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Recent Work

Title

The US DOE Joint Genome Institute Microbial Genome Program

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The US DOE Joint Genome Institute Microbial Genome Program

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DOE Joint Genome Institute
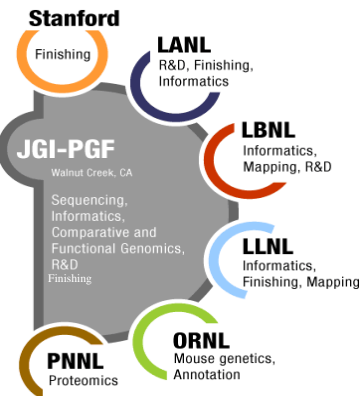
Programs:

DOE Microbial Program

DOE GTL Program (GTL)

Community Sequencing Program (CSP)

JGI Internal Program

LSP- Lab Science Program

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

The Community Sequencing Program

http://www.jgi.doe.gov/CSP/index.html

Types of projects:

A wide range of projects.
The most important factor for acceptance is a project's scientific merit.
The deliverables can range from raw sequence traces to well-annotated assembled genomes

JGI is a leader in performing sequences to support the number of U.S. Department of Energy (DOE) Microbial Programs. The Microbial Genome and GTL programs were established to determine the complete genome sequence of a number of microbes selected for their relevance to DOE missions. Community Sequencing Program recently started by JGI (http://www.jgi.doe.gov/CSP/index.html) also includes sequence and detailed analysis of the genomes of the different representatives of the microbial world.

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 300 microbes to draft quality, finished over 60 and is currently working on more than 100 additional microbial projects. Most projects are now targeted for complete finishing.
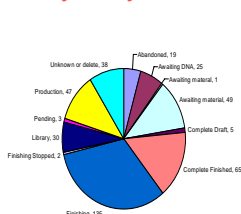
A completely sequenced, high quality genome is a perfect starting point for the genome annotation (http://img.jgi.doe.gov/v1.1/main.cgi), microarrays, knockout experiments, etc. Despite the fact that draft genomes are useful on their own, a completed genome is, overall, a better product, especially if it will be used to analyze previously unknown and difficult-to-cultivate microbes; for the comparative analysis of 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. 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.

The Integrated Microbial Genomes (IMG) system was created to provide a framework for comparative analysis of the genomes sequenced by the Joint Genome Institute. Its goal is to facilitate the visualization and exploration of genomes from a functional and evolutionary perspective. Currently IMG includes 674 genomes from archaea to eukarya sequenced by JGI (134) and other centers.
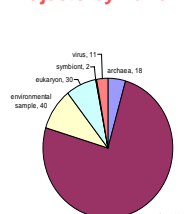
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Genome Sequencing

Start with genomic DNA → Make sheared fragments → Sequence both ends of fragments

Genome assembly and finishing

Genome Annotation

Steps in the Sequencing Process
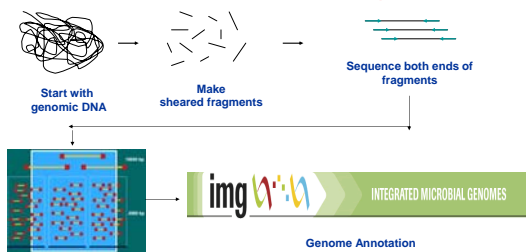
Finished Genomes

2005 DOE Microbe Projects
Rhodopseudomonas palustris HaA2
Acidobacterium Ellen 345
Rhodopseudomonas palustris BisB18
2005 CSP Microbe Projects
Ignicoccus sp. KIN4/I
2005 WFO Microbe Projects
Chlamydia trachomatis Ds2923
Chlamydia trachomatis G9301
2004 DOE Microbe Projects
Pelodictyon luteolum DSM 273
Methanospirillum hungateii, JF1
Nitrosospira multiformis Surinam
Nitrosococcus oceani ATCC 19707(ex Nitrosomonas oceani)
Nitrobacter winogradskyi, Nb-255
Frankia sp., Ccl3
Anaeromyxobacter dehalogenans, 2CP-C
Thiomicrospira crunogena XCL-2
Thiomicrospira denitrificans
Jannaschia sp.CCS1
Thiobacillus denitrificans, ATCC 25259
Polaromonas JS666 (ex b-proteobacterium sp., JS666)
Synechococcus sp., CC9902 (Coastal)
Synechococcus sp., CC9605 (Oligotrophic)
Prochlorococcus sp., NATL2A
Chromohalobacter salexigens, DSM3043
Psychrobacter cryohalolentis K5 (ex Psychrobacter cryopegella)
Nitrobacter hamburgensis
2004 GTL
Rhodoferax ferrireducens DSM 15236
Pelobacter carbinolicus DSM 2380
Organsim: 2003 Microbes
Prochlorococcus sp. MIT9312
Methylobacillus flagellatus
Chlorobium chlorochromatii CaD3 (ex Chlorochromatium aggregatum)
Moorella thermoacetica ATCC 39073
Anabaena variabilis
Synechococcus elongatus
Methylobium petroleophilum PM1(ex Rubrivivax gelatinosus PM1)
Burkholderia strain 383(ex R-18194)

2002 Microbes
Ehrlichia canis
Saccharophagus (ex Microbulbifer) degradans 2-40
Ralstonia eutropha JMP134
Dechloromonas aromatica RCB
Pseudomonas syringae B728a
Rhodospirillum rubrum ATCC 11170
Desulfovibrio desulfuricans G20
Geobacter metallireducens GS-15
Psychrobacter sp. 273-4
Methanococcoides burtonii
Haemophilus somnus 129PT

2001 Microbes
Cytophaga hutchinsonii ATCC 33406
Methanosarcina barkeri fusaro
Pseudomonas fluorescens PfO-1
Rhodobacter sphaeroides 2.4.1
Thermobifida Fusca YX
Burkholderia xenovorans LB400 (ex Burkholderia fungorum)
Nostoc punctiforme ATCC 29133
Novosphingobium (ex Sphingomonas) aromaticivorans
Synechococcus WH8102
Rhodopseudomonas palustris CGA009
Nitrosomonas europaea
Prochlorococcus marinus MED4
Prochlorococcus marinus MIT9313
Bacillus anthracis Sterne
Bacillus thuringiensis 9727
Bacillus thuringiensis ALH
Bacillus thuringiensis Zebra killer
Brucella abortus 2308
Francisella philomiragia 2773039
Francisella tularensis OR-960463
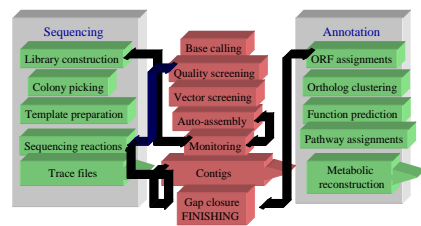
JGI-wide Finishing Standards

- All low quality areas (<Q30) should be reviewed and re sequenced.
- Final error rate should be < 0.2 per 10 Kb.
- No single clone coverage, i.e. minimum of 2X depth everywhere.
- Manually inspect and quantify single stranded regions.
- Check all high quality discrepancies.
- Verify all repeats (paired ends and PCR if necessary).
- Make sure to check ends of final contigs (chromosomes, plasmids)
- Using Assembly Viewer and phrapViewer tools check correctness of final assembly. Confirm questionable areas with PCR.

135 Microbial projects in finishing
65 – Microbial genomes finished

Genome Analysis

finished/draft

	JGI	Total
Bacteria	43/87	256/117
Archaea	1/3	23/3
Eukarya	0/0	12/3
Viruses	0/0	260/0
All Organisms	44/90	551/123
Grand Total	134	674

Next IMG release: March 1, 2006

Projects by Status

Projects by Taxonomy