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# ORIGINAL ARTICLE

## Exploring nucleocytoplasmic large DNA viruses in Tara Oceans microbial metagenomes

Pascal Hingamp<sup>1,11</sup>, Nigel Grimsley<sup>2</sup>, Silvia G Acinas<sup>3</sup>, Camille Clerissi<sup>12</sup>, Lucie Subirana<sup>1</sup>, Julie Poulain<sup>1</sup>, Isabel Ferrera<sup>1,12</sup>, Hugo Sarmiento<sup>13</sup>, Emilie Villar<sup>1</sup>, Gipsi Lima-Mendez<sup>1,14</sup>, Karoline Faust<sup>1,15</sup>, Shinichi Sunagawa<sup>16</sup>, Jean-Michel Claverie<sup>17</sup>, Hervé Moreau<sup>18</sup>, Yves Desnues<sup>19</sup>, Peer Bork<sup>20</sup>, Jérôme Raes<sup>21</sup>, Colomban de Vargas<sup>22</sup>, Eric Karsenti<sup>23</sup>, Stéphanie Kandels-Lewis<sup>24</sup>, Olivier Jallot<sup>25</sup>, Fabrice Not<sup>26</sup>, Stéphane Pesant<sup>27</sup>, Patrick Wincker<sup>28</sup> and Hiroyuki Ogata<sup>1,10,11</sup>

<sup>1</sup>CNRS, Aix-Marseille Université, Laboratoire d'Information Génétique et Structurale (UMR 7256), Mediterranean Institute of Microbiology (FR 3479), Marseille, France; <sup>2</sup>CNRS and Université Pierre et Marie Curie (Paris 06), UMR 7232, Observatoire Océanologique, Banyuls-sur-Mer, France; <sup>3</sup>Department of Marine Biology and Oceanography, Institute of Marine Sciences (ICM), CSIC, Passeig Marítim de la Barceloneta, Barcelona, Spain; <sup>4</sup>CEA, Institut de Génétique, Genoscope, Evry, France; <sup>5</sup>Department of Structural Biology, VIB, Brussels, Belgium; <sup>6</sup>Department of Applied Biological Sciences (DBIT), Vrije Universiteit Brussel, Brussels, Belgium; <sup>7</sup>European Molecular Biology Laboratory, Heidelberg, Germany; <sup>8</sup>CNRS, Université Pierre et Marie Curie (Paris 06), UMR 7144, Station Biologique de Roscoff, Roscoff, France; <sup>9</sup>MARUM—Center for Marine Environmental Sciences, Universität Bremen, Bremen, Germany and <sup>10</sup>Education Academy of Computational Life Sciences, Tokyo Institute of Technology, Tokyo, Japan

NCLDVs in Tara Oceans metagenomes  
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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 (HaV) affects the population dynamics of their unicellular algal host, which forms seasonal harmful blooms in coastal areas (Tamaru 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 to separate free viruses from other organisms (Van Etten, 2011). The prototype of such large viruses, also referred to as *Aratharnax* (Claverie et al., 2008), is the amoeba-infecting *Aratharnax 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 been found in

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<sup>6</sup> viruses ml<sup>-1</sup> depending on the season and the distance from the shore (Belloc et al., 2010). The abundance of EBVs could reach over 10<sup>6</sup> viruses ml<sup>-1</sup> 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

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