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Interactive comment on “Mats of psychrophilic thiotrophic bacteria associated with cold seeps of the Barents Sea” by S. Grünke et al.

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This interesting and comprehensive study describe the bacterial diversity of 2 visually different type of microbial mats of 3 cold seep sites of the Norwegian margin based on both microscopic observation data and molecular survey (16SrRNA gene sequencing, molecular fingerprints..) in regards with geochemical gradients. This paper presents a huge set of data exploited in a very elegant manner.

My remarks are as follow : 1-I wonder if, as (according to the supplementary table 2) chemicals data (pore water analysis, oxygen profiles), and molecular data (ARISA, sequencing) some time came from different cores (sometimes sampled during different cruises), a map or figure presenting the spatial distribution of core samples for each sampled habitats would have been helpful.

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Reply: We thank this reviewer for the helpful comments and suggestions. Molecular and chemical samples for one type of mat generally came from sets of pushcores taken together (within decimetre to metre distance) during one dive, at relatively small cold seep structures (Supp. Tab. 1). We have added a respective comment to line 110 f. Precisely which pushcores were taken together is indicated in Table 3 and Suppl. Tab. 2. All precise positions have been deposited in the Pangaea database and are retrievable via their event labels (Suppl. Tab. 2). We have also detailed the numbers of replicates, which are rather high for a deep-sea study (Suppl. Tab. 4). Originally, we had considered a visual display of the data, but as the three cold seep sites investigated are far away from each other, and the many replicate cores at each site very close by, a composite map is not adding more information compared to the tables (e.g. points for the cores overlap in the graphical display).

2-On figure 3 Phylogenetic tree the addition recent obtained sequences from the Lucky strike vent field (Crepeau et al, 2011) would have been of interest to asses a possible "temperature dependant" speciation within *Beggiatoa* sp!

Reply: We have added this sequence to Fig. 3. According to the study by Crepeau et al. (2011), two sequences were closely associated with filamentous species from White Point (acc. AY496953; Kalanetra et al., 2004) and the Escanaba Trough (acc. AY883934; Kalanetra and Nelson, 2010), which are representatives of the group of "Candidatus Marithrix spp." within the family Beggiatoaceae that is also presented in the tree of this study. The sequence identities between LSmat.B40 (acc. FR670387) presented by Crepeau et al. (2011) and "Candidatus Marithrix sp." ST-E1935 (acc. FR847874) as well as "Candidatus Marithrix sp." Menez Gwen (acc. FR827864) presented in this study were only 97.1%, which is below the sequence identities between these species and "Candidatus Marithrix sessilis" from Juan de Fuca (99.0-99.1%).

Interactive comment on Biogeosciences Discuss., 9, 3917, 2012.

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