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van der Maarel, Marc; Huber, R; Damste, JSS; Sinninghe Damsté, Jaap S.

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NOTE

2,6,10,15,19-Pentamethylcosenes in *Methanobacterium bombayensis*, a marine methanogenic archaeon, and in *Methanosarcina mazei*STEFAN SCHOUTEN¹, MARC J. E. C. VAN DER MAAREL²,
ROBERT HUBER³ and JAAP S. SINNINGHE DAMSTÉ¹¹Department of Marine Biogeochemistry and Toxicology, Netherlands Institute for Sea Research (NIOZ), PO Box 59, 1790 AB Den Burg, Texel, The Netherlands, ²Department of Microbiology, Centre for Ecological and Evolutionary Studies, University of Groningen, Kerklaan 30, 9751 NN Haren, The Netherlands and ³Lehrstuhl für Mikrobiologie, University of Regensburg, Universitätstrasse 31, D-93053 Regensburg, Germany*(Received 3 January 1997; returned to author for revision 3 February 1997; accepted 6 February 1997)*

Abstract—2,6,10,15,19-Pentamethylcosenes (PMEs) containing three to five double bonds have been found in the methanogenic archaea *Methanosarcina mazei* (DSM 3338), a strain isolated from sewage sludge, and in *Methanobacterium bombayensis* (OCM 438), a non-extremophilic archaeon isolated from a marine sediment. This finding gives additional support for the use of compounds with the PME carbon skeleton as markers for methanogenic activity in marine environments. © 1997 Elsevier Science Ltd

Key words—2,6,10,15,19-pentamethylcosane, methanogenic archaea, *Methanobacterium bombayensis*, *Methanosarcina mazei*, archaeal biomarkers

INTRODUCTION

Steroids and hopanoids are specific biomarkers for eukaryotes and prokaryotes, respectively (e.g. Ratledge and Wilkinson, 1989). Biomarkers for the third domain of life, archaea, include ether-linked lipids with isoprenoid side chains such as phytanyl (I) and biphytanyl (II) (e.g. de Rosa and Gambacorta, 1988). These compounds have been encountered frequently in hypersaline sediments, where they have been attributed to halophilic archaea (e.g. Teixidor *et al.*, 1993), and in lacustrine sediments, where they have been attributed to methanogenic archaea (e.g. Pauly and van Vleet, 1986).

Another compound considered to be a biomarker for methanogenic archaea is the irregular tail-to-tail isoprenoid 2,6,10,15,19-pentamethylcosane (PME*, III; Brassell *et al.*, 1981). This assumption was based on the identification of PME and 2,6,10,15,19-pentamethylcosanes with one to four double bonds in several methanogens, including the thermophilic methanogenic archaeon *Methanobacterium thermoautotrophicum* (Holzer *et al.*, 1979; Tornabene *et al.*, 1979). However, Risatti *et al.* (1984) showed, using authentic standards, that this thermophilic archaeon

(strain ΔH) indeed biosynthesizes C₂₅ isoprenoid alkenes with one to two double bonds but possesses the 2,6,10,14,18-pentamethylcosane carbon skeleton (IV). The reason for these contradictory findings is unclear and may be due to the use of different strains of *Methanobacterium thermoautotrophicum* or different culture conditions. However, the mesophilic methanogenic archaeon *Methanosarcina barkeri*, which is considered to be predominantly a freshwater species (Maestrojuan *et al.*, 1992) but which can also live under more saline conditions (Sowers and Gunsalus, 1988), was unambiguously shown to biosynthesize PME (Holzer *et al.*, 1979; Risatti *et al.*, 1984). Holzer *et al.* (1979) also reported the tentative identification of pentamethylcosenes in low amounts in *Methanobacterium ruminantium*, a methanogenic archaeon isolated from bovine rumen, and *Methanococcus vannielii*, a mesophilic methanogenic archaeon.

PME (III) is frequently encountered in the marine water column (e.g. Wakeham, 1990) and in marine sediments (e.g. Brassell *et al.*, 1981; Kohnen *et al.*, 1992). In these environments its origin remains unclear since organisms which biosynthesize PME, and commonly live under non-extreme marine conditions, have not yet been conclusively identified. The stable carbon isotopic composition of PME is sometimes similar to that of photoautotrophic biomarkers (Kohnen *et al.*, 1992; Freeman *et al.*, 1994), which suggests an origin other than from

*Earlier literature refer to this compound as 2,6,10,15,19-pentamethyleicosane. However, IUPAC rules are now different but for reason of compatibility the acronym PME is still used.

Table 1. Cultured methanogenic archaea

Species	Culture no.	Origin
<i>Methanosarcina mazei</i>	DSM 3338	Sewage sludge
<i>Methanobrevibacter smithii</i>	DSM 162	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 163	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 164	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 165	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 166	Human feces
<i>Methanobrevibacter smithii</i>	DSM 167	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 168	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 169	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 170	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 171	Human feces
<i>Methanobrevibacter smithii</i>	DSM 172	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 173	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 174	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 175	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 176	Human feces
<i>Methanobrevibacter smithii</i>	DSM 177	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 178	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 179	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 180	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 181	Human feces
<i>Methanobrevibacter smithii</i>	DSM 182	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 183	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 184	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 185	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 186	Human feces
<i>Methanobrevibacter smithii</i>	DSM 187	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 188	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 189	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 190	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 191	Human feces
<i>Methanobrevibacter smithii</i>	DSM 192	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 193	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 194	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 195	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 196	Human feces
<i>Methanobrevibacter smithii</i>	DSM 197	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 198	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 199	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 200	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 201	Human feces
<i>Methanobrevibacter smithii</i>	DSM 202	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 203	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 204	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 205	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 206	Human feces
<i>Methanobrevibacter smithii</i>	DSM 207	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 208	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 209	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 210	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 211	Human feces
<i>Methanobrevibacter smithii</i>	DSM 212	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 213	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 214	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 215	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 216	Human feces
<i>Methanobrevibacter smithii</i>	DSM 217	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 218	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 219	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 220	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 221	Human feces
<i>Methanobrevibacter smithii</i>	DSM 222	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 223	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 224	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 225	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 226	Human feces
<i>Methanobrevibacter smithii</i>	DSM 227	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 228	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 229	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 230	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 231	Human feces
<i>Methanobrevibacter smithii</i>	DSM 232	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 233	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 234	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 235	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 236	Human feces
<i>Methanobrevibacter smithii</i>	DSM 237	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 238	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 239	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 240	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 241	Human feces
<i>Methanobrevibacter smithii</i>	DSM 242	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 243	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 244	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 245	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 246	Human feces
<i>Methanobrevibacter smithii</i>	DSM 247	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 248	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 249	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 250	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 251	Human feces
<i>Methanobrevibacter smithii</i>	DSM 252	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 253	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 254	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 255	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 256	Human feces
<i>Methanobrevibacter smithii</i>	DSM 257	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 258	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 259	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 260	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 261	Human feces
<i>Methanobrevibacter smithii</i>	DSM 262	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 263	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 264	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 265	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 266	Human feces
<i>Methanobrevibacter smithii</i>	DSM 267	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 268	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 269	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 270	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 271	Human feces
<i>Methanobrevibacter smithii</i>	DSM 272	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 273	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 274	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 275	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 276	Human feces
<i>Methanobrevibacter smithii</i>	DSM 277	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 278	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 279	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 280	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 281	Human feces
<i>Methanobrevibacter smithii</i>	DSM 282	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 283	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 284	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 285	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 286	Human feces
<i>Methanobrevibacter smithii</i>	DSM 287	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 288	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 289	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 290	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 291	Human feces
<i>Methanobrevibacter smithii</i>	DSM 292	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 293	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 294	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 295	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 296	Human feces
<i>Methanobrevibacter smithii</i>	DSM 297	Human feces
<i>Methanobrevibacter ruminantium</i>	DSM 298	Human feces
<i>Methanobrevibacter formiciferus</i>	DSM 299	Human feces
<i>Methanobrevibacter coccooides</i>	DSM 300	Human feces
<i>Methanobrevibacter burtonii</i>	DSM 301	Human feces
<i>Methanobrevibacter smithii</i>	DSM 302	Human feces

methanogenic archaea. However, in other instances the ^{13}C content of PME may differ substantially from that of photoautotrophic biomarkers (Schouten *et al.*, in press).

Here we report the presence of unsaturated compounds with the PME carbon skeleton not only in a strain of *Methanosarcina mazei*, but also in the marine methanogenic archaeon *Methanobrevibacter smithii*, confirming previous ideas on a methanogenic archaeal origin for compounds possessing the PME carbon skeleton in marine environments.

EXPERIMENTAL

Culture conditions

Cell masses of *Methanosarcina mazei* G1 were grown at 37°C with stirring (50 rpm) at pH 6.9 in a 100 l enamel-protected fermentor (HTE Bioengineering, Wald, Switzerland) pressurized with 200 kPa N_2/CO_2 (80:20, v/v). For cultivation, modified M3-medium (Balch *et al.*, 1979) supplemented with methanol (0.5%, final concentration) was used. Cells were harvested by continuous centrifugation (3000 rpm).

The following strains (see Table 1) were cultivated according to the 1993 catalog of the Deutsche Sammlung von Mikroorganismen und Zellkulturen: *Methanosarcina acetivorans* and *Methanosarcina* sp. strain MTP4 (30°C), *Methanosarcina siciliae* and *Methanococcoides methylutens* (30°C). *Methanobrevibacter smithii* (30°C) was grown in mineral medium according to the Oregon Collection of Methanogens guidelines. All strains were grown on a combination of (tri)methylamine (50 mM) and methanol (50 mM) as growth substrates at 37°C, unless otherwise indicated. Cells were harvested by centrifugation at 16 000 g for 10 min and the pellet was washed twice with a 25 mM potassium phosphate buffer (pH 7.1) containing 30 g/l NaCl and 3.5 g/l $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$. After washing, the pellet was resuspended in 1 ml sterile doubly-distilled water. Subsequently the cells were lyophilized.

Analysis of lipids

The freeze-dried biomass was ultrasonically extracted with methanol (3 \times), methanol/dichloromethane (DCM) (1:1, v/v; 3 \times) and DCM (3 \times). The extracts were combined and separated into an apolar and a residual fraction using column chromatography (Al_2O_3 as stationary phase) with hexane/

DCM (9:1, v/v) and DCM/methanol (1:1, v/v) as eluents. Fractions were hydrogenated by dissolving in ethyl acetate, adding PtO_2 and bubbling H_2 through for 1 h. The mixture was then stirred for an additional 24 h. The samples were analysed by gas chromatography (GC) and gas chromatography-mass spectrometry (GC-MS).

Gas chromatography

GC was performed using a Hewlett-Packard 5890 equipped with an on-column injector. A fused-silica capillary column (25 m \times 0.32 mm) coated with CP Sil-5 (film thickness 0.12 μm) was used with helium as carrier gas. A flame ionization detector (FID) was used for detection. The samples were dissolved in ethyl acetate and injected at 70°C. Subsequently the oven was programmed to 130°C at 20°C/min and then at 4°C/min to 320°C, at which it was held for 15 min.

Gas chromatography-mass spectrometry

GC-MS was performed using a Hewlett-Packard 5890 gas chromatograph interfaced with a VG Autospec Ultima mass spectrometer operated at 70 eV with a mass range of m/z 40–800 and a cycle time of 1.7 s (resolution 1000). The gas chromatograph was equipped with a fused-silica capillary column (25 m \times 0.32 mm) coated with CP Sil-5 (film thickness 0.2 μm). The carrier gas was helium. The samples were injected on column at 60°C and subsequently the oven was programmed to 130°C at 20°C/min and then at 4°C/min to 300°C at which it was held for 10 min.

RESULTS AND DISCUSSION

Six different methanogenic archaea were cultured and analysed for apolar lipids (see Table 1). Only two cultures, *Methanosarcina mazei* and *Methanobrevibacter smithii*, were found to contain significant amounts of apolar hydrocarbons.

Table 2. Pseudo Kovats indices of unsaturated PMEs

Archaea	Number of double bonds	Pseudo Kovats index (CP Sil 5)
<i>Methanosarcina mazei</i>	4	2336
	5	2347
<i>Methanobrevibacter smithii</i>	3	2290, 2314
	4	2326, 2333
	5	2347, 2366

Methanosarcina mazei, a strain isolated from sewage sludge, was found to contain only a limited number of compounds which, on the basis of their mass spectra and retention indices (Table 2), are

thought to be 2,6,10,15,19-pentamethylcosenes containing four or five double bonds (Figs 1 and 2B). The carbon skeleton of these compounds was confirmed by hydrogenation of the apolar fraction,

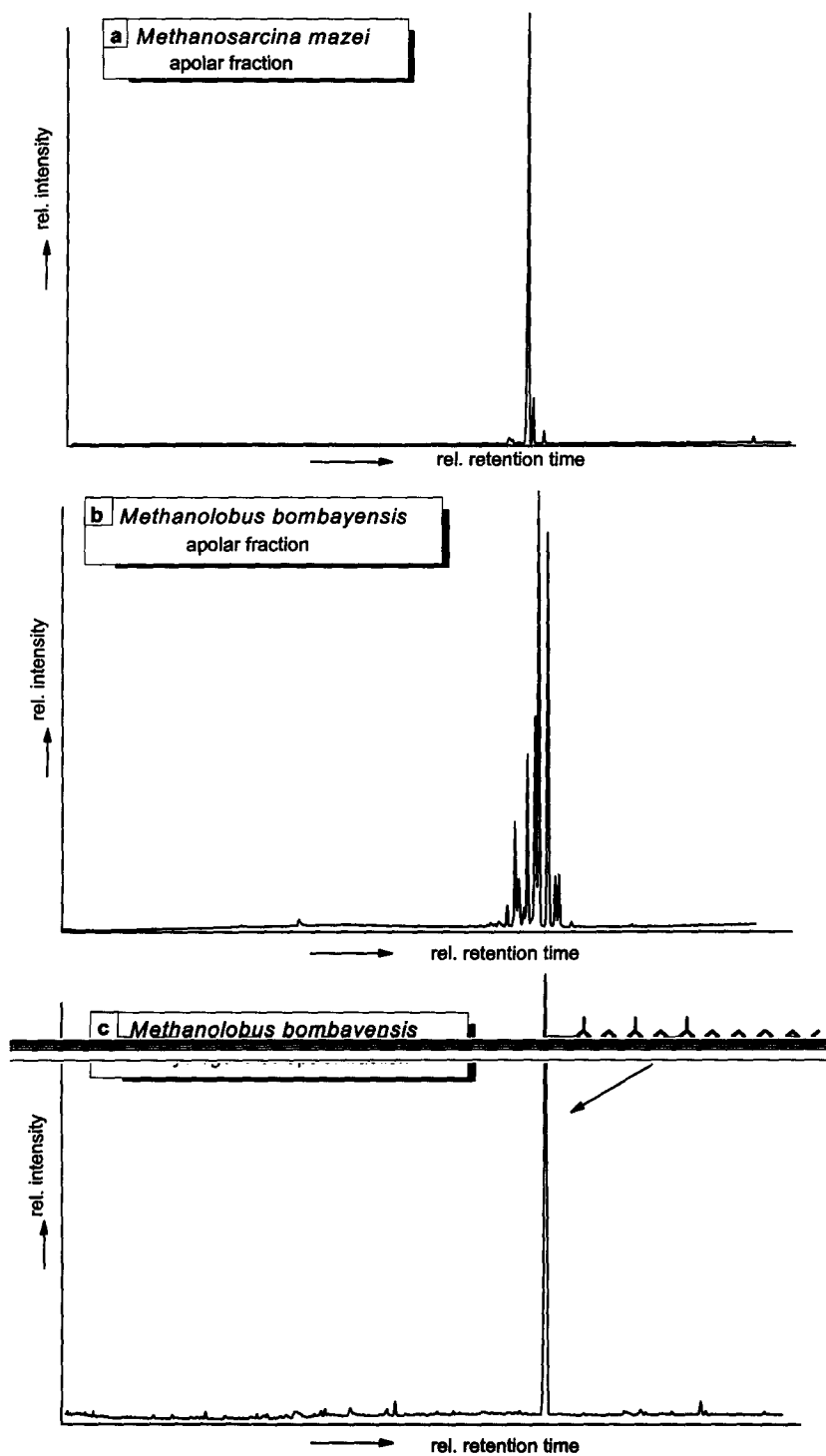


Fig. 1. Gas chromatograms of (a) apolar fraction of lipid extract from *Methanosarcina mazei*, (b) apolar fraction of lipid extract from *Methanolobus bombayensis* and (c) hydrogenated apolar fraction of lipid extract from *Methanolobus bombayensis*.

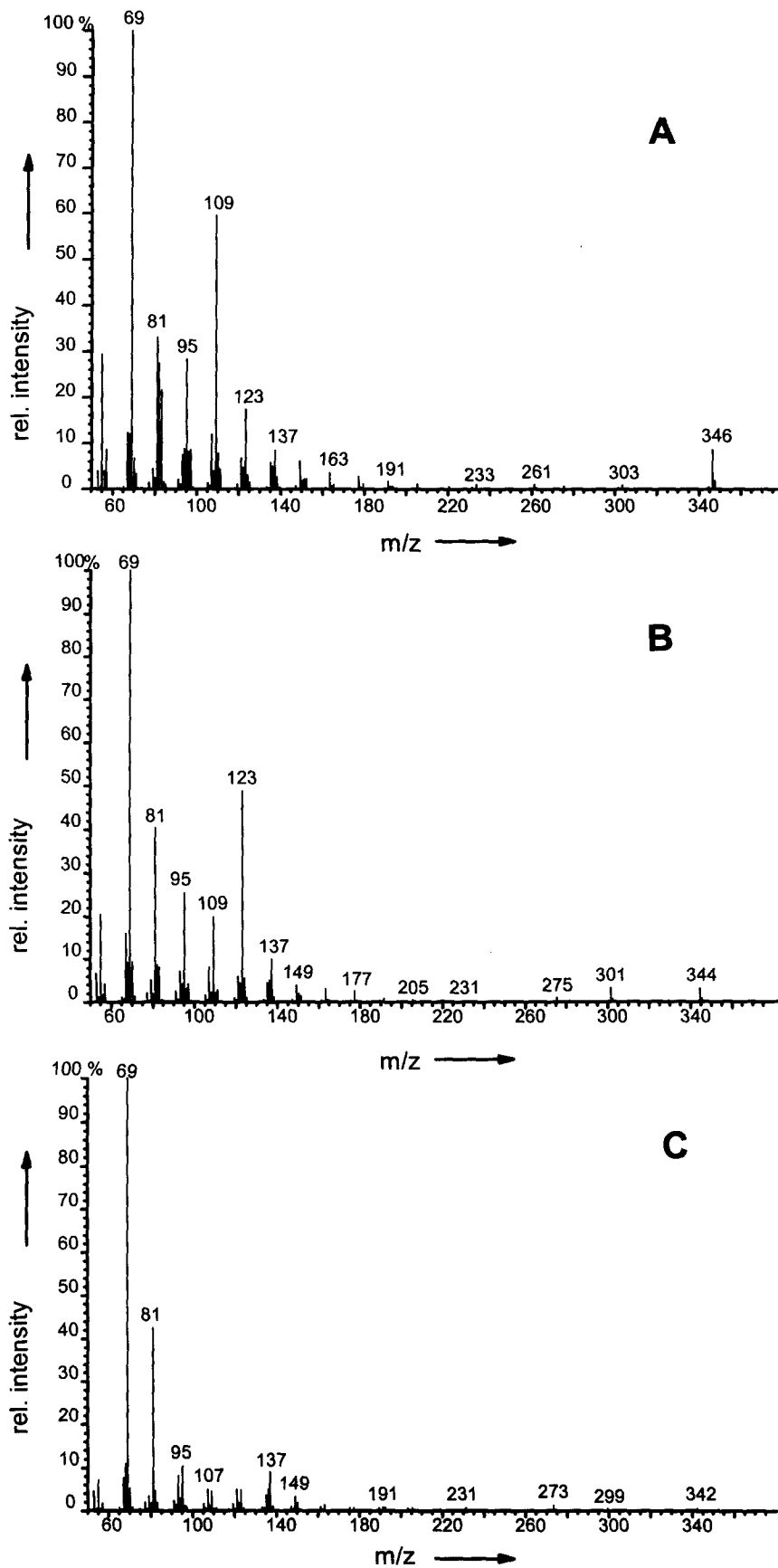


Fig. 2. Mass spectrum of (A) 2,6,10,15,19-pentamethylcosenes with three double bonds present in *Methanolobus bombayensis*, (B) 2,6,10,15,19-pentamethylcosenes with four double bonds present in *Methanosarcina mazei* and (C) 2,6,10,15,19-pentamethylcosenes with five double bonds present in *Methanolobus bombayensis*.

which yielded PME as the only compound as identified by comparison with the mass spectrum and retention index of synthetic PME (Rowland *et al.*, 1982; Risatti *et al.*, 1984). When the apolar fraction of the extract of *Methanobolus bombayensis* was analysed, a cluster of compounds was found which were identified as 2,6,10,15,19-pentamethylcosenes containing three to five double bonds (Fig. 1b, 2b and 2c). Indeed, hydrogenation of the fraction yielded PME as the only compound (Fig. 1c). *Methanosarcina* sp. MPT4 and *Methanosarcina siciliiae* contain only trace amounts of pentamethylcosenes with three and four double bonds, respectively, but their low amounts prevented any firm identification through hydrogenation of the fractions. The apolar fractions of the lipid extracts of *Methanosarcina acetivorans* and *Methanococcoides methylutens* did not contain any significant amounts of apolar hydrocarbons.

The identification of alkenes with the PME carbon skeleton in *Methanosarcina mazei*, a species which can thrive under mesophilic conditions (Maestrojuan *et al.*, 1992), and, more importantly, in *Methanobolus bombayensis*, an archaeon isolated from a marine sediment of the Indian Ocean (Kadam *et al.*, 1994), gives additional support for the hypothesis that compounds with this carbon skeleton can serve as a marker for methanogenic activity in marine environments (Brassell *et al.*, 1981). Previous unambiguous identifications of compounds possessing the PME carbon skeleton were either in an archaeon living at temperatures of 60–80°C (*Methanobacterium thermoautotrophicum*) or in archaea living predominantly in freshwater or mesophilic conditions (*Methanosarcina barkeri*, *Methanobacterium ruminantium*, *Methanococcus vannielii*). Although it cannot be excluded that other organisms are biosynthesizing this compound, methanogenic archaea are the only organisms known to date which biosynthesize this particular carbon skeleton. Furthermore, it has been shown for a few marine sediments that the stereochemistry of the sedimentary PME is in full accordance with a biological origin from methanogenic archaea (Rowland *et al.*, 1982; Risatti *et al.*, 1984). The fact that this compound has been found in oxygenated upper parts of the water column (Wakeham, 1990) does not invalidate this hypothesis since methanogenic archaea have been isolated from such environments (Cynar and Yayanos, 1991; Sieburth, 1993); also methanogenic activity is known to occur in oxygen-rich waters (Karl and Tilbrook, 1994), possibly in the guts of zooplankton or in anoxic micro-environments inside particulate organic matter.

To date, only PME has been reported in sediments or in the water column (e.g. Brassell *et al.*, 1981; Wakeham, 1990; Kohnen *et al.*, 1992) whilst there are no reports of unsaturated PMEs or of sulphur-bound PME (incorporation of sulphur

requires the presence of functionalities in the original lipid; e.g. Kohnen *et al.*, 1992). Our results and those of Tornabene *et al.* (1979) show that methanogens in culture produce abundant unsaturated PMEs, although Risatti *et al.* (1984) found only the saturated compound in their culture of *Methanosarcina barkeri*. It is unclear why in their case and possibly also in the natural environment only PME is biosynthesized. This may be due to the particular environments where they thrive or due to the nutrients and carbon sources supplied to the methanogenic archaea. Growth of methanogen cultures under different conditions may help to explain this observation.

CONCLUSION

2,6,10,15,19-Pentamethylcosenes containing three to five double bonds have been found in high amounts in the methanogenic archaeon *Methanosarcina mazei*, a strain isolated from sewage sludge, and in *Methanobolus bombayensis*, a strain isolated from marine sediments of the Indian Ocean. This result gives additional support to the contention that compounds possessing a PME carbon skeleton are biomarkers for past methanogenic activity in marine environments.

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APPENDIX

