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Role of phytoplankton in aquatic mercury speciation and transformations

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15 **Environmental Context**

16 Understanding mercury transformations in the aquatic environment is of utmost importance for
17 the improvement of mercury biogeochemical modelling and sound environmental risk assessment.
18 In such a context, we discuss critically the advancement in the knowledge on the role of the
19 phytoplankton (algae and cyanobacteria) in mercury cycling and transformations in the aquatic
20 environment. Important research advances revealed that different microalgal species and
21 cyanobacteria contribute: to biotic reduction of inorganic mercury to elemental mercury; to
22 demethylation of methylmercury and transformation of inorganic mercury into metacinnabar; and
23 to production of different biomolecules which can contribute to abiotic mercury reduction.

24



Thibaut Cossart is a Ph.D. student in Environmental Science at the University of Geneva, Switzerland. He got a MSc in marine biodiversity and biomolecules from the University of Toulon, France. His research is focused on the interactions between phytoplankton and mercury. He

highlighted the role of phytoplankton in the biogeochemical cycle of mercury by (i) evaluating the biotic transformations performed by a cyanobacterium and natural phytoplankton communities, (ii) determining the effects of thiols bioligands on the bioaccumulation of Hg species by cyanobacteria.



João P. Santos holds a BSc in Biology and a MSc in Ecology, Environment and Landscape, and a MSc in Marine Sciences from the University of Porto, Portugal. He worked with the nitrogen cycle communities until he started his Ph.D. Currently, he is a Ph.D student in the

Slaveykova's lab at the University of Geneva, Switzerland. He studies the interaction of diatoms and natural phytoplankton communities with different mercury species, and explores their capability to accumulate, transform and detoxify mercury.



Dr. Isabelle A.M. Worms is a senior scientist of environmental biogeochemistry and ecotoxicology at the University of Geneva. She is a biochemist with a MSc in molecular chemistry. Since her Ph.D., her research interests include (i) understanding of the bioavailability of trace metals; (ii)

developing of AF4-ICP-MS to assess the role of natural organic matter on the binding and dispersion of trace metals in surface water; and (iii) identifying key processes involved in nanoparticle stability using quantitative approaches.



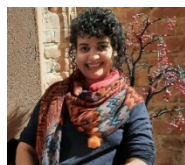
Dr. David Amouroux is a research director at the French CNRS appointed at IPREM, CNRS-UPPA. He is responsible of the Research Unit for Environmental Chemistry and Microbiology. He is an environmental and analytical chemist, specifically

interested in the cycling and reactivity of contaminants in the environment. Some of his research lines include: (i) transformations and transfer of mercury; selenium and other metal(loid)s at aquatic environment interfaces and (ii) development of analytical and experimental methods using stable isotopes of trace elements to investigate biogeochemical mechanisms in the environment.



Javier García Calleja is a Ph.D. student in the Amouroux lab at the IPREM, CNRS-UPPA, Pau, France. He holds a BSc in chemistry and a MSc in analytical and bioanalytical chemistry from the University of Oviedo, Spain. His research includes (i) development of

mathematical approaches based on isotope pattern deconvolution for studying Hg compound reactivity in *in situ* Hg incubation experiments and (ii) characterization of bioligands involved in Hg speciation in phytoplankton by hyphenated techniques based on elemental and mass spectrometry.



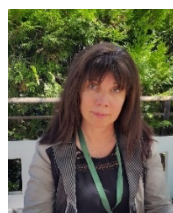
Dr. Elaheh Lotfi Kalahroodi is a postdoctoral researcher in Environmental Geochemistry at the Umeå University in Sweden. Her research is focused on studies the biogeochemical mechanisms of organic

and inorganic contaminants in the environment through isotope fractionation of stable non-traditional isotopes. She evaluates and optimizes methodologies to trace and quantify the spread of Hg from contaminated sediment sites to surrounding sediment and pelagic and benthic biota using Hg stable isotope measurements.



Dr. Zoyne Pedrero ZAYAS is a research scientist at the French CNRS appointed at IPREM, CNRS-UPPA. She is analytical chemist and her work principally focuses on metal speciation (mainly Hg and Se) by hyphenated chromatography-based

separation mass spectrometry techniques and isotopic analyses in living organisms. Her research interest comprises, among others, the interaction of Hg and Se in biota as wells as pollution sources and metabolic processes tracking.



Dr. Vera I. Slaveykova is a full professor at University of Geneva and president of the School of Earth and Environment Sciences. She works on the development of concepts and tools for a better understanding of the fundamental processes governing the behavior and

impact of trace elements and nanoparticles in the aquatic environments. Her current research interests and portfolio include (i) speciation and bioavailability of trace elements, and nanoparticles in the aquatic environment; (ii) aquatic toxicology of inorganic contaminants and nanoparticles; transcriptomics and metabolomics.

Abstract

Phytoplankton may directly influence biogeochemical cycling and transformations of mercury (Hg) through biotic transformations of the accumulated metal via methylation/demethylation and reduction/oxidation, and indirectly, through the excretion of low and high molecular weight ligands, likely triggering or influencing different abiotic transformation pathways as well as the transformations carried by bacteria. However, unlike the extensive work already done on the role of bacteria in Hg transformations, the current knowledge about the influence of phytoplankton (algae and cyanobacteria) on such processes is still limited.

Critical evaluation of the existing advances in the research topic revealed that different microalgal species and cyanobacteria contribute to the biotic reduction of inorganic mercury (iHg or Hg^{II}) into elemental Hg (Hg^0), monomethylmercury (MeHg) demethylation, and transformation of iHg into metacinnabar. The low and high molecular weight biomolecules released by phytoplankton can complex Hg species and contribute to abiotic mercury reduction. Despite these advances, the underlying mechanisms and their importance in the aquatic environment are to be explored and detailed. The development of the novel molecular, stable isotope-based, and multi-omics approaches would provide further impetus for the understanding of the key interactions between Hg species and phytoplankton. Such understanding will be of utmost importance for the improvement of the Hg biogeochemical modelling, mitigation strategies, and rational environmental risk assessment in the changing aquatic environment.

Keywords: Mercury cycling, methylmercury, speciation, methylation, demethylation, reduction, oxidation, algae, cyanobacteria

1. Introduction

Mercury is naturally present in the environment, however, since the industrial revolution, anthropogenic activities have increased the global Hg emissions by a factor of 2-15 and disturbed the Hg biogeochemical cycle (Driscoll *et al.* 2013, Ariya *et al.* 2015, Asaduzzaman *et al.* 2019, Branfireun *et al.* 2020), leading to a significant increase in the concentration of various Hg compounds in the aquatic environment.

In aquatic environments, mercury is commonly found as oxidized Hg^{II} (iHg), reduced elemental mercury (Hg⁰), and monomethyl mercury (MeHg, MMHg, CH₃Hg⁺) with their relative abundances being controlled by numerous chemical, physical and biological processes (Branfireun *et al.* 2020). Mercury species interact with different biotic and abiotic constituents forming complexes with inorganic ligands such as the hydroxide, chloride anions (Powell *et al.* 2005), low molecular weight thiols (Hsu-Kim and Sedlak 2005) and dissolved organic matter (DOM) (Ravichandran 2004, Wang *et al.* 2015, Jiang *et al.* 2017, Liem-Nguyen *et al.* 2017, Klapstein and O'Driscoll 2018, Lavoie *et al.* 2019, Poulin *et al.* 2019). Among all chemical functional groups present in DOM, mercury binds preferentially the –SH groups (Ravichandran 2004). Given the very strong tendency of iHg to form complexes, the estimated value of the mercury free ion concentrations in surface waters is $< 10^{-26}$ mol L⁻¹ (Le Faucheur *et al.* 2014). In addition, Hg species are subject of various transformations, which results in a distribution that is usually follows the order of iHg>Hg⁰~MeHg in freshwater and iHg>Hg⁰>MeHg in seawater (Le Faucheur *et al.* 2014). The major transformation pathways involve the reduction/oxidation of iHg/Hg⁰, and the methylation/demethylation of iHg/MeHg. iHg and MeHg can accumulate in the aquatic organisms and MeHg biomagnifies along the food webs, presenting a hazard to higher consumers, including humans (Sheehan *et al.* 2014, Yang *et al.* 2020). The bioconcentration of Hg by phytoplankton represents one of the main entry steps of Hg into the food web (Dranguet *et al.* 2014, Le Faucheur *et al.* 2014, Wu *et al.* 2019). The knowledge of various transformation processes determined by photochemical, chemical, and biologically mediated reactions (such as

those performed by phytoplankton) is also crucial for understanding the global Hg⁰ fluxes (Jiskra *et al.* 2021).

Exploring mercury transformation pathways in the aquatic environment is an active research area. Extensive studies have been already done on the role of bacteria in Hg transformations, as comprehensively reviewed by (Hsu-Kim *et al.* 2013). Several recent reviews deal with specific transformation mechanisms and influencing factors, including advances in the knowledge regarding the methylation (Paranjape and Hall 2017, Gallorini and Loizeau 2021, Wang *et al.* 2021), demethylation (Barkay and Gu 2022), production/degradation of MeHg in the cryosphere (Ghimire *et al.* 2019), biotic and abiotic degradation of MeHg (Du *et al.* 2019) and photochemical transformation of Hg species (Luo *et al.* 2020). The role of phytoplankton (algae and cyanobacteria) in Hg cycling (i. e., alteration of Hg redox state, Hg scavenging, the potential for methylation), as well as the description of the cellular and molecular targets involved in the toxicity of Hg in phototrophs, were thoroughly discussed previously (Grégoire and Poulain 2014, Beauvais-Flück *et al.* 2018). Hg bioavailability to phytoplankton (Dranguet *et al.* 2014, Le Faucheur *et al.* 2014) and its toxicity to primary producers were also reviewed (Nuzzi 1972, Wu and Wang 2011, Chen *et al.* 2014, Dranguet *et al.* 2014, Beauvais-Flück *et al.* 2017, Beauvais-Flück *et al.* 2018). In this context, the importance of phytoplankton in aquatic mercury transformations was always questioned but never systematically addressed.

In the present review, we focussed on the possible controls exerted by phytoplankton on the key transformations of mercury in the aquatic environment (Fig. 1). In particular, we critically discuss (i) the role of biomolecules released by phytoplankton in Hg speciation, (ii) different abiotic transformation pathways triggered or influenced by phytoplankton and (iii) biotic transformation pathways and cellular speciation of Hg species.

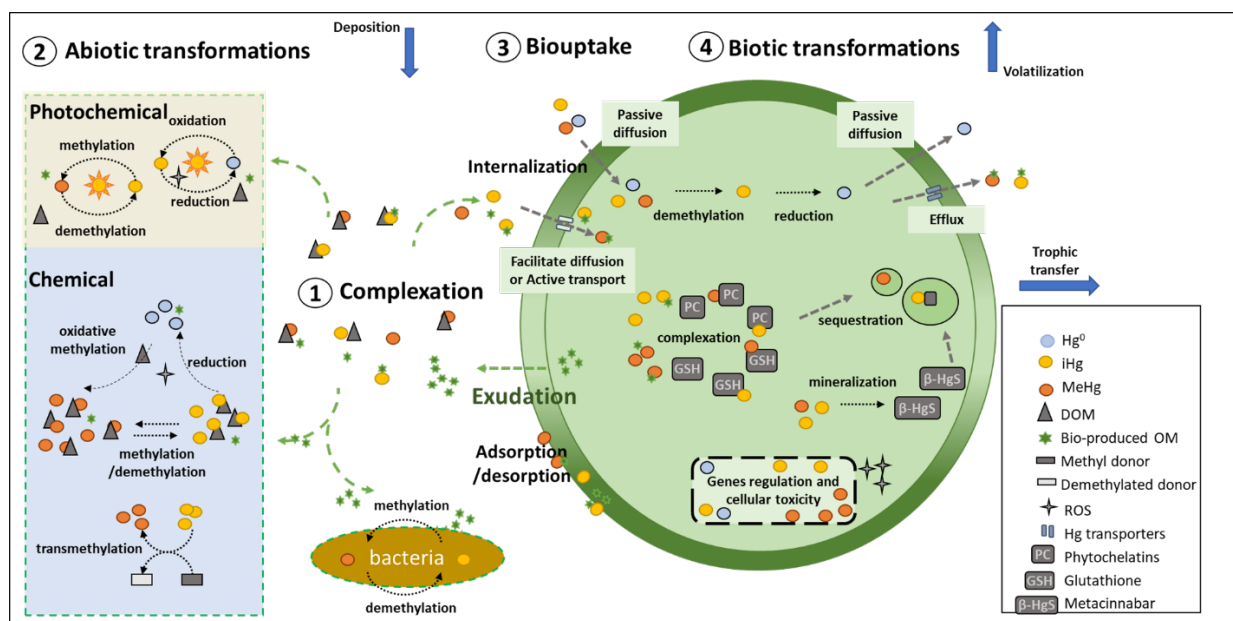


Figure 1. Conceptual view of main processes involved in aquatic Hg biouptake and biotic transformations by phytoplankton, and abiotic transformations influenced or triggered by phytoplankton species.

2. Mercury complexation by biomolecules produced by the phytoplankton

Phytoplankton produces various small molecules, including fatty acids, carboxylic acids, amino acids, and extracellular polymeric substances (EPS, such as polysaccharides, nucleic acid, and proteins) (Seymour *et al.* 2017). EPS represent up to 25% of natural organic matter in freshwaters, especially during algal blooms (Wilkinson *et al.* 1997, Shou *et al.* 2018). The EPS components comprise diverse anionic groups (e.g., $-SH$, $-NH_2$, $-COOH$), thus providing metal-binding properties (Babiak and Krzemińska 2021). Phytoplankton is also known to release small thiols with strong capacities to bind metals in their ambient environment (Liu *et al.* 2020), which are expected to affect the speciation and thus Hg abiotic and biotic transformations. The nature and concentration of such small biomolecules vary with the algal species and environmental factors (Mangal *et al.* 2019a). For example, the diatom *Phaeodactylum tricornutum* has been reported to release cysteine-like exudates, whereas the coccolithophore *Emiliana huxleyi* excreted both glutathione- and cysteine-like compounds (Vasconcelos *et al.* 2002). The effects of biomolecules

released by algae on Hg speciation (Fig. 1 ①) have been examined in the field, where dissolved organic carbon and algal exudates are the predominant ligands of Hg in the rivers and lakes of Long Island Sound, USA (Lamborg *et al.* 2004). Six thiols (mercaptoacetic acid, cysteine, homocysteine, N-acetyl-cysteine, mercaptoethane-sulfonate, and glutathione) were detected with total concentrations of 7-153 nM in boreal lake waters (Bouchet and Björn 2014, Liem-Nguyen *et al.* 2015). Recent studies have shown that several green algae excrete some ligands, particularly thiol-containing ligands that form strong complexes with Hg species and thus modify Hg speciation and bioavailability (Mangal *et al.* 2016, Ly *et al.* 2017, Mangal *et al.* 2019a). The interaction of Hg species with EPS is poorly documented although recognized to have a unique molecular character (Mangal *et al.* 2016, Ly *et al.* 2017). EPS were shown to complex significantly different metals, including Hg (Naveed *et al.* 2019). Indeed Hg was found to bind to protein-like material produced by *Chlorocochus* (molecular weight, MW > 3.5 kDa) (Song *et al.* 2014), and EPS from activated sludge (MW > 3.5 kDa) presumably by electrostatic interactions (Zhang *et al.* 2013). Biomolecules released by several microalgae with apparent molecular mass > 1kDa, likely prevented the induction of Hg microbial biosensor, whereas the presence of smaller biomolecules (MW 0.3 kDa-1 kDa) allowed the induction of Hg controlled fluorescence (Mangal *et al.* 2019a). Nevertheless, further studies are necessary to explore the relative importance of the biomolecules released by the phytoplankton species, including thiols and EPS, in Hg speciation and their role in its transformations in aquatic environments.

3. Abiotic transformation pathways of mercury triggered or influenced by phytoplankton

In oxic waters, Hg species can be subjected to a series of abiotic transformations (Fig. 1 ②), such as reduction/oxidation and methylation/demethylation, as influenced or not by incident light. The extent of these transformations depends on the environmental factors and biological activity of aquatic living microorganisms (Hsu-Kim *et al.* 2013, Grégoire and Poulain 2014).

Photochemical reactions are responsible for the **abiotic reduction** of iHg to Hg⁰ and Hg⁰ oxidation to iHg (Vost *et al.* 2012). The extent of these reactions depends on the intensity of ultraviolet (UV) radiation (Black *et al.* 2012) and the ambient water composition (Lalonde *et al.* 2001, Whalin *et al.* 2007). Although the importance of each reaction is not resolved yet, it is recognized that their kinetics is strongly affected by Hg speciation, which in turn is modulated by the nature and concentrations of ligands present in surface waters (Zhang and Hsu-Kim 2010, Tai *et al.* 2014). For example, it was shown that the biogenic DOM produced by the marine diatom *Chaetoceros* sp. was involved in the photoreduction of iHg (Lanzillotta *et al.* 2004). A recent review highlighted that the **photooxidation** of Hg⁰ is mainly mediated by reactive oxygen species (ROS) (Luo *et al.* 2020). The ROS generation can also occur by the absorption of UV-B radiation by humic and fulvic-like DOM resulting in various photochemical transformations involving oxygen. High production of dissolved gaseous mercury (DGM) was correlated to the high concentration of DOM, in particular thiols binding sites (Ariya *et al.* 2015). On the other hand, the Hg redox cycle in oxic surface waters is mainly dominated by photochemical iHg reduction (Amyot *et al.* 1997).

Abiotic methylation can occur through transmethylation with organometallic species (methylated Pb, I, etc.) and methyl- donors such as methylcobalamin, but these pathways are not considered predominant compared to biotic methylation (Weber 1993, Celo *et al.* 2006). Indeed, experimentation in productive or organic-rich natural waters, incubation in filtered water enriched with iHg at environmental levels demonstrated no production of MeHg even if some methylation was detected in some particular conditions (Monperrus *et al.* 2007, Alanoca *et al.* 2016). Physico-chemical parameters of the aquatic environment greatly impact the extent of abiotic methylation. For example, in Canadian Lakes, DOM having molecular sizes lower than 5 kDa and between 30 kDa and 300 kDa have been reported to mitigate abiotic methylation occurring through solar irradiation (Siciliano *et al.* 2005).

Demethylation occurs by multiple and complex processes, which can be mediated by different biotic and abiotic mechanisms (Barkay and Gu 2022). Two abiotical processes are commonly evoked: (i) photodemethylation, which is believed to be responsible for a significant part of MeHg degradation in surface waters (Hammerschmidt and Fitzgerald 2010, Zhang and Hsu-Kim 2010); and (ii) chemical demethylation, most likely due to e.g. reaction with H₂S or sulfide minerals (Jonsson *et al.* 2016, Kanzler *et al.* 2018) and selenoamino acids (Khan and Wang 2010). The photodemethylation of MeHg and dimethylmercury is well-described and considered to be central in the MeHg degradation in surface waters (Barkay and Gu 2022). The extent of MeHg photodemethylation was observed to depend on the type of solar radiation, the concentration of DOM and the structure of MeHg binding sites, which in turn could influence the generation of free radicals and ROS (e.g. •OH or ¹O₂) (Sellers *et al.* 1996, Hammerschmidt and Fitzgerald 2006, Lehnher and Louis 2009, Luo *et al.* 2020). However, there are still some controversies about the role of DOM in photodemethylation. For example, low DOM concentration promoted, whereas very high DOM concentration inhibited MeHg photodemethylation by DOM (Klapstein and O'Driscoll 2018). However, using Hg compound-specific stable isotope analysis it was shown in situ that MeHg photodegradation in natural waters mostly occurred in waters exposed to UV radiation and was modulated by the DOM level (Bouchet *et al.* 2022). The photodemethylation of MeHg to iHg was shown to increase in the presence of fulvic acids while this process was limited in the presence of humic acids (Luo *et al.* 2020). Labile Fe and photochemically produced ROS were shown to play a role in MeHg photodecomposition (Hammerschmidt and Fitzgerald 2010), although demonstrated to be not compulsory as thiol and phenyl may be the major moieties in DOM-mediated MeHg photodegradation (Zhang *et al.* 2018).

The production of biomolecules by phytoplankton was also shown to affect the Hg transformations *indirectly* by affecting mercury methylation/demethylation by bacteria. For example, organic matter derived from phytoplankton is considered “a fuel” for methylating

organisms and shapes the community structures of periphytic biofilms (Xing *et al.* 2018). The symbiotic presence of *Chlorella* increased the methylation by *Geobacter sulfurreducens* PCA (Zhao *et al.* 2021). However, the biomolecules released by *Chlorella* had only limited effects on iHg methylation by *G.sulfurreducens* PCA but significantly increased the MeHg production by *D. Desulfovibrio desulfuricans* (Yin *et al.* 2022). A clear positive correlation between the activity of methylating microorganisms in sediments and algal productivity was proven in several aqueous systems (Bravo *et al.* 2017, Ortega *et al.* 2018, Wu *et al.* 2022). However, further studies are needed since the quality and quantity of the produced biomolecules are species-specific and dependent on the environmental conditions.

4. Biotic transformation pathways mediated by phytoplankton

Biotic transformations of Hg are considered as intracellular processes (Hsu-Kim *et al.* 2013), therefore the **uptake** (Fig. 1 ③) of iHg and MeHg species by phytoplankton is an important first step in the overall transformation processes. Nonetheless, the uptake pathways and their kinetics are still not well understood for phytoplankton species. Evidence are supporting passive diffusion of uncharged complexes (Bienvenue *et al.* 1984, Mason *et al.* 1996, Kim *et al.* 2014), facilitated diffusion (Wang *et al.* 2004, Le Faucheur *et al.* 2011, Moreno *et al.* 2014) as well as possible active transport pathways (Miles *et al.* 2001, Moye *et al.* 2002, Pickhardt and Fisher 2007). Assimilation of MeHg by diatoms, chlorophyte, dinoflagellate and coccolithophore by passive diffusion is considered the most plausible uptake mechanism considering the high surface-area-to-volume ratio of algal cells. However, the uptake of MeHg by dinoflagellate *Prorocentrum minimum* was suggested to be an active process (Lee and Fisher 2016).

The biouptake of Hg by aquatic microorganisms is recognized to be affected by the complexation by DOM and different ligands (Chiasson-Gould *et al.* 2014, Le Faucheur *et al.* 2014, Bravo *et al.* 2017, Grégoire *et al.* 2018). Nevertheless, the influence of the EPS on the mercury species' biouptake is still poorly understood. EPS produced by 5 algae (*Scenedesmus obliquus*, *Chlorella*

vulgaris, *Chlamydomonas reinhardtii*, *Euglena gracilis*, and *Euglena mutabilis*) were shown to reduce the Hg gene lux induction used as a surrogate for the uptake for modified *E. coli* but in a way which depends on the species and molecular mass of the EPS: low molecular weight fractions likely participate to bacterial Hg uptake, whereas high molecular weight fractions decrease the uptake (Mangal *et al.* 2019b). Thiol ligands, such as 2-mercaptoethanol, dithiothreitol, and glutathione reduced the uptake of MeHg by a cyanobacterium, *Nostoc calcicole* (Pant *et al.* 1995). MeHg uptake by a green alga *Selenastrum capricornutum* was decreased in the presence of cysteine, mercaptoacetic acid, 2-mercaptopropionic acid, glutathione, *N*-acetyl-L-cysteine and *N*-acetyl-penicillamine (Skrobonja *et al.* 2019).

Phytoplankton was reported to trigger different mercury transformation processes (Fig. 1 (4)), including reduction, demethylation, and sequestration of Hg as β -HgS. The **reduction of iHg** to gaseous Hg^0 has been demonstrated in laboratory experiments with several phytoplankton species (Mason *et al.* 1995, Poulain *et al.* 2004, Kelly *et al.* 2006, Poulain *et al.* 2007, Morelli *et al.* 2009, Oh *et al.* 2011, Grégoire and Poulain 2014, 2016). The volatilization rates varied between the algal species, Hg concentration and exposure duration (Devars *et al.* 2000, Morelli *et al.* 2009). Early works demonstrated that the exposure of various phytoplankton species to very high iHg concentrations resulted to Hg^0 production, observations often linked to the detoxification mechanisms (Ben-Bassat *et al.* 1972, Ben-Bassat and Mayer 1975, Macka *et al.* 1978, Wilkinson *et al.* 1989, Kelly *et al.* 2007). Diatom *T. weissflogii* was shown to produce DGM under light and dark conditions suggesting that biological rather than photochemical processes or photosynthetic metabolites mediate this transformation (Morelli *et al.* 2009). Production of DGM was observed for 3 other diatoms species (Wu and Wang 2014), suggesting an important role of intracellular thiols. The reduction of iHg was, however, observed in cultures of *Chlorella vulgaris*, but the organic matter released or obtained after cell degradation was shown to reduce more iHg than living algal cells themselves (Liang *et al.* 2022). Nevertheless, the fundamental mechanisms

involved in the biological reduction process remain poorly understood.

Recent advances revealed the activation of a *MerR*-like transcription factor, Slr0701 when cyanobacterium *Synechocystis* sp. PCC6803 is exposed to iHg (Singh *et al.* 2019). The activation of this transcription factor promotes the expression of the mercuric reductase, *MerA*-like coded by the Slr1849 gene, which allows the reduction of iHg into the volatile form Hg⁰ (Boyd and Barkay 2012, Singh *et al.* 2019). This process of Hg reduction could enhance the Hg tolerance of this cyanobacterium. The reduction of iHg to Hg⁰ followed by its volatilization is the process responsible for the evasion of Hg from both terrestrial and aquatic systems (Gonzalez-Raymat *et al.* 2017). Hg⁰ production by phytoplankton has been thus evidenced in the field (Grégoire and Poulain 2014) and the formation of DGM was correlated with phytoplankton dynamics and blooms (Poulain *et al.* 2004, Poulain *et al.* 2007). It was also shown that phototrophic bacteria use iHg as an electron sink to maintain redox homeostasis to produce Hg⁰ (Grégoire and Poulain 2016). However, it is still unclear whether algae and cyanobacteria are directly involved in DGM production or mediate this process by triggering bacterial activity or releasing biogenic organic ligands.

Hg ***methylation/demethylation*** by phytoplankton was investigated in the laboratory. For instance, the potential MeHg demethylation was seen in the different species of algae and cyanobacteria (Bravo *et al.* 2014, Franco *et al.* 2018, Li *et al.* 2022, Yin *et al.* 2022) however, no evidence of methylation was found. Indeed, a specific gene cluster (*hgcAB*) used as a proxy for the microorganism's capability to methylate iHg (Gilmour *et al.* 2013), is not found in phytoplankton species. Similarly, no methylation was observed by pico-nanoplankton from a eutrophic lake (Cossart *et al.* 2021). Although there is no direct evidence that phytoplankton microorganisms can methylate Hg itself, numerous studies have highlighted the importance of algae in MeHg production (Lázaro *et al.*, 2019). Several studies have reported a positive correlation between phototrophic productivity and an increase in MeHg (Tsui *et al.* 2010, Lázaro *et al.* 2013, Xing *et al.* 2018, Lázaro *et al.* 2019). Strong links have been uncovered between methylation rates in open

oceans and the presence of nano- and pico-phytoplankton (Heimbürger *et al.* 2010). iHg methylation rates were measured at the maximum chlorophyll depth (i.e. maximum phytoplankton biomass) in oxic surface seawater and were shown to be influenced by pelagic microorganism abundance and activities (phyto- and bacterioplankton)(Monperrus *et al.* 2007). iHg methylation in the water column was shown to account for around 47% of the MeHg present in polar marine waters (Lehnherr *et al.* 2011). The Hg methylation rates have been linked to the presence of thiols produced by phytoplankton species and the decomposition of algal-derived organic matter (Bravo *et al.* 2017, Bouchet *et al.* 2018, Zhao *et al.* 2021).

Demethylation in oxic surface waters has been reported to be partially biologically mediated besides being induced by solar radiation (Whalin *et al.* 2007). Reduction and demethylation of Hg were also demonstrated in the diatom *T. weissflogii* (Devars *et al.* 2000, Morelli *et al.* 2009) and green alga *C. reinhardtii* (Bravo *et al.* 2014). However, the transformation yields and demethylation rate constants are still to be elucidated and quantified. Very recently, the demethylation capacity of 15 algae species was investigated, and 6 out of 15 species (dinoflagellates, chrysophytes, and diatoms) tested were able to demethylate MeHg (Li *et al.* 2022). The demethylation was also demonstrated in natural pico-nanoplankton communities from a eutrophic lake (Cossart *et al.* 2021) as well as in productive coastal waters (Sharif *et al.* 2014) and maximum phytoplankton biomass depth of marine waters (Monperrus *et al.* 2007). Overall, the current understanding of methylation and demethylation of Hg species by phytoplankton is rather limited. Yet, recent results have highlighted phytoplankton direct or indirect implications for both processes.

Phytoplankton species could control **intracellular Hg speciation** and thus affect the intracellular transformations by cytosolic ligands. It has been shown that the quantity and the quality of the intracellular metabolites, which could interact with Hg species, are altered by iHg exposure (Mangal *et al.* 2022). Glutathione (GSH) content, which is the most prevalent thiol in algae, was found to increase in algae exposed to iHg (Howe and Merchant 1992, Devars *et al.* 2000, Morelli

et al. 2009). MeHg exposure was also seen to induce the synthesis of GSH in *Thalassiosira weissflogii*, but it was iHg that contributed to higher levels of other thiol compounds, such as cysteine and phytochelatins (PCs) (Wu and Wang 2012, 2013). More recently, GSH was identified as the main low molecular weight binding ligand to iHg and MeHg in the cytosolic fraction of cyanobacterium *Synechocystis* sp. PCC 6803 (Garcia-Calleja *et al.* 2021). PCs enzymatically produced from glutathione are additional thiols used by algae to counteract Hg negative effects (Mehra *et al.* 1996). For example, the PC₂₋₃ have been reported to be synthesized by *T. weissflogii* when exposed to 5 and 150 nM Hg while MeHg seems to be a poor inducer (Howe and Merchant 1992, Ahner and Morel 1995, Knauer *et al.* 1998, Morelli *et al.* 2009). A comparison of diatom *T. weissflogii* with the green alga *Chlorella autotrophica* revealed that PCs induction is highly dependent on the phytoplanktonic species with higher biological responses seen in *T. weissflogii*, and low PCs induction observed for *C. autotrophica* (Wu and Wang 2014). The sequestration of iHg bound to PCs was identified in the microalga *Chlorella sorokiniana* exposed to high iHg concentrations (Gómez-Jacinto *et al.* 2015). However, the role of these thiols in cellular transformations of iHg and MeHg still needs to be confirmed under lower environmentally realistic exposure Hg concentrations.

Hg sequestration as β -cinabar (HgS) has been demonstrated as a detoxification mechanism in a variety of cyanobacteria *Limnothrix planctonica*, *Synechococcus leopoldiensis*, and *Phormidium limnetica* (Kelly *et al.* 2006, Kelly *et al.* 2007). Green algae *Chlorella autotrophica*, flagellate *Isochrysis galbana*, and marine diatom *Thalassiosira weissflogii* could transform iHg into metacinnabar (β -HgS) (Wu and Wang 2014). Sunlight was also shown to facilitate the transformation of Hg to less bioavailable species, such as β -HgS and Hg-PCs (Liang *et al.* 2022). Overall, phytoplankton can sequester high quantities of Hg as a detoxification strategy without apparent harmful effects. The tolerance to Hg species toxicity has been related to the capacity of the phytoplankton to capture Hg in subcellular compartments as vacuoles which serve as a sink for mineralized forms or low molecular weight thiol compounds. Nevertheless, no information

has been ever provided at environmentally relevant concentrations or even in real environmental conditions in various aquatic systems.

The examples presented above demonstrated the important role of thiol compounds in intracellular handling of iHg and MeHg and the existing research gaps in understanding the underlying mechanisms and interplay between iHg and MeHg transformation and thiol pathways. However, the recent developments allowing direct quantification of both low and high molecular weight thiols and their Hg complexes (Pedrero *et al.* 2011, Pedrero Zayas *et al.* 2014, Garcia-Calleja *et al.* 2021) open new opportunities for exploring the effect of intra- and extracellular ligands in Hg uptake and biotic transformation. On the other hand, the exposures of green alga *C. reinhardtii* to low (5 nM) and high (50 nM) iHg and MeHg concentrations induced metabolic perturbations in amino acid and nucleotide synthesis and degradation, fatty acids, carbohydrates, tricarboxylic acids, antioxidants and photorespiration (Slaveykova *et al.* 2021).

5. Conclusion and perspectives

Important research advances confirmed that phytoplankton could affect Hg speciation and transformations directly, e.g. via biotic transformations of the accumulated mercury species and/or indirectly via the release of low and high molecular weight molecules which could complex mercury and affect both abiotic and biotic transformations of Hg compounds. The up-to-date studies revealed that different microalgal species and cyanobacteria contribute to iHg biotic reduction into Hg⁰, MeHg demethylation and transformation of iHg into metacinnabar, as well as produce different biomolecules which can contribute to abiotic mercury reduction. Nevertheless, numerous questions remain open concerning the underlying mechanisms of Hg species interactions with phytoplankton in terms of their uptake mechanisms and cellular handling, including the release of biomolecules, which can be the focus of future research. The mechanisms behind the potential transformations of mercury species in aquatic environment mediated by the

phytoplankton are still not fully understood and further research studies are needed. The role of the phytoplankton in biotic transformations of mercury species and their significance compared to other microorganisms such as bacteria are overlooked and need to be further explored especially combining both phototrophic and heterotrophic microorganisms in specific experiments. Therefore, studies that quantitatively examine different transformation processes and identify the phytoplankton species or groups of species able to demethylate or reduce mercury in situ are highly sought.

The development of the Hg stable isotope fractionation approach opens up the possibility to decipher the contribution of interconnected abiotic and biotic transformation (Kritee *et al.* 2013) and to track further the processes controlling origin and cycling of Hg before its incorporation in the foodweb (Bouchet *et al.* 2022). Since the biotic transformations are considered prevailing, the development of the novel -omics approaches would provide key information on the interactions between Hg and phytoplankton species (Beauvais-Flück *et al.* 2016, Beauvais-Flück *et al.* 2018, Slaveykova *et al.* 2021, Mangal *et al.* 2022). These approaches can be used to design the strategies to understand the mechanisms of Hg-induced metabolic perturbations and to explore their relationship with cellular transformations of Hg species. A combination of the chromatography-based separation with mass spectrometry detection for quantification of both low and high molecular weight cellular molecules and their Hg complexes (Garcia-Calleja *et al.*, 2021) with the cellular effects could contribute to uncover the relationship between transformations and toxicological outcomes of Hg exposure. Furthermore, the relationship between different cellular transformation processes and different detoxification mechanisms merits deeper insight. Identifying specific organelles and cellular compartments where Hg species accumulate and can be transformed could be also of added value, given the importance of cellular speciation and distribution in the toxicity, detoxification and trophic transfer of mercury (Wu and Wang 2011). In addition to the mechanistic studies with model microorganisms, the above-mentioned approaches can be used to address key questions on the interactions between Hg species and the

phytoplankton community and, to improve the current understanding of their contributions to Hg species transformations in natural environment.

The understanding of the cellular transformations and speciation is central for the elucidation of the role of phytoplankton in Hg biogeochemical cycle and is of high importance to better predict the long-term changes in Hg bioavailability to food webs. Indeed, a global circulation 3D model of MeHg in seawater showed that diatoms and picocyanobacterium *Synechococcus* sp. are the most important phytoplankton categories for the transfer of MeHg from seawater to herbivorous zooplankton, contributing 35% and 25%, respectively (Zhang *et al.* 2020). Given the interconnection between the global change and biogeochemical cycling of mercury (Chetelat *et al.* 2022), a deeper understanding of the mercury transformation processes triggered by phytoplankton, measured both in the laboratory and in situ and the development of mechanistic models coupling primary production, Hg transport, abiotic and biotic transformations and climate models would allow projections under various climate change scenarios at a global scale. This will further constrain the efficiency of the measures taken by the Minamata convention to reduce mercury emissions. This is important given continuous anthropogenic Hg inputs to aquatic ecosystems and considerable shifts in the phytoplankton dynamics predicted with global change.

Data Availability Statement

Data sharing is not applicable as no new data were generated or analyzed during this study.

Conflicts of Interest

The authors declare no conflicts of interest.

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