GENOMIC AND MORPHOLOGIC CHARACTERIZATION OF THE MYCOBACTERIUM SMEGMATIS BACTERIOPHAGE EAGLE

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# BACKGROUND

- Course taught with 3 sections
- Started with enrichment protocol
- All students isolated new bacteriophages from environment

# ENRICHMENT

- Soil samples were collected from the UMW campus
- 1 sample from each group of 3 students used for enrichment
- Enrichment protocol of Erin Sanders-Lorenz (UCLA) followed

# PHAGE ISOLATION

- Plaques were picked after 24 hours incubation at 37°C, using micropipette tip
- Phages resuspended in 100 μL phage buffer
- 10-fold dilutions performed and plated
- Plaques picked after 24 hr incubation, resuspended and plated

# **EAGLE PLAQUES**



# PHAGE ISOLATION (CONT'D)

- All plaques picked through at least three iterations to ensure purity
- Final plates were counted to determine pfu/mL of phage preparation
- 10 plates prepared for web lysis

# PHAGE ISOLATION (CONT'D)

- 2 ml of phage buffer added to each of the 10 plates
- Top agar and phage buffer scraped from plates and transferred to 50 mL centrifuge tube
- Agar-lysate mixture centrifuged at 4000 rpm for 15 minutes
- Supernatant filtered through 22 μm filter, collected, and titered

## **ELECTRON MICROSCOPY**

- I0 mL of phage preparation transferred to copper EM grid
- Washed 2X with sterile water
- Stained with 1.0% uranyl acetate
- Examined with F.E.I. Morgagni Transmission Electron Microscope





KLB.tif Katie Belfield Print Mag: 298000x @7.0 in 14:29 11/19/08 TEM Mode: Imaging

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# **DNA ISOLATION**

- 10 mL of phage lysate treated with 40 μL of nuclease mixture
- Incubated 30 minutes at 37°C and 1 hour at room temp.
- 4 mL of phage precipitant added and incubated at 4°C overnight
- Sample centrifuged at 10,000 rpm for 20 minutes

# DNA ISOLATION (CONT'D)

- Pellet retained and drained
- Pellet resuspended in Promega DNA clean up resin
- Pellet subjected to Promega mini-column
  DNA isolation procedure
- DNA quantitated using Perkin-Elmer Lambda 40 UV/Vis spectrophotometer

## **RESTRICTION ANALYSIS**

- 0.5mg of Eagle DNA mixed with restriction endonucleases
  - *Bam*H1  *Hae*III
  - Clal HindIII
  - *Eco*R1
- Incubated at 37°C for 2 hours
- Run on 0.8% agarose gel for 2 hours

### EAGLE RESTRICTION DIGEST



### **EVALUATE GENOMIC QUALITY**

#### • 1 μL of Eagle DNA run on 1% JGI gel



# SEQUENCING

- Genome sent to JGI for sequencing
- Rough sequence used to determine ambiguous region
- Primers designed using Primer 3
- Primers ordered from Fisher Scientific
- Sequencing performed using Beckman
  Coulter CEQ 8000 Genetic Analysis System

PCR Product after amplification with Primers



# **GENOME ANALYSIS**

- Finished JGI sequence analyzed and annotated
- Genome length was approximately 52 kb
- The genome was divided into ~7 kb sections and pairs of students analyzed each section
- Each pair generated a poster, and lab classes compared their annotations

### **POSTER PRESENTATION**









# ANNOTATION

- 42 genes called and annotated
- Used BLASTx to determine matches and E values
- Used E value cutoff of 10<sup>-25</sup>

#### **GBROWSE COMPARISON**



# **PUTATIVE GENE PRODUCTS**

- Tape measure protein
- Major and minor tail proteins
- Capsid protein
- DNA helicase
- DNA polymerase
- Full integrase
- Lysozyme
- Terminase

## OTHER MYCOBACTERIOPHAGE MATCHES

#### • Vast majority in cluster A2:

- Pukovnik
- Bxz2
- D29
- **L**5
- Che12

# OTHER MYCOBACTERIOPHAGE MATCHES

#### • Several matches in cluster A1:

- Bethlehem
- Bxb1
- **U**2
- Single matches:
  - Tweety (F1)
  - TM4 (unclustered)
  - Ms6

# CONCLUSIONS

#### • We believe Mycobacteriophage Eagle

- is a Siphoviridae based on the micrograph
- is a fairly small mycobacteriophage
- is probably not a linear genome
- belongs to Cluster A2