

Reply to the comment on "New insights into the biomineralization of mercury selenide nanoparticles through stable isotope analysis in giant petrel tissues" by A. Manceau, J. Hazard. Mater. 425 (2021) 127922. doi: 10.1016/j.jhazmat.2021.127922

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2 mercury selenide nanoparticles through stable isotope analysis in giant

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27 ABSTRACT

28 In the comments reported by A. Manceau [1], relating to our recent paper on mercury (Hg) 29 species-specific isotopic characterization in giant petrel tissues [2] two critical questions were 30 raised. Firstly, according to A. Manceau, our method of extraction and isolation of nanoparticles 31 was not able to efficiently isolate mercury selenide nanoparticles (HgSe NPs) and therefore the δ^{202} Hg values measured are not species-specific, but rather δ^{202} Hg of mixtures of complexes such 32 33 as MeHgCys, Hg(Sec)₄, and HgSe. Secondly, he suggests that our main findings showing that 34 no isotopic fractionation is induced during the HgSe NPs biomineralization step from the 35 precursor-demethylated species is erroneous because it contradicts the conclusion of two recent 36 articles by A. Manceau and co-workers [3,4]. In this reply we defend our scientific findings and 37 respectively respond to the questions and comments raised by A. Manceau.

38

39 1. DISCUSSION

40 Firstly, we address the comment questioning the purity of the isolated HgSe NPs fraction. 41 Manceau is suggesting that this fraction is a mixture of MeHgCys, Hg(Sec)₄ and HgSe, therefore 42 leading to a non-species-specific HgSe NPs isotopic characterization. We would like to point out 43 that the NPs isolation approach, as detailed in the manuscript, is based on the published research 44 by Bolea-Fernández and co-workers for Hg isotopic characterization of Tiemannite in pilot whale 45 tissues [5,6]. We have done slight modifications to their method including a heating step at 85°C 46 for 2 hours with formic acid to remove any organic molecules. Even if a small amount of Hg could 47 be found in the solid residual resulting fraction, it is also a product of Hg (bio)demethylation. In 48 addition, as detailed in our article, the cut-off filter with isolated HgSe NPs fraction was abundantly 49 washed with MQ-water until complete elimination of total soluble Hg was achieved and verified 50 by CV-AFS measurements. Therefore, by using such sample treatment, the absence of the 51 concomitant Hg species mentioned by Manceau is guaranteed and it is unlikely it will modify the 52 interpretation of the obtained data. Manceau supports his criticism regarding HgSe NPs purity, 53 probably based on those values where the δ^{202} Hg _{bulk} is equivalent to species-specific δ^{202} Hg of isolated HgSe NPs. However, in more than 50% of the samples the absolute shift $\delta^{\rm 202} Hg$ (Bulk -54

HgSe NPs) is larger than 0.20 ‰), all having been treated with the same procedure and
demonstrating that labile-Hg was removed from that fraction.

57 The second comment addressed by Manceau questions our main hypothesis that HgSe NPs 58 biomineralization from the precursor-demethylated species does not induce Hg isotopic 59 fractionation due to its conflict with two research investigations conducted by himself and his co-60 workers [3,4]. In this regard, we would like to state that our premise is solidly based on high 61 precision measurements of the Hg isotopic composition in the tissues of 11 giant petrels (40 62 tissues in total, with HgSe NPs extracted from 37 tissues, all except three blood samples). In 63 contrast, the two recent publications by Manceau and co-workers [3,4], based their hypothesis on 64 a mathematical calculation approach which has not yet been experimentally validated by 65 measurements of species-specific Hg isotopic composition.

In each tissue, the bulk Hg isotopic composition results from the contribution of different Hgspecies as outlined in equation 1:

68 $\delta^{202} \text{Hg}_{\text{bulk}} = \sum_{i=\text{Hg species}} f_i \times \delta^{202} \text{Hg}_i \quad (\%) \qquad \text{Eq. 1}$

69 where δ^{202} Hg_{bulk} represents the isotopic composition of total mercury in the tissue, f_i is the fraction 70 of i-species in the corresponding tissue, and δ^{202} Hg_i represents the species-specific isotopic 71 composition of Hg in i-species. The resolution of this equation requires the knowledge of a series 72 of data that have been over simplified in the aforementioned mathematical works [3,4] with the 73 following assumptions: i) the isotopic composition of each Hg species is only species-dependent, 74 and it does not vary between individuals or between tissues; ii) Hg species in tissues are 75 exclusively limited to three different forms, viz.: MeHqCys, Hq(Sec)₄ and HqSe. Regarding the 76 invariance of Hg isotopic composition, to the best of our knowledge there is no research to date 77 that supports the theory that there is a specific δ^{202} Hg value that is solely dependent on the nature 78 of the species. So far, in cases where different Hg species have been extracted, no unique and constant δ^{202} Hg value has been obtained for all tissues or in all individuals studied. This has not 79 80 been experimentally proven neither for MeHg [4,7–9] or HgSe NPs [2,5] in different living 81 organisms. A study developed by our group (IPREM CNRS Pau) and co-workers is the only one 82 to jointly report Hg isotopic compositions for MeHg and inorganic mercury (iHg) [9] in aquatic 83 mammal tissues. These values reflect a large variability between individuals and tissues for the

species-specific δ^{202} Hg values in beluga whales (δ^{202} Hg_{MeHg} variation of ~3.5‰) and seals 84 85 $(\delta^{202}$ Hg_{MeHg} variation of ~1.7‰). This aspect of the mathematical approach has also been recently 86 questioned by Wiederhold and Jiskra [10], which makes it clear that this assumption remains 87 questionable for the seabird tissues. So far the number of studies dealing with Hg species-specific 88 isotopic composition is limited mainly due to the great challenge associated with the 89 extraction/isolation of the different Hg species while preserving the original isotopic pattern [2,5,7– 90 9,11]. The Hg species-specific approach in animal tissues has been mainly applied on the isotopic 91 characterization of MeHg [4,7–9]. Meanwhile Bolea-Fernández and co-workers together with our 92 article [2,5] reported the unique Hg species-specific isotopic composition relative to HgSe NPs. 93 The obtained Hg species-specific isotopic data has been key to obtain information on metabolic 94 processes [2,5,7-9].

95 The comments of Manceau about the δ^{202} Hg in HgSe NPs values experimentally determined in 96 our article comes from the differences with the values estimated by a mathematical approach 97 considering exclusively three species of Hg (MeHgCys, Hg(Sec)₄ and HgSe). However, the 98 analysis of the water-soluble fraction from the different seabird tissues by size exclusion 99 chromatography (SEC)-ICP-MS presented in Figure 4 of our recent article [2], evidenced that Hg 100 binds several (unknown) biomolecules that probably play key roles on MeHg demethylation. The 101 unambiguous characterization of Hg binding biomolecules/proteins represents an important 102 analytical challenge, which explain the limited number of publications reporting Hg-metabolites 103 [12–19]. The crucial role of speciation in understanding metabolic processes is undoubtedly an 104 additional dimension to Hg isotopic characterisation. Thus, we consider that a mathematical 105 approach which simplifies the number of Hg species and the possibly large variability of δ^{202} Hg in 106 different tissues and individuals, cannot be used in a general way to estimate Hg isotopic values 107 to improve our understanding of the pathways and fate of Hg in biota.

108 Moreover, we would also like to highlight this statement by Manceau: "that the ²⁰²Hg isotope is 109 actually fractionated during the Hg(Sec)₄ \rightarrow HgSe reaction, and therefore that this isotope can be 110 used to trace the Hg metabolic pathways between tissues in a single individual and in different 111 animals". This argument is independent of whether there is isotopic fractionation at that stage, 112 and even transcends this study, as δ^{202} Hg (MDF) has already been used in several works to trace 113 metabolic pathways in living organisms [5,9,20–25]. Even the fact that there is no isotopic 114 fractionation of Hg at this stage characterizes the (metabolic) process, therefore, this statement 115 for us means a trivialization of the scientific results of this research.

Additionally, our hypothesis related to the absence of isotopic fractionation during the biomineralization step from the precursor (demethylated) species, can be supported by the combination of δ^{202} Hg values measured in giant petrels and estimated with equation 1. The δ^{202} Hg species-specific experimental data (table 1) reported [2,4,25,26] for MeHg (δ^{202} HgMeHg) and for HgSe NPs (δ^{202} Hg_{HgSe}) were combined by applying equation 2 (adapted from equation 1) in the estimation of δ^{202} Hg_{bulk} as follows:

 $122 \qquad \delta^{202}Hg_{\text{bulk estimated}} = f(\text{MeHg}) \times \delta^{202}Hg_{\text{MeHg}} + f(\text{HgSe}) \times \delta^{202}Hg_{\text{HgSe}} + f(\text{HgSe} (1:4)) \times \delta^{202}Hg_{\text{HgSe} 1:4} \quad (\text{\rohese}) \quad Eq.2$

where δ^{202} Hg_{bulk} represents the estimation of isotopic composition of total mercury in the tissue and f is the fraction of the three main species (MeHg, precursor HgSe (1:4), and HgSe NPs) determined by HR-XANES [26]. The δ^{202} Hg_{HgSe (1:4)} will be considered equivalent to δ^{202} Hg_{HgSe}, in line with our observation in the preceding article. The obtained δ^{202} Hg _{bulk} estimated reported in table 1 and the measured values (average between δ^{202} Hg _{bulk} measurements in different sections of the tissues) [2,4] show a good agreement when assuming the lack of Hg isotopic fractionation in the biomineralization and approximating the δ^{202} Hg_{HgSe (1:4)} to the δ^{202} Hg_{HgSe}.

In summary, the complexity of Hg pathways in biota calls for a combination of complementary analytical techniques to contribute to their elucidation. The analytical approaches addressed on this discussion (species-specific isolation, liquid chromatography separation, HR-XANES identification and high precision isotopic analyses) demonstrates the potential of such synergy to go further on the understanding of Hg processes in biota.

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Table 1. Estimation of the δ^{202} Hg_{bulk} based on the species-specific δ^{202} Hg of the three main species according to HR-XANES measurements. The measured

236 δ^{202} Hg_{bulk} value for comparison has been calculated as an average of the two published values for these tissues. The δ^{202} Hg_{HgSe (1:4)} has been approximated to

237 the δ^{202} Hg_{HgSe} experimentally measured in the corresponding tissues.

		δ ²⁰² Hg _{bulk} (‰) ^[4]	δ ²⁰² Hg _{bulk} (‰)	Mean δ ²⁰² Hg _{bulk} (‰)	δ ²⁰² Hg _{MeHg} (‰) ^[4]	δ^{202} Hg _{HgSe} = δ^{202} Hg _{HgSe (1:4)} (‰) ^[2]	f MeHg (%) ^[26]	f HgSe (1:4) (%) ^[26]	f HgSe (%) ^[26]	δ ²⁰² Hg _{bulk estimated} (‰)
Individual 1	Kidneys	0.15 ± 0.02	0.11 ^[2]	0.15 ± 0.03	2.70 ± 0.03	-0.08	0.07 ± 0.03	0.32 ± 0.09	0.61 ± 0.08	0.11
	Muscle	-0.76 ± 0.03	-0.48 [2]	-0.76 ± 0.20	2.78 ± 0.03	-0.70	-	0.67 ± 0.08	0.33 ± 0.08	-0.70
Individual 2	Liver	0.04 ± 0.04	-0.08 [2]	0.04 ± 0.08	1.87 ± 0.03	-0.05	-	0.09 ± 0.06	0.91 ± 0.06	-0.05
	Muscle	-0.57 ± 0.02	-0.51 ^[2]	-0.54 ± 0.04	2.07 ± 0.03	-0.55	0.07 ± 0.03	0.60 ± 0.09	0.33 ± 0.09	-0.37
Individual 3	Muscle	-0.73 ± 0.06	-	-0.73 ± 0.06	0.90 ± 0.04	-	-	0.40 ± 0.08	0.60 ± 0.08	-
Individual 4	Brain	0.50 ± 0.04	0.10 [8]	0.30 ± 0.28	2.58 ± 0.04	-0.32	0.13 ± 0.05	0.16 ± 0.10	0.71 ± 0.08	0.06

238

239 $\delta^{202}Hg_{bulk estimated} = f_{MeHg} \times \delta^{202}Hg_{MeHg} + f_{HgSe} \delta^{202}Hg_{HgSe} + f_{HgSe (1:4)} \delta^{202}Hg_{HgSe 1:4}$ (‰)

240 Individual 1: P2^[26]=P3^[2]; Individual 2: P3^[26]=P4^[2]; Individual 3: P5^[26]=P8^[2]; Individual 4: P8^[26]=PGA03^[2,25]