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Finishing of *Spirochaeta aurantia* M1

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Shotgun sequencing and finishing of an isolate of the *Spirochaeta aurantia* M1 genome, a free-living nonpathogenic Spirochete, is in process at the Joint Genome Institute. *S. aurantia* M1 is being sequenced due to its proximity on the phylogenetic tree to bacteria present in the termite hindgut that were partially sequenced during a metagenomic project at the JGI, and, for improving the understanding of pathogenic Spirocheates through comparative genomic studies. The assembly is currently in 3 contigs and most of the finishing has been done using fosmid templates to close gaps. The shotgun assembly is a combination of fosmid sequencing, a novel Sanger approach, 454 sequencing, and Solexa data. The novel Sanger approach takes advantage of a bulk cloneless library preparation method involving the amplification of long DNA fragments onto beads, by emulsion PCR, and the subsequent sorting of individual beads by flow cytometry for seeding the Sanger chemistry process.

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