Assembly and Annotation Strategies for Three Microbial Genomes Sequenced Through the Genome Consortium for Active Teaching – NextGen Sequencing Group (GCAT-SEEK).


Our Projects – de novo sequencing and assembly of microbial genomes
- Flavobacteriaceae sp. JJC – Isolated from a PA creek, Possible novel genus to be named Lycomia zaccaria.
- Chryseobacterium haisense DSM 19056 T – Does not produce Flexirubin pigments, probably incorrectly classified, to be renamed Lycomia haisense
- Kaistella koreensis CCUG 49689 T – Moved into genus Chryseobacterium in 2009, based on similarity to C. haisense

Reference Strains – with Genome sequences available
- Flavobacteriaceae sp. 3519-10 – Isolated from ice core over Lake Vostok, not yet officially classified, to be named Lycomia vostokensis.
- Chryseobacterium gleum ATCC 35910 T – Sequenced as part of the human microbiome project

1. Sequence based comparison with related genomes suggests adjacent contigs/supercontigs.
2. Contigs/supercontigs can be reassembled and reversed complemented in Artemis.
3. Detailed sequence/ORF analysis can determine if contigs/supercontigs overlap, or if gap exists to be closed by PCR and sequencing during finishing.
4. Comparison of genes allows identification of specific genes, genes shared by different groups.

References

Acknowledgements
This work was supported by support from NSF Award DBI-1061893 to Michael D Boyle. The authors also thank Deb Grove and the staff of the Penn State University Genomics Core Facility.