

The Marine Microbial Eukaryote Transcriptome Sequencing Project marinemicroeukaryotes.org

The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP) is an online reference database for the transcriptomes of marine microbial eukaryotic organisms. The goal of this project is to create an online category of genes that specify how the microbes live in and influence the marine ecosystems. The over 650 assembled, functionally annotated and mostly well-defined transcriptomes allow scientists to explore the physiology, interpret metagenomics and illuminate the evolutionary relationships of marine microbial eukaryotic organisms.

Microbial eukaryotes, like diatoms or dinoflagellates, are crucial to the marine ecological web. They perform vital functions such as CO₂ absorption, photosynthesis, predation and parasitism.

Unfortunately, they are often excluded from studies because their genomes are structurally complex and enormous in size. The MMETSP is focused on transcriptomes. Transcriptomes are the expression content of a genome and can provide a wealth of genomic information but from less sequence data.

Other data available, even databases that emphasize microbial life, focus on other species. The MMETSP is tasked with countering this bias by not only providing an online reference database, but also directly sequencing and annotating important transcripts of microbial eukaryotes.

With MMETSP, researchers can access the molecular data of the missing piece of the puzzle in the communities they are studying and illuminate the complex interactions of marine web.

Project Statistics

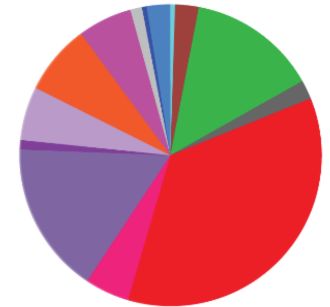
Unique Genera:	210
Unique Species:	305
Unique Strains:	396
Number Approved:	678

Taxon assignments for a sample from the surface waters of the North Pacific Ocean



Better Match

Taxon breakdown of MMETSP



Poor Match

Taxonomic diversity of eukaryotes from the other microbial focused databases

