

ORIGINAL ARTICLE

Exploring nucleocytoplasmic large DNA viruses in Tara Oceans microbial metagenomes

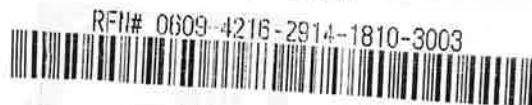
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viruses (NCLDVs).
2012) constitute an
apparently monophyletic group of eukaryotic viruses
with a large double-stranded DNA (dsDNA) genome
ranging from 100 kb up to 1.26 Mb. Their hosts show a

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Received 8 November 2012; revised 28 February 2013; accepted 6
March 2013; published online 11 April 2013

hosts or flow cytometry (FSC) the volume.
HaVs infecting the rhizodiphyte *H. akashiwo* could
reach 10^4 viruses ml^{-1} in natural sea water during
the period of host blooms (Tomaru et al., 2004).

sampling of planktonic organisms ranging in size from
expedition, planktonic organisms ranging in size from
viruses to fish larvae together with physico-chemical

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
(Pegarete 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
giant viruses (Claverie et al., 2006), is the amoeba-infecting
virus (Acanthamoeba polyphaga mimivirus) with a 0.75-µm

The abundance of viruses (*Ostreococcus tauri* virus
(Otv)) infecting the smallest free-living green alga
O. tauri could vary from undetectable levels to over
 10^4 viruses ml^{-1} depending on the season and the
distance from the shore (Belloc et al., 2010). The
abundance of EhVs could reach over 10^4 viruses ml^{-1}
in rapidly expanding host populations in mesocosm
experiments simulating host blooms (Schroeder
et al., 2003; Pegarete 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 lysis evaluation or on relatively simple
community compositions amenable to PCR 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