Diversity of carbonic anhydrase in Symbiodiniaceae and its different expression

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Background

The marine algae contribute about 46% of global primary productivity through photosynthesis. However, limited by inorganic carbon in aquatic environments and RubisCO’s low affinity for CO2, photosynthetic algae have evolved a carbon concentrating mechanism (CCM) to improve carbon sequestration efficiency.

Carbonic anhydrase (CA) catalyzes the reversibility of HCO3~ with CO2, is a key enzyme in CCM, and plays a crucial role in CCM.

The CA family belongs to a class of metalloenzymes with rich diversity, including metal cofactors, gene sequences, protein structures, and researchers currently have an in-depth understanding of the carbon concentration mechanism and the role of carbonic anhydrase in the model algae Chlamydomonas reinhardtii. Dinoflagellate is limited by its large genome, and its understanding of CA type and physiological function is extremely limited.

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Hypothesis and Methods

The research subject in this study was the Symbiodiniaceae found in corals. Material exchange between Symbiodiniaceae and host corals is the material basis of coral reef ecosystems. The host provides the inorganic carbon needed for photosynthesis, hence CA is crucial in the transfer of inorganic carbon for corals.

Therefore, we proposed the hypothesis: Differences in the subcellular distribution of different types of CA play an important role in the mechanism by which Symbiodiniaceae obtain inorganic carbon from the host.

Result-1: Four types of CA exist in Symbiodiniaceae

- clustered to four types: α, β, γ, and δ.
- β-CA: the most abundant type

Result-2: Differences in the distribution of CA in Symbiodiniaceae

Finally, a total of 86 CA sequences were determined in the Symbiodiniaceae genome, of which β-CA sequences were the most, followed by α-CA, and γ-CA were the least. F. kawagutii contains the highest number of CA sequences at 36, while Symbiodiniaceae Clade C has the fewest CA sequences with only 9.

Almost 4 CA encoding gene sequences were identified in 3 species of Symbiodiniaceae among which sfβCA has two Open reading frame (ORF), each encoding a protein, which is a common tandem repeat phenomenon in dinoflagellate functional genes.

Result-3: Different expression of CA in different environment

- Dynamic transcriptional expression of different types of CA genes in Symbiodiniaceae under different environmental conditions.
- β-CA: more significant changes > α-CA and β-CA, indicating a more important role in the physiological process of Symbiodiniaceae.
- N limitation induces up-regulation of α-CA, β-CA gene expression.
- P limitation induces down-regulation of δ-CA gene expression.
- Warming induces down-regulation of α-CA gene expression.

Future Work

In order to further explore the role of CCM and CA in Symbiodiniaceae, it is necessary to identify the distribution of Symbiodiniaceae CA genes. Phylogenetic analysis and transcriptome data analysis of Symbiodiniaceae showed that β-CA may play an important role in the physiological process of Symbiodiniaceae, so the future work will focus on the identification of the gene distribution of β-CA in Symbiodiniaceae, and further analyze the expression of Symbiodiniaceae CA under different environmental conditions, so as to provide data support for the role of coral-Symbiodiniaceae symbiosis in the process of coral reef carbon sink, and provide new insights for coral reef ecosystems to cope with climate change.