In this manuscript, Gaye and colleagues measure amino acid (AA) concentration in a large sample set including particulate, sedimentary, and dissolved organic matter to assess the utility of AA molar abundance-based degradation proxies. Based on trends in AA molar abundance, they suggest suspended and particulate OM undergo separate degradation pathways, and that current degradation indices do not function as expected for suspended particulate matter (SPM). They suggest two new indices which can be calculated from AA molar abundance. The first, the sediment degradation indicator (SDI) is suggested as an alternative to the degradation index (DI) for sinking particles and sediments. The second, the residence time indicator (RTI) is proposed as an indicator specific to the degradation of SPM. Clearly, a lot of work went into the impressive dataset presented in this manuscript. I believe the authors' exploration of existing AA-based degradation proxies as well as the introduction of new proxies is of interest to the wider biogeochemistry community. However, I feel there are some issues that should be addressed prior to publication, including tightening of the introduction, clarification of some methodologies, and providing additional support for some conclusions. Below are my specific suggestions.

Reply: We thank the referee for taking the time to review our manuscript and for the detailed comments which will help to improve the manuscript. The referee has indeed identified the points which need to be specified, further discussed or corrected.

General comments:

- DI application to SPM and DOM: The authors note that the classic calculation of DI according to Duawe et al., 1999 does not seem applicable to SPM and DOM. However, there is an alternative DI calculation suggested by Kaiser and Benner 2009 specific for DOM. This calculation is more appropriate for DOM samples and based on their argument that SPM cycling is more similar/linked to DOM cycling than suspended particles, may also be more appropriate for their SPM samples. I suggest the authors add this calculation to their analyses before arguing existing DI calculations are not appropriate for their sample set. Comparisons with the RTI should also be included.

Reply: we already approached the authors and will calculate their DOM specific DI and check its suitability for our data set and also compare it to our RTI.

- "Residence time" terminology: I'm not convinced the RTI is an indicator of "residence time", as suggested by the name and by section header 4.2.2. All the RTI indicates is changes to AA molar abundance. Throughout section 4.2.2, residence time is only mentioned once (lines 589-591). Instead, most of this discussion focuses on hypothesized relationships between SPM and DOM. Additionally, as the authors note, water mass age can vary significantly below 200 m (line 590), while the RTI is relatively constant at these depths. If the authors want to claim that the RTI is an indicator of residence time, I think they need to make a clearer connection/stronger argument in this section. Otherwise, a connection to hypothesized degradation seems more consistent with their data.

Reply: The connection of changes in the "RTI" with residence time is indeed speculative. It is based on the observation that samples from water depths below about 200 m show no depth dependent trend in AA composition while there is a trend of increasing "RTI" in the upper 200 m. The referee is right that according to our theory the equilibrium with ambient DOM drives the changes and is evidently taking place relatively fast (about 100 years or faster according to water

mass ages and the fact that fresh organic matter is constantly supplied/produced in near surface water). We will think about a better term for this SPM-DOM specific new index and also work on its discussion. Checking the DI of Kaiser and Benner 2009 may also help here.

- Range of sampling locations: One strength of this paper is the very large dataset they use for their analyses. However, their samples come from a very wide range of sampling environments. The authors do mention that there is more variation between sample types than between similar sample types from different regions (lines 460, 637), but this appears to be almost an afterthought. I think it would be helpful if a brief description of variation within each sample type between the different locations was presented in the results and/or earlier in the discussion.

Reply: we will include a section on the different sample times and briefly about the possible variations between working areas.

Specific comments:

Figures:

Overall: The authors are inconsistent with their use of identifying colors/symbols/etc in figure captions. Per the journal guidelines, “A legend should clarify all symbols used and should appear in the figure itself, rather than verbal explanations in the captions (e.g. "dashed line" or "open green circles").”

Reply: We will check all Figures and supply legends instead of descriptions in the text.

Figure 3: A legend should be included for the red vs. black symbols.

Reply: legend will be included in the Figures.

Figure 4: This figure seems to have some repeated information and unclear legend entries. The caption says 4b compares AA mol% of “plankton, SPM, and water samples”, while figure legend says “dissolved” (instead of water samples). For 4c, the caption says, “water samples and pore water”, but here the legend says “water” instead of “dissolved” or “water samples.” The authors need to be clearer about dissolved vs. water vs. pore water (does “dissolved” include water column and pore water combined?). Also, the caption notes what the colors mean for part c, but not for parts a and b. Finally, plankton data is presented in both panels a and b, and it is unclear if there is repeated water column data in b and c. While repeating some data in multiple panels allows direct comparison between certain sample types, it appears the discussion text only directly compares sediment traps and SPM (line 439), which are noton the same plot in any panels. Would it be possible to remove repeated info and condense the figure to two panels? Finally, including an asterisk for significant differences might help aid the eye to see which differences are important.

Reply: We will add the explanations of colours of Fig.4a and b into the caption. Fig. a and b both, contain plankton sample composition. Plankton is shown in duplicate in order to clarify the trends from plankton via trap samples to sediments as well as from plankton to SPM and further to DOM. However, several of the remarks of the referee ask us to work on the trends observed in SPM. We will check if splitting SPM into shallow and deep samples would make more sense and in case show this in Figure 4b. Figure 4c splits the dissolved AA results into samples from the water column and from pore waters. Both groups are indeed quite similar in composition so that 4c could be deleted, especially as further and more detailed information on the differences between these two groups of samples is provided in supplement S3.

We will also add asterisks to indicate AA which show changes to aid the eye looking at many columns.

Figure 5c: It appears two or three of the box and whisker plots are cut off.

Reply: We will redraw Figure 5a and c.

Figure 6a: would it be possible to separate the overlapping amino acid labels to improve readability? (Perhaps with an arrow pointed to exactly where the factor loadings are for that AA).

Reply: We will separate the overlapping labels according to the suggestion.

Figure 7: The text in most of the figures is small, but the text in 7a and b is so small it is almost illegible. It is also inconsistent with the text size in 7c. Additionally, I suggest the authors include the regression line in figure 7a.

Reply: We will increase the font of the text in this Figure and also check the other Figures with small texts. Regression line will be included in Fig. 7a.

Figure S2: Could the regression lines be plotted on these figures? It's possible part of the regression line can be seen in figure S2a, though if this is the case it is mostly hidden by the data points in the same column. Perhaps a separate color could be used?

Reply: We will add regression lines in different colours.

Text:

Line 112 (and other places throughout the manuscript): change citation to say "McCarthy"

Reply: Will be changed.

Lines 117-124: Considering the authors do not use/test different hydrolysis conditions, this seems like a lot of unnecessary detail in an already long introduction.

Reply: Will be deleted here and moved partly to the discussion.

Lines 126-128: This is methods text, it does not belong in the introduction.

Reply: Will be moved to methods

Section 2. This section feels like a long mix of introduction, discussion, and methods. I think in general the whole introduction could be shortened. One way to do this which may improve readability is to move the calculations for each index to a separate methods subsection and only include a concise summary of different in the introduction. Any remaining details necessary for the discussion of results could be moved to the relevant discussion sections (some of which are repeated in the discussion anyway).

Reply: Calculation methods of indicators will be moved as a much smaller section to the methods. Other parts will be moved to the discussion where appropriate.

Line 170: Conversion of Asp and Glu via hydrolysis is methods text (and is repeated in the methods). Should be deleted here.

Reply: Will be deleted

Line 190: This additional discussion of Asp and Glu seems to come out of nowhere. I would consider including this with the previous paragraph about Asp Glu.

Reply: Will be deleted

Line 217: As noted above, a separate DOM-specific calculation was suggested which is more applicable to DOM.

Reply: See reply to the first general comments above; we will calculate the DOM specific degradation index of Kaiser and Benner (2009) and then compare it with our "RTI" and decide which index is best applicable.

Lines 252, 284: While the authors mention use of Whatman GF/F filters, it might be helpful for readers to also provide the pore size rather than assuming they will know. Overall, I think a clear size range for each sample type would be helpful (similar to that provided in lines 254-255 for sediment trap samples).

Reply: We will add the pore size of these glass microfiber filters of 0.7 µm.

Line 258-261: Based on this text, it appears the only water sampling was pore-water samples and 18 water samples off Namibia. However, Figure S3 implies there were additional water column samples collected not mentioned here. If so, the authors should describe those sampling procedures here as well. Additionally, it would be helpful if the authors provide a pore size for the rhizon samplers.

Reply: We will add information on the water samples which are from the southern Indian Ocean and from the central Pacific.

Line 370-370: "particles and sediments have increasing mol%..." Increasing with what? Greater than plankton samples? Or is this meant to reflect some relationship with depth or some other variable?

Reply: This is indeed imprecise. We will clarify that this trend of increasing mol% is depth dependent.

Line 387: This sentence is hard to follow. It begins with a comparison between SPM and sed trap samples, but rather than giving any data for sed trap samples transitions to comparing AA/HA in shallow and deep SPM with Gluam/Galam ratios in SPM.

Reply: We will rewrite the sentence and explain it better.

Line 397: "significantly different" implies a statistical difference. If this is what the authors mean, the statistics should be included.

Reply: The significance could be tested by a discriminant analysis which is too much effort. We will instead remove "significantly" and refer to the close mean values and overlapping standard deviations (Fig. 5c and d).

Line 436: "shares" is a confusing term here. Do the authors mean mol%?

Reply: Will be changed.

Line 436-437: There is no depth data in figure 4b to support this claim.

Reply: We will change this statement. In Figure 4b only the trends from plankton via sinking particles to sediments are visible while the trends within the sample groups are not shown in this paper. We will rethink how to refer to the trends within the sample groups in this paper. This is related to some of the earlier remarks (see above).

Line 443: This feels like a jump in logic to me. The authors note at the end of the results that most calculated indices don't show major differences in SPM with depth, but I think they need to expand on this in discussion prior to making the claim that SPM has a different degradation pathway that is not captured by these indices. Especially because many of the AAs which are enriched with water depth in SPM (Gly, beta-Ala, gamma-Aba, Orn) are also enriched with depth in sediments.

Reply: beta-Ala and gamma-Aba are not enriched in SPM with depth which is one of the reasons why we think that it is not the classical degradation which drives changes in SPM. Anyway, this discussion will be expanded in the revised version (see comments and replies above).

Line 490: There is no information regarding depth in Fig. 6. This can only be seen in figure S1.

Reply: We will change this and refer only to S1.

Line 505: The topic sentence for this paragraph suggests there will be discussion regarding if individual AA can be used in place of SDI and RTI, but there is no further mention of this in section 5.2.1 (though there is section 5.2.2).

Reply: In line 576 (section 5.2.2) we mention that mol-% Gly or Ser could be used instead of the RTI to characterise the relative changes in suspended matter. We find this important as several groups do not measure beta-Ala and gamma-Aba which are needed to calculate our SDI and RTI.

Line 524: is this also referencing figure S2?

Reply: A reference to S2 will be added.

Lines 525-530: There appear to be three separate arguments in this sentence, but the overall reasoning/data to support these arguments is unclear to me. Could the authors break this down, so each argument is presented separately with the data to support it? I think would improve readability and help convince readers that SDI is in fact an improvement over the DI and ox/anox ratio.

Reply: Thank you for this comment. The three arguments will be presented separately in a more logical order.

Line 651-652: AA are not the main identifiable contributors to all global nitrogen- a qualifier, such as sedimentary or particularly organic N is necessary.

Reply: We will add that this is the case in most particulate organic matter samples.

Line 660: I believe this is referencing the same paper as the line above (McCarthy 2007), as there is no McCarthy 2006 paper is in references. The citation should be corrected and probably only needs to be cited once at the end of the sentence.

Reply: This reference will be corrected.

Line 672: should this say water depth above 200m?

Reply: Yes, the 200 m will be added.

Line 698: Can the authors discuss how these calculations compare with past work and direct measurements of %OC and ON which is AAs? For instance, Bronk 2002 suggests dissolved combined AAs only represent ~ 7% of total DON, and Kaiser and Benner 2009 suggest amino acids, amino sugars, and neutral sugars collectively account for 1% to 5% of TOC in the Pacific and Atlantic gyres. Perhaps their values are higher because most of their sampling locations are coastal rather than the open ocean?

Reply: Lines 113-124 contain some more information on % AAN of N which will be moved to the Discussion. The above mentioned references will also be added.

Line 748: I think it would be helpful to mention in paratheses which biogeochemical indicators are not better than POC, as there are others which are not investigated in this study.

Reply: The indicators not better than POC % (and DI and SDI) used in this work will be added.