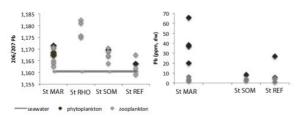
## Pb concentrations, stable isotopes and <sup>210</sup>Pb in seawater, phytoplankton, zooplankton, sardines, anchovy from the Gulf of Lion

EMILIE STRADY<sup>1</sup>, ALAIN VERON<sup>1</sup>, JEAN FRANCOIS CHIFFOLEAU<sup>2</sup> AND OLIVIER RADAKOVITCH<sup>1</sup>

 <sup>1</sup>University Paul Cezanne, CEREGE laboratory, Aix en Provence, France (strady@cerege.fr, radakovitch@cerege.fr, veron@cerege.fr)
<sup>2</sup>IFREMER, LBCM, Nantes, France (jfchiffo@ifremer.fr)

## Introduction

The COSTAS project aims at understanding the trophic transfer of metallic contaminants through seawater, phytoplankton, zooplankton, sardine and anchovy populations in the Gulf of Lion (NW Mediterranee). Its originality is to combine the ecology of the trophic web and the biogeochemistry of the metallic contaminants. We present here preliminery results of bioaccumulated lead in each compartment at four stations, which were emphasized by analysing for the first time and in the same samples <sup>210</sup>Pb activity as a proxy of natural lead and <sup>204, 206, 207, 208</sup> Pb stable isotopes as proxy of anthropogenic Pb in the environment.



**Figure 1:** preliminary <sup>206/207</sup>Pb and Pb concentrations in seawater, phytoplankton and zooplankton in the Gulf of Lion.

## **Results and discussion**

Higher Pb concentrations in phytoplankton than in zooplankton (Fig 1) confirm the low ability of Pb to bioaccumulate in zooplankton. Pb isotopes ratios show different signatures among stations, despite constant Pb concentrations, close to the seawater signal in station far from the coast (St REF) and close to the radiogenic signal (1.175) in the Rhone station (St RHO). Emphasis on the relation between isotopes signals, Pb concentrations and plankton size/species will conduct to better understand the assimilation of Pb by plankton.

## Review on biogeochemistry of microbial coal-bed methane

DARIUSZ STRĄPOĆ<sup>1,2,3</sup>

<sup>1</sup>Dariusz BioGeoChem LLC, Houston, TX 77077 USA

(strapoc@gmail.com) <sup>2</sup>Indiana University, Bloomington, IN 47405, USA <sup>3</sup>Formerly: ConocoPhillips, Houston, TX 77079 USA

Microbial methane accumulations have been discovered in multiple coal-bearing basins over the past two decades. Such discoveries were originally based on unique biogenic signatures in the stable isotopic composition of methane and carbon dioxide. Basins with microbial methane contain either low-maturity coals with predominantly microbial methane gas or uplifted coals containing older, thermogenic gas mixed with more recently produced microbial methane. Recent advances in genomics have allowed further evaluation of the source of microbial methane, through the use of high-throughput phylogenetic sequencing and fluorescent in situ hybridization, to describe the diversity and abundance of bacteria and methanogenic archaea in these subsurface formations. However, the anaerobic metabolism of the bacteria breaking coal down to methanogenic substrates, the likely rate-limiting step in biogenic gas production, is not fully understood. Coal molecules are more recalcitrant to biodegradation with increasing thermal maturity, and progress has been made in identifying some of the enzymes involved in the anaerobic degradation of these recalcitrant organic molecules using metagenomic studies and culture enrichments. In recent years, researchers have attempted lab and subsurface stimulation of the naturally slow process of methanogenic degradation of coal [1].

Discussion includes description of (i) how occurrences of microbial methane accumulations in coal beds are identified through the use of geochemical tools such as stable isotopes; (ii) geological and hydrogeological constraints of such accumulations; (iii) the origin and composition of coal as the substrate and implications to microbial methane formation; (iv) methods of analysis of microbial methane formation; (iv) methods of analysis of microbial metabolic pathways and microbial communities involved in biodegradation of various moieties of coal's organic matter; (v) attempts of stimulation of enhanced microbial methane generation in coals.

[1] Strapoc et al. (2011) Annu. Rev. Earth Planet. Sci **39** 617-656

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