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Study and Analysis of Prokaryotic Communities and CH₄ Changes in the Arctic Kongsfjorden, Svalbard

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Abstract

The fast Arctic warming is having a profound impact on prokaryotes as the basis of microbial food loop. However, we still do not know much of these microbes, especially their environmental function and their environmental regulation mechanisms in the high Arctic Kongsfjorden. All these have restricted our knowledge in prokaryotic feedback on climate and environmental change. As the second most greenhouse gas, methane (CH₄) is sensitive to temperature changes; and seafloor hydrates are huge reservoirs of CH₄. These CH₄ are usually produced by prokaryotes. Despite the importance of both prokaryotes and CH₄, we still know little about the activity of prokaryote community and their correlations with CH₄ in Kongsfjorden. This paper is to make a comprehensive description of research status in both prokaryotes and CH₄ in the Arctic Kongsfjorden. Several topics that need to study in future were put forward at the end of this paper.

Keywords: Arctic high latitude; Prokaryotes; Methane; Omics; High-through put sequencing

Short Communication

The Arctic Kongsfjorden (79°N, 12°E) is an inner bay on the northwest coast of Svalbard. Kongsfjorden is influenced by both North Atlantic Current and glacial melt water [1]. In recent years, there has been a significant increase in the input of the warm Atlantic current [2]; its presence was detected of even in winter [3]. There has been non-icebound in winter in the past decade [4]. In addition, the stratification and salinity in the bottom of Kongsfjorden are increasing, which have a great impact on the biota there [5-7]. The sensitivity of Kongsfjorden to changes makes it an ideal place to study the effects of climate change on Arctic coastal ecosystems [5,8].

Prokaryotes are important microbes in Kongsfjorden, which experience extreme temperature and seasonal light changes. Although the abundance of prokaryotes decreases from low to high latitudes, their abundance in Kongsfjorden is estimated to be about 10⁸-10⁹ cells/L [9]. Prokaryotes are key components of the marine microbial food loop; and their metabolic pathways play an important role in microbial circuits of biogeochemical processes such as the carbon, nitrogen and phosphorus cycles [10]. In Kongsfjorden, about

19% of particulate organic carbon and 36% of particulate matter are composed of bacteria [11]. Prokaryotes are sensitive to environmental changes. However, they can also have a lasting impact on the microenvironment in which they live through the microphoretic and metabolic pathways, i.e., feedback to environmental changes [12,13]. During the summer of the peak melt season, large amounts of glacial melt water can change the community structure [14]. Because glacial melt water will bring a large number of glacial and terrestrial organic and inorganic substances into Kongsfjorden, so that the temperature and salt of the sea water decreases significantly, the seawater stratification increased, both the transmittance and euphotic layer of the sea water decreased. This leads to a negative effect of low temperature and osmotic pressure on the plankton individuals. The input of terrestrial organisms alters the original plankton community structure [15,16]. In addition, the increase of warm Atlantic water also led to an alteration of the prokaryotic community [17].

In Kongsfjorden, the core groups of prokaryotes are Verrucomicrobia and Bacteroidetes, whose community compositions are strongly affected by the content of

carbohydrate in the particulate organic matter. However, the core groups of prokaryotes are α -Proteobacteria and γ -Proteobacteria, whose community composition is influenced by glacial melt water inflow and particulate organic carbon [16]. Bacteroidetes is the most abundant bacteria group in spring [18], while Proteobacteria and Bacteroidetes are the dominant bacteria group in summer [19]. Our research shows that with the change of climate, Bacteroidetes is gradually replaced by Actinobacteria in summer. In summer, the prokaryotes in both water and sediments are mainly Proteobacteria, Bacteroidetes, Verrucomicrobia, and Actinobacteria [20]. Cyanobacteria are mainly present in glaciers, and enter Kongsfjorden with glacial meltwater. Cyanobacteria are also found in the warm Atlantic water mass, although they belong to different species.

CH₄ is second only to carbon dioxide as a greenhouse gas that accelerates global warming [21]. Arctic seafloor hydrates are large CH₄ reservoirs, which are highly sensitive to temperature [21,22]. These CH₄ are usually formed by a microbiome-mediated process called Methanogenesis of CH₄ [21], and were buried in sediments through long-term fermentation [21]. In surface sea water, CH₄ formed in local anaerobic microenvironment (such as zooplankton gut, inside particles of copepod feces, etc.) also becomes an important source of CH₄ in seawater and atmosphere [23-25], these CH₄ are ultimately produced by prokaryotes. Cyanobacteria with nitrogen fixation were also strongly associated with CH₄.

Generally, there have been several studies on distribution of prokaryotic community and CH₄ in Kongsfjorden. For example, there is abundant CH₄ in seabed of the Svalbard shelf, which has a certain response and feedback to climate changes. However, little is known about the activities of prokaryotic communities and their relationship with CH₄, which makes it difficult to analyze the functions of prokaryotic communities in the production and consumption of CH₄, thus not knowing their accurate role in climate and environmental changes. The 16S rRNA and methyl-coenzyme M-reductase (mCRA) genes of prokaryotes (bacteria/archaea) in seawater and sediments from Kongsfjorden were quantitatively analyzed [21,26], combined with isotopic methods [27], sources and exports of CH₄ can be effectively traced to assess the impact of environmental changes in coastal waters on CH₄ production and release. Progresses in technology, especially in high-throughput sequencing of omics (metagenomics, metatranscriptome, and metabolomics) have enabled us to better understand the environmental functions of different groups of prokaryotes. Therefore, in the face of increasingly

significant global changes (glacier melting, permafrost melting, etc.), it is urgent to study the mechanism of CH₄ migration and transformation and its relationship with prokaryotes in Kongsfjorden. On the basis of the existing studies, we need to further answer the following questions:

1. With the rapid warming of the Arctic and the total environmental changes of Ny-Alesund, how will the composition of the prokaryotic community in Kongsfjorden change? How do the living and active populations change, and what are their internal correlations?

2. What is the proportion of CH₄ contributed by prokaryotes in the coastal marine ecosystem?

3. How does the rapid warming of the Arctic affect the composition of prokaryotic communities in seawater and sediments of Kongsfjorden, and thus the change of CH₄? What are the implications for global change?

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