Response to Editor Initial Decision: Reconsider after major revisions (27 Jun 2014) by Toby Tyrrell

Comments to the Author:

1. The main request of the reviewer, to more clearly acknowledge that sexual reproduction does take place in nature, even if it is not very important in blooms, has not been addressed in the revised MS. The reviewer asked, reasonably in my opinion, for acknowledgement that E. huxleyi has an identified sexual life cycle, that haploid E. huxleyi cells have been detected in nature, and that the haploid cells may even have a different ecological niche. Brief mention of these points will be useful in framing the conclusions of your study.

*We’ve included text (lines 82-86) in the introduction describing the presence of haploid gametes of E.hux during bloom events. We however, don’t wish to overstate or labour the significance of the haploid life stage because our study clearly demonstrates that sexual reproduction is not responsible for bloom development. By doing so, it would detract from the main finding of the paper.*

1. Although most of the minor comments of the second reviewer have been addressed, again the major comments (“essential revision” or “major revisions” or area of “major concern” in the words of the reviewer) have not been addressed in the MS. Firstly, the review of past work has not been extended as requested, although reasons for not doing so have been given.

*We decided not to include the papers suggested by the Reviewer as we don’t believe its good practice to use data that is presented in an inadequate way.*

Secondly, the revised MS does not include a more careful description of the experimental protocol (isolation method) in order to defend against the alternative interpretation that the observed higher frequency of clones is an artefact of the protocol rather than showing the reality in nature. It appears that there are two arguments to defend against: (1) that the cells divided after dilution leading you to pick multiple clonal descendants of the same original cell, and (2) that your technique inadvertently included an artificial selection pressure towards certain types of clones. These possibilities should be explained in the revised MS and then either admitted to (and ramifications briefly examined) or else discounted (including an explanation of why the argument is not valid, if that is what you think). The changes to the MS could build upon the public response to reviewer 2 but, in my view, an even clearer defence against these alternative possibilities would be very helpful. The reader should be able to understand the possible artefacts and be given enough information to assess whether or they may have played a role in producing the results. Please note that it is not relevant that “Our public response dealt with this sampling issue bias concern” because the MS needs to stand alone.

*We inserted new text (lines 224 -227) to circumvent any fears pointed out by the Reviewer. That said, the point that we made was that the argument raised by this reviewer was/is a red herring. The methodology is well established and closer scrutiny of our data bears this out. Expanding and reviewing all the nuances of single cell isolation methodologies will overcomplicate the manuscript and therefore detract from the core finding of our study.*

1. By “between 7x10-3 to 142” do you mean “between 7x10-3 and 142x10-3” ? The text needs to be changed to be unambiguous, or if this is nor possible then should be deleted.

*Deleted this text.*

1. For points number 9 and 10 of your reply, please resolve in the MS also.

*Point 9: Modified lines 696 and 698. This should avoid further misinterpretations.*

*Point 10: To deny syngamy in Ehux is to go directly against Frada et al. findings. We chose to rather cite Frada et al. observations. (lines 82-86).*

1. Biogeosciences strongly promotes the full availability of the data sets reported in the papers that it publishes in order to facilitate future data comparison and compilation as well as meta-analysis. This can be achieved by uploading the data sets in an existing database and providing the link(s) in the paper. Alternatively, the data sets can be published, for free, alongside the paper as supplementary information. All or most of the other manuscripts in the special issue cite doi’s for their data. Please consider how your genetic data could be made available.

*We included the source of our data (lines 193-194) into the manuscript*

1. Please cite other manuscripts in the special issue where applicable, since this is one of the advantages of collecting papers together into a special issue. The most obviously relevant papers are those by Young et al and by Poulton et al. Young et al could usefully be cited for the morphometrics, for instance (section 2.6).

*Done, now cite both Young & Poulton et al. throughout the manuscript. In addition, new text was also included (lines 709-713 & 744-748)*

1. Funding support through UKOA should be acknowledged as follows: “We are grateful for funding support from NERC, Defra and DECC to the pelagic consortium of the UK Ocean Acidification programme (grant no. NE/H017348/1\*). [the grant no. is different for each institute; the above one is for University of Southampton only – the grant no. for MBA should be used instead]

*Done*

1. Typographical corrections need to be made to the following lines: 7 (not the corresponding author), 56 (change “generation time” to “growth rate”? - a time cannot be in units of day-1), 69 (predominants), 78 (,), 91, (1959 and 2011), 93 (decreases in carbonate ions), 189 (off the coast, in the Bay), 436-438 (“), 541 (the ability of Lohbeck’s strains to calcify), 542 (,,), 644 (italics), 673 (conceivable to predict), 772 (Pälike), 804 (Holligan), 856/859 (consistency of name), footnote to Table 4 (coccolithosphere).

*Done*