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***Interactive comment on “Seasonal and interannual study of volatile reduced sulfur compounds (VRSC) in coastal environment: the Bay of Quiberon (Brittany, France)” by A. Cozic-Houly et al.***

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1. The variations of the two main algal groups - dinophyceae and bacillariophyceae - were detailed from May 2004 to August 2006. We only considered these algae families because they accounted for more than 92% of the phytoplankton cells present at all seasons. Moreover, dinophyceae synthesize significant amounts of DMSP (Turner et al. 1988). Bacillariophyceae were also followed because their density was the highest observed whether the seasonal period. No coccolithophorid was observed in the bay of Quiberon from 2004 to 2006. Therefore, the impact of coccolithophorid on the DMSP

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synthesis (Charlson et al. 1987; Malin et al. 1993) and its role in the sulfur cycle was not highlighted in the manuscript.

2. Indeed, zooplankton may transform the DMSP from phytoplankton to zooplankton body, fecal material and dissolved DMSP by grazing (Keller et al. 1989; Simo et al. 2002). Unfortunately, the density and variability of zooplankton were not followed in the bay of Quiberon. Only the phytoplankton was monitored by through the REPHY (i.e., French network to survey the phytoplankton and phycotoxins densities on coastal environments) because toxic algae develops regularly in this coastal area.

3. Our data suggest that phytoplankton is the principal origin of biogenic sulfur compounds (e.g., DMS, DMDS, MeSH). Jean et al. (2009) highlighted that the particulate DMSP in the oligotrophic Niel Bay originated principally from phytoplankton. Although bacteria play an important role in sulphur cycle, the manuscript was based on the distribution of volatile sulfur compounds in an oligotrophic environment, not on the DMSP degradation. Moreover, no monitoring of bacteria density exists in the Bay of Quiberon.

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