



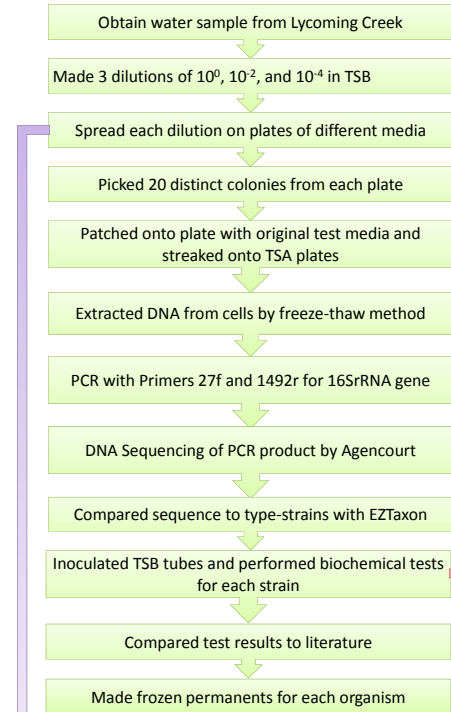
A Survey of Culturable Microbial Diversity from the Lycoming Creek.

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Abstract

The purpose of our study was to survey the bacterial diversity of Lycoming Creek in Lycoming County, PA with a systematic approach. We obtained a water and sediment sample from Lycoming Creek near where it empties into the Susquehanna River and grew bacteria on several types of media under different conditions, selecting for single colonies. We then amplified the 16S rRNA genes from the organisms by PCR and analyzed their sequences to determine their identity. Here we present data showing the different types of organisms isolated from the same source using different types of growth media and incubation conditions. Our secondary purpose was to identify potentially novel organisms (<98.5% 16S rRNA sequence identity) for subsequent polyphasic characterization.

Methods



Strain designations derived from original growth conditions:
 ABI = blood agar
 ALK = LB Kan
 AH = HEA
 AE44 = EG and LB Arab 44°C
 ALAm = LB Amp
 AA30 = LB Arab 30°C
 AAan = LB Arab anaerobic
 AArt = LB Arab room temperature

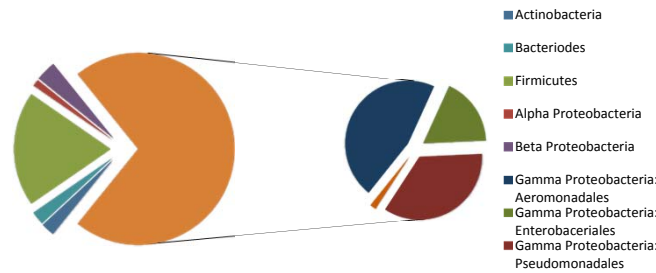
Biochemical Tests:
 Glucose, MR, VP, citrate, phenyl ethanol, urea, nitrate, gas pak, catalase, oxidase, growth at 4°C, 20°C, 37°C, 45°C, lipid, EMB, HEA, MSA, denitrification, gas glucose, starch, blood, Endo, MacConkey, Milk

Survey Results

Table 1. Types of Bacteria found in Lycoming Creek

Group	Number of Organisms
Actinobacteria	2
Bacteriodes	2
Firmicutes	17
Alpha Proteobacteria	1
Beta Proteobacteria	3
Gamma Proteobacteria	60

Figure 1. Pie Chart of Families Found in Lycoming Creek

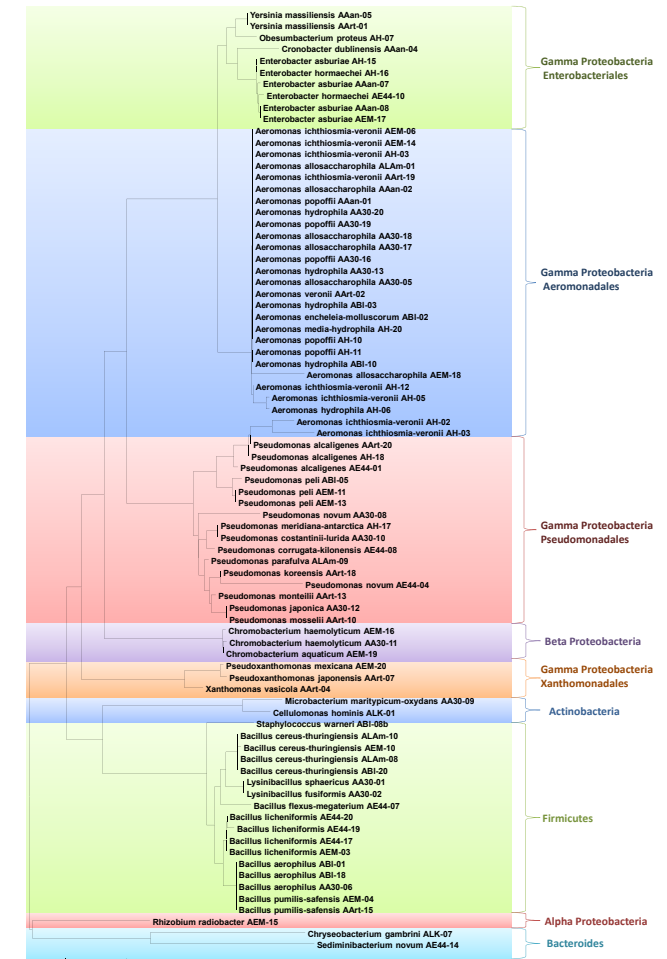


Novel Organism Results

Table 2. List of Potentially Novel Organisms and %ID to known organisms

Organism	% Identity
Sediminibacterium novum AE44-14	92.3
Bacillus flexus-megaterium AE44-07	98.8
Chromobacterium haemolyticum AA30-11	98.9
Aeromonas popoffii AA30-14	98.6
Aeromonas popoffii Aaan-01	98.7
Cronobacter dublinensis Aaan-04	98.7
Enterobacter asburiae Aaan-08	98.6
Obesumbacterium proteus AH-07	98.5
Yersinia massiliensis Aaan-05	98.4
Yersinia massiliensis AArt-01	98.4
Pseudomonas alcaligenes AE44-01	98.7
Pseudomonas novum AA30-08	95.4
Pseudomonas novum AE44-04	94.8

Figure 2. Phylogenetic Tree of Organisms found in Lycoming Creek



Conclusions

- Most of the bacteria found in the survey of the microbes from Lycoming Creek were members of Gamma Proteobacteria and Firmicutes.
- Several potentially novel species were identified.

Ongoing and Future Research

Several of the novel species are being further characterized by API tests, complete 16S rRNA sequencing, and other family-specific tests.

References

- Chun, J., Lee, J.-H., Jung, Y., Kim, M., Kim, S., Kim, B. K. & Lim, Y. W. (2007). EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. *Int J Syst Evol Microbiol* 57, 2259-2261.
- Stackebrandt, E., Ebers, J. (2006) Taxonomic Parameters Revisited: Tarnished Gold Standards. *Microbiol. Today*. 33:152-155.