**Richardson Egyirifa**

**Title:** Quantification and Characterization of *Microcystis*-Specific Cyanophages in Lake Erie

**Research Question(s)**

* What is the spatial and temporal distribution of *Microcystis*-specific cyanophages in Lake Erie?
* How does viral diversity change across different locations and seasons?
* What are the gene functions associated with dominant cyanophage variants?

**Objective(s)**

* To quantify *Microcystis*-specific cyanophages in Lake Erie across spatial and temporal scales.
* To analyze viral diversity using high-throughput sequencing and identify gene functions relevant to host-virus interactions.

**Approach**

Environmental water samples collected from various locations and time points in Lake Erie will be analyzed using qPCR to quantify *Microcystis*-specific cyanophages. R will be used to load and clean qPCR data, handling missing values and ensuring consistency across datasets with packages like *tidyverse* and *janitor*. Exploratory data analysis will be conducted using *ggplot2* for visualization of viral abundance trends over time and space.

For viral diversity assessment, sequencing data from high viral load samples will be preprocessed in R, including quality filtering, trimming, and normalization using packages such as *phyloseq* and *vegan*. Statistical analyses, including alpha and beta diversity measures, will be performed to compare viral communities across sites and seasons. Functional annotation of viral genes will be conducted, and R will be used to map gene function distributions, conduct enrichment analysis, and visualize relationships through network diagrams.

Amplicon sequencing of viral off-bands will be analyzed using R-based bioinformatics pipelines like *dada2* for sequence variant inference and *DECIPHER* for taxonomic classification. Comparative analyses will be performed using multivariate statistical approaches, with R supporting clustering and ordination techniques. The entire workflow will be structured in R for reproducibility, integrating statistical modeling, exploratory data analysis, and dynamic reporting through R Markdown.

**5. Selected References**

* Ewa Miśkiewicz, Alexander G. Ivanov, John P. Williams, Mobashsher U. Khan, Stefan Falk, Norman P.A. Huner, Photosynthetic Acclimation of the Filamentous Cyanobacterium, *Plectonema boryanum* UTEX 485, to Temperature and Light, *Plant and Cell Physiology*, Volume 41, Issue 6, June 2000, Pages 767-775, <https://doi.org/10.1093/pcp/41.6.767>
* Francoeur SN, Biggs JF, Smith RA, Lowe RL. 1999. Nutrient limitation of algal biomass accrual in streams: seasonal patterns and a comparison of methods. J North Am Benth Soc.18(2):242–260. doi:10.2307/1468463
* Bayer T, Schallenberg M, Martin CE. 2008. Investigation of nutrient limitation status and nutrient pathways in Lake Hayes, Otago, New Zealand: a case study for integrated lake assessment. N Z J Mar Freshwater Res. 42:285–295.doi:10.1080/00288330809509956