Title
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 Spirochetes through comparative genomic studies.

Illumina for polishing

Part of finishing at the JGI is polishing. Our current standards require that each base has to meet quality thresholds. We have begun to use Illumina data to polish in a time and cost effective manner. Our group has developed a tool to align Illumina data to a 454-sanger hybrid assembly. This takes care of a vast number of reactions. However, often there are still areas that need additional verification. These remaining areas are verified using traditional Sanger sequencing.

Part A of the screenshot below shows an area of the genome covered by 454 and partially covered by 1 low quality read. Part B shows the Illumina reads aligned to the reference. Bases that are “solexa supported” don’t need further verification.

Further improvements:

Further improvements include making a larger insert library. In terms of repeat resolution and gap spanning a 2kb library isn’t an ideal size. The Sanger/454 hybrid process could also be developed further by sorting the emulsions rather than the 454 beads.

Other applications:

The flow sorter can be used with anything that can be fluorescently labeled or sorted by size. This can allow you to sort a single population out of a community. The flow sorter can also be used in single cell genomics.