

The abundance of viruses (*Ostreococcus tauri* virus [OTV]) infecting the smallest free-living green alga (*O. tauri*) could vary from undetectable levels to over 10^6 viruses ml⁻¹, depending on the season and the distance from the shore (Belloc et al., 2010). The abundance of EHV could reach over 10^6 viruses ml⁻¹ in rapidly expanding host populations in mesocosm experiments simulating host blooms (Schroeder et al., 2003; Pagarete et al., 2011). A typical observation in these studies was an episodic sudden increase (> several orders of magnitude) in virus concentration. 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 FC analysis. Currently, no direct method is available to assess the abundance of diverse NCLDVs in a complex microbial assemblage dominated by an overwhelming amount of bacterial cells and phages.

To better understand the diversity and geographical distribution of marine NCLDVs, we analyzed a subset of metagenomic sequence data (0.2–1.6 μm size fraction) generated by Tara Oceans, an international 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, Chelate, through the Indian Ocean (Table 1).

Remarkably wide taxonomic spectrum from microscopic unicellular eukaryotes to larger animals, including humans. Certain NCLDVs are known to have important roles in marine ecosystems. For instance, *Heterosigma akashiwo* virus (HkV) 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 population 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 (Van Etten, 2011). The viruses from other organisms (Van Etten, 2011). The prototypic of such large viruses, also referred to as *Acetiviruses* (Claverie et al., 2006) is the amoeba-infecting *Acetiviruses polyphaga* Mimivirus (Roault 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

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ORIGINAL ARTICLE

Exploring nucleocytoplasmic large DNA viruses in Tara Oceans microbial metagenomes

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