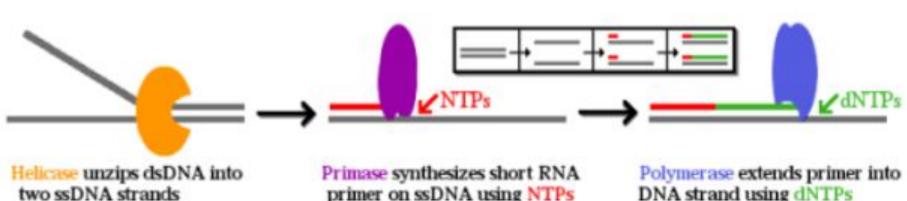
Background

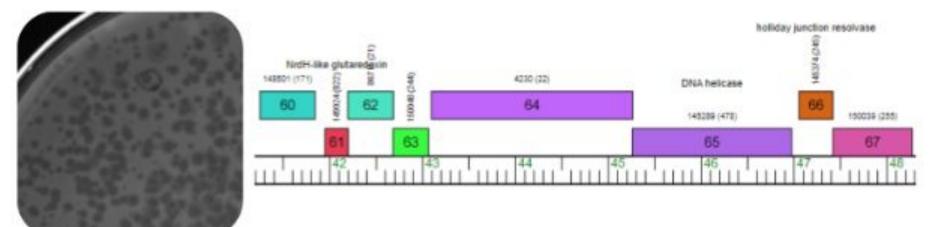
Primase-polymerases, more commonly known as primpols, are enzymes that possess the properties of a primase and polymerase for DNA replication in the same enzyme. DNA replication is an essential biochemical component of all cellular life, and in some viruses. The main aspect that makes something alive is its ability to reproduce, of which replication of DNA to form another organism or to repair itself is of paramount importance. DNA replication usually requires three separate enzymes: a helicase, a primase, and a polymerase. Each of these enzymes play an essential role, with the helicase "unzipping" the double stranded DNA, primase forms a small strand of RNA on both pieces of the now unzipped DNA, to which the DNA polymerase will start at the 3'-end of the RNA primers to form complementary DNA. These trifecta of enzymes work together to form two identical strands of double-stranded DNA (1).



While some primpols require a helicase to unzip the DNA, many have the ability to both unzip, prime and polymerize the DNA to undergo DNA synthesis. The three-for-one property of primpols is intriguing as it may offer a look into the early origins of DNA replication (1). There have been recent studies that have suggested that certain primpols can function as a helicase as well to undergo strand displacement synthesis (2). Strand displacement synthesis refers to a DNA synthesis that only replicates one side of the DNA strand and releases a piece of single stranded DNA which then becomes double stranded in random fashion. The ability for a singular enzyme to serve multiple roles in DNA synthesis provides impetus for research into primpols.

Primpols are found in a number of bacteriophages. Bacteriophages are viruses that infect solely bacteria, and have the potential as an alternative for antibiotics and in the treatment of antibiotic-resistant bacterial infections. Bacteriophages are the most abundant biological entities on planet Earth, making up an incredibly rich genomic and proteomic landscape to explore. The emerging public health crisis of antibiotic resistant bacteria has resulted in increased interest and research into bacteriophages as clinical therapies (3). Studies of viral genome replication and host-virus interactions can help tailor and adapt bacteriophages for eventual pharmaceutical applications.

Actinophages are typically linear dsDNA viruses that infect bacteria belonging to the Actinobacteria phylum. Mycobacteriophages are of particular interest in the realm of actinophages as they infect certain Mycobacterium hosts. Notable members of the Mycobacterium genus include Mycobacterium tuberculosis and Mycobacterium leprae, the bacteria responsible for tuberculosis and leprosy (4). Further investigation into mycobacteriophage genomic replication, where primpols are a subject of interest, can potentially help lead to more effective phage treatments against antibiotic resistant infections. Many bacteriophages contain genes annotated as primpols based on domain conservation software; however, when compared to the amount of bacteriophages being discovered and annotated every year, primpols in bacteriophage are largely understudied. Mycobacteriophage Larva was isolated from Mycobacterium smegmatis mc²155 in Williamsburg, VA. It is classified as a temperate phage of the Siphoviridae morphotype belonging to cluster K5 (5).



Larva's gene 64 (Larva64) encodes a primpol, and is the only encoded DNA polymerase of the phage. Thus, Larva64 is the presumed sole source of Larva's endogenous genetic replication abilities, and prime for study. Previous research at WCU by Nathan Folse in 2020 expressed and purified Larva64and observed de novo enzymatic activity by Larva64, as well as protein-protein interactions between Larva64 and M. smegmatis proteins via a two-hybrid assay (6). The enzymatic activity of Larva64 however was not quantified, rather only shown to be present via gel-based assay and that the enzyme appeared to be Mg²⁺ dependent. The two-hybrid assay shed light on potential interactions between Larva64 and M. smegmatis proteins, but did not explore protein-protein interactions within the virus itself.

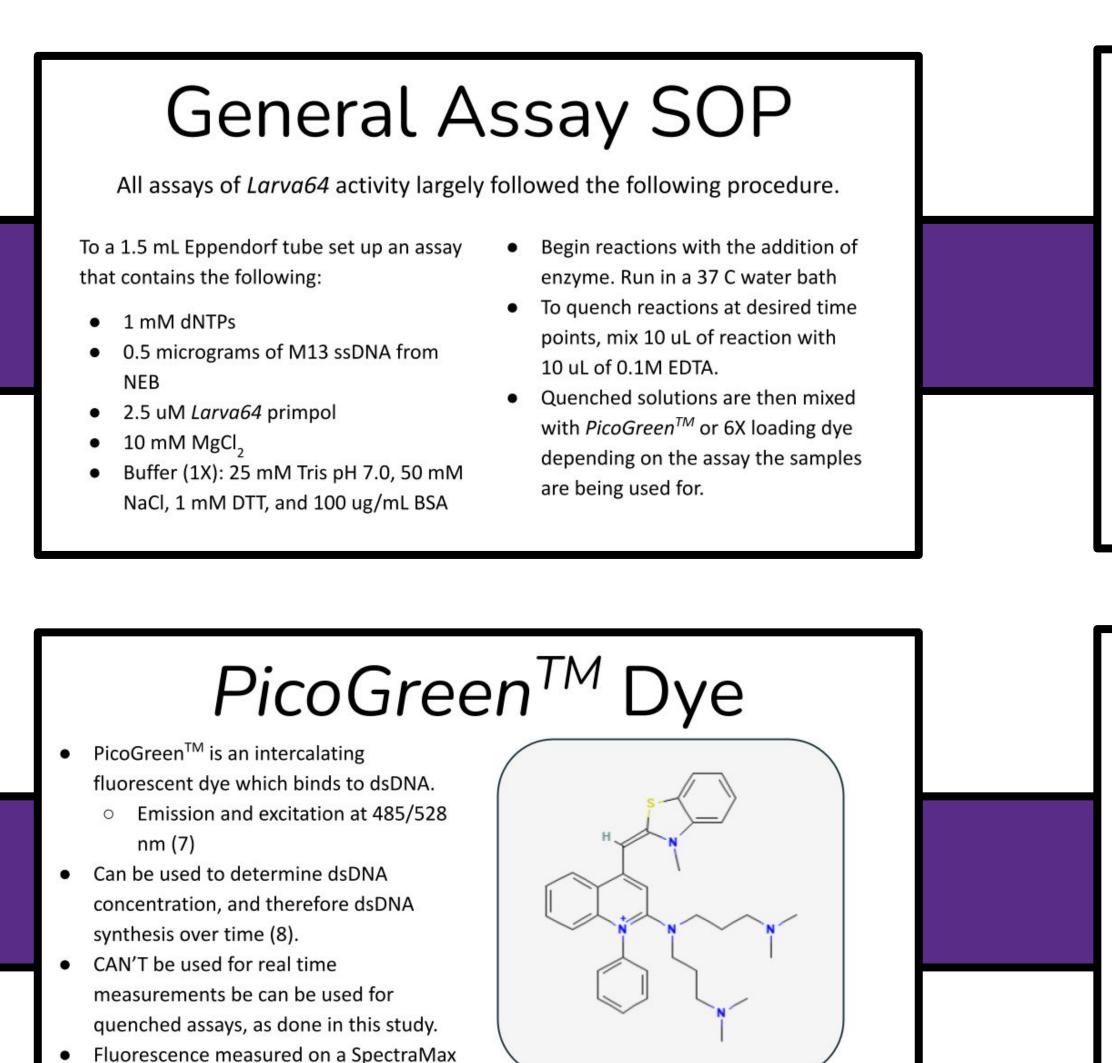
Moreover, Folse using CRISPRi was able to show that Larva64 is necessary for the survival of phage Larva. However, qualitative data from agarose gel assays and quantitative data from PicoGreen[™] fluorescence assays have shown that the enzyme works at a speed too slow to fully replicate the roughly 62 kb viral genome in a timely manner. This indicates other interactions or proteins assist in Larva's genome synthesis.

Goals

- Quantify the DNA synthesis activity of Larva64 via a fluorescence assay
- Identify variables that could potentially increase the speed of *Larva64*
- Determine by what mechanism phage Larva's genome is replicated, and what role Larva64 plays in that replication given its extremely slow speed.

Quantification and Characterization of Larva64 **Primpol Activity** H. Chase Bishop and Dr. Jamie Wallen Department of Chemistry and Physics at Western Carolina University

Methods



tional Center for Biotechnology Information (2023). PubChem Compound Summary fo

CID 16071083, Picogreen. Retrieved November 8, 2023 from

Characterization of Activity

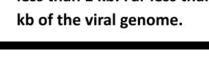
Mg²⁺ Dependence

iD5 plate reader.

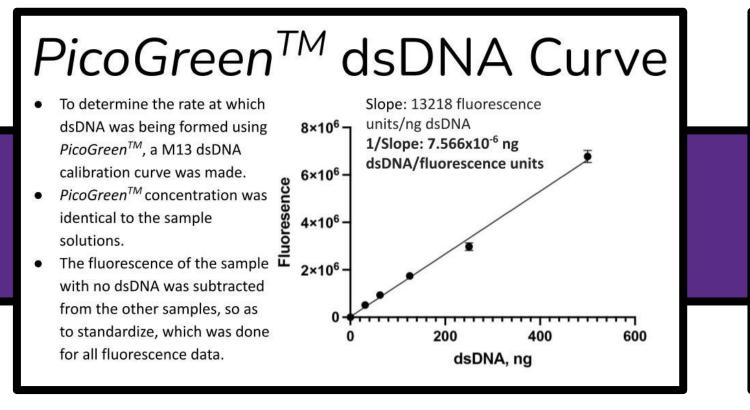
- unable to substitute Mn²⁺ ir lieu of Mg²⁺
- To confirm and expand on that result, a gel assay wa run with different divalent metal salts replacing MgCl MnCl,, CaCl,, NiCl,
- CoCl₂, ZnSO No substitute metal salt allowed for activity.

Long Run Timepoints Gel

- determine a relative size the dsDNA product formed at a given time, a long run gel based assay was ran.
- Quenched at 10 minute intervals the gel shows the DNA synthesis activity of the primpol over time.
- Bands above the later time points may indicate strand displacemen The product formed after 2 hours is less than 1 kb. Far less than the 62

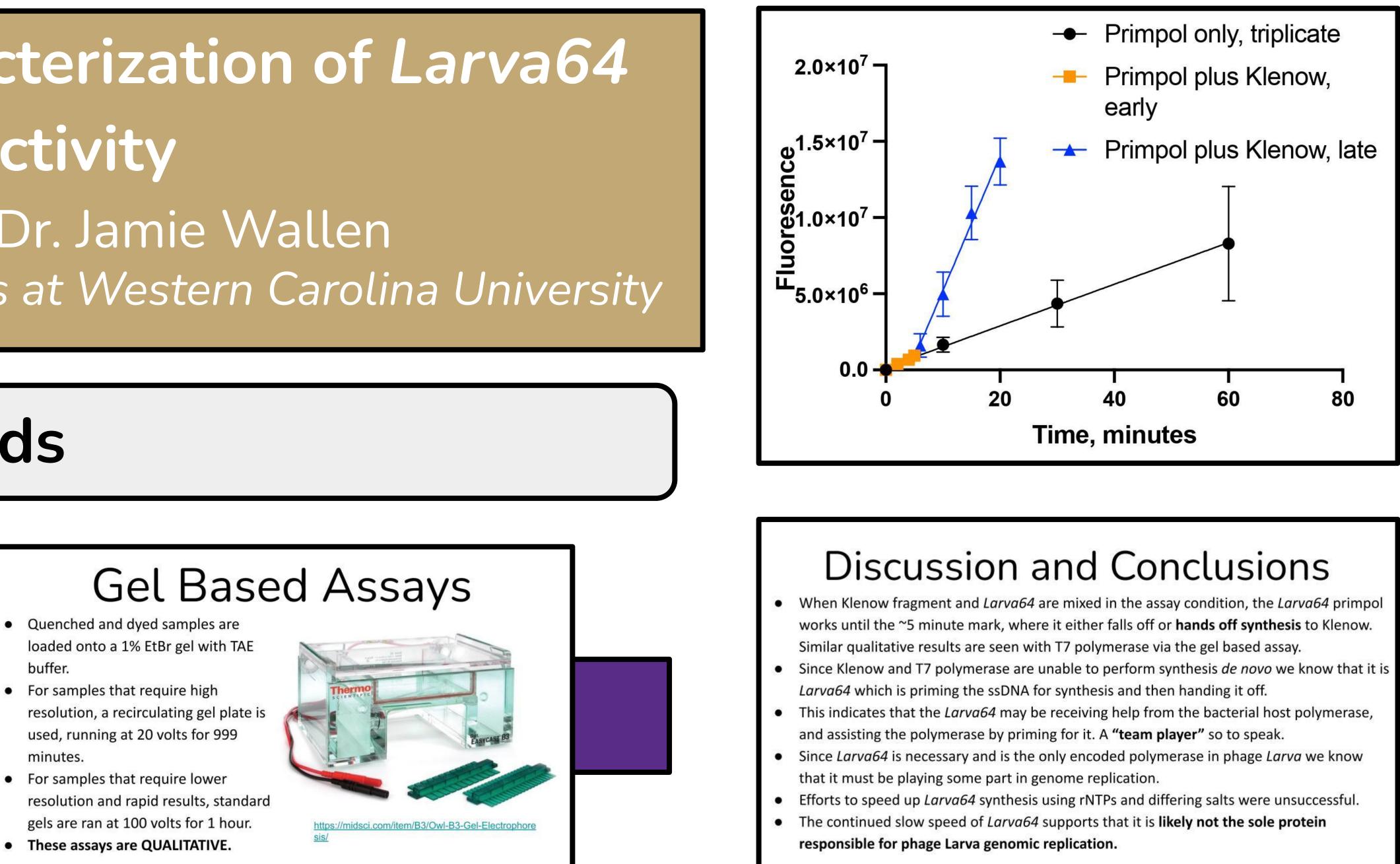






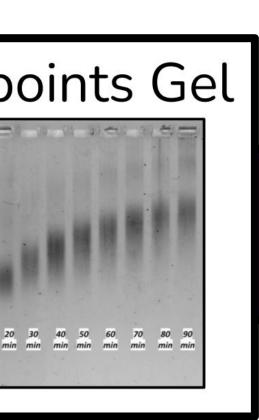
Larva64 Rate and Klenow

- Multiplying the inverse slope of the dsDNA curve slope of the kinetic data (fluorescence/minute), you get a rate with units of ng dsDNA/minute.
- Triplicate data of *Larva64* activity using the *PicoGreen*[™] assay was gathered. The slope of which is 144611
- fluorescence units per minute. Rate: 1.1 ng dsDNA/minute
- Given Larva64's slowness, we decided to see if it could hand off synthesis to a faster bacterial polymerase that is unable to perform *de novo* synthesis: Klenow fragment. Many phages utilize host polymerases for replication.
- The resulting fluorescence chart can be seen in the top right of the poster.



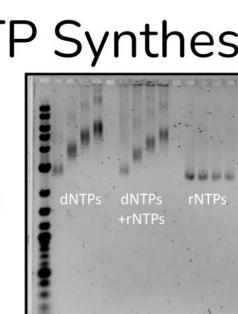
Fluorescence Based Assay

- Quenched samples are mixed with a 5X solution of *PicoGreenTM* on a 96 well plate reader plate and given 10 minutes in the plate reader to allow the dye to bind to dsDNA and temperature equilibrate. Plate reader settings:
- Ex, Em: 485, 535 nm (filter engaged) PMT Gain: Low
- A 60 ppb quinine solution (Ex, Em: 349, 461 nm) served as a fluorescence standard between days to account for differing instrument
- emission intensity. These assays are QUANTITATIVE.

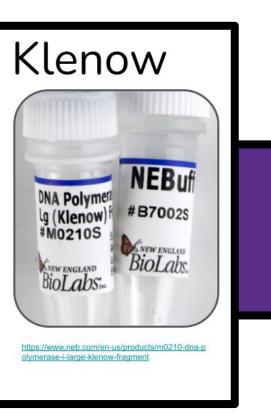


rNTP and dNTP Synthesis

- region which utilizes rNTPs, we investigated if Larva64 would be able to synthesize a
- double stranded using just rNTPs. Standard assay was ran as with rNTPs replacing dNTPs, dNTPs only, and both rNTPs
- and dNTPs
- rNTPs were unable to form a double stranded product, and the addition of rNTPs neither inhibited or assisted dsDNA
- rNTPs did not speed up synthesis.







Larva64 and T7 Polymerase The addition of a faster polymerase with Larva64 results in a short period of dsDNA synthesis by our primpol,

followed by the rapid synthesis of dsDNA by the faster protein. This result was seen quantitatively with the bacterial

polymerase Klenow, and qualitatively with the phage T7 polymerase. Larva64 was able to hand off

synthesis to both polymerases.

Future Work

 Work is underway to utilize a bacterial two-hybrid assay to identify endogenous protein-protein interactions between Larva64 and other genes in the Larva genome that are predicted to interact with DNA.

• Example: Interaction between Larva primpol and Larva sliding clamp protein. • These protein-protein interactions could potentially assist in the replication of the Larva genome at a higher rate and shed light on the mechanism of genome replication in phage Larva.

 The peculiar inefficiency of Larva64 may be due to an uncharacterized novel function of it. Bioinformatic analysis will shed light on primpols in cluster K5, and their potential as a CRISPR-adjacent primase polymerase (CAPP).

• Utilizing non-quneching dsDNA dyes, a real time assay of DNA synthesis could be performed, giving a cleaner and more precise rate.



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Hatfull, G. F. Mycobacteriophages. Microbiology Spectrum 2018, 6 (5). DOI:10.1128/microbiolspec.gpp3-0026-2018. Dana, R.; Gray, V. The Actinobacteriophage Database: Larva https://phagesdb.org/phages/Larva/ (accessed Oct 29, 2023). lathan Folse. BIOINFORMATIC AND IN VITRO CHARACTERIZATION OF PRIMASE-POLYMERASE ENZYMES FROM VIRUSES THAT INFEC ACTINOBACTERIAL HOSTS. Masters Thesis, Western Carolina University, Cullowhee, NC, April 2020 Held, P. https://www.agilent.com/cs/library/applications/fluorometric-guantitation-dsDNA-using-PicoGreen-5994-2888EN-agilent.pdf (accessed 2023-11-01).

(8) Dragan, A. I.; Casas-Finet, J. R.; Bishop, E. S.; Strouse, R. J.; Schenerman, M. A.; Geddes, C. D. Characterization of PicoGreen Interaction with Dsdna and the Origin of Its Fluorescence Enhancement upon Binding. Biophysical Journal 2010, 99 (9), 3010-3019. DOI:10.1016/j.bpj.2010.09.012.

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