SUPPLEMENTAL ONLINE INFORMATION

For publication in conjunction with the following:

Viral dynamics in a high rate algal pond reveals a burst of *Phycodnaviridae* diversity correlated with episodic algal mortality

Chase EE1,2,3, Pitot T4, Bouchard S1, Triplet S5, Przybyla C5, Gobet A5, Desnues C1,2, and Blanc G1.

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**SUPPLEMENTAL FIGURES**

A screenshot of a graph

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**Figure S10.** Investigation of *Nucleocytoviricota* and PLV relationships through **(A)** principal component analyses using combined and normalised qPCR data and 18S rDNA ASVs (*i.e.,* metabarcoding) on tracked putative viruses and potential alga (Chlorophyta) hosts for *Mimiviridae* (M), *Phycodnaviridae* (P), andpolinton-like viruses (PLV). Cos2 reports the strength of the principal component for the observations (*i.e.* virus or potential hosts), where a higher value depicts a stronger relationship between them or a “good representation”. The vector length of each observations represents the contribution they make to the ordination. Dates are represented by numbered objects, where 2017 is composed of 1–5 (April is 1 and 2, May is 3, June is 4 and 5), and 2018 is composed of 6–16 (April is 6, May is 7–9, August is 9, September Is 10–13, and October is 14–16). A second analysis: **(B**) Hierarchical clustering (SIMPROF,  = 0.1) of potential hosts (Chlorophyta) and viruses of interest, where colours represent different groups clustering at our minimum. Bolded text signifies hosts and viruses mentioned within the manuscript.

![A diagram of a computer code

Description automatically generated with medium confidence]()

**Figure S11.** Putative Nucleocytoviricota phylogeny based on the DNA polymerase B gene (PolB). Reference sequences were downloaded by NCBI GenBank (accession numbers as indicated) and sequenced recovered from the HRAP are included (in bold). Bootstrap values are indicated by circle size.