Response to Reviewer #2

We thank the two anonymous reviewers for their useful comments on the paper. Please find below our corresponding responses (in blue color) to the comments one by one embedded in the original review. We have also revised the manuscript accordingly.

Anonymous Referee #2
Received and published: 13 October 2013
The paper describes the CO2 dynamics in two cyclonic eddies resulting in upwelling sites. While most of the relevant parameters have been measured, one particular, albeit important parameter is only poorly constraint, i.e, microbial respiration. This is deduced from leucine incorporation measurements, assuming a prokaryotic growth efficiency of 8%. Clearly, this microbial respiration should have been measured directly via CO2 production or O2 consumption assays. As shown in a number of studies, the prokaryotic growth efficiency can vary substantially. Hence, taking a reported value and applying it for the specific eddy conditions might result in major deviations from the actual rate. While the paper presents two conceptual models on the CO2 dynamics in upwelling regimes, it does not discuss the CO2 dynamics in the light of the remineralization depth' concept. I think the authors needs to thoroughly discuss the remineralization depth concept and the model exercise given in Kwon et al, 2009, Nature Geosci. The Kwon et al paper appears to be the most useful paper to compare their findings and conclusions with and even use the modeling approach for their data.
Also, the paper needs some editing of the English.
Response:
We admit that direct measurements of respiration rates would be the best; we actually tried O_2 consumption assays on board, but could not obtain enough data for valid comparison due to detection limitations in the oligotrophic environment as documented in the literatures. We then turned to calculating bacterial respiration rates based on bacterial production measurements via BGE, which has been widely applied in the literature with an appropriate range (Giorgio and Cole, 1998, Bacterial Growth Efficiency in Natural Aquatic Systems, Annual Review of Ecology and Systematics, 1998, Vol. 29: 503-541).
Although applying a reported BGE value might take the risk of deviating from the actual respiration rate, the calculated results (mainly determined by bacterial production measurements) are indicative of each individual site and comparable between different sites. In addition, the BGE factor is not a fixed parameter for BR calculations and there is a broad positive relationship between bacterial respiration and production according to various models equations, e.g. $BR = 3.70 \times BP^{0.41}$; $BR = 3.42 \times BP^{0.61}$ (Giorgio and Cole, 1998).

Thanks for the suggestion to take Kwon et al 2009 paper into our discussion. We have

done so in the revised version. A major part added in the section 3.5 is as below:
Taken together POC sinking and microbial respiration, a comprehensive parameter, the remineralization depth can be referred. A three-dimensional global ocean biogeochemistry model has shown that a modest change in remineralization depth can have a substantial impact on atmospheric CO_2 concentrations (Kown & 2009). As upwelling processes influence nutrients temperature, and oxygen concentration, as well as stratification and community composition, and the all these variables influence the remineralization depth (Kown et al., 2009), so upwelling scenario models should be established to better illustrate the effects of upwelling on ocean carbon sink/source.

Table 1: for bacterial abundance, the n=2, nevertheless, the standard deviation is given. This is wrong since for calculating SD, an n of at least 3 is needed. For some of the estimates there, the SD is large compared to the mean and it remains unclear whether there are statistical differences between the sampling sites. Some statistics should be included here in the table.

Response:

We have deleted SDs of bacterial abundance and respiration in Table 1, since SD calculated based on 2 values is not meaningful. Since normal distribution of the individual data sets was not met, we used the non-parametric Kruskal-Wallis Test for comparison of variables between sites by SPSS software. The relevant description was added in the Material and methods section (paragraph 2.7). Statistics were added in Table 1.

In addition, we found some wrong N values in the original Table 1, and have corrected them in the revised version.

Table 1. Hydrographic characteristics, phytoplankton, particle export parameters, bacterial abundance and respiration and air-sea CO_2 flux in CE1, CE2 and surrounding waters. CE1: cyclonic eddy #1; CE2: cyclonic eddy #2. Error bars indicate standard deviation. TChl a: total chlorophyll *a*; SS: stable state; POC: particle organic carbon; BA: bacterial abundance; BR: bacterial respiration rate. Non-parametric Kruskal-Wallis Test was used for comparison of variables between sites.

Parameters	**CE1**	**CE2**	**Reference site**
Hydrography			
Depth of mixed layer (m)	~25 [a]	~15 [b]	~40 [c]
Euphotic depth (1% light level, m)	~62 [a]	~63 [b]	~78 [c]
Nitracline depth (m)	~20 [a]	~10 [b]	~70 [c]

Temperature (°C, at 25 m)	27.72[a]	23.33[b]	29.63[c]
Salinity (PSU, at 25 m)	34.12[a]	34.08[b]	33.99[c]
AOU (mol m^{-2}, 50-100 m)	4.83[a]	5.89[b]	2.31[c]
Phytoplankton[d]			
TChl *a* (mg m^{-2}, 0-50m)**	12.3±3.68 (N=23)	13.8±4.91 (N=11)	10.1±7.89 (N=47)
Fucoxanthin (mg m^{-2}, 0-50 m)	0.60±0.26 (N=22)	1.14±1.10 (N=11)	1.07±1.89 (N=47)
Divinyl chorophyll *a* (mg m^{-2}, 0-50 m)**	2.88±1.13 (N=22)	1.97±2.02 (N=11)	1.72±0.90 (N=47)
Particle export[d]			
SS ^{234}Th flux @100 m (dpm m^{-2} d^{-1})*	712±521 (N=8)	1609±572 (N=6)	1279±697 (N=22)
POC (×10^2 mol C m^{-2}, 0-100 m)*	1.76±0.26 (N=8)	2.18±0.38 (N=6)	1.78±0.35 (N=17)
POC/^{234}Th @100 m (μmol C dpm^{-1})	3.43±1.00 (N=8)	3.66±1.00 (N=6)	3.66±1.12 (N=22)
POC export @100 m (mmol C m^{-2} d^{-1})*	2.50±2.03 (N=8)	6.16±3.74 (N=6)	4.92±3.63 (N=22)
Bacteria			
BA (10^5 cells ml^{-1})	2.41[d] (N=2)	1.73[b]	2.14[c]
BR (mg C m^{-2} d^{-1}, 0-100 m)	327[d] (N=2)	255[b]	292[c]
Air-sea CO_2 flux[d]			
CO_2 flux (mmol m^{-2} d^{-1})**	4.15±0.84 (N=9112)	3.43±0.59 (N=1330)	2.82±0.65 (N=13754)

[a] Data from the CE1 center site TS1;
[b] Data from the CE2 center site Y12;
[c] Data from the reference site SEATS;
[d] Data were mean ± SD (standard deviation) from the CE1 and CE2 regions and the reference sites of surrounding waters;
** $P < 0.01$;
* $P < 0.05$.

Fig. 3: in the legend of the 2 left hand panels, liter is given as ’l’ while everywhere else it is given as ’L’. Also, it is unclear what the number of samples is.

Response:
Fig.3 is revised and the number of samples is added in the figure legend.

Fig. 5: instead of ’unicellular’ Leu-uptake use the term ’cell-specific’
Response: Revised as suggested.