

Genome sequence of the dissimilatory metal ion-reducing bacterium *Shewanella oneidensis*

Heidelberg, J. F., Paulsen, I. T., Nelson, K. E., Gaidos, E. J., Nelson, W. C., Read, T. D., ... & Fraser, C. M. (2002). Genome sequence of the dissimilatory metal ion-reducing bacterium *Shewanella oneidensis*. *Nature biotechnology*, 20(11), 1118-1123. doi:10.1038/nbt749

Mary Alverson
Josh Kuroda

Biological Databases
Loyola Marymount University
November 24th, 2015

Outline

- **The Genome Features of *S. oneidensis***
- ***S. oneidensis* compared to other Organisms**
- **The identification of phages**
- ***S. oneidensis* can be used for
bioremediation**
- **Ensembl is the Model Organism database**

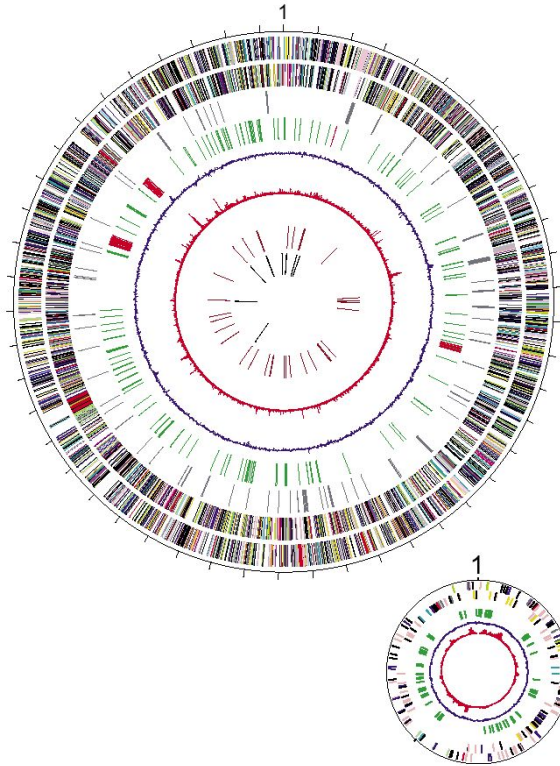
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The Genome Was Sequenced

- The whole-genome sequencing method was used.
- The *S. oneidensis* was grown in a single, isolated colony.
- A plasmid library and a shotgun library were sequenced and joined.
- Sequencing reactions were used to close gaps and improve coverage.

Figure 1 Shows the Circular Genome of *S. oneidensis*



- predicted coding regions on the plus and minus strand
- genes involved in the electron transport chain
- transposon-related genes and the phage-related genes
- percentage of G+C in relation to the mean G+C
- χ^2 values for trinucleotide composition
- tRNAs and the rRNAs

Table 1 Shows the Genome Features of *S. oneidensis*

Table 1. General features of the *Shewanella oneidensis* genome

	Chromosome	Plasmid
Size (bp)	4,969,803	161,613
G+C percentage	46.0	43.7
Number of predicted CDSs	4,758	173
Average size of CDS (bp)	893	742
Percentage coding	85.5	79.5
Number of rRNA operons (16S-23S-5S)	9	0
Number of tRNAs ^a	102	0
Number of CDSs similar to known proteins	2,430	91
Number of CDSs similar to proteins of unknown function ^b	371	7
Number of conserved hypothetical proteins ^c	843	28
Number of hypothetical proteins ^d	1,114	47
Number of rho-independent terminators	833	13

^aThere is one selenocysteine tRNA likely to be important in translation of the selenium-containing, nitrate-inducible formate dehydrogenase (SO0101).

^bProteins of unknown function have substantial similarity (homology) to a named protein for which there is currently no known function.

^cConserved hypothetical proteins have sequence similarity to a translation of another CDS, but there is currently no evidence a protein is expressed.

^dHypothetical proteins have no substantial similarity to another protein.

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The Genome of *S. oneidensis* was compared to Other Genomes

- Glimmer software was used to identify open reading frames that were likely to encode proteins.
- The open reading frames were used to identify likely proteins from the amino acids.
- The final genome was compared to all other complete genomes available.

Figure 2 Compares the *S. oneidensis* Open Reading Frames With Those of Sequenced Organisms

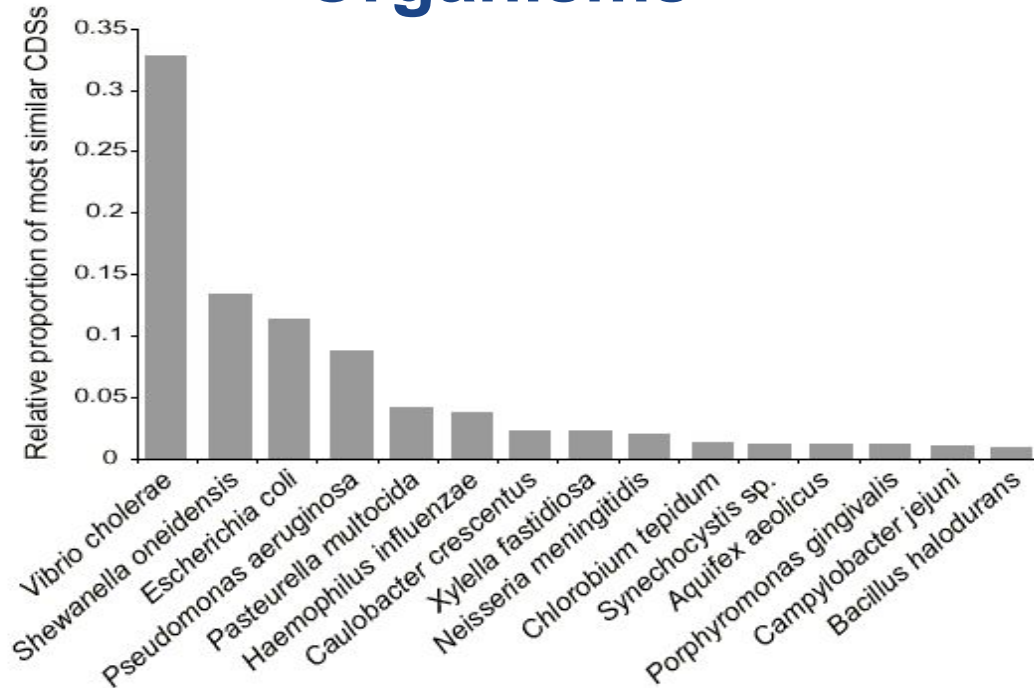
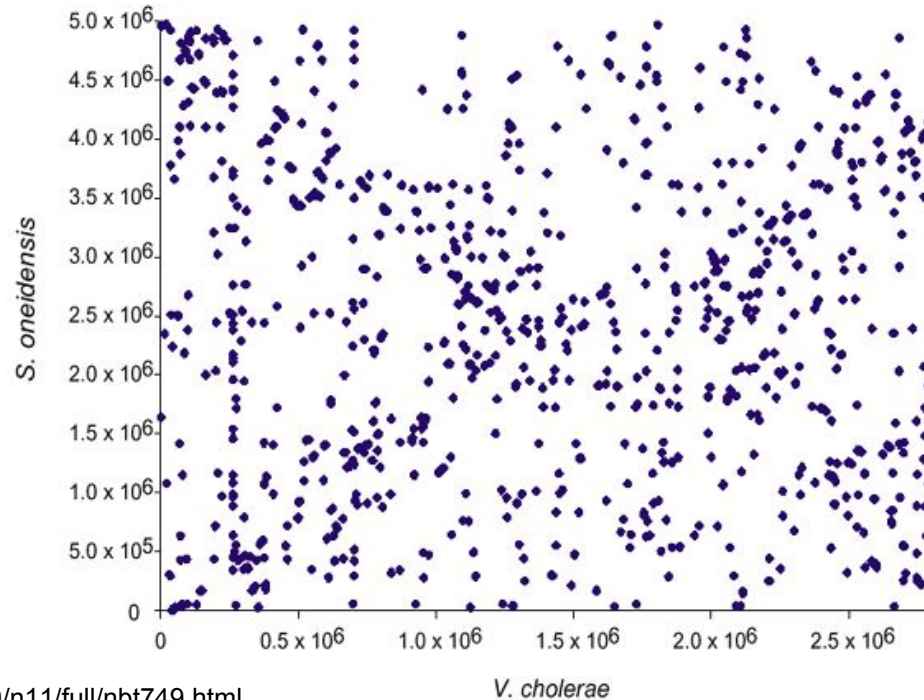


Figure 3 Illustrates Whole-genome Proteome Alignments Between *S. oneidensis* and *V. cholerae*



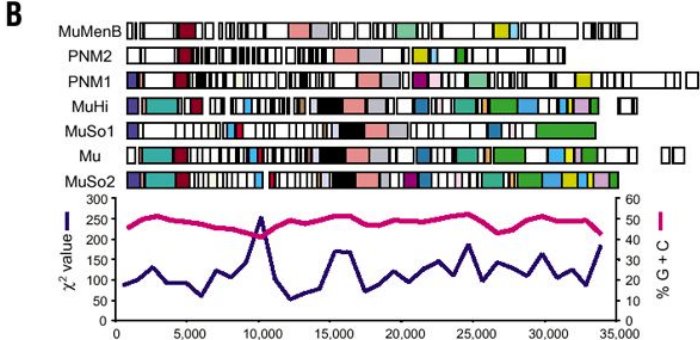
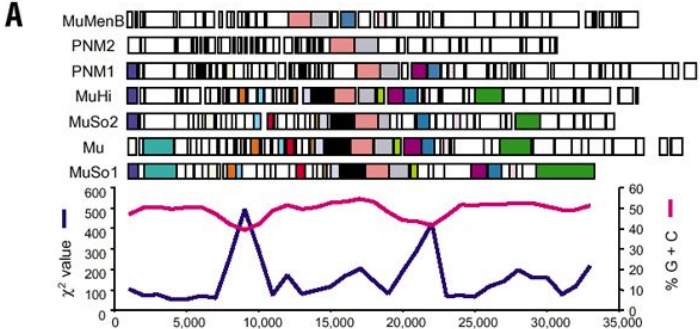
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Phages Were Found

- A lambda-like phage genome was discovered, both integrated in the *S. oneidensis* genome and present in nonintegrated form.
- This *Shewanella* phage is an important tool for *Shewanella* genome engineering.
- Two phages related to the *Escherichia coli* were also discovered.

Similarities Were Found Between Phages



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S. oneidensis Can Be Used For Bioremediation

- S. oneidensis can reduce the levels oxidized metals.
- S. oneidensis is infrequently a human pathogen.
- The lambda-like phage introduces the possibility of genetically manipulating the genes.
- Others can now conduct experiments with the genome in order to better predict the behaviors of S. oneidensis.


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Ensembl is the Model Organism Database

- You can search for genes, regions of the chromosome, or description such as enzymes or proteins, along with splice variants, cDNA and protein sequences, and non-coding RNAs.
- This is a meta database; it gets data regarding *S. oneidensis* from the European Nucleotide Archive.
- Data is curated both electronically and manually (in-house).
- It is maintained at the EMBL-European Bioinformatics Institute under the guidance of the INSDC International Advisory Committee and a Scientific Advisory Board.
- There are no restrictions to accessing the database.

Ensembl is User-friendly

 BLAST | Tools | Downloads | Documentation | Website help Login/Register

Shewanella oneidensis MR-1


Shewanella oneidensis MR-1

Shewanella oneidensis MR-1


Provider [European Nucleotide Archive](#) | Taxonomy ID [211586](#)


e.g. [prpC](#) or [Chromosome:350116-351467](#) or [synthetase](#)


About *Shewanella oneidensis* MR-1


 Information and statistics

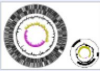
Genome assembly: [GCA_000146165.2](#)

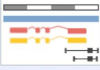
 More information and statistics

 Download DNA sequence (FASTA)

 Convert your data to GCA_000146165.2 coordinates


 Display your data in Ensembl Bacteria


 View karyotype


 Example region


Gene annotation


What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

 More about this genebuild

 Download genes, cDNAs, ncRNA, proteins - FASTA - GFF3


 Update your old Ensembl IDs


 Example gene


 Example transcript

Comparative genomics

What can I find? Gene families based on HAMAP and PANTHER classification. Homologues and gene trees including species across the pan-taxonomic range.


 More about comparative analyses

 Gene families



Variation

This species currently has no variation database. However you can process your own variants using the Variant Effect Predictor:

Variant Effect Predictor 

http://bacteria.ensembl.org/shewanella_oneidensis_mr_1/Info/Index?db=core

Acknowledgements

Dr. Dioniso

Dr. Dahlquist

Questions?