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Assembly and identification of novel viruses in the aquatic invertebrate *Daphnia magna*

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Background

- *Daphnia magna*: A model host organism for multiple fields including ecotoxicology and host-parasite interactions
- *D. magna* is relatively easy to study due to low variation in bacterial microbiome
- Microbiome studies do not focus to characterize viral species within *D. magna*

Questions

- Can shotgun sequencing be used to identify novel viruses in the microbiome of a zooplankton?
- If phages are present, what Baltimore classification might they fall under?

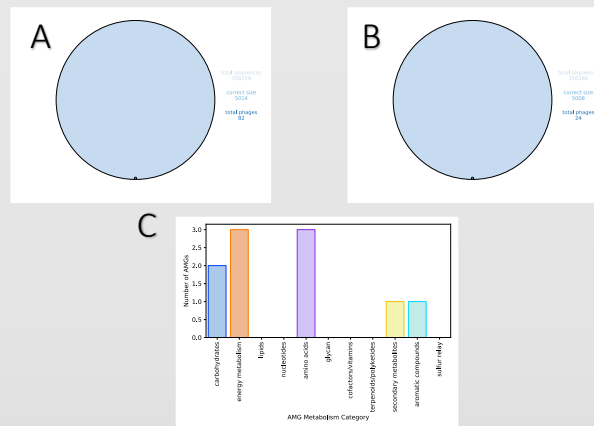
Methods

- Co-assembled shotgun sequencing data from four samples of 100 *Daphnia magna* using metaSPAdes
- Filtered out host DNA with BWA-MEM
- Analyzed deep sequencing data to identify novel viruses, using VIBRANT
- BLASTP was used to compare VIBRANT data with viral protein databases, and only proteins that fell under an E-value below 1e-100 were further analyzed

Acknowledgements

- Support from the UCARE undergraduate research program

Results



Quantitative analysis of genomic sequences identified by VIBRANT: (A) 82 contigs & (B) 24 scaffolds were identified as putative phage sequences from an initial set of 356,759 initial contigs. (C) VIBRANT indicates that the following auxiliary metabolic genes (AMGs) may increase phage fitness.

Conclusions

- VIBRANT confirmed that viruses are present within *D. magna*
- One fully intact, circular phage was identified
- The taxonomic identification of the phage proteins suggest that it may have a host range of varying organisms including *Paraburkholderia*

Results

Protein	Taxonomic Identification	E-Value	Bit Score
AAA family ATPase	Verrucomicrobiaceae bacterium	2.92E-150	436
DNA polymerase A	uncultured virus	0	875
putative DNA polymerase	Prokaryotic dsDNA virus sp.	0	552
DNA-directed DNA polymerase I	uncultured Mediterranean phage uvMED	3.55E-113	361
PD-(D/E)XK nuclease family protein	Verrucomicrobiaceae bacterium	1.15E-109	323
DEAD/DEAH box helicase, partial	Acidobacteriales bacterium	0	573
DEAD/DEAH box helicase	<i>Pseudomonas mediterranea</i>	1.35E-123	381
DEAD/DEAH box helicase	<i>Paraburkholderia</i> sp. BL1012N1	2.42E-123	380
ATP-dependent helicase	Gammaaproteobacteria bacterium	3.17E-119	370
DEAD/DEAH box helicase	<i>Spirochaetes</i> bacterium	5.00E-116	362
DEAD/DEAH box helicase	Desulfurellales bacterium	5.06E-116	362

Complete putative genes identified in the lytic phage: 47 proteins were identified in the 65.551 kb-long lytic phage. 10 of the 47 proteins are listed above. The phage is shown to have a taxonomic identification in accordance with a dsDNA viral species – falling under a Group I or Group VII Baltimore Scheme classification.