Expansion of the Genomic Encyclopedia of Bacteria and Archaea

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Abstract

To date the vast majority of bacterial and archaeal genomes sequenced are of rather limited phylogenetic diversity as they were chosen based on their physiology and/ or medical importance. The Genomic Encyclopedia of Bacteria and Archaea (GEBA) project (Wu et al. 2009) is aimed at systematically filling the gaps of the tree of life with phylogenetically diverse reference genomes. However more than 99% of microorganisms elude current culturing attempts, severely limiting the ability to recover complete or even partial genomes of these largely mysterious species. These limitations gave rise to the GEBA uncultured project. Here we propose to use single cell genomics to massively expand the Genomic Encyclopedia of Bacteria and Archaea by targeting 80 single cell representatives of uncultured candidate phyla which have no or very few cultured representatives. Generating these reference genomes of uncultured microbes will dramatically increase the discovery rate of novel protein families and biological functions, shed light on the numerous underrepresented phyla that likely play important roles in the environment, and will assist in improving the reconstruction of the evolutionary history of *Bacteria* and *Archaea*. Moreover, these data will improve our ability to interpret metagenomics sequence data from diverse environments, which will be of tremendous value for microbial ecology and evolutionary studies to come.

Scientific Questions/ Goals

Diversity
Discovery of novel genes, protein families, pathways

Ecology
Functional roles of candidate phyla?
Are phyla functionally homogeneous?

Phylogenetic distribution of functions
Photosynthesis? CO_2 fixation?

DOE relevance:
Functions of DOE interest in novel lineages of single cell genomes?

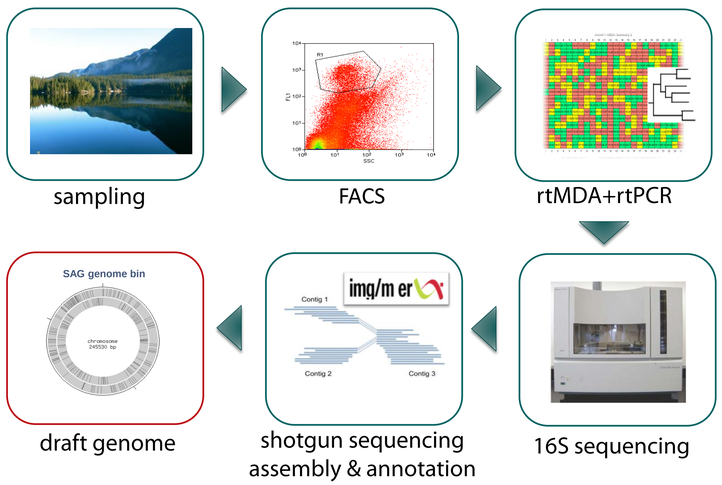
Evolution
Improved understanding on evolutionary diversification.
How did the bacterial domain evolve?

Diversity

Function

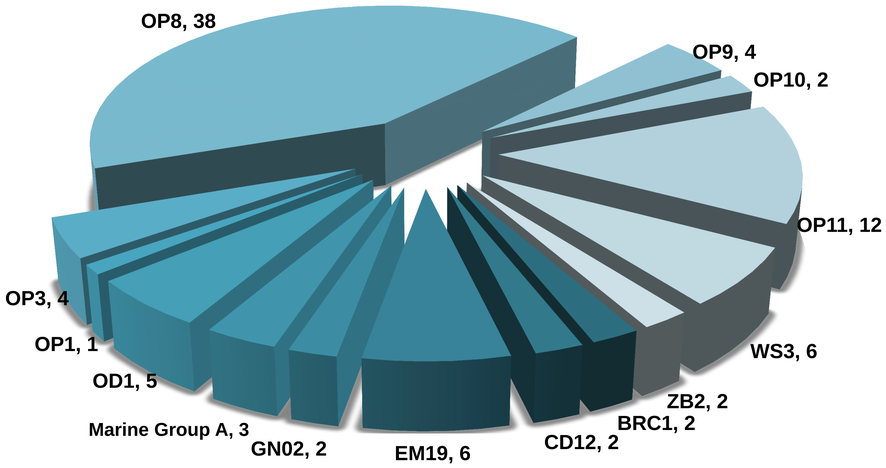
Evolution

Single Cell Genomics Pipeline

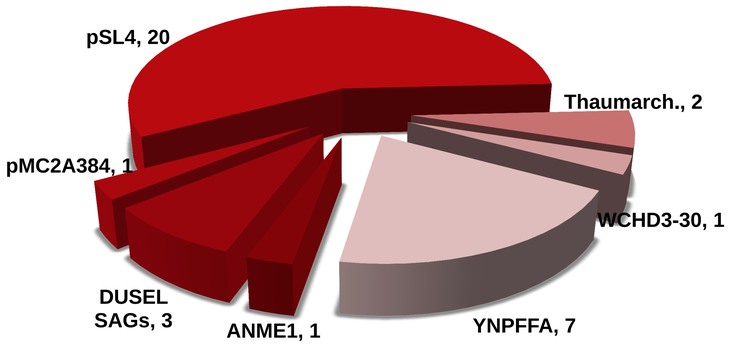


Results - Single Cell 16S Sequences

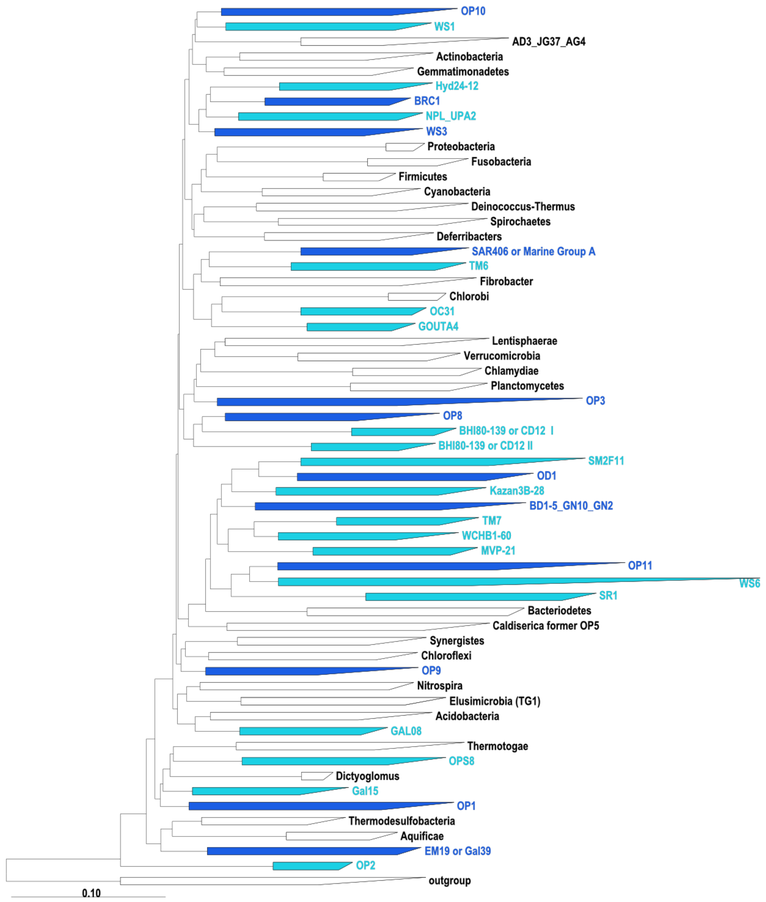
Novel Bacterial Lineages (89 total)



Novel Archaeal Lineages (35 total)

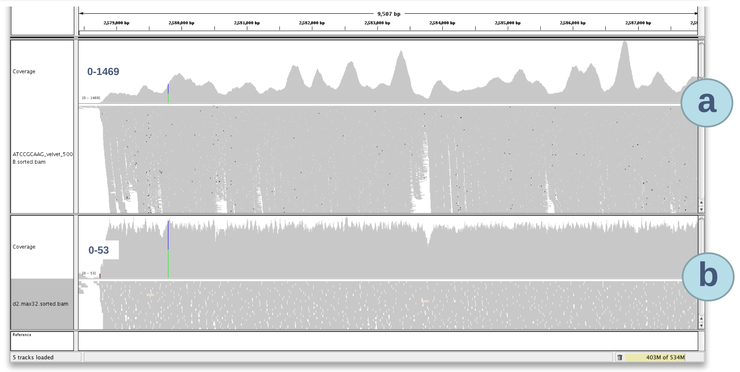


A total of 124 short 16S rRNA gene sequences of Single Amplified Genomes (SAGs) are available and will undergo low level shotgun sequencing in order to evaluate SAGS for deeper sequencing.

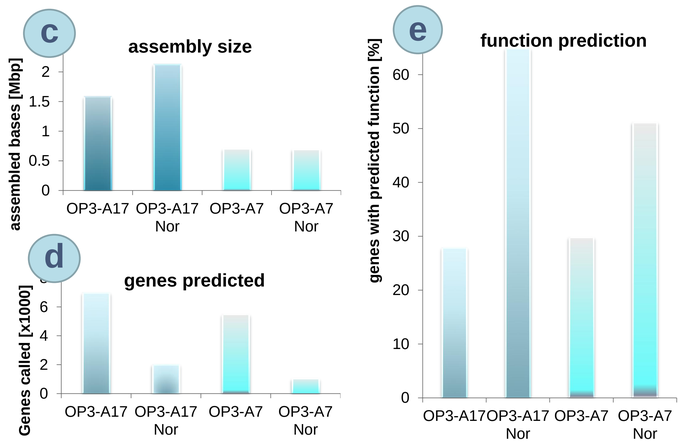


16S rRNA gene phylogenetic neighbor-joining tree of *Bacteria* based on the SILVA ARB database (www.arb-silva.de). Novel lineages of uncultivated representatives known only from environmental sequences are in blue: dark blue lineages are covered by the GEBA uncultured project, light blue lineages are not yet covered.

Results – Sequencing/Assembly



(a) MDA bias causes uneven genome coverage as shown by mapping the reads back to reference (velvet assembly). (b) Computational normalization based on k-mer frequency scales down coverage. (c) Assembly size of normalized reads (Nor) is equal to non- normalized reads. (d) Number of predicted genes is too high for non normalized assemblies. (e) Percentage of genes with a predicted function is higher for normalized assemblies.



Conclusion

Our single cell genomics pipeline allows amplification of genomes from microbial single cells directly from environmental samples, and thus the exploration of novel uncultured lineages.

References:
Wu D, et al. (2009) A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. Nature 462(7276):1056-60.

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