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Editorial

Microbial methylation of mercury in the water-level fluctuation zone of the Three Gorges Reservoir, China

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Methylmercury (MeHg) is an organic form of the global pollutant mercury (Hg) which readily accumulates in fish tissue. A majority of Hg methylation is a result of microbial activity and the abundance of inorganic Hg within the water reservoirs (Eckley et al., 2017). Compared to natural lakes and rivers, reservoirs have elevated Hg levels from the decomposition of recently flooded organic material which promote Hg release and enhance microbial methylation of Hg (Eckley et al., 2017). Microorganisms containing the gene clusters *hgcA* and *hgcB*, such as sulfate reducing bacteria (SRB) and iron reducing bacteria (FeRB), have been demonstrated to be contributors to MeHg (Du et al., 2017; Eckley et al., 2017; Xiang et al., 2018). Reservoirs with seasonal water-level fluctuations similar to floodplains and wetlands have been demonstrated to stimulate Hg methylation due to enhanced decomposition of organic matter (Eckley et al., 2017). The Three Gorges Reservoir (TGR), located in the upper reaches of the Yangtze River, China, is one of the largest reservoirs around the world. The flooded area of TGR changed seasonally from 350 to 632 km². The water level in the winter could be 30 m higher than that in the summer (Fig. 1) (Chen and Schaffer, 2017).

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Comparing the diversity, distribution and abundance of microorganisms with MeHg in a reservoir with a large, dynamic water-level fluctuation is essential to determining strategies to reduce MeHg levels. To date, many studies have independently focused on the identification of microbial methylators or the concentration of MeHg in reservoir areas that are permanently inundated and non-inundated (Du et al., 2017; Eckley et al., 2017). However, it is essential to determine if certain microorganisms positively correlate with elevated MeHg in reservoirs. Previous studies of the Three Gorges Reservoir (TGR) identified a positive correlation between the abundance of microorganisms containing the *hgcA* and *dsrB* genes and elevated levels of MeHg in sediments and non-inundated areas (Du et al., 2017). To gain further understanding of the effect of seasonal water-level fluctuations on microbial composition, Xiang et al. (2018) quantified the MeHg, total-mercury (THg) concentrations, as well as soil bacterial and archaeal diversity and abundance in the TGR, China.

Soil THg and MeHg were determined via Direct Mercury Analyzer and Gas chromatography cold vapour atomic fluorescence spectrometry. Soil physiochemical parameters were also analyzed. THg concentrations were the highest in seasonal drying and flooding alternating areas (DFA), most likely due to the higher abundance of soil organic matter and sedimentation from flooding – both are major contributors to Hg in the TGR. MeHg and ratio of MeHg to THg (MeHg%) demonstrated a similar pattern to THg, in which the DFA had the highest concentrations. The results indicate that water-level fluctuation is an important factor in affecting MeHg production in reservoir soils. Considering the major contributors to MeHg are Hg methylator microbes, the authors further determined which microbes were the dominant contributors to this trend.



Fig. 1 – Water-level fluctuation zone of the Three Gorges Reservoir, showing flooding (top picture) and drying (bottom picture) seasons. Photo courtesy of Dr. Dingyong Wang and Deliang Yin, Southwest University, China.

To understand soil microbial abundance and diversity at different altitudes, Xiang et al. (2018) analyzed microbes in soil samples using high-throughput pyrosequencing of 16S ribosomal RNA (16S rRNA). They obtained 153,262 high-quality sequences from 15 samples, and aligned with known microbe databases for classification. The abundance of each species was reflected by the copy number of the same sequence. Results showed that the abundance and diversity of bacteria were relatively higher in seasonal drying and flooding alternating areas (DFA) than those in permanently non-inundated and inundated areas, which might be a result of the seasonal water level fluctuation.

Not all microbes work as Hg methylators. Gene related to Hg methylation were found in species in *Deltaproteobacteria*,

Firmicutes, and *Methanomicrobia*. Thus, Xiang et al. (2018) analyzed the abundance of the species in this phylum and classes in samples. Hg methylation ability was found in 8 families in the class of *Deltaproteobacteria*. Among them, 6 families were found in the Three Gorges Reservoir, with the highest relative abundance equal to 0.85% of total bacteria in a sample. The abundance of these strains is higher in drying and flooding conditions than non-inundated and inundated areas. In the *phylum* of *Firmicutes*, all 4 families that work as methylators were found in soils, their abundances were lower than 0.26%. *Methanomicrobia* in *Archaea* also has the Hg methylation activity. Both families that can methylate Hg in *Methanomicrobia* exist in the Three Gorges Reservoir. The relative abundance of one of the two families was high in

DFA, and it was 1-2 orders of magnitude higher than other methylators.

In seasonal drying and flooding alternating areas, the high relative abundances of strains in *Deltaproteobacteria* and *Methanomicrobia* were consistent with the methylation level of Hg. Although the *Methanomicrobia* was dominant, its low Hg methylation capacity compared to other strains might account for the low total MeHg levels in all samples to be less than 1%.

The results of the Xiang et al. (2018) study demonstrated an enhanced methylmercury production in soil areas with seasonal water level fluctuations compared to permanent inundated and non-inundated areas in the Three Gorges Reservoir. This research denotes a relationship between the diversity and distribution of microorganisms with mercury methylation. Future studies could consider the variation of microorganism diversity and abundance over longer periods of time to aid in monitoring and reducing methylmercury levels. The methods of determining methylmercury abundance and microorganism diversity can be transferable to studies of other reservoirs. Because methylmercury is a major bioaccumulative environmental toxicant in fish and food

chain, it is crucial to minimize its formation and reduce its concentration within water reservoirs.

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