Biogeosciences Discuss., 11, C7197–C7203, 2014
www.biogeosciences-discuss.net/11/C7197/2014/

Biogeosciences Discussions Open Access

Interactive comment on "Origin and fate of particulate and dissolved organic matter in a naturally iron-fertilized region of the Southern Ocean" *by* L. Tremblay et al.

L. Tremblay et al.

luc.tremblay@umoncton.ca

Received and published: 8 December 2014

(1) comments from Referees, (2) author's response, (3) author's changes in manuscript

C. Panagiotopoulos (Referee) christos.panagiotopoulos@mio.osupytheas.fr Received and published: 9 October 2014

(1) A. General comments Southern Ocean plays an important role to CO2 sequestration, while it is considered as one the largest HNLC oceanic regimes. Although several studies and many international projects have been undertaken in the Southern Indian Ocean, very few accessed the dynamics of DOM and POM at the molecular level in relation with bacterial degradation. The authors present an extremely valuable dataset

on the distribution of amino acids in POM and DOM in 5 representative stations of the Southern Ocean around the Kerguelen plateau. AA were used to assess the origin and fate of POM and DOM and the authors speculate about the mechanisms regarding the slower degradation of the organic matter in the HNLC waters. The whole discussion is well supported by the data and this study is a nice contribution to the field of marine biogeochemistry. Below are some minor comments that will help the authors to improve their MS.

(1) B. Minor comments Abstract line 12. . . .. and other markers revealed that. . .. Which other markers do you mean? Be more specific.

(2) (3) To clarify, “and other markers“ was removed and, as requested, these other markers were indicated by the addition of this sentence : “Alteration state was also assessed by trends in C/N ratio, %D-AA and degradation index.“.

(1) Introduction, line 7. , the largest HNLC ocean. I would change this as : . . .., the largest HNLC oceanic regime.

(2) (3) To clarify, “ the Southern Ocean, the largest high-nutrient low chlorophyll (HNLC) ocean“ was replaced by “ the Southern Ocean having the largest high-nutrient low chlorophyll (HNLC) zone“.

(1) Introduction, line 30. . . ..at ambient concentrations and provide numerous indicators on OM origin. I would change this as:. . .. . .. and may provide wealthy information. . ..

(2) We believe our expression is more precise and thus we prefer not to make the change as suggested.

(1) Materials & Methods. I would advise the authors to give a figure with the sampling stations because in Blain et al., 2014 paper there are several sampling stations from transects during the cruise and it is not easy for the reader to locate quickly the sites of sampling.

BGD
11, C7197–C7203, 2014

(2) The map provided in Blain et al. (2014) is cited by many different articles of the same special issue. Moreover, the coordinates of all the sampling sites are provided in Table 1 and thus their position on a map can easily be obtained using readily available tools such as Google Map. We believe that adding a figure will not be a cost effective use of valuable journal space.

(1) Discussion. 4.1 Amino acids in the Southern Ocean. The authors can include in the reference list the following papers : Shen et al. 2012; Biogeosciences 9: 4993-5005. Distribution of AA in DOM in the Beaufort Sea (Arctic Ocean). Panagiotopoulos et al. 2002. Org. geochem. 33: 985-1000. Bulk AA in POM in the polar front zone (Southern Ocean).

(2) (3) As suggested, these two references were added to Section 4.1 and in the reference list. These references appear in the following sentences: “The measured concentrations, yields, and relative distributions of AA in POM and DOM were in the range of values previously found in the open equatorial Pacific (Lee et al., 2000), the coastal waters of the Arctic (Dittmar et al., 2001; Shen et al., 2012) and Northern Atlantic oceans (Bourgoin and Tremblay, 2010), and in the polar front zone of the Southern Ocean (Panagiotopoulos et al., 2002).“ “Here, AA accounted for only 0.9 to 4.4% of DOC, which is in the range of values found in other regions (Benner, 2002; Bourgoin and Tremblay, 2010; Shen et al., 2012).“

(1) Origin and fate of POM, line 10-15 page 14114. I am sceptical with the idea that you explain POM export during the bloom when you sampled POM with Niskin bottles and not with sediment traps.

(2) It is true that POM export and export efficiency must be calculated using sediment traps. However, in our study we assessed POM reactivity and diagenetic state by using water samples collected by Niskin bottles at different depths. At the bloom site A3-2, we observed a more rapid decrease of POM and particulate THAA concentrations and of amino acid yields with depth. Although it is true that not all particles sink in

BGD
11, C7197–C7203, 2014

the water column, we can say with confidence that most POM collected in deep water originated from the surface. Because most particles collected in deep waters sank from the surface, our statement is valid "...but was more rapidly degraded during sinking than the POM from the HNLC site". We make no quantification of export or degradation rates.

(1) Fig.5. It will be really interesting if you can include in this Figure AA data (if you have any) from diatoms (phaeocycstis) or autotrophic bacteria (Synechococcus) from the sampling stations. Diatoms or coccoliths from other studies -I do not know if it does make any sense- are simply indicative of AA composition.

(2) No AA analysis was done on diatoms or bacteria collected at the sampling site. However, it is important to note that this figure shows mol% of individual AA (relative composition) and not AA concentrations. We don't expect major differences in AA relative composition in the same organism from different areas of the oceans. This consistency was demonstrated by Cowie and Hedges (1992, L&O, 37, 703-724) "Amino acid analyses were performed on a suite of potential organic matter sources to coastal marine environments. They yielded no source-indicative compositional parameters,...". This is why, the values for diatoms and bacteria we use in our Fig. 5 were also used by Salter et al. (2010, L&O, 55, 2207-2218). These values come from Muller et al. (1986).

(1) Discussion. Line 23 page 14114; line 15 page 14115. The term refractory should be used with great caution. It is hard for me to believe that D-AA are refractory simply because they come from living organisms such as bacteria. The term "refractory" should be accompanied with Δ14C measurements. In my knowledge there are not yet Δ14C measurements on individual D-AA (compound specific radiocarbon analysis) and therefore I would avoid using this term. You can use instead the term, less degradable compounds, less labile compounds etc. A compound that is not easily degradable, this does not imply that it is necessarily refractory.

(2) (3) We agree. These are all the parts of the entire manuscript were the term "re-

BGD
11, C7197–C7203, 2014

fractory“ was used: p. 14114 lines 22-23: “. . .probably in more refractory structures.“ p. 14115 line 15: “. . .indicates that bacterial DOM has an average reactivity similar to bulk DOM and contributes to all DOM fractions, from labile to refractory DOM.“ p. 14116 line 22: “. . . the microbial carbon pump concept in which marine microbes transform labile DOM into refractory DOM (Jiao et al., 2001).“ We thus never describe our DOM as “refractory“. In the first case, we use the term “more refractory“, which is the same as “less degradable or less labile“. Nevertheless, to avoid confusion, the term “refractory“ was replaced by “recalcitrant“. In the second case, we specifically indicate that bacterial DOM is made of molecules having a wide range of reactivity, from labile to refractory. This is in agreement with this reviewer's comment “It is hard for me to believe that D-AA are refractory simply because they come from living organisms such as bacteria. In the third case, the term “refractory“ is used because it is in the definition of the microbial carbon pump concept described in the cited reference (Jiao et al., 2001).

Anonymous Referee #2 Received and published: 13 November 2014

(1) Tremblay et al, present an interesting and timely discussion on dissolved and particulate amino acids in the Southern Ocean. The area sampled is naturally fertilized by iron and the amino acid data presented fills in a gap in the understanding of organic nitrogen dynamics in this area. One interesting observation is the DOM in the HNLC was less altered than DOM from the bloom waters and showed no signs of alteration. The authors then point to unfavorable conditions for bacterial degradation of DOM in HNLC waters. I was curious though if the authors have any supporting measurements (optics, radiocarbon age or other molecular markers such as lipids) to justify their hypothesis of contrasting DOM sources (section 4.3).

(2) Our results in Fig. 5 and in Table 3 suggest that DOM sources are similar in all studied sites. As a result we never make the hypothesis of contrasting DOM sources in section 4.3 as indicated by this reviewer. Instead, we present numerous markers of contrasting DOM fates or dynamics (e.g., AA yields, %D-AA, DI) as discussed in section 4.3. We do not have other supporting measurements.

BGD

11, C7197–C7203, 2014

(1) Lastly, section 4.2 describes D-AA yields estimating total bacterial biomass. The author's make some assumption based upon literature but did they do any actually sampling to validate their model? If not, how valid are bacterial biomass estimates?

(2) (3) This approach was validated in previous studies. We realise that very little description of this approach was provided. Thus, we added this sentence in the introduction (p. 14100, lines 24-26) where it was introduced: "The description of this approach and its limitations are presented in previous studies (Tremblay and Benner, 2006; 2009; Kaiser and Benner, 2008; Kawasaki et al., 2011)." In addition, we discussed the validity of those estimates in section 4.2 in this part of the original manuscript: "Extreme values or the disagreement between D-AA yields are probably caused by the fact that yields in POM were calculated by difference between the chromatographic peaks measured in unfiltered and filtered water samples. In many samples, this difference was very small, because of the very low POM concentrations, increasing the uncertainty of these yields. Different dynamics between D-Asx, D-Glx et D-Ala in the studied POM could also explain inconsistent values."

(1) A minor note, but please make sure all paragraphs are either indented or not. Also, please do not start off a paragraph with an abbreviation.

(2) The manuscript was formatted by Biogeosciences and thus some paragraphs must be indented while other should not. Some paragraphs start with acronyms (not abbreviation) such as AA, DOC, and HPLC. We think this is a common and acceptable practice. If this practice is not accepted by Biogeosciences, we will make these changes.

(2) Final comment: In our revised MS Word file of the manuscript, uploaded with this letter, we tried to incorporate all the corrections that were made by Biogeoscience and us when producing the typeset manuscript version (bg-2014-447-discussions-typeset_manuscript-version1). However, we probably missed some of them and thus the revised MS Word file uploaded should be used to show the new modifications that should be done on the typeset version (and not on the old MS Word file).

BGD
11, C7197–C7203, 2014

Interactive comment on Biogeosciences Discuss., 11, 14097, 2014.