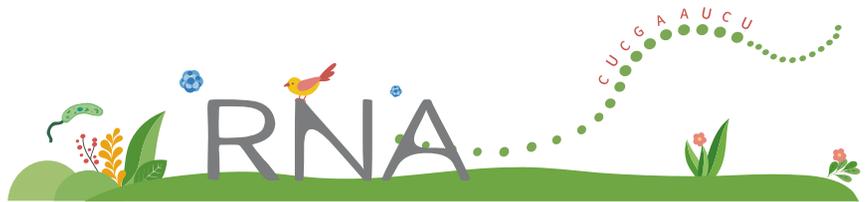


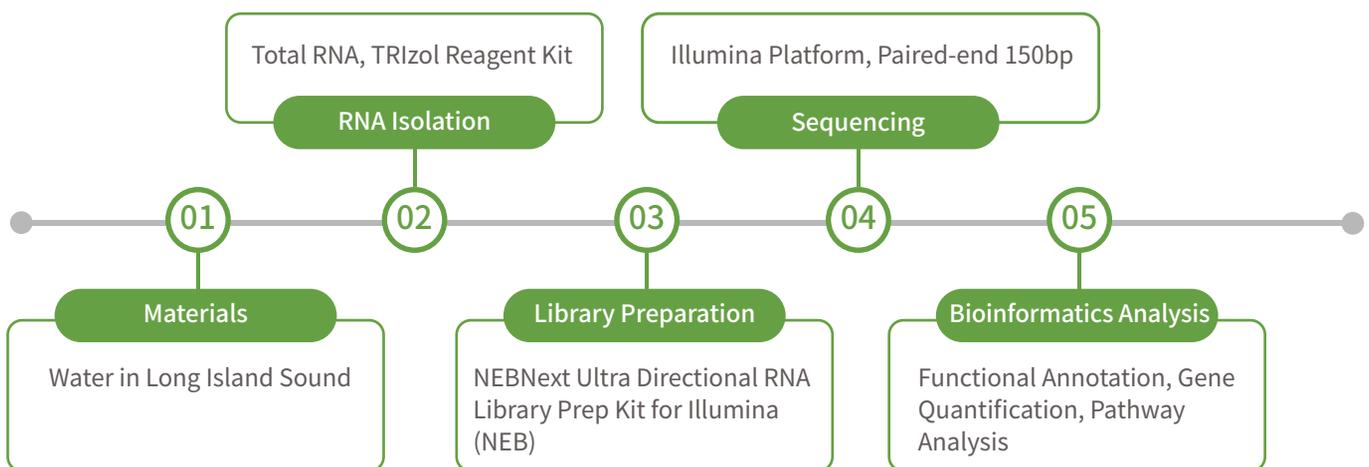
Cryptophyte farming by symbiotic ciliate host detected *in situ*



Background

Protist–alga symbiosis is much more widespread in the marine ecosystem than previously thought, both spatially and taxonomically. Field and laboratory observations have documented a wide range of host integration of symbionts, from enslaving transiently kept chloroplasts to permanent intact-cell endosymbionts. However, the degree of host integration and function of endosymbionts in natural plankton assemblages *in situ* is poorly understood and severely understudied.

Research Pipeline



Research Results

1 *Mesodinium rubrum* was verified as the causative species of the bloom

A red-tide bloom occurred in Long Island Sound (Figure 1A). Microscopic examination revealed *M. rubrum* as the causative species of the bloom (Figure 1B). Researchers picked *M. rubrum* cells from samples under the microscope and obtained a 1,581-bp rRNA gene (rDNA) small subunit (SSU) sequence and plastid rDNA SSU sequences, which phylogenetically verified the bloom organism as *M. rubrum* (Figure 1C).

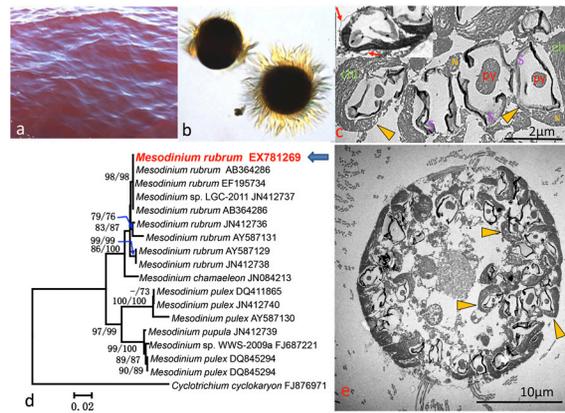


Figure 1. Red-tide bloom and the causative organisms. (A) Photograph of the red tide. (B) Light microscopic image of the causative ciliate. (C) 18S rDNA phylogenetic tree verifying that the causative ciliate was *M. rubrum*.

2 RNA-seq and gene annotation

Researchers extracted RNA from the bloom sample and conducted metatranscriptome sequencing. About 55.18% of the unigenes were functionally annotated and the rest were novel genes. The annotated portion of the metatranscriptome was predominated by cryptophyte genes, mainly matching *Guillardia theta* but also *Rhodomonas sp.*

3 Metabolic pathways analysis in a cryptophyte

The metatranscriptome allowed us to provide detailed documentation of core metabolic pathways in a cryptophyte, including the tricarboxylic acid (TCA) cycle, pyruvate metabolism, glyoxylate metabolism, glycolysis/gluconeogenesis, etc. The crucial connections from the TCA cycle to starch and PRPP in the pentose phosphate pathway, and from carbohydrates, amino acids, and lipids to the TCA cycle, were uninterrupted (Figure 2).

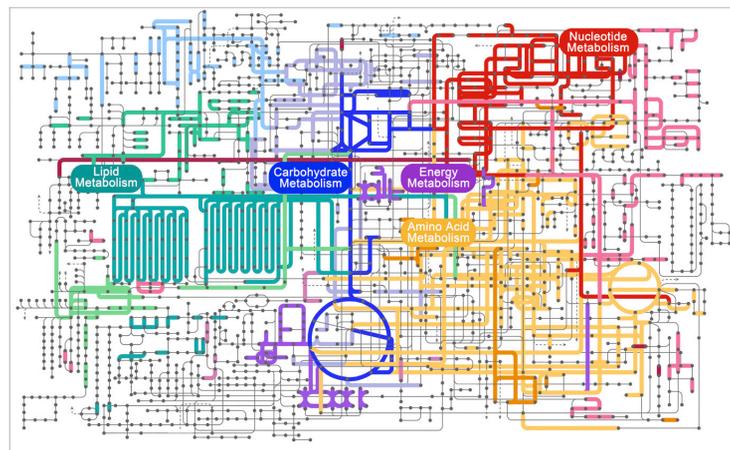


Figure 2. Metabolic circuit map constructed from the cryptophyte subset of the metatranscriptome. Highlighted in this circuit are pathways of nucleotide metabolism (red), carbohydrate metabolism (blue), energy metabolism (purple), lipid metabolism (cyan), and amino acid metabolism (yellow) in cryptophytes.

Reference

Qiu DJ, Huang LM, and Lin SJ. Cryptophyte farming by symbiotic ciliate host detected *in situ* [J]. *Proceedings of the National Academy of Sciences of the USA*, 2016, 113(43): 12208-12213.



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