Metabolic potential of eukaryotic communities off the coast of southern California

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Goals

- We present preliminary results of a metatranscriptomic survey of the microbial eukaryotic community from the San Pedro Ocean Time-series station (May 2015)
- Relative gene expression was inferred from transcript abundance to examine how protistan physiological ecology varied with respect to community composition and depth
- Concurrent microscopy and RNA-based taxonomic assignment characterized the total community composition

Diversity

- Proportion of reads attributed to ciliate and other eukaryotes at 150 m compared to MMETSP. Large proportion of surface 150 m 890 m compared to 150 m and 890 m.
- Differences in diversity in (A) and (B) attributed to gene copy number variation with RNA, use of different reference databases, or low relative abundance of transcripts with RNA reads.

Approach

- Collection → Sequencing
- 3-5 replicates per sample (7.5 um filtrates)
- <30 minute filtration
- Total RNA extraction
- mRNA stranded KAPA library preparation
- HiSeq 125bp PE Hi output

Preparatory Analysis

- Non-rRNA [mRNA]
- Assembled in MetaHIT
- Taxonomy assignment in QiIME2 against the SILVA database
- BWA alignment with MMETSP via BWA
- BWA required a 95% alignment
- Alignment rate ranged from 1-14%, total of 3.8 million transcripts
- KEGG annotation performed on transcripts of > 5 count

Collections:

- Carbohydrate metabolism
- Carbon metabolism
- Biosynthesis of amino acids
- Carbon fixation
- Amino acid metabolism
- Metabolism of cofactors and vitamins
- Carbohydrate metabolism
- Fatty acid metabolism
- Lipid metabolism
- Oxidative phosphorylation
- Methane metabolism
- Metabolism of other amino acids
- Purine metabolism
- Lipid metabolism
- Pyrimidine metabolism
- N-glycan metabolism
- Sulfur metabolism
- Signal transduction
- Membrane transport
- Transport and catabolism
- N-glycan metabolism
- Protein turnover
- Phagosome
- Gene expression and motility
- Astrocytosis
- Tight junction
- Pervicose

Environmental Information Processing

- Gene expression (all three depths)
- Process groups on the left, then singles out (G) Specific pathways annotated from mapped genes from all taxonomic groups on the left, then singles out chlorophytes (middle), and ciliates (right). Overall, there was a larger total number of annotated pathways detected at surface – likely due to better representation in databases. Similar pattern was upheld with chlorophytes, but more pathways were detected at 150 and 890 m with ciliates. Specific modules are missing in chlorophyta and ciliate only KEGG annotations.

References


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