

Resource Summary Report

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Microbial Genetics Resource at JGI

RRID:SCR_000570

Type: Tool

Proper Citation

Microbial Genetics Resource at JGI (RRID:SCR_000570)

Resource Information

URL: <http://genome.jgi.doe.gov/programs/bacteria-archaea/index.jsf>

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Description: Mission: Dynamically evolve sequencing, finishing, annotation and analysis processes, exploit new technologies, and develop expertise to deliver high quality and high throughput sequence-based microbial science by listening to and responding to DOE Users and scientific community needs. GOALS 1. Expand product catalog and increase sample throughput while maintaining highest quality The MGP has been expanding its product catalog beyond a finished microbial genome and has projected to significantly up ramp throughput for the majority of its current products namely Draft Genomes, Single Cell Genomes, Quick Draft Genomes, Resequencing projects and RNAseq Project. This projected increase in microbial genomes is going hand-in-hand with and has been stimulated by new high throughput technologies and capabilities (de novo microbial Illumina assemblies, single cell genomics, Genologic sample tracking). The increased throughput will support the user community as well as JGI scientists by enabling DOE-relevant science at a grander scale. As the Program aims to generate hundreds of microbial genomes per year, our goal is to scale our production efficiency and maintain our trademark quality to best support our science mission. 2. Expand sequence space One of the ongoing missions of the MGP is to expand the coverage of the phylogenomic sequence space by generating reference genome datasets from highly diverse branches in bacterial and archaeal tree of life. The value of such effort includes the generation of phylogenetic anchors for metagenomic datasets, the improvement of annotation, an increased insight into phylogenetic distribution of functions, the discovery of novel genes, protein families, pathways and a better understanding on evolutionary diversification. 3. Make Single Cell Genomes a robust User product As the vast majority of microbes are uncultured to date, single cell genomics will be a crucial component of the MGP over the next several years to drive not only JGI science but also User community proposed single cell research. Going hand-in-hand are R&D efforts in selective single cell isolations, testing the effects of fixation of single cell sequencing, as well as single cell transcriptomics. 4. Sequence Pangenomes Combining similar genomes together creating pangenomes will allow more compact genome sequence storage and visualization and

expedite analysis and annotation. Moreover, the pangenome as a representation of the whole group of organisms may be more representative of a given species within the environment. The MGP thus thrives to enable the sequencing and analysis of pangenomes. Current technology allows the sequencing of one organism strain at a time. Assuming that for most cases, several dozen strains may need to be sequenced in order to generate a more accurate pangenome for every microbial species, it becomes evident that the cost for doing so may be prohibitively high. Our goal here will be to explore new approaches and technologies for generating these pangenomes at a very low cost and analogous to what is the cost today for a single strain.

5. Expand and improve microbial annotation using transcriptomic data To improve annotation of gene structure, establish accurate transcription level and timing, provide information on gene regulation and generate information for expanding understanding of systems biology, the MGP strives to generate transcriptomics data for larger sets of Bacteria and/or Archaea. This will enable the identification of novel regulator RNAs, as well as facilitate the understanding of uncharacterized protein families.

6. Maintain and evolve a top quality data management system To enable state of the art and world class comparative analysis of internal and external scientific projects, the JGI data integration and visualization management system for comparative analysis of microbial genomes, namely IMG, needs to be maintained and continuously evolved. The system needs to be able to support and integrate all data generated by JGI (WGS, reseq, RNAseq, -other omics data), as well as by the user community, enabling annotation and manual curation of the annotation, comparative analysis, gene-centric and pathway centric analyzes. The system should also facilitate the integration of associated metadata, enable data sharing and distribution, as well as automated data GenBank submissions. Lastly, the system needs to have the ability to scale enabling the annotation of thousands of genomes per year.

7. Drive Flagship projects To stay at the forefront of microbial genomic research, be recognized as such and enable the development new methods and tools, the MGP aims to drive DOE mission relevant flagship projects. Novel tools and methods developed will ultimately serve the user community if proven useful and implemented as part of a larger pipeline. MGP flagship projects are the GEBA and GEBA uncultured projects, as well as the GEBA-RNB, the proposed Microbial Earth and the Microbial Dark Matter Projects.

Abbreviations: JGI Microbial Genetics Program

Synonyms: Microbial Genetics Program - Exploration of Microbial Diversity, Microbial Genetics Program at JGI

Resource Type: data or information resource, database

Keywords: genomics, microbe, bacteria, archaea, sequencing, annotation, genome, microbial

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Ratings and Alerts

No rating or validation information has been found for Microbial Genetics Resource at JGI.

No alerts have been found for Microbial Genetics Resource at JGI.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.