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Research paper

Sources of organic matter and microbial community structure in the sediments of the Visakhapatnam harbour, east coast of India

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ABSTRACT

Organic matter in the coastal sediments originates from various terrestrial and marine sources. Within the sampling sites, relative inputs from these sources may vary and can influence the microbial community structure. In order to identify the sources of organic matter, and its influence on microbial community structure in coastal environment, 19 surface sediment samples were collected from various stations in the Visakhapatnam harbour, east coast of India. These samples were analyzed for organic carbon (OC) content, bulk δ13C signatures, and the concentration and composition of phospholipid fatty acids (PLFAs). Contents of OC, δ13C, and PLFA concentrations varied spatially and ranged from 0.6 to 7.6%, -29.32 to -23.75%, and 0.30 to 33.30 μg g⁻¹ dw sediment, respectively. The bulk δ13C of sediments reflected mixed carbon sources from marine and terrestrial end members with dominance of the latter at most of the stations. The PLFA community was not influenced by concentration and source of OC. Saturated PLFAs were the most abundant followed by monounsaturated fatty acids (MUFAs), branched PLFAs, and polyunsaturated fatty acids (PUFAs). MUFAs indicate the abundance of Gram negative bacteria, cyanobacteria and microalgae. Branched PLFAs (iso and anteiso) suggest the presence of Gram positive bacteria, and sulfate reducing bacteria. Similarly, PUFAs indicate the presence of eukaryotes. Moreover, the presence of trans-monounsaturated PLFAs in the harbour sediments imply that PLFA community was under stress due to contamination of the sampling sites by sewage and industrial waste, sulfur and petroleum products. Principal component analysis (PCA) based on concentrations of PLFAs established three factors that accounted for 81% of the total variance. The first factor contributed 57% of variance, and was mostly influenced by MUFAs and branched PLFAs. The second factor was controlled by PUFAs such as C20:3n6, C18:3n3, C20:4n6, C20:5n3, and C22:6n3, whereas the third factor was influenced by C20:3n6, C22:1n9. PLFA community in the Visakhapatnam harbour sediments was mostly dominated by bacteria along with some contribution from eukaryotes.

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. Introduction

Organic matter (OM) in the near shore and coastal sediments is derived from various sources including primary production by phytoplankton or benthic microalgae, terrestrial plants, river runoff, municipal sewage and industrial discharge, etc. (Hedges and Keil, 1995; Hedges et al., 1997). Stable carbon isotope (δ13C) signatures of various carbon sources are often different, and despite some overlap between different sources, they are powerful tracers of carbon inputs in various environments (Fry and Sherr, 1984; Prahl et al., 1994; Leyers, 1994; Schelske and Hodell, 1995). Geochemical biomarkers such as n-alkanes, alcohols, sterols, alkenones, and fatty acids also are often used to identify the carbon inputs from various organisms in marine environments (Volkman et al., 1992; Tolosa et al., 2003).

However, these geochemical biomarkers and stable carbon isotopes do not differentiate between dead and live organisms.

In marine environment, living biomass consists of a complex mixture of prokaryotes and eukaryotes, whose combined activity determines nearly all of the elemental biogeochemical cycling (Boschker et al., 2001). The nature and sources of OM, nutrient status and pollution may influence the microbial community structure (Cuckert et al., 1986; Bäath et al., 1995; Pennanen, 2001). Traditional techniques of isolation and culturing have not been adequate for characterization of microorganisms in environmental samples, especially in evaluating the natural microbial diversity (Fang et al., 2000; Delong and Pace, 2001). Thus, to detect changes in bacterial biomass and natural microbial communities, culture-independent techniques such as phospholipid fatty acid (PLFA) analysis (Pennisanen et al., 1996; Pinkart et al., 2002), and genetic fingerprinting (Polymenakou et al., 2005), are routinely used.

PLFAs are the central component of the microbial cell membranes. They are present in reasonably constant amounts over a wide range of growth conditions and are rapidly hydrolyzed upon cell death (White
Sources of hydrocarbons in sediments of the Mandovi estuary and the Marmugoa harbour, west coast of India

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A B S T R A C T

Surface sediments were collected from various locations of the Mandovi estuary and the Marmugoa harbour. Sediments were analysed for organic carbon (OC), total lipids, n-alkanes concentration and composition. Concentrations of OC, total lipids and n-alkanes varied spatially and ranged from 1 to 2.5%, 176 to 1413 pg/g dry weight (dw) sediments, and 0.8 to 3.2 µg/g dw sediments of the Mandovi estuary, respectively; and from 0.6 to 2.9%, 233 to 1448 µg/g dw sediments, and 1.6 to 10.7 µg/g dw sediments in the Marmugoa harbour, respectively. Long chain odd carbon n-alkanes (C19-C21) in the Mandovi estuary, whereas short chain, even carbon n-alkanes (C11-C17) in the Marmugoa harbour sediments were more abundant. The total HC concentrations, n-alkane composition, CPI, UCM and other evaluation indices suggest the dominance of terrestrial hydrocarbons in the estuarine while petroleum derived hydrocarbons in the harbour sediments. This conclusion was further supported by the abundance of hopanes with C25 to C29 α, β compounds and steranes with C23, C24 and C25 compounds in the harbour sediments.

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1. Introduction

Organic matter (OM) in coastal sediments is derived from various sources such as terrigenous, marine, atmospheric and anthropogenic (Gogou et al., 2000; Wang et al., 2006). However, the fate of autochthonous and terrigenous derived OM in estuarine environments is not well understood (Hedges et al., 1997; Wu et al., 2004). The information about processes controlling the delivery of organic matter to coastal environments, and how the signatures of these inputs are reflected in newly deposited sediments is important to our understanding of global biogeochemical cycles.

Lipid molecules such as n-alkanes, fatty acids, alcohols and steroids are used to identify the sources of organic matter in marine and terrestrial samples (Volkman et al., 1992; Tolosa et al., 2003; Wu et al., 2004). Of these, the n-alkanes are commonly used to characterize organic matter of water, suspended matter and sediments from various environments (Ou et al., 2004; Gao et al., 2007). This is because n-alkanes are easy to analyse, and many are source specific. For example, bacteria normally show predominance of even carbon n-alkanes, mainly C18 and C20 (Han and Calvin, 1969). Elias et al. (2000) reported that even carbon n-alkanes in the C14-C22 range originate from diatoms. On the other hand, planktonic organisms such as cyanobacteria and green, red and brown algae generally produce a simple mixture of odd carbon n-alkanes dominated by C15, C17, and C19 with predominant compound being species dependent

(Clarck and Blumer, 1967; Gogou et al., 2000). Whereas, abundance of straight chain odd carbon n-alkanes C25, C27, C29 and C31 has been used extensively as an indicator of terrestrial or land derived organic matter (Pearson and Eglington, 2000; Zhao et al., 2003).

A number of other indices such as concentrations of total hydrocarbons, major n-alkanes, the ratios of short chain/long chain n-alkanes, total n-alkanes/n-C15, n-C17/Pristane and n-C18/Phytane, carbon preference index (CPI) and the presence of an unresolved complex mixture (UCM) also have been used to identify the sources of n-alkanes in environmental samples (Bouloubassi et al., 2001; Ou et al., 2004; Gao et al., 2007). Similarly, because of their greater thermodynamic stability, hopanes with the 17α, 21β-configuration, and steranes with 5α, 14α and 17α configuration are useful to identify petroleum derived n-alkanes (Zaghden et al., 2005; Gao et al., 2007). Furthermore, δ13C analysis is yet another useful technique to identify the sources of n-alkanes (Pearson and Eglington, 2000; Wu et al., 2004; Wang et al., 2006).

There are numerous studies on the physical, chemical and biological characterization of the waters of the Mandovi estuary and the Marmugoa harbour (Selvakumar et al., 1980; Qasim and Gupta, 1981; Shirodkar and Sengupta, 1985; Chanda et al., 1996). There also are studies on the total organic carbon (TOC) and the mineralogy of the surficial sediments of the Mandovi estuary, and total petroleum hydrocarbons in the coastal waters of Goa (Murty et al., 1976; Fondaker et al., 1980; Alagarsamy, 1991). In contrast, little is known about molecular level characterization of OM, especially n-alkane concentration and composition in the sediments of the Mandovi estuary and the Marmugoa harbour. Therefore, the aims of the present
Degradation of alkenones by aerobic heterotrophic bacteria: Selective or not?

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Abstract

Four bacterial communities were isolated from Emiliania huxleyi strain TWP1 cultures before and after the algal cells had been treated with different antibiotics. Incubation of E. huxleyi with these bacterial communities resulted in dramatically different extents of alkenone degradation, ranging from effectively none to extensive. Selective degradation of the more unsaturated alkenones was observed in experiments using the total bacterial community and one of the communities isolated from antibiotic-treated algal cells. The observed increases in δ¹³C are equivalent to a +2 °C and +3.3 °C change in the inferred temperature. Our results clearly show that intense aerobic microbial degradative processes have the potential to introduce a significant ‘warm’ bias in palaeotemperature reconstruction and could explain apparent anomalies in palaeotemperatures inferred from alkenone distributions in strongly oxidizing sedimentary environments. The results show that aerobic bacteria capable of selectively degrading alkenones are not limited to particular environments such as microbial mats and can be actually associated with living E. huxleyi cells. The detection of epoxyketones in some cultures indicates that metabolic pathways involving attack at the terminal groups of the molecule are essentially non-selective, while those acting on alkenone double bonds are selective. The epoxyketones resulting from bacterial epoxidation of alkenone double bonds could be useful indicators of aerobic bacterial alteration of the alkenone unsaturation ratio in situ. The production of alkenols during incubation with one of the bacterial communities demonstrated for the first time that bacterial reduction of alkenones can be a potential source of these compounds in the environment. The intriguing production of small amounts of monounsaturated alkenones by one of the bacterial communities also raises the possibility of a bacterial reduction of alkenone double bonds.

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1. Introduction

Alkenones are a class of unusual, very long chain mono-, di-, tri- and tetraunsaturated methyl and ethyl ketones synthesized by a limited number of haptophyte microalgae (Volkman et al., 1980a;
Biomarkers derived from heterolytic and homolytic cleavage of allylic hydroperoxides resulting from alkenone autoxidation

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Abstract

Laboratory incubation of alkenone mixtures with tert-butyl hydroperoxide and di-tert-butyl nitroxide (radical initiator) in hexane, as a means to simulate alkenone autoxidation processes, rapidly led to the formation of allylic hydroperoxides, whose presence was recently demonstrated in Emiliania huxleyi cells. After incubation in seawater and subsequent reduction with NaBH 4 (to reduce residual hydroperoxides before analysis), these reaction products quickly disappeared and were replaced by complex mixtures of n-alcohols, fatty acids, alkyldiols and hydroxyacids. Methyl alkenones produced saturated n-alkan-1-ols and fatty acids ranging from C 13 to C 16 and two series of C 13 -C 16 (ω-1)-hydroxyacids and (1,ω-1)-diols. Ethyl alkenones also afforded C 13 -C 16 saturated n-alkan-1-ols and fatty acids, accompanied by the production of C 14 -C 17 (ω-2)-hydroxyacids and (1,ω-2)-diols. Deuterium labelling allowed us to show that most of the n-alkan-1-ols, hydroxyacids and alkyldiols resulted from the reduction during the NaBH 4 treatment of the corresponding aldehydes, ketoxyacids and ketoxyaldehydes formed from heterolytic or homolytic cleavages of allylic hydroperoxyl groups resulting from the oxidation of the double bonds of di- and trisaturated alkenones. Amongst these products, the (ω-1)- and (ω-2)-hydroxyacids formed after NaBH 4 reduction of the (ω-1)- and (ω-2)-ketoxyacids were selected as potential biomarkers for alkenone autoxidation. Re-examination of lipid extracts of post-bloom seawater particulate matter samples from the DYFAMED station in the Ligurian Sea (where strong autoxidative alteration of the lipid distributions had previously been detected) showed the presence of significant amounts of 12-hydroxytetradecanoic, 13-hydroxytetradecanoic, 14-hydroxyhexadecanoic and 15-hydroxyhexadecanoic acids thus providing good evidence that these autoxidative processes occur in natural samples.

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Keywords: Alkenones; Autoxidation products; Heterolytic and homolytic cleavages; Markers; (omega-1) and (omega-2)-hydroxyacids

1. Introduction

Di-, tri- and tetraunsaturated long-chain alkenones (n-C 37 -C 39 ) are biosynthesized by a very few species of phytoplankton, including the cosmopolitan coccolithophorid Emiliania huxleyi and the subtropical Geophycus capsica oceanica in the open ocean (Conte et al., 1994, 1998; Volkman et al., 1980, 1995), and some other members of the Haptophyceae such as Isochrysis galbana and Chrysothoe lamellosa (Marlowe et al., 1984; Patterson et al., 1994; Rontani et al., 2004) in...