

Lawrence Berkeley National Laboratory

Recent Work

Title

Microbial Finishing at JGI

Permalink

<https://escholarship.org/uc/item/48s447w8>

Authors

Lapidus, Alla
Chain, Patrick
Han, Cliff
[et al.](#)

Publication Date

2005-08-10

Microbial Finishing at JGI.

[Alla Lapidus](#), [Patrick Chain](#), [Cliff Han](#), [Eugene Goltsman](#), [Michele Martinez](#), [Stephanie Malfatti](#), [Olga Chertkov](#), [Stephan Trong](#), [Tom Brettin](#), [Roxanne Tapia](#), [Alex Copeland](#), [Paul Richardson](#).

The U.S. Department of Energy (DOE) established the Microbial Genome and GTL programs to determine the complete genome sequence of a number of microbes that may be useful to DOE in carrying out its missions (which include research of new energy sources, sequester excess atmospheric carbon affecting global climate, and to clean up contaminated environments). Another program was established to study hard-to-culture individual microbes and microbial communities. They are very difficult to study but play critical roles in the Earth's ecology.

JGI is a leader in performing sequences to support these programs.

Another important specialization of the JGI is the recently started Community Sequencing Program (<http://www.jgi.doe.gov/CSP/index.html>).

All of the above projects include sequence and detailed analysis of the genomes of the different representatives of the microbial world.

A completely sequenced, high quality genome is a perfect starting point for the genome annotation (<http://img.jgi.doe.gov/v1.1/main.cgi>), microarrays, knockout experiments etc. Despite the fact that drafted genome contains a sufficiently large amount of information to be usable, a completed and polished one is overall a better product especially if it will be used to analyze previously unknown and difficult-to-cultivate microbes; for the comparative analysis of the clinical isolates or for the creation of microbial strains overproducing different proteins and amino acids. Knowledge of the completely finished genome will allow scientists to modify specific regions of the genome and therefore to affect the expression of the gene being studied. The study of the potential usage of microorganisms as new energy sources requires a complete knowledge of the genomes sequence as well.

Thus in order to be able to realize these and many other studies, it is necessary to close most (if not all) of the genomes being sequenced at JGI.

To this date JGI has accumulated a significant amount of experience closing the microbial genomes. During the last two years the combined efforts of three groups (LANL, LLNL and PGF) allowed to finish 41 microbial projects. Our goal is to fulfill the needs of all of the projects undertaken by JGI and complete no less than 50 genomes per year.

This work was performed under the auspices of the US Department of Energy's Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Livermore National Laboratory under Contract No. W-7405-Eng-48, Lawrence Berkeley National Laboratory under Contract No. DE-AC02-05CH11231 and Los Alamos National Laboratory under Contract No. W-7405-ENG-36.