

industry. (<http://www.tigr.org/tdb/mdb/mdbcomplete.html>, <http://www.ornl.gov/microbialgenomes/organisms.html> and http://www.jgi.doe.gov/JGI_microbial/html/). Nonetheless, most of our current knowledge of microbiology still is derived from individual species that either cause disease or grow easily and readily as monocultures under laboratory conditions and are thus easy to study. The preponderance of species in the environment remains largely unknown to science. Many are thought to grow as part of interdependent consortia in which one species supplies a nutrient necessary for the growth of another. Virtually nothing is known of the organization, membership, or functioning of these consortia, especially those involved in environmental processes of DOE interest. Fungi and small multicellular eukaryotes play important roles in the environment as well.

Genomic analyses of sequenced microbes have suggested that processes such as lateral gene transfers at various times in the evolutionary history of some microbial lineages may have blurred the understanding of their phylogenetic relationships. For this notice, groups of microbes that may have exchanged (or may be exchanging) genetic information via lateral gene exchange or plasmid mediated exchanges can be proposed if the processes of genetic exchange result in functions relevant to DOE missions noted above.

Genomic analyses are badly needed of microbial consortia and species refractory to laboratory culture that play important roles in environments challenged with metals, radionuclides, chlorinated solvents, or are involved in carbon sequestration. The candidate(s) must mediate or catalyze metabolic events of energy or environmental importance. Priority will be given to studies on those microbes or microbial consortia that can bioremediate metals and radionuclides, degrade significant biopolymers such as celluloses and lignins, produce potentially useful energy-related materials (H₂, CH₄, ethanol, etc.), or fix or sequester CO₂.

For this notice, candidate organisms (either individual organisms, consortia of organisms, or eukaryotes with small genomes) comprised of archaea, bacteria, fungi, algae, and other eukaryotes with genome sizes not greater than 100Mbp can be proposed for draft sequencing. For a current list of microbes that have been and are being sequenced see <http://www.ornl.gov/microbialgenomes/organisms.html> and <http://www.ornl.gov/microbialgenomes/seq2003.html>.

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Aims: This request for nominations of candidate sequencing targets has two broad foci:

(1) Single culturable organisms. These may be bacteria, archaea, fungi, microalgae or multicellular organisms with genomes not larger than 100Mb. The criteria that will be used to evaluate proposed candidates for draft sequencing will include:

(a) The candidate has significant relevance to the DOE missions noted above;

(b) The genome size and structure are known;

(c) The source of genomic DNA (*i.e.*, strain or isolate, and researcher) is identified, and a clonal sample (or samples with low and characterized polymorphism) are available;

(d) A brief description of post sequencing follow-up work (*e.g.*, a data use plan and how will data be annotated to enable rapid and open use) is included;

(e) The availability of a DNA/gene transfer system supporting genetic analyses is known;

(f) Biological novelty or uniqueness (*i.e.*, unusual genetically determined characteristics pertinent to DOE missions) is described;

(g) Place in the currently understood, 16s RNA based, "Tree of Life" is identified, *e.g.*, is the proposed candidate in a sparsely populated or more heavily populated section of the tree?

(h) A brief description of the user community is given;

(i) The potential impact on the scientific community is large;

(j) Explicit commitment to a data-release schedule, consistent with the guidelines given below is provided.

(2) Currently unculturable or hard-to-culture organisms and environmental consortia. The review criteria that will be used to evaluate proposed candidates for draft sequencing will include most of the criteria listed above for single culturable organisms (with less emphasis on genome size/structure, presence/absence of a genetic system, or position in the "Tree of Life" since it is recognized that few data on these attributes will be available), but in addition, the following considerations will be included:

(a) Some measure of the "complexity" of the target consortium being proposed, *e.g.*, approximate number of species, size(s) of genomes, and proportions of different members (it is understood that in most cases, only estimates of these parameters may be available) is discussed. When the environmental

consortia are complex, approaches should be described to normalize the DNA libraries in order to reduce the amount of sequencing required and assure adequate sampling of the complexity of the consortia. Additionally, the proposer(s) should be prepared to work together with JGI scientists to optimize the yield from the sequencing effort required;

(b) Past attempts to cultivate consortium members are described, *e.g.*, have any members of this consortium been successfully cultured;

(c) Some spatial/temporal/hydrochemical/geochemical or other characterization of the environment is given, *e.g.*, the physicochemical parameters of the site from which the selected community is derived; a description of the site contaminants; the accessibility of the site for future sampling; the adequacy of site documentation;

(d) If proposed, technical approaches and technology development specific for defining and isolating members of a given consortium are described;

(e) Some indication of the biological function of the relationships, within consortium members, where available along with a discussion of the scientific and programmatic importance of understanding these relationships is given;

(f) Information where available is given about the phylogenetic position(s) of the members of the consortium and what is known about closely related organisms.

(g) Available informatics tools and annotation plan (*e.g.*, for annotating genes from a consortium analysis or grouping identified genes into a putative "consortium phenotype" within the chosen environment) are described;

(h) Explicit commitment to a data-release schedule, consistent with the guidelines given below is provided.

Scientific community standards regarding access to sequencing data are evolving. BER conforms to the general guidance contained within the Draft Rapid Data Release Policy (<http://www.genome.gov/page.cfm?pageID=10506537>) for "community resource projects." The usual and customary practice for the JGI is to put all sequencing data up on its web site (<http://www.jgi.doe.gov/>) at frequent and periodic intervals. However, for the purposes of this notice, BER does not regard individual genome sequencing efforts involving less than 50Mb, or microbial community sequencing efforts, as requested herein, as "community resource projects" within the definition of the Draft Rapid Data Release policy. BER's position,