

PROPOSITION DE SUJET DE STAGE M2

Comparaison de la biodiversité microbienne en lien avec la méthylation du mercure par une approche métagénomique

1- Contexte : Le mercure reste un métal problématique pour la santé publique de nos jours car sa forme organique, le méthyl-mercure, est biomagnifié dans la chaîne trophique (Bravo et al., 2014; Bravo et Cosio, 2019). De fait, ce métal est souvent retrouvé en concentrations dépassant la norme environnementale en vigueur pour les poissons de nombreux lacs en Europe et ailleurs, malgré l'absence de source locale (Eagles-Smith et al., 2016). Le rôle des microbes est essentiel dans la production et la dégradation de méthyl-mercure (Park et al., 2013 ; Barkay et al 2003), mais leur abondance et rôle précis reste à comprendre. Nos travaux récents ont montré que la méthylation du mercure avait lieu dans les sédiments du lac Léman (Suisse ; Capo et al. 2023 ; Gascon et al 2016).

2- Objectifs du travail : Le but de ce projet est de caractériser la biodiversité et la fonctionnalité de la communauté microbienne de sédiments par une analyse bioinformatique de métagénomique et de comparer les résultats de différentes méthodes.

3- Déroulement : Le projet inclut les tâches suivantes: (i) analyse bioinformatique, (ii) interprétation des résultats.

4- Lieu de travail : Le stage se déroulera intégralement dans le laboratoire partenaire à Barcelone.

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Références bibliographiques :

- Barkay T, Miller SM, Summers AO. 2003. Bacterial mercury resistance from atoms to ecosystems. *FEMS Microbiol Rev.* Jun;27(2-3):355-84
- Bravo AG, Cosio C., 2019 Biotic formation of methylmercury: a bio-physico-chemical conundrum, *Limnology and Oceanography*, 65:1010–1027
- Bravo, A. G., C. Cosio, D. Amouroux, J. Zopfi, P.-A. Chevalley, J. E. Spangenberg, V.-G. Ungureanu, and J. Dominik. 2014. Extremely elevated methyl mercury levels in water, sediment and organisms in a Romanian reservoir affected by release of mercury from a chlor-alkali plant. *Water Res.* 49: 391–405.
- Bravo AG, Zopfi J, Buck M, Xu J, Bertilsson S, Schaefer JK, Poté J, Cosio C., 2018. Geobacteraceae are important members of mercury-methylating microbial communities of sediments impacted by waste water releases. *ISME J.* 12(3):802-812
- Capo E, Cosio C. ..., Bravo AG, 2023, Anaerobic mercury methylators inhabit sinking particles of oxic water columns, *Water Research.* 229:119368
- Eagles-Smith, C. A., J. T. Ackerman, J. J. Willacker, and others. 2016. Spatial and temporal patterns of mercury concentrations in freshwater fish across the Western United States and Canada. *Sci. Total Environ.* 568: 1171–1184. doi:10.1016/j.scitotenv.2016.03.229
- Gascón Díez, E., J. L. Loizeau, C. Cosio, S. Bouchet, T. Adatte, D. Amouroux, and A. G. Bravo. 2016. Role of settling particles on mercury methylation in the oxic water column of freshwater systems. *Environ. Sci. Technol.* 50: 11672–11679.
- Parks, J. M., A. Johs, M. Podar, and others. 2013. The genetic basis for bacterial mercury methylation. *Science* 339: 1332–1335.



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Internship

Comparison of microbial biodiversity in relation to mercury methylation by a metagenomic approach

1- Background : Mercury remains a problematic metal for public health because its organic form, methyl mercury, is biomagnified in the trophic chain (Bravo et al., 2014). Currently, this metal is often found in concentrations exceeding the current environmental standard for fish in many lakes in Europe and elsewhere, despite the absence of a local source (Eagles-Smith et al., 2016). The role of microbes is essential in the production and degradation of methyl mercury (Park et al., 2013; Barkay et al 2003), but their abundance and precise role remains to be understood. Our recent work has shown that mercury methylation happened in the Lac Léman (Gascon et al., 2016).

2- Objectives: The goal of this project is to characterize the biodiversity and functionality of the microbial community through a bioinformatic analysis of metagenomics and compare outcomes of different methods.

3- Implementation: The project includes the following tasks: (i) bioinformatic analysis of sequences, (ii) interpretation of the results.

4- Location: The internship will take place entirely in the partner laboratory in Barcelona.
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