Variability of methane in the epilimnion of Lake Kivu

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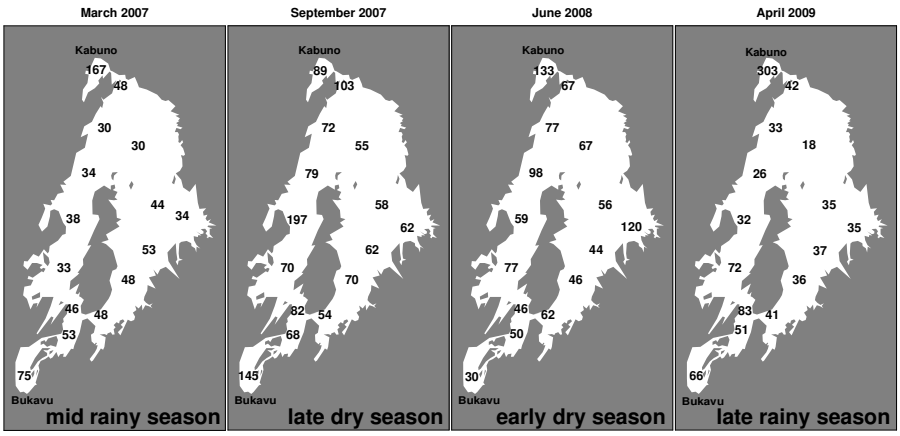
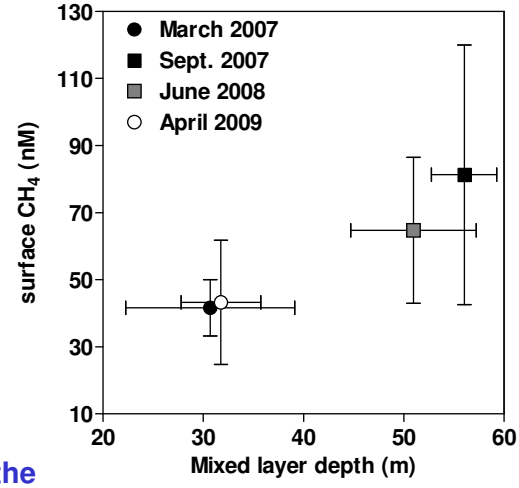
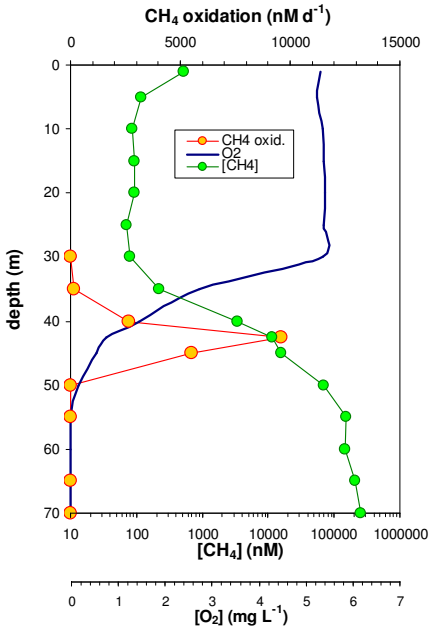
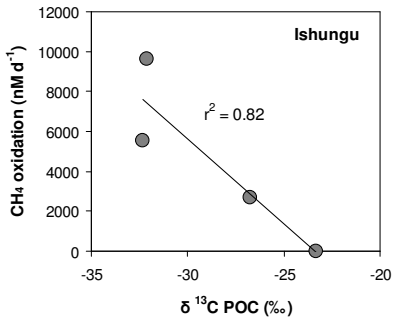




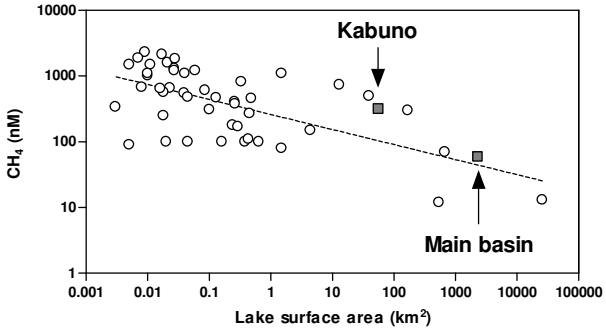
We report a data-set of methane concentrations (CH_4) in the surface waters of Lake Kivu obtained during four cruises covering the two main seasons (rainy and dry). Spatial gradients of CH_4 concentrations were modest in the surface waters of the main basin. In Kabuno Bay (a small sub-basin), CH_4 concentrations in surface waters were significantly higher than in the main basin. The likely higher contribution of deepwater springs in Kabuno Bay than in the main basin increases the upward flux of solutes and might explain the higher CH_4 concentrations we observed in Kabuno Bay than in the main basin.



Seasonal variations of CH_4 in the main basin were strongly driven by deepening of the mixolimnion and mixing of surface waters with deeper waters rich in CH_4. On an annual basis, both Kabuno Bay and the main basin of Lake Kivu were over-saturated in CH_4 with respect to atmospheric equilibrium (7330% and 2510%, respectively), and emitted CH_4 to the atmosphere (39 mmol m^{-2} yr^{-1} and 13 mmol m^{-2} yr^{-1}, respectively). A global cross-system comparison of CH_4 in surface waters of lakes shows that both Kabuno Bay and the main basin are at the lower end of values in lakes globally, despite the huge amounts of CH_4 in the deeper layers of the lake (concentrations 10^6 higher than in surface). This is related to the strongly meromictic nature of the lake that promotes an intense removal of CH_4 by bacterial oxidation. Indeed, the average CH_4 oxidation rate (7200 µmol m^{-2} d^{-1}) in the main basin of lake Kivu is 200 times higher than the average CH_4 emission to the atmosphere in the main basin.



Available CH_4 oxidation rates (June 2011) were low or undetectable at CH_4 concentrations < 3300 nM. CH_4 oxidation rates were undetectable in the anoxic layer during this cruise. Hence, maximal CH_4 oxidation rates were observed in lower part of the oxycline. CH_4 oxidation rates were well correlated with $^{13}\delta$POC, confirming the presence and probable dominance of methanotrophs among the bacterial community characterized by these negative $^{13}\delta$POC signatures



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