

Programs:

- DOE Microbial Program
- DOE GTL Program (GTL)
- Community Sequencing Program (CSP)
- JGI Internal Program

Goal: to provide the scientific community access to high throughput sequencing and to operate as a Genomic Infrastructure for American Science

In February 2004, the JGI launched the Community Sequencing Program (CSP).

2004: 24 proposals accepted, 10 microbial projects

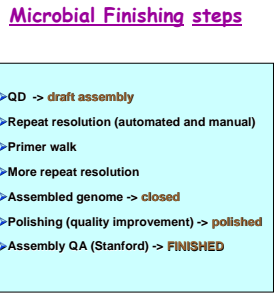
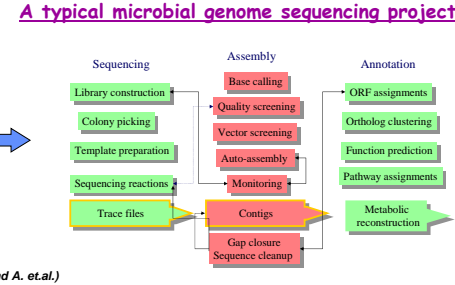
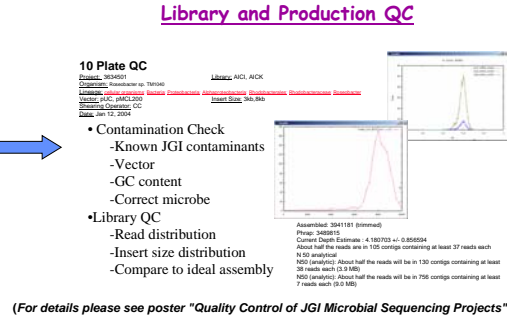
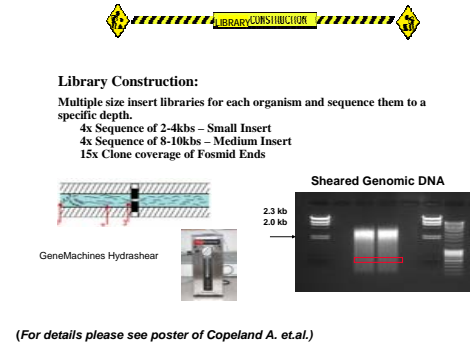
2005: 135 applications; 50 – microbes

<http://www.jgi.doe.gov/CSP/>

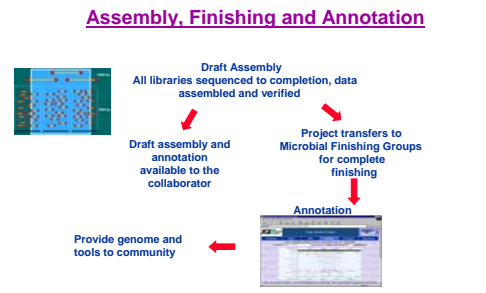
The Department of Energy established the Microbial Genome Program (MGP, <http://microbialgenome.org>) in 1994 as a spin-off of the Human Genome Program. A principal goal of this project is to determine the complete genome sequence of a number of microbes that may be useful to DOE in carrying out its missions including energy production, carbon sequestration and bioremediation.

The JGI is responsible for sequencing, assembling, finishing and annotating microbial genomes of interest to the DOE through the MGP and other programs. A workflow procedure for all microbial programs has been formalized to process samples from DNA prep through sequencing, assembly, finishing, quality assurance, annotation and analysis. To date, the JGI has sequenced over 100 microbes to draft quality, finished over 30 and is currently working on more than 60 additional microbial projects. Most projects are now targeted for finishing at one of three JGI locations. Finishing groups will resolve repeat discrepancies, close all gaps, and improve low quality regions. The final assembly is then passed to the Quality Assurance group to assess the integrity and overall quality of the genome sequence. The finished sequence then receives a final annotation and this package is used as the basis for analysis and publication.

The Integrated Microbial Genomes (IMG) system was just created to provide a framework for comparative analysis of the genomes sequenced by the Joint Genome Institute. The goal is to facilitate the visualization and exploration of genomes from a functional and evolutionary perspective. There are two main approaches to using the system: genes and genomes. Genes can be found by keyword or BLAST query via the Gene Search and then analyzed in the context of their chromosomal, metabolic, and phylogenetic neighborhoods. Genomes of multiple organisms can be selected with the Organism Browser. Genomes can be compared using the Phylogenetic Profiler to identify common or unique properties. The first release of IMG (www.jgi.doe.gov) includes 101 genomes sequenced at JGI together with most publicly available complete microbial genomes.



- All low quality areas (<Q30) reviewed and re sequenced.
- Final error rate < 0.2 per 10 Kb.
- No single clone coverage, i.e. minimum of 2X depth everywhere.
- Manually inspected and quantified single stranded regions.
- Checked all high quality discrepancies.
- Final sequence has a base at every position (no strings of xxxx anywhere).
- All repeats verified (paired ends and PCR if necessary).
- Make sure to check ends of final contigs (chromosomes, plasmids)
- Final Assembly QC



Finished Genomes: 31 Draft Genomes: 97