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Authors

Richardson, Paul
Bruce, David
Lucas, Susan
et al.

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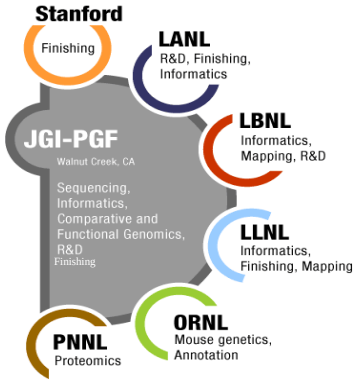
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Advancing Science with DNA Sequence

The Joint Genome Institute User Facility Sequencing Programs

Paul Richardson*, David Bruce, Susan Lucas, Thomas Brettin, Paul Gilna, Jim Bristow, Eddy Rubin and the JGI Sequencing Staff
*Corresponding Author (PMRichardson@lbl.gov)

DOE JOINT GENOME INSTITUTE
US DEPARTMENT OF ENERGY
OFFICE OF SCIENCE



The Joint Genome Institute (JGI) is a high-throughput sequencing center and user facility funded primarily by the US Department of Energy (DOE). The JGI sequences genomes and environmental samples of interest to the scientific community in response to applications to several peer-review programs. The primary programs that review suggestions for sequencing from the research community are the DOE Microbial Genome Program (MGP) and the JGI Community Sequencing Program (CSP). The main goal of these programs is to utilize genomics to advance science related to DOE missions in bioenergy production, environmental remediation, and carbon management. Any research scientist may send in proposals to these programs to suggest targets for sequencing. Successful applicants do not receive monetary awards, but receive an allocation of JGI sequencing capacity and are expected to provide the DNA and other information to complete the project.

The JGI activities include DNA sequencing, assembling, and annotating genomes of prokaryotes, eukaryotes and environmental samples. The DNA sequences are made publicly available on the JGI website (www.jgi.doe.gov), and deposited in public databases such as GenBank. Virtually all genome projects are sequenced by the whole genome shotgun method. The process begins by shearing purified genomic DNA and ligating size selected fragments into different vector systems to produce multiple subclone libraries for sequencing. The libraries are sequenced by the production group to approximately 8.5X coverage. The resulting reads are trimmed for vector sequences and aligned with one another to produce a consensus draft genome assembly. There are various Quality Control checkpoints during the process to ensure the genome assembly accurately reflects the DNA sequence of the organism under study. Much of the sequencing capacity is devoted to microbial genomes and to date, the JGI has sequenced over 250 microbes and metagenomic samples to draft quality and completely finished over 70 microbial genomes. Genomes are annotated using automated pipelines that identify potential genes and these are assigned putative function based on similarity to known genes. Annotated genomes are uploaded to the JGI Integrated Microbial Genome database (IMG) tool for pathway analysis and comparative genomic approaches (http://img.jgi.doe.gov).

The JGI has sequenced a number of microbes relevant to DOE missions. These include organisms involved in Carbon production or sequestration including a variety of species of Chorobia and Chloroflexi, marine organisms such as Prochlorococcus, Synechococcus Micromonas, and Tholassiosira pseudonana. The JGI sequences a large number of organisms that live in diverse environments and can process heavy metals or other toxic compounds. Examples include Bukholderia, Acidobacteria, Dehalococcoides, Deinococcus, Shewanella, and Geobacter. In addition, the JGI has sequenced organisms that may be important in biofuel production. These include several Methanogens and Clostridia, Microbulbifer degradans, Phanerochaete chrysosporium, Postia placenta, and Pichia stipitis. A complete list of organisms, their sequence and annotations can be found at: http://www.jgi.doe.gov/. The JGI is made up of affiliates from a number of national laboratories including Lawrence Berkeley National Laboratory, Lawrence Livermore National Laboratory, Los Alamos National Laboratory, Oak Ridge National Laboratory, and Pacific Northwest National Laboratory as well as Stanford Human Genome Center.

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Programs:

DOE Microbial Program

DOE GTL Program (GTL)

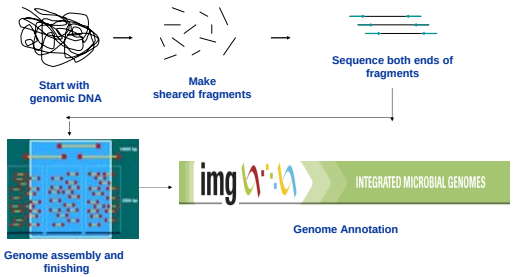
Community Sequencing Program (CSP)

JGI Internal Program

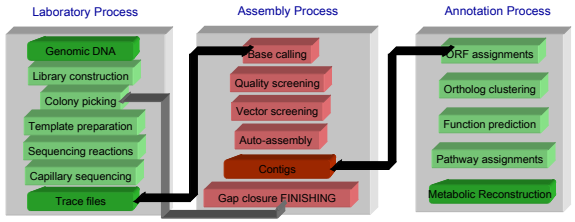
LSP- Lab Science Program

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

Whole Genome Shotgun Sequencing



Steps in the Sequencing Process



U.S. DEPARTMENT OF ENERGY

JGI DOE JOINT GENOME INSTITUTE

BIOENERGY

Harnessing DNA to Fuel Energy Security

The U.S. Department of Energy Joint Genome Institute (DOE JGI) occupies a unique niche as a U.S. based user facility dedicated to harnessing the power of information embedded in microbes and plants through DNA sequencing. In the field of bioenergy, DOE JGI is attempting to make alternative fuels cheaper and easier to produce.

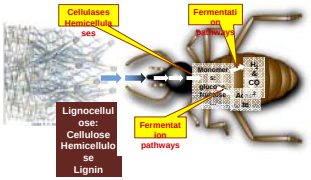
The Poplar Tree: Advancing Alternative Energy Sources



Forest trees contain more than 90% of the Earth's terrestrial biomass, providing such environmental benefits as carbon sequestration, renewable energy supplies, improved air quality, and biodiversity. However, little is known about the biology of forest trees in comparison to the detailed information available for crop plants. DNA sequence information will enable forest tree biologists to perform large-scale analyses of genes, leading to improved plant materials for the forest products industry and eventually to the selection of genetic traits for addressing questions related to the DOE's energy-related mission. DOE JGI has already identified candidate genes that will help domesticate poplar for biomass and reduce costs from $50 down to about $20 per ton.

The black cottonwood, *Populus trichocarpa*, is used in activities such as carbon sequestration research, free-air CO2 enrichment studies, and the development of fast-growing trees as a renewable bioenergy resource. The sequencing effort will also inform applications of phytoremediation, where trees can be used to remediate hazardous waste sites.

Termites: Fueling the Future



One of DOE's most enduring goals is to replace fossil fuels with renewable sources of cleaner energy, such as hydrogen produced from plant biomass fermentation. The lowly termite is capable of cranking out two liters of hydrogen from fermenting just one sheet of paper, making it one of the planet's most efficient bioreactors.

Termites accomplish this Herculean task by exploiting the metabolic capabilities of microorganisms inhabiting their hindguts. Sequencing the community of microbes in the termite hindgut, providing a better understanding of the biochemical pathways, may lead to more efficient strategies for converting biomass to fuels and chemicals. Harnessing the pathways directly involved in hydrogen production in the termite gut may make it possible for biological production of this alternative fuel source.

Soybeans: Translational Genomics for Clean Energy



The soybean, Glycine max, is the principle source of biodiesel, a renewable, alternative fuel. Biodiesel has the highest energy content of any alternative fuel and is much more environmentally friendly than comparable petroleum-based fuels. Biodiesel degrades rapidly in the environment and burns more cleanly than conventional fuels, releasing only half the pollutants and reducing the production of carcinogenic compounds by more than 80%.

Detailed knowledge of the soybean genetic code will allow for crop improvements and the effective application of this plant to clean energy generation. Knowing which genes control specific traits, researchers could change the type and quantity of oil produced by the crop, and lead to soybean plants that are more resistant to drought or disease. Through DOE JGI's efforts, it may be possible to develop a customized biomass production platform for combining oil seed production for biodiesel with enhanced vegetative growth for ethanol conversion—doubling the energy output of the crop.

In 2004, over 3.1 billion bushels of soybeans were grown on nearly 75 million acres in the US, with an estimated annual value exceeding $17 billion—second only to corn, and about twice that of wheat.

JGI Microbial Sequencing Projects

