**1. Title**  
Functional Genomics and Host-Specific Gene Identification in Cyanophage-Cyanobacteria Interactions

**2. Research Questions**

* What functional genes in cyanophages contribute to host specificity and infection dynamics in cyanobacteria?
* How do these genes influence cyanophage-host interactions in the context of environmental and ecological factors?

**3. Objectives**  
i. Identify key functional genes in cyanophages that determine host specificity through comparative genomics and transcriptomic analysis.  
ii. Characterize the role of host-specific genes in infection dynamics using controlled laboratory experiments.  
iii. Assess the ecological implications of cyanophage-host interactions by integrating genomic data with environmental metagenomic datasets.

**4. Approach**  
This research will employ a combination of genomic, transcriptomic, and bioinformatics approaches to investigate cyanophage functional genes associated with host specificity. Whole genome sequencing of cyanophages and their cyanobacterial hosts will be conducted, followed by comparative genomic analysis to identify host-specific genes. RNA sequencing during infection cycles will elucidate gene expression patterns linked to host interactions. Functional validation experiments will include gene knockout and overexpression studies to determine the impact of specific genes on infection efficiency. Environmental metagenomics will provide context for the ecological significance of identified genes in natural cyanophage-cyanobacteria populations.

**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. Nutrientlimitation 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 ofnutrient limitation status and nutrient pathways in LakeHayes, Otago, New Zealand: a case study for integratedlake assessment. N Z J Mar Freshw Res. 42:285–295.doi:10.1080/00288330809509956.
* Sullivan, M.B., et al. (2018). "Genomic insights into cyanophage-host dynamics." Annual Review of Virology.