

**SHOTGUN LIBRARY UTILIZATION FOR MICROBIAL SEQUENCING PROJECTS AT THE JGI**

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To date, the US Department of Energy's Joint Genome Institute has produced shotgun libraries for more than 150 microbial whole genome sequencing projects. In an effort to better span repeats and link contigs we now utilize a 3 library approach for all whole genome shotgun projects. Here, we describe the construction, sequencing, and analysis of our 3 library cloning approach with the goal of producing high quality draft assemblies with greater genome coverage and fewer gaps. The libraries were constructed from randomly sheared whole genomic DNA that was size selected to approximately 3Kb, 8Kb or 40Kb and ligated into the appropriate high, low, or single copy cloning vector. The libraries were sequenced to an approximate depth of 4X for the 3Kb and 8Kb libraries, and approximately 15X clone coverage for the 40Kb fosmid library. Analysis to date of a wide array of microbial projects indicates our cloning strategy has been successful in spanning repeat regions and producing longer-range contiguity. These assemblies reduce the amount of finishing required to complete the genome sequence.

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