

# Mercury speciation at the oxic/anoxic transition of a meromictic lake

## (Lake Pavin, Massif Central, France)

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### Introduction

Lake Pavin is a unique permanently stratified maar lake in France with anoxic bottom waters. It is stratified with an oxygenated mixolimnion overlying an anoxic monimolimnion from ~55m to the bottom at 92m. A turbidity layer enriched with Fe and Mn (oxy)hydroxides is located around 55m (Fig.1).

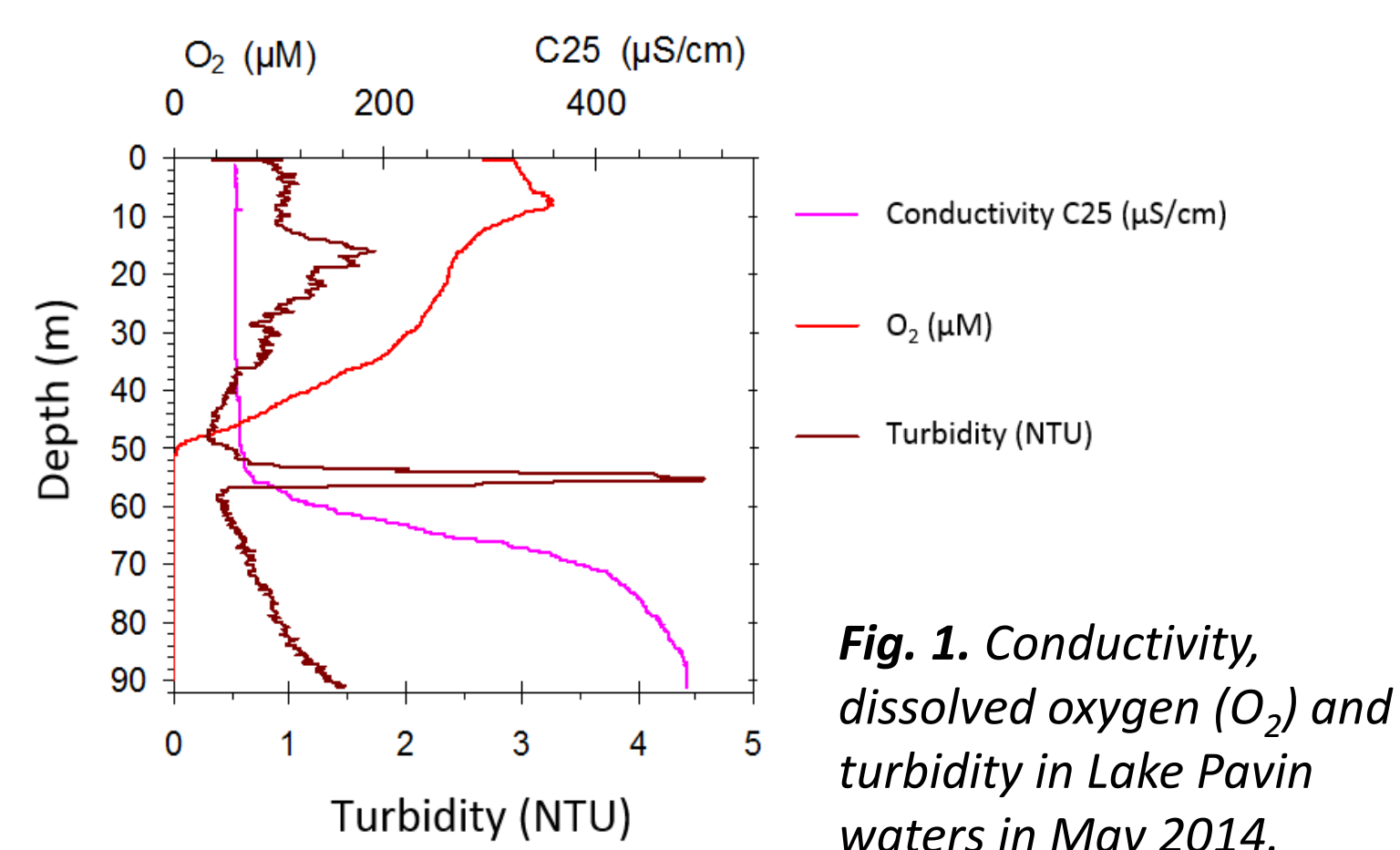


Fig. 1. Conductivity, dissolved oxygen ( $O_2$ ) and turbidity in Lake Pavin waters in May 2014.

Mercury (Hg) speciation in aquatic systems consists of zero and divalent species, namely elemental Hg ( $Hg^0$ ), inorganic ( $Hg^{II}$ ), monomethylmercury (MMHg), dimethylmercury (DMHg). MMHg is a neurotoxic species and has the ability to bioaccumulate and bioamplify throughout the aquatic food chain, leading to human exposure. It is thus of major importance to understand how and where methylation processes take place. The aim of our study is to determine Hg speciation on filtered (F) and unfiltered waters (UNF), including dissolved gaseous Hg ( $DGM=Hg^0+DMHg$ , UNF), total mercury  $THg_F$  and  $THg_{UNF}$ , and total methylated mercury ( $MeHg=MMHg+DMHg$ , F and UNF), to understand Hg transformations near the oxic-anoxic interface in relation with Fe, S chemistry, and bacterial activity.

### Methods

Sampling was performed from the surface to the bottom, at the middle of the lake on a 3x3m sampling platform, using a Niskin bottle. Samples were unfiltered (UNF) and filtered (F, 0.45µm PVDF membranes) on site, stored in acid-cleaned Teflon bottles following ultra-clean techniques. Samples were collected at 10m-intervals and at < 5m-intervals near the oxycline.



Quantification at ultra-trace levels (pM) were performed on site for DGM and at the laboratory for  $THg$  and  $MeHg$  using atomic fluorescence spectrometers (Tekran 2500) following US-EPA standard method 1631 [1] for  $THg$  and a derivatization method for  $MeHg$  [2].

Samples below 55m depth underwent HCl acidification to 15% (v/v) and 1 min of stirring prior to  $MeHg$  analyses to minimize analytical bias due to high sulfidic water. Acid Volatile Sulfide (AVS) were performed on site on unfiltered waters within few hours after sampling: samples were kept under anoxia until analysis following a purge and trap technological innovation designed at ISTerre.

### Results and Discussion

Major elements ( $Na^+$ ,  $K^+$ ,  $Mg^{2+}$  and  $Ca^{2+}$ ) analysis shows the stratification of the lake with increasing concentrations downward the oxycline starting at around 55m depth (Fig.2A).  $THg_F$  and  $THg_{UNF}$  ranged from 0.5 to 11.8 pM (Fig.2B), DGM ranged from 0.02 to 1.10 pM (Fig.2C).  $MeHg_F$  and  $MeHg_{UNF}$  ranged from < LD to 3.2 pM (Fig.2D).  $MeHg$  represented up to 44% of  $THg$  on filtered waters at 60m depth, which is high compared to other studies [3, 4, 5]. Both  $THg$  and  $MeHg$  maxima were located below the maximum turbidity.

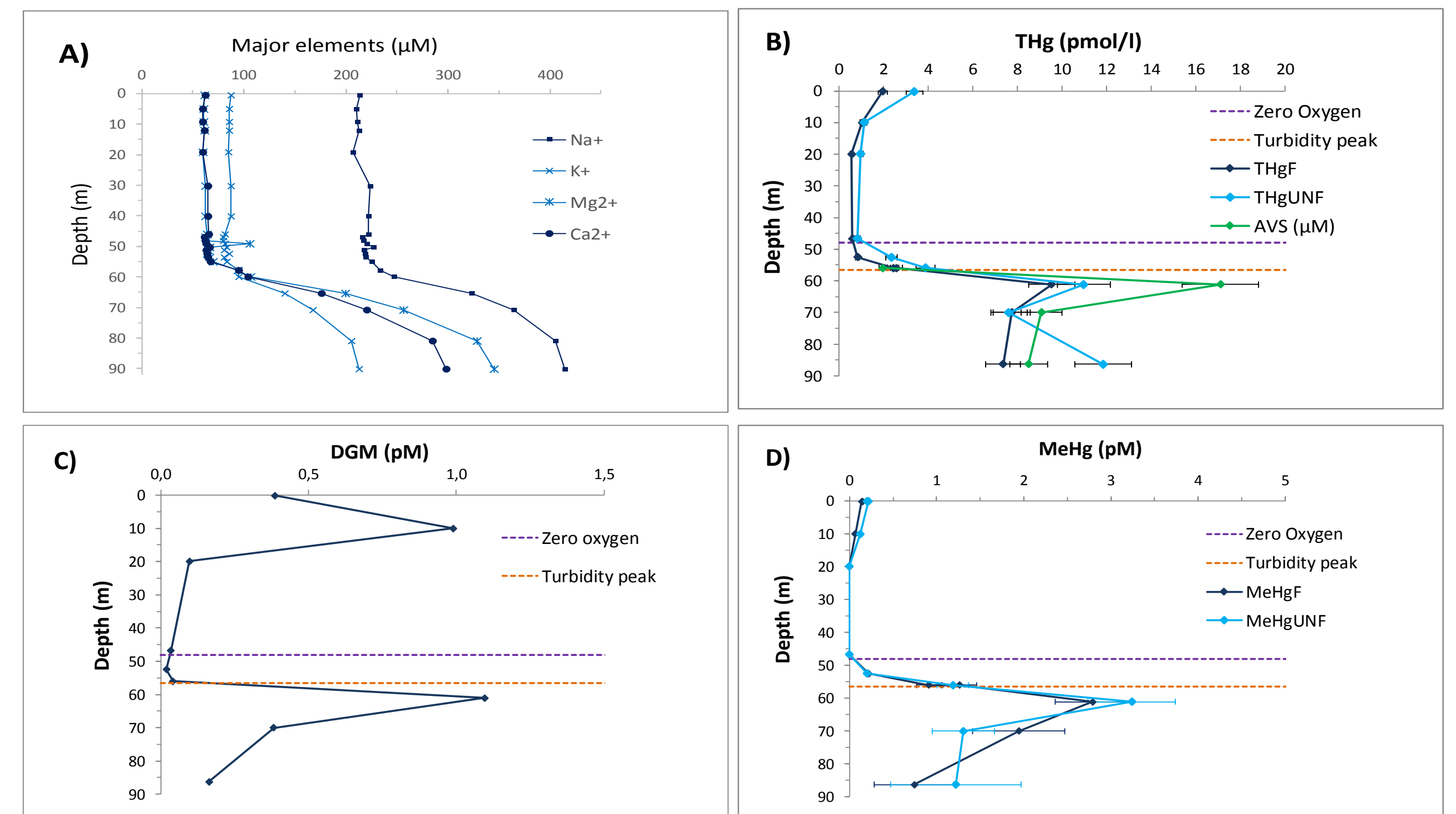


Fig. 2. Vertical concentration profiles: A) Major elements from May 2015 campaign, B)  $THg_F$  &  $THg_{UNF}$ , C) DGM and D)  $MeHg_F$  &  $MeHg_{UNF}$  and AVS concentrations sampled in October 2016.

- Calculations using PhreeqC (without organic species), reveal that in oxic conditions,  $Hg(OH)_2$  and  $HgOHCl$  are the dominant aqueous species, whereas in sulfidic and anoxic waters, aqueous  $HgS$  is the major specie (Fig.3) that could play an important role for methylation [6, 7].
- Highest  $MeHg_F/THg_F$  and  $MeHg_{UNF}/THg_{UNF}$  ratios are reached at the turbidity peak (Fig.4), whereas maximum concentrations are located below. This suggests that methylation is favored by Fe (oxy)hydroxides reduction (*via* iron reducing bacteria, IRB). Below 60m, precise  $MeHg$  quantification is disturbed by matrix effect and thus results in high error bars that can get to 61% (Fig.2D).
- In anoxic waters, AVS exist as free sulfides ( $H_2S/HS^-$ ) and disordered  $FeS$  [8]. AVS concentrations measured on unfiltered waters follow the same tendency as  $THg$  with a maximum reached at 61m depth. The correlation between AVS and  $THg$  and the maximum of DGM at 61m suggest (1) a link between  $FeS$  and Hg [9] and (2) that bacteria (possibly Sulfate Reducing Bacteria, SRB, highlighted in the lake [10]) or  $Fe^{2+}$  could be involved in the reduction of inorganic  $Hg^{II}$  to  $Hg^0$  (DGM) [11, 12].
- $THg$  and  $MeHg$  were mainly present in the filtered phase indicating that these species are either totally dissolved or could be hosted by sulphide filter passing nanoparticles present in the lake [13,14].  $THg_F$  and  $THg_{UNF}$  evolve in parallel except at the bottom of the lake where much higher  $THg_{UNF}$  suggests that Hg could be hosted by particles bigger than 0.45µm.
- $MeHg$  and Hg maxima suggest that  $MeHg$  production depends of the simultaneous presence of methylation agents (IRB/SRB) and  $Hg^{II}$  availability [11,15].

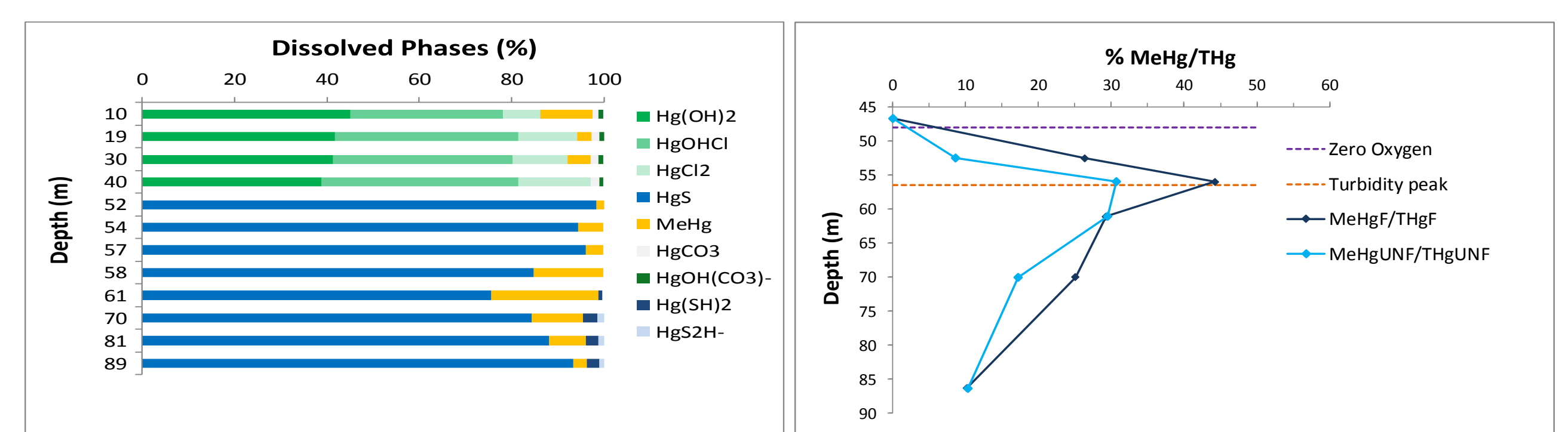


Fig. 3, 4. Calculations from PhreeqC for Hg speciation within the aqueous phase and  $MeHg/THg$  ratios.

The perspective of this study is to develop a more reliable analytical method to quantify  $MeHg$  in pM range in high sulfidic zone in order to delete the bias encountered with the derivatization method. Secondly, we will determine what is the Hg partitioning between aqueous and solid mineral phases with the identification of particles that host Hg. A third question is to determine which solid species favor or restrict the availability of Hg for methylation/demethylation at the interface and in the anoxic zone.

### References

- [1] Telliard et al., 2001 [4] Muresan et al., 2006 [7] Chen et al., 2017 [10] Jézéquel et al., 2008 [13] Viollier et al., 1997  
[2] Leopold et al., 2010 [5] Cossa et al., 2017 [8] Bura-Nakić et al., 2009 [11] Lamborg et al., 2008 [14] Miot et al., 2015  
[3] Guedron et al., 2014 [6] Mikac et al., 2000 [9] Hellal et al., 2015 [12] Charlet et al., 2002 [15] Bravo et al., 2016

### Acknowledgments

This work was funded by Geochemistry group, which is part of Labex OSUG@2020.