

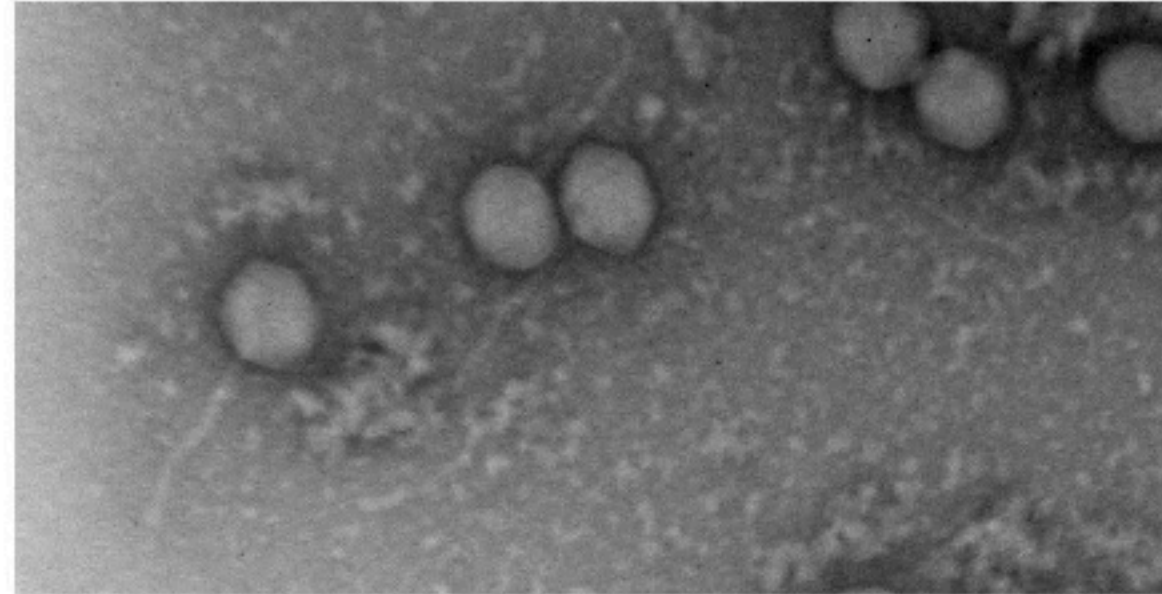
The Annotation Process of the Mycobacterium Phage: Stagni



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Abstract

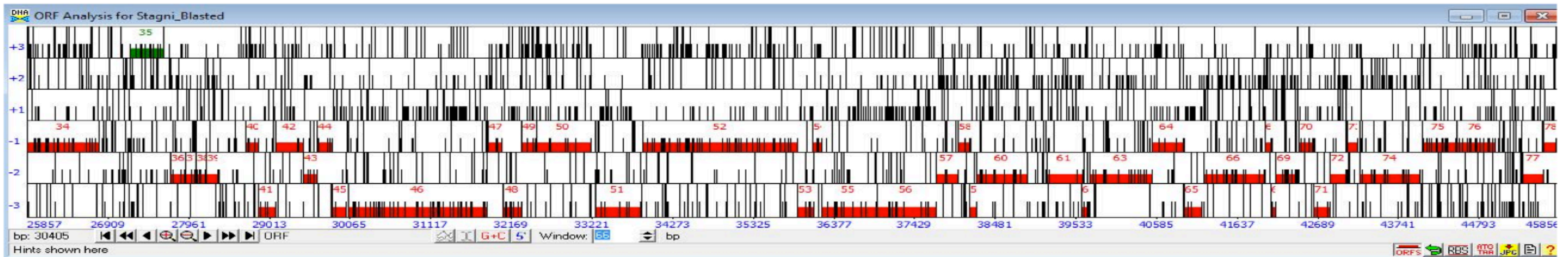
In our research we have went in depth looking at each gene within our given phage, Stagni. We were able to compare our phage to others that have been put into the database. We looked into the start and stop codons and made sure that they were correct. Our research is all based around the fact that we are trying to use bacteriophages to cure bacterial infections. We used Starterator and DNA master to take a closer look at what the DNA within our phage. The phage we are looking into is one that one of our classmate isolated last semester. We were able to go through the entire process of the lives of our phage. We collected them from soil and went through a 20 week process to get it pure and isolated away from all surrounding substances. After we did this we sent it's DNA to a testing center so we can begin the in depth research we have just completed. We now have annotated the genome and corrected anything that we felt to be an error. Our phage will soon be over looked and added into the database.



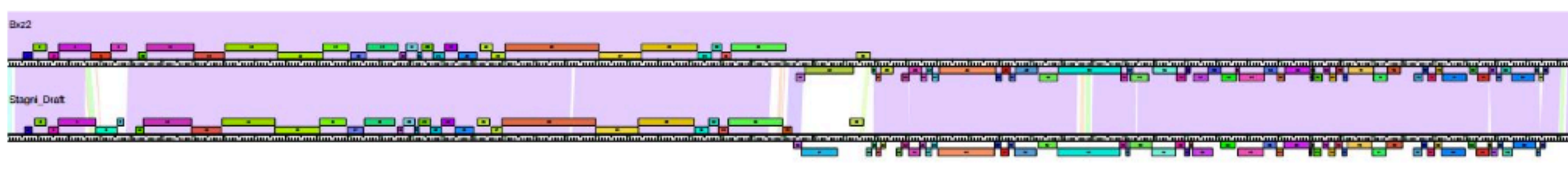
Shown above: Electron microscopy image of the Phage Stagni, taken at Wayne State University

Introduction

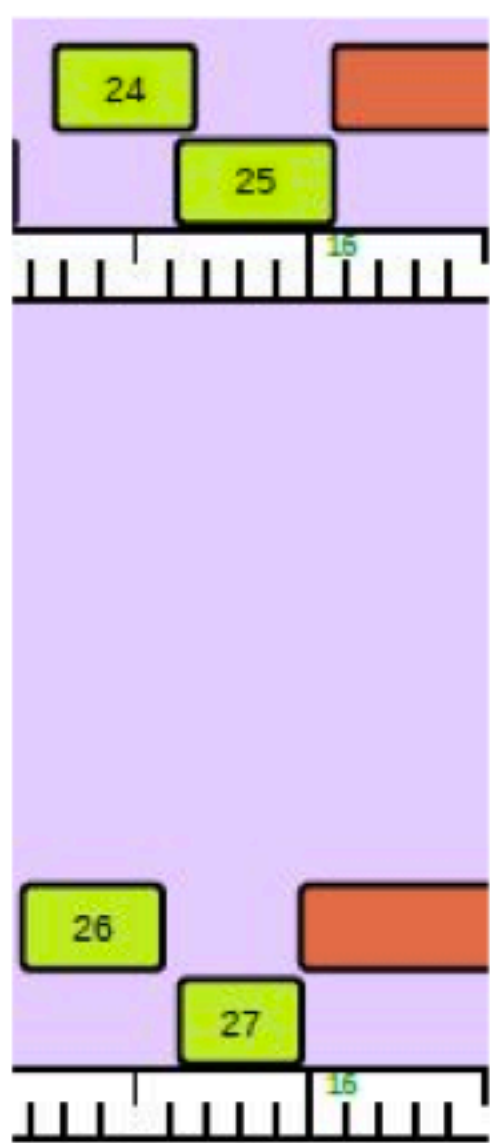
- Phage can be used to treat overgrowth of bacteria
- Isolated from soil in Livonia, Michigan
- 15 week lab in attempt to isolate pure phage in order to test DNA
- Used programs DNA Master, Phamerator and Staterator
- Compared our Phage in the Sea-Phages database with other phages discovered around the world



Shown above: Predicted genes in DNA Master. We used this program to find the predicted start and finish for each gene. For some genes we had to readjust the given codons to make them more fitting, going along with the most probable.



Shown above: This is an image comparing our phage Stagni to the other phage we found to be the most similar, Bzx2, as you can see the genetic makeup appears to be very similar.

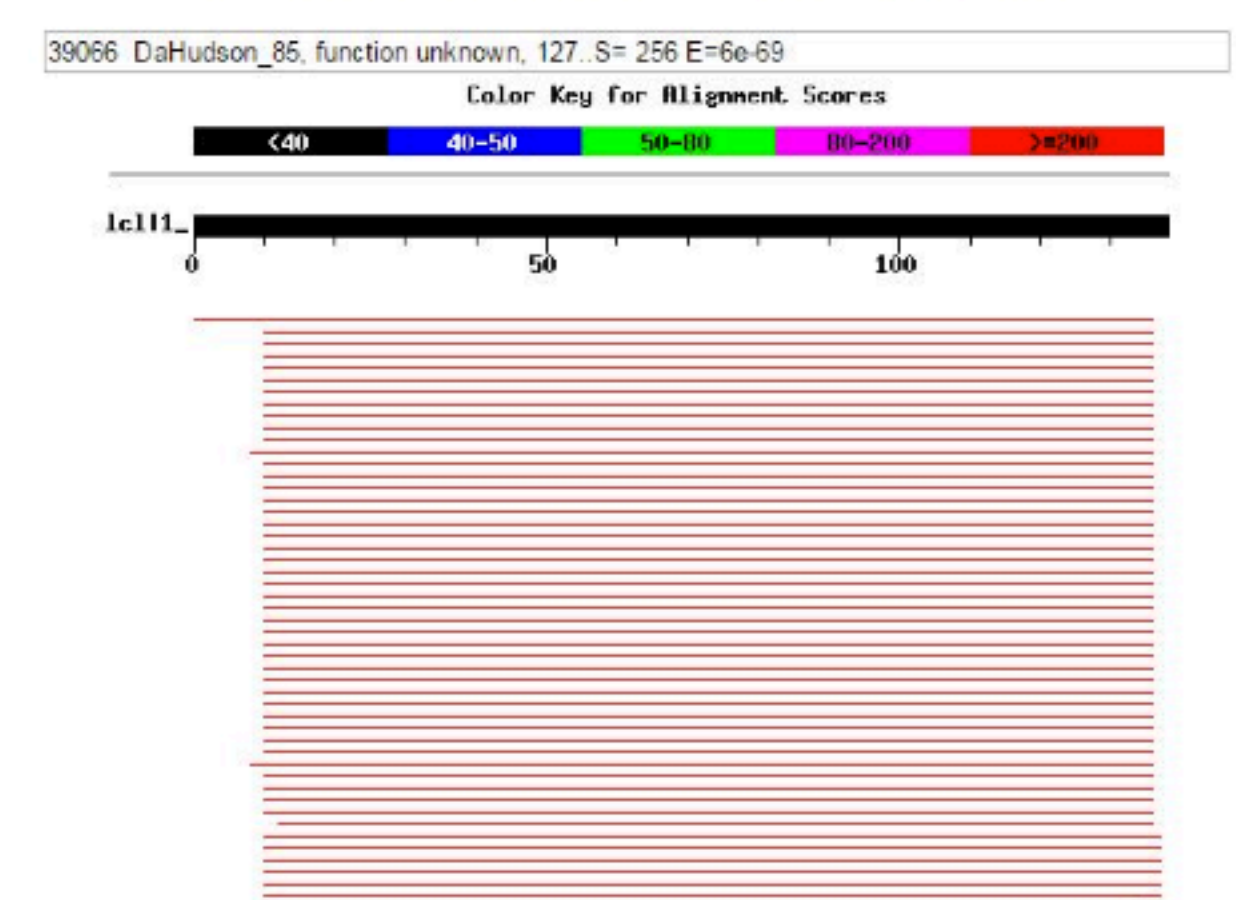


Shown left: This was one of the most interesting frame we discovered throughout this research. DNA master failed to realize that in Stagni genes 26 & 27 were meant to all be in one gene. The top image shows how it is supposed to look.

Conclusion

More research can be done to continue on the journey of finding useful phages to cure bacterial infections. Now that we know the DNA sequence of the Phage Stagni, we can use it to see the specific functions and characteristics of the phage.

Distribution of 100 Blast Hits on the Query Sequence



Shown above: Example of a Blast search done at <http://phagesdb.org/blast/results/blast.cgi>. The key is color coordinated with the dark red meaning that it has the closest relationship with the inserted gene, which in this case was gp83 from bacteriophage Stagni.



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