Cornell Undergraduate Research Board with the Cornell Pre-Vet Society

~ Presents ~

3rd Annual Fall Research Forum

CORNELL UNDERGRADUATE RESEARCH BOARD
CURB

November 13th 2013

Proceedings and Abstracts

Alburuj Rahman '15
College of Agriculture and Life Sciences
Arr75@cornell.edu
Columbus, OH

Biological Sciences, Computational
Advisor: James Shapleigh
Cornell University, Microbiology

Study of modular denitrification in microbial communities through sequence analysis

Denitrification is a critical part of the nitrogen cycle and is predominantly carried out by bacteria. Complete denitrification is the reduction of nitrate to nitrogen gas. A unique reductase is used for each of the four steps: (i.) nitrate reductase (Nar or Nap), (ii.) nitrite reductase (Nir), (iii.) nitric-oxide reductase (Nor), and (iv.) nitrous-oxide reductase (Nos). While previous work has suggested most denitrification is carried out by bacteria with all four reductases, new research suggests the denitrifier community is made up of incomplete denitrifiers.

To determine if modularity is important in soil, DNA samples were collected from the soil of the Hubbard Brooke Experimental Forest, a site reserved for ecosystem studies. Soil was collected from three distinct locations of different pH, altitude with respect to a body of water, and soil properties. The DNA was sequenced using the Illumina sequencing platform. Trimmed and paired reads were imported into MG-RAST, a metagenomic database sequence analysis tool. Based on analysis of the data so far, more organisms have had hits – that is, their sequences were linked to possessing a certain reductase – to Nor than they did to Nir. Also, the most common organisms with hits to Nor were not found to have hits to Nir. This reinforces the notion of modularity.

Going forward, we plan to validate the MG-RAST based taxonomic classifications and functional characteristics of the sequenced DNA. This will be done by studying the collected DNA sequences using local NCBI blastx and blastn searches. We have also recently found that MG-RAST misassigns many of the proteins labeled as nitrate reductase and consequently we will work on building more appropriate databases and validation tools to allow reasonable determination of nitrate reductase distribution at Hubbard Brook.