

Cornell Undergraduate  
Research Board

~ Presents ~

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Proceedings and Abstracts

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Food preparation is a complex process that mediates food choice and dietary intake, a contributor to common lifestyle-related diseases like diabetes, cardiovascular disease, and cancer. Altered life course context can affect the food choice process, motivating the development of culinary adaptive strategies addressing constraints. The objective of this study is to identify and describe how older adults use the culinary adaptive strategy of altering ingredients during home food preparation. Seventeen adults ages 61-91 were interviewed using a semi-structured interview guide and the transcripts were coded for emergent themes. Culinary adaptive strategies were reported throughout the life course. Participants most often adapted their ingredient choices when they were faced with health concerns or because they felt limited to using ingredients that were present in the home due to access or financial limitations. Culinary adaptive strategies used to alter ingredient choice included substituting healthier ingredients, adapting to available foods, and participating in formal or formal food exchanges. Because dietary modifications are often a way to treat common lifestyle-related diseases, understanding how people adapt their food preparation behavior in response to constraints can contribute to improving nutrition counseling.

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### Sequence analysis through alignment: modular denitrification in microbial communities

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.

We have been developing additional methods to validate the MG-RAST based taxonomic classifications and functional characteristics of the sequenced DNA. Through PLAN, a public blast navigator, blastx and blastn searches were carried out on FASTA files created after compiling sequences collected from several datasets, and including the paired-ends used to validate assignments. In Excel, PLAN results were organized for analysis. Differences between blastx and blastn assignments were examined. For blastn, lack of classification and inconsistencies with blastx and paired-ends led to use of blastx results almost exclusively. Paired-ends were compared for consistency of taxonomic classification. NirK classification appeared to be more taxonomically sound than that of Nor. We suspect the sequences examined in NirK to be less conserved than those of Nor, allowing for higher specificity for identifying protein sequences. The alignments will be examined through the use of semi-quantitative tests to measure differences in levels of conservation between NirK and Nor, and to ultimately determine which classifications can be trusted and used for further analysis.