

Genomic Sequencing of Prokaryotic Type Strains: GEBA III October 5, 2017

The Genomic Encyclopedia of Bacteria and Archaea (**GEBA**) III is a project of the Community Science Program (CSP) of the DOE Joint Genomes Institute. Its goal is to obtain draft genomic sequences of the **type strains** of prokaryotes associated with soil or plants and their close relatives as well as type strains from newly described species prior to publication. Strains of human pathogens and human associated species and strains with a Biosafety Level greater than 1 are not eligible.

In this project, DOE-JGI will provide a draft genome sequence using the Illumina technology with an automatic annotation, yielding on average ~50 contigs. Data will become publically available and made available to the investigator as soon as it passes the final QC analysis at DOE-JGI.

Requests for sequencing should be sent to Barny Whitman at whitman@uga.edu. Include in the subject line 'JGI genome sequencing'. Requests should include: 1) A list of the type strains to be sequenced with a short description of each strain identifying the source of the strain, any particularly interesting properties, reference for the validating or effective publication, and the strain designation in at least one international culture collection. The description of each strain does not need to be longer than 2-3 sentences. All strains have to have been deposited in a culture collection, including proposed type strains prior to publication. If a culture collection number is not available, please attach a copy of the Certification of Availability. If the species description is already accepted for publication, cite the publication as in press.

If the request for sequencing is approved, you will be asked to provide 500 ng of high molecular weight, RNA-free DNA from each type strain. The identity and purity of the type strain and the DNA to be sent should be confirmed by nearly complete (>1300 bp) sequencing of the 16S rRNA gene. The DNA can be prepared according to a variety of protocols, and some recommendations on the purification will be provided upon acceptance of your proposal.

The sequencing of type strains of prokaryotes is an international effort and proceeding rapidly in many different laboratories. To determine if a genome project is currently underway for organisms of your interest, please check the NCBI [<http://www.ncbi.nlm.nih.gov/>] and GOLD [<http://genomesonline.org/cgi-bin/GOLD/index.cgi>] databases for existing sequencing projects prior to requesting sequencing through this program.

For questions, contact Barny Whitman, University of Georgia (whitman@uga.edu).