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Genome sequences of two giant viruses infecting Prymnesium kappa (Haptophyta)

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Nucleocytoplasmic large DNA viruses (NCLDV) infect hosts across the entire eukaryotic tree of life. Large genome size and atypical gene content have fostered genomic studies of these viruses. PkV RF01 and PkV RF02 are two putative members of the Mimiviridae family[1]. They infect Prymnesium kappa, a single-celled organism of the Haptophyte eukaryotic super-group, thereby extending the known phylogenetic breadth of NCLDV's hosts. Here we report their genome sequences, assembled from Illumina short paired-end reads. PkV RF01 and PkV RF02 genome sequences are 816 kb and 487 kb long with 756 and 493 protein-encoding genes, respectively. This makes them the first and third largest marine NCLDV described so far. Their gene content will be presented with a special focus on the ones involved in DNA repair[2]. References:1.Johannessen, T. V. et al. Characterisation of three novel giant viruses reveals huge diversity among viruses infecting Prymnesiales (Haptophyta). Virology 476, 180 ? 188 (2015).2.Blanc-Mathieu, R. & Ogata, H. DNA repair genes in the Megavirales pangenome. Curr. Opin. Microbiol. 31, 94 ? 100 (2016).