Lawrence Berkeley National Laboratory
LBL Publications

Title
Metagenomic Finishing at the JGI

Permalink
https://escholarship.org/uc/item/9pv1r8g0

Authors
Lapidus, Alla
Lowry, Stephen
Clum, Alicia
et al.

Publication Date
2008-11-03

eScholarship.org Powered by the California Digital Library
University of California

Metagenomic Finishing at the JGI

Stephen Lowry, Alicia Clum, Eugene Goltsman, Hector Garcia Martin, Phil Hugenholtz, Susan Lucas, **Alla Lapidus** (alapidus@lbl.gov)
US DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598

Normally, complete genomes are obtained by growing the organism of interest in pure culture, generating the shotgun sequencing and closing the gaps. In case of metagenomic samples, it is difficult to expect a completed, ungapped genome, considering the organism is being sequenced directly from the environment. Despite this fact, finishing of three dominant populations within the metagenome datasets of different complexity that had draft level coverage was successfully performed. This was possible due to 1) the enrichment of the target organism in the population; 2) generation of draft sequence using traditional metagenomics; 3) computational identification of sequences derived from the target organism; 4) gap closure; 5) use of pyrosequencing. The complexity of the community, the quantity of genomic DNA available as well as the size of the fraction of the total DNA, which represented the organism under study all added on to the normal difficulty level of having to establish a complete sequence.

At the JGI we have managed to complete the sequence of three metagenomic organisms, and are investigating a fourth, presenting a considerable range of difficulty.

Candidatus Korarchaeum cryptofilum OPF8, (low complexity case; 1.59MB; 49%GC), is the first of this apparently ancient hyperthermophilic phyletic group to be sequenced (3). The ability to obtain ample DNA of near-monocultural purity and low strain complexity made this the most straightforward sort of metagenomic subject. The target organism constitutes ~40% of the Yellowstone thermal Obsidian Pool community. The community could be maintained in culture, and it was found that *K. cryptofilum* was the most resistant member to SDS lysis, thus allowing DNA purification to better than 90%. Its strain complexity was low as indicated by a SNP rate of ~0.2%.

Some organisms have remote or difficult habitats limiting the availability of source material. This is the case with the thermophile *Desulforudis audaxviator*, (limited amount of source material; 454 pyrosequencing to compensate for the cloning bias of Sanger libraries), from fractures in the earth's crust at a depth of 2800 meters in a South African gold mine (4).

The bacteria were collected on filters through which large amounts of subterranean water was passed. The surprising fact that this ecosystem contained but one species fortunately meant that the DNA yield of this one-time-only collection was sufficient to complete the genome.

Considerably more complex situations are the rule, as illustrated by the case of *Candidatus Accumulibacter phosphatis Type IIA str. CU-1* . This and closely related species are the principal actors in the sequestration of inorganic phosphate as intracellular polyphosphate in wastewater treatment facilities. Bioreactor sludge derived from a working facility in Wisconsin is a physically unresolvable mixture of organisms, with *A. phosphatis* predominating at about 40%. The entire DNA sample was sequenced and the resulting data then subjected to phylogenetic parsing using the Phylopythia (2) binning technique, greatly reducing the complexity of the subclone libraries.A single 5Mb chromosome was successfully sequenced, along with 3 plasmids of 167, 42 and 38kb.

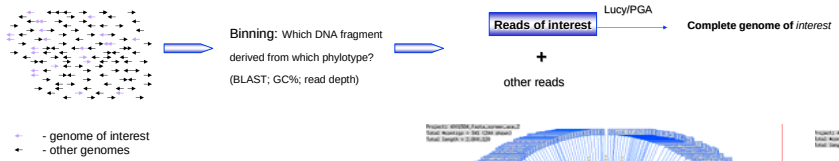
We are now approaching a still more difficult genome. *Candidatus Endomicrobium trichonymphae* is an intracellular symbiont of a flagellate protist, itself part of the normal hindgut community of a termite host. It is of interest in the pursuit of the efficient breakdown of cellulose and lignin necessary in the hoped-for use of bulk plant materials as CO2-neutral fuel stocks.

Again partitioning with Phylopythia was absolutely necessary. So far this has yielded some 42,000 Sanger reads. Of these about 40% of the assembled contigs are similar to related organisms. Also contigs from 454 pyrosequencing contributed about 750,000 bp of additional coverage (~0.5x).

Additional difficulty arises from sample size and strain complexity. There are several closely related organisms with substantial representation. There are several hindguts in the sample, and the lines of descent may be relatively independent even at the protist level.

1. Martin, H.G., Hugenholtz, P., et al. 2006. *Metagenomic Analysis of two Enhanced Biological(EBPR) sludge communities Phosphorous Removal*, Nature Biotechnology, v24, no.10, 1263-69
2. McHardy et al. Appl, 2000, *Accurate phylogenetic classification of variable-length DNA fragments.* Environ Microbiol, 66 (3):1175-1182
3. James G. Elkins, et al.,2008, *A korarchaeal genome reveals insights into the evolution of the Archaea*, PNAS, Jun 10;105(23):8102-7
4. Dylan Chivian, et al., 2008, *Environmental genomics reveals a single-species ecosystem deep within Earth.* Science, Oct 10;322(5899):275-8

Finishing approach (binning/reassembly):

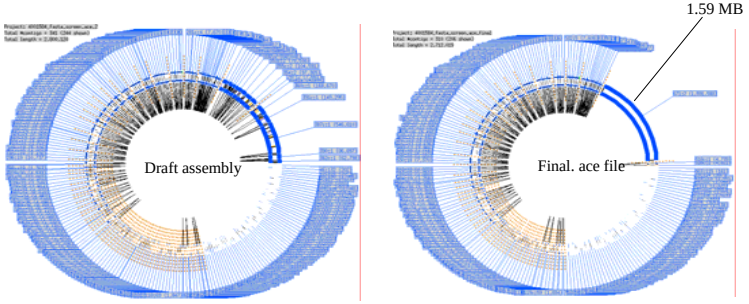


Korarchaeum cryptofilum OPF8

From a more complex thermophilic community, it was maintained as a community in the lab, and enriched by differential lysis. This organism was finished by conventional means. Its small size was helpful.

Though there was considerable enrichment, there is a great deal more representation of other species in this project than with *D. audaxviator*.

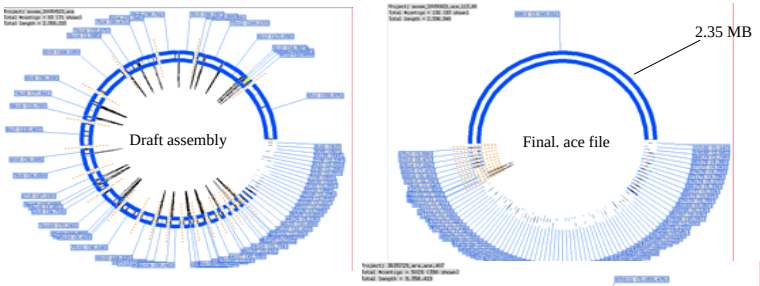
These first two organisms certainly represent the unusually straightford end of the community finishing spectrum.



Desulforudis audaxviator

Described as a 'one organism ecosystem'(4), which is to say it has been environmentally enriched. The representations in Orchid (available from the Stanford Genome Center) at right show clearly the low complexity of this community. (Orchid displays an ace file distributed around a circle, the heavy blue sections being continuous sequence.)

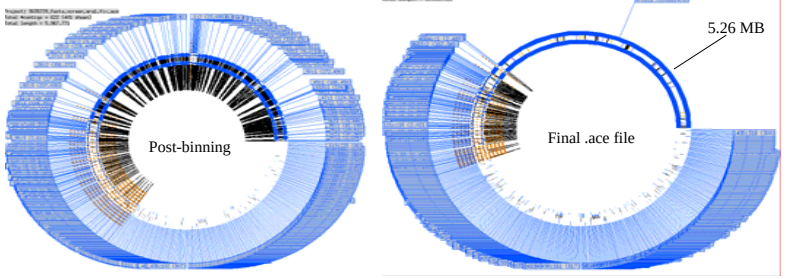
The left hand image is a representation of the contigs in the earliest assembly ace-file, while the right is of the final. Only about 100 reads remain unincorporated out of 28000.



Accumulibacter phosphatis Type IIA str. CU-1

A more difficult, and undoubtedly more typical situation was presented by *A. phosphatis*. It was the first community subjected to PhyloPythia binning, reducing th number of reds by more than half and which eventually produced the assembly illustrated at right. One can see that after completion about 45% of the initial reads have fused into the final consensus.

There is moderate polymorphism. It was our good fortune that 454 sequencing came on the scene as we considered finishing the genome. It allowed the bridging of many small gaps, and confirmed other only moderately supported regions.



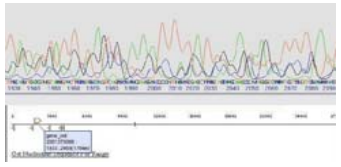
Data QC and assembly: Trimmer + PGA

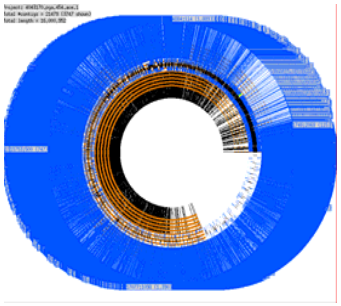
cross_ match

VS

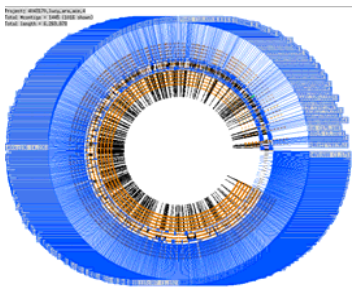
trimming (Lucy)

Poor quality data can also be annotated!!!





Pre-binning



Post-binning

Endomicrobium trichonymphae

A more challenging situation exists with *E. trichonymphae.* The sequence obtained from the combined hind-guts of a group of termite nest-mates was binned targeting a bacterial symbiote of a symbiotic flagellate protist. The enrichment reduced the read number by about 60%. The pertinent portion of the assembly at this point seems to consist of a number of strains considererably more distant from each other than the polymorphic members of the previous projects.

This can be illustrated by the cartoon on the right. In it, contigs with clear BLAST related sequence to a very closely related organism are aligned against that genome (AP009510.1), which is represented by the left vertical bar. The coloring is arbitrary to make contigs distinct.

This work was performed under the auspices of the US Department of Energy's Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Berkeley National Laboratory under contract No. DE-AC02-05CH11231, Lawrence Livermore National Laboratory under Contract No. DE-AC52-07NA27344, and Los Alamos National Laboratory under contract No. DE-AC02-06NA25396.