess the
abundance of diverse NCLDVs in a complex micro-
bial assemblage dominated by an overwhelming
amount of bacterial cells and phages.

To better understand the diversity and geographi-
cal distribution of marine NCLDVs, we analyzed a
subset of metagenomic sequence data (0.2–1.6 µm
size fraction) generated by Tara Oceans, an interna-
tional multidisciplinary scientific program aiming
to characterize ocean plankton diversity, the role of
these drifting microorganisms in marine ecosystems
and their response to environmental changes
(Karsenti et al., 2011). Samples were collected during
the first year of the expedition from the Strait of
Gibraltar, through the Mediterranean and Red Sea

remarkably wide taxonomic spectrum from micro-
scopic unicellular eukaryotes to larger animals,
including humans. Certain NCLDVs are known to
have important roles in marine ecosystems. For
instance, *Heterosigma akashiwo* virus (HaV) affects
the population dynamics of their unicellular algal
host, which forms seasonal harmful blooms in coastal
areas (Tomaru et al., 2004). Another well-known virus
(*Emiliania huxleyi* virus (EhV)) controls the popula-
tion of the ubiquitous haptophyte *E. huxleyi*, which
can form vast oceanic blooms at temperate latitudes
and exerts complex influence on the carbon cycle
(Pagarete et al., 2011). Other NCLDVs cause diseases
in fishes and can lead to economic damages in
aquaculture industries (Kurita and Nakajima, 2012).
NCLDVs include viruses with very large virion
particles, which do not pass through 0.2-µm filters
typically used in viral metagenomics to separate free
viruses from other organisms (Van Etten, 2011). The
prototype of such large viruses, also referred to as
gigaviruses (Claverie et al., 2006), is the amoeba-infecting
Acanthamoeba polyphaga Mimivirus with a 0.75-µm
virion particle and 1.18-Mb genome (Raoult et al.,
2004). Since the discovery of the giant Mimivirus from
fresh water samples, NCLDVs have become a subject
of broader interest. This has led to several conceptual
breakthroughs in our understanding of the origin of
viruses and their links to the evolution of cellular
organisms (Claverie, 2006; Forterre, 2006; Raoult and
Forterre, 2008; Forterre, 2010; Legendre et al., 2012).

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