The Cellular Fatty Acids of the Sulphate-reducing Bacteria, *Desulfobacter* sp., *Desulfobulbus* sp. and *Desulfovibrio desulfuricans*

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The fatty acid profiles of *Desulfobacter* sp. grown on acetate and *Desulfobulbus* sp. grown on propionate, lactate and H_2/CO_2 were analysed. *Desulfobacter* sp. grown on acetate and *Desulfobulbus* sp. grown on H_2/CO_2 gave mainly even numbered straight chain acids but odd numbered acids predominated in *Desulfobulbus* sp. grown on propionate, reflecting the use of the growth substrates provided as chain initiators for fatty acid biosynthesis. The cellular fatty acids of *Desulfobulbus* sp. grown on lactate were distributed approximately evenly between even and odd straight chain acids. In contrast those of *Desulfovibrio desulfuricans*, were dominated by branched chain iso and anteiso fatty acids, when grown on either lactate or H_2/CO_2 . On the basis of the fatty acid biosynthetic pathways these sulphate-reducing bacteria could be separated into two groups, one comprising *Desulfobacter* sp. and *Desulfobulbus* sp. and the other more primitive *Desulfovibrio desulfuricans*.

INTRODUCTION

Dissimilatory sulphate reduction has been shown to play a major role in the degradation of carbon within marine sediments (Jørgensen, 1977; Sørensen *et al.*, 1979). Until recently, however, the few known genera of sulphate-reducing bacteria (*Desulfovibrio* and *Desulfotomaculum*, Postgate, 1979) which have restricted nutritional capacities, tended to contradict the field observations. The isolation of several new genera of sulphate-reducing bacteria (Widdel, 1980) with greater catabolic diversity than previous isolates has tended to resolve this apparent contradiction. The distribution of these new genera of sulphate-reducing bacteria in the environment and which of them are important in terms of carbon cycling is still unclear.

Several techniques may be used to enumerate and identify bacterial types present in marine sediments but all suffer from various limitations. Culture techniques using selective media may be able to enumerate the bacterial types present (Laanbroek & Pfennig, 1981) but this technique can both distort and underestimate the *in situ* population. Microscopic analysis of the sediment can provide data on bacterial distribution but morphology gives very little indication of the types of organism present. Radioactive tracer experiments provide information regarding substrates being utilized but give no direct information about the actual bacteria present.

Another approach to this problem of identification of bacteria in sediments is to analyse them for bacterial components which are specific for individual species. Fatty acids have been used extensively in this respect (Parkes & Taylor, 1983; Bobbie & White, 1980; Perry *et al.*, 1979; van Vleet & Quinn, 1979; King *et al.*, 1977; Cranwell, 1976*a, b*) and in this study we report the fatty acid profiles of two of the newly described sulphate-reducing bacteria, *Desulfobacter* sp. and *Desulfobulbus* sp. and compare their profiles to that of *Desulfovibrio desulfuricans*. The effect of varying growth substrate on the cellular fatty acid distributions of these nutritionally limited sulphate reducers was also studied. The aim of this work was to identify fatty acids characteristic of the different sulphate-reducing bacteria that might enable their distribution within marine

sediments to be estimated. *Desulfobacter* sp., which can utilize acetate, and *Desulfobulbus* sp., which can utilize propionate, were chosen as Sørensen *et al.* (1981) had shown that these substrates were important electron donors for sulphate reduction in marine sediments, being responsible for 50% and 10–20%, respectively, of sulphate reduction.

METHODS

Bacterial isolates and culture conditions. *Desulfobacter* strain 3 ac 10 and *Desulfobulbus* strain 3 pr 10 were both isolated from the anaerobic mud flat of the Jadebusen (North Sea) and were kindly supplied by Dr F. Widdel, University of Konstanz, West Germany (Widdel & Pfennig, 1981, 1982). Although the marine strains are morphologically and nutritionally similar to the type strains *Desulfobacter postgatei* and *Desulfobulbus propionicus*, further investigation is required to decide whether 3 ac 10 and 3 pr 10 are strains of *Desulfobacter postgatei* and *Desulfobulbus propionicus*, respectively, or whether they are other species of these genera (F. Widdel, personal communication) and hence can only be designated so far as *Desulfobacter* sp. and *Desulfobulbus* sp. These organisms were grown on a marine medium as described (Widdel & Pfennig, 1981, 1982) but in a 2.5 l fermenter (L.H. Engineering, Stoke Poges). The substrate for *Desulfobacter* sp. was acetate (30 mM) and for *Desulfobulbus* sp. was either propionate (18.7 mM), lactate (13.2 mM) or H_2/CO_2 + acetate (2 mM). The pH was constantly monitored but not controlled as the pH remained relatively constant during growth (7.2–7.6 for *Desulfobacter* and 7.2–7.5 for *Desulfobulbus*). Both strains were grown at 29 °C which was at (*Desulfobulbus*) or near (*Desulfobacter*, 31 °C) their temperature optimum in order to facilitate comparison of their fatty acid profiles (Oliver & Colwell, 1973). Cells were harvested at the end of the exponential growth phase.

Desulfovibrio desulfuricans was isolated from the anaerobic sediments of Loch Eil, Scotland, using Postgate's liquid medium B, and was kindly supplied by N. Battersby, Heriot-Watt University, Edinburgh. Purification and identification were conducted as described by Postgate (1979) except that the 'roll-tube' technique of Hungate (1969) was used for growth on solid medium. This marine isolate was grown on a medium based on Postgate's medium E (Postgate, 1979) which contained extra NaCl, (23.4 g l⁻¹), and no lactate, but with an atmosphere of H_2/CO_2 (80:20, v/v). At the end of exponential growth the culture was harvested leaving approximately 100 ml in the fermenter, the gas phase was switched to N₂, the fermenter was thoroughly flushed with N₂, and the same medium supplemented with lactate (21 mM) was added. The culture was once more harvested at the end of exponential growth. *Desulfovibrio desulfuricans* was grown at 30 °C and the pH during growth was approximately 7.3 for both the substrates used. Purity checks were conducted as described by Postgate (1979).

Extraction and isolation of fatty acids. Bacterial cultures were harvested by centrifugation at 34000 g for 20 min and lipids extracted by a modified Bligh & Dyer procedure (Boon *et al.*, 1977). The bacterial cells were homogenized in 40 ml water, 80 ml methanol and 160 ml chloroform. Centrifugation yielded a pellet which was ultrasonically extracted with 100 ml methanol and 60 ml chloroform. The combined extracts yielded a monophasic solution, which separated into two layers on addition of 80 ml water. The lipids were recovered in the chloroform phase, the solvent was removed under vacuum and the fatty acids were released by refluxing for 3 h with 2 M-KOH in methanol (50 ml). After cooling, methanol was removed under vacuum, 40 ml distilled water was added and the non-acidic fraction was extracted with 30 ml portions of dichloromethane. The fatty acids were obtained from the aqueous layer by acidification to pH 2 with concentrated HCl and extracted with three 30 ml portions of dichloromethane. After removal of the solvent under vacuum, the acids were methylated with BF₃/CH₃OH (Metcalf & Schmitz, 1961). Preparative TLC on silica gel (Merck 7731) developed with hexane/diethyl ether (9:1, v/v) yielded the monocarboxylic acid methyl esters (R_F : 0.56–0.69). These were further separated by argentation TLC on silica gel (Merck 7731), impregnated with 5% (w/v) AgNO₃ into saturated esters (R_F : 0.56–0.69) and monounsaturated esters (R_F : 0.40–0.45) by development with n-hexane/diethyl ether (9:1).

Analysis of fatty acids. Fatty acids were analysed as their methyl esters by GLC using a Carlo Erba FTV 4160 gas chromatograph fitted with either a MEGA OV-1 glass capillary column (25 m, 0.1–0.15 µm, Erba Science) or a MEGA carbowax 20 M glass capillary column (25 m, 0.1–0.15 µm, Erba Science). The carrier gas was hydrogen with a flow of 2.5 ml min⁻¹. The OV-1 column was programmed from 80 to 290 °C at 4 °C min⁻¹ and the carbowax 20 M column from 70 to 210 °C at the same rate. Injection was on column and detection was by flame ionization, with a detector temperature of 335 °C. Quantitation was achieved by using an electronic computing integrator (Hewlett Packard 1360). Mass spectral data were obtained by a computer linked gas chromatograph-mass spectrometer using a Finnigan 4000 instrument under standard conditions (Volkman *et al.*, 1981).

The fatty acid methyl esters were identified from their GLC retention times and where possible coeluted with standards (Applied Science Laboratories) on both OV-1 and carbowax 20 M columns. The order of elution of saturated and unsaturated fatty acid methyl esters on the OV-1 column is the reverse of that obtained on the carbowax 20 M column, providing a useful cross-check on identifications. Confirmation of structural assignments were obtained by comparison of mass spectral results with published data (Parkes & Taylor, 1983 and references therein).

RESULTS

The fatty acid composition of pure cultures of the three genera of sulphate-reducing bacteria *Desulfobacter* sp., *Desulfobulbus* sp. and *Desulfovibrio desulfuricans* grown on various substrates are presented in Table 1. In each case their fatty acids fall in the C₁₂–C₁₉ range commonly found in bacteria (Kates, 1964; Shaw, 1974) and the monounsaturated acids exhibit double bond positional isomers indicative of biosynthesis by the anaerobic metabolic pathway (Erwin & Bloch, 1964).

Table 1. Percentage fatty acid composition of the three genera of sulphate-reducing bacteria

The important fatty acid concentrations are shown in bold type.

Growth substrate acid*	ECL		<i>Desulfobacter</i> sp. Acetate	<i>Desulfobulbus</i> sp.			<i>Desulfovibrio</i> <i>desulfuricans</i>	
	OV-1	Carbowax 20 M		Propionate	Lactate	H ₂ /CO ₂	H ₂ /CO ₂	Lactate
*12:0	12.00	12.00	2.99	0.71	2.70	1.93	3.06	0.58
*iso-13:0	12.50	12.60	0.56	tr	—	—	—	—
*anteiso-13:0	12.60	12.70	0.04	tr	—	—	—	—
13:0	13.00	13.00	0.02	0.40	0.08	0.12	—	—
iso-14:0	13.68	13.60	0.12	0.06	—	0.24	—	—
*14:1 ω 7	13.77	14.20	0.04	0.03	0.08	0.24	—	—
14:0	14.00	14.00	22.52	2.27	4.57	9.53	2.68	0.71
*iso-15:1 ω 7	14.45	14.65	—	—	—	—	2.94	2.84
*anteiso-15:1 ω 7	14.49	14.75	—	—	—	—	0.13	0.32
iso-15:0	14.76	14.65	4.32	0.03	0.04	0.08	9.89	12.60
anteiso-15:0	14.84	14.75	0.17	0.03	0.92	0.24	0.59	0.93
15:1 ω 10	14.88	15.05	—	0.80	1.95	—	—	—
15:1 ω 8	14.92	15.25	—	1.81	3.42	0.60	—	—
15:1 ω 6	14.95	15.35	—	0.22	—	—	—	—
15:0	15.00	15.00	0.65	23.01	6.47	5.23	0.40	0.03
iso-16:1 ω 7	15.53	15.79	—	—	0.08	0.80	—	0.26
iso-16:0	15.77	15.75	0.17	0.14	0.04	0.08	0.20	0.52
16:1 ω 9	15.80	16.15	0.20	—	—	—	—	—
16:1 ω 7	15.85	16.27	3.80	1.09	3.83	7.96	1.34	2.32
16:1 ω 5	15.90	16.35	—	—	—	—	—	—
16:0	16.00	16.00	44.27	5.93	11.47	20.34	9.61	3.40
*10 Me-16:0	16.67	16.60	10.80	—	—	—	—	—
iso-17:1 ω 7	16.60	16.75	—	—	—	—	38.36	40.72
anteiso-17:1 ω 7	16.77	16.85	—	—	—	—	4.48	3.75
iso-17:0	16.80	16.75	0.50	tr	tr	—	9.78	15.46
anteiso-17:0	16.90	16.86	0.10	tr	tr	—	2.82	3.75
17:1 ω 10	16.88	17.04	—	1.30	2.21	0.20	—	—
17:1 ω 8	16.95	17.15	—	52.01	39.70	10.95	—	—
17:1 ω 6	16.97	17.20	—	0.08	0.35	—	—	—
*V17:0	16.95	17.10	2.73	—	—	—	—	—
17:0	17.00	17.00	0.26	3.81	0.72	0.74	0.60	0.32
iso-18:1 ω 7	17.55	17.69	—	—	—	0.28	0.27	0.29
iso-18:0	17.70	17.65	0.10	—	0.15	0.20	1.95	0.13
18:1 ω 9	17.75	18.00	0.80	0.47	1.32	0.88	—	0.03
18:1 ω 7	17.80	18.07	1.97	2.92	6.30	22.60	1.43	2.42
18:1 ω 5	17.85	18.17	—	—	—	—	—	—
18:0	18.00	18.00	2.86	0.93	2.28	4.50	6.47	4.89
iso-19:1 ω 7	18.35	18.53	—	—	—	—	1.72	1.58
anteiso-19:1 ω 7	18.45	18.65	—	—	—	—	0.27	0.29
iso-19:0	18.55	18.53	—	—	—	—	0.92	1.74
anteiso-19:0	18.70	18.65	—	—	—	—	0.07	0.06
19:0	19.00	19.00	—	—	—	—	—	—

* Fatty acid abbreviations exemplified by: 12:0, dodecanoic; iso-13:0, 11-methyldodecanoic; anteiso-13:0, 10-methyldodecanoic; 14:1 ω 7, 7-tetradecenoic; iso-15:1 ω 7, 13-methyltetradec-7-enoic; anteiso-15:1 ω 7, 12-methyltetradec-7-enoic; 10 Me-C16:0, 10-methylhexadecanoic; V17:0, 9,10-methylenehexadecanoic.

Table 2. *Structural correlations between chain initiator substrates and cellular fatty acid percentages for the three genera of sulphate-reducing bacteria*

Growth substrate acid type	Chain initiator	<i>Desulfobacter</i> sp. Acetate	<i>Desulfobulbus</i> sp.			<i>Desulfovibrio</i> <i>desulfuricans</i>	
			Propionate	Lactate	H ₂ /CO ₂	H ₂ /CO ₂	Lactate
Even normal acids n-C ₁₂ -C ₁₄ -C ₁₆ -C ₁₈	Acetyl-CoA	93.0*	16.0	43.8	78.9	24.6	14.5
Odd normal acids n-C ₁₃ -C ₁₅ -C ₁₇ -C ₁₉	Propionyl-CoA	0.9	83.4	54.9	17.8	1.1	0.4
Even iso acids iso-C ₁₂ -C ₁₄ -C ₁₆ -C ₁₈	Isobutyryl-CoA	0.4	0.2	0.3	1.6	2.4	1.2
Odd iso acids iso-C ₁₃ -C ₁₅ -C ₁₇ -C ₁₉	Isovaleryl-CoA	5.4	0.0	0.0	0.1	63.6	74.9
Odd anteiso acids anteiso-C ₁₃ -C ₁₅ -C ₁₇ -C ₁₉	α-Methylbutyryl-CoA	0.3	0.0	0.9	0.2	9.3	9.1

* 10 Me-C_{16:0} and ∇17:0 are assumed to arise biosynthetically from C_{16:1} and hence use acetyl-CoA as chain initiator.

The three sulphate-reducing species studied exhibit gross differences in their cellular fatty acid compositions. The major cellular fatty acids (79%) of *Desulfobacter* sp. grown on acetate were even numbered straight chain acids with C_{14:0} (23%) and C_{16:0} (44%) dominating (Table 1). In contrast, *Desulfobulbus* sp. exhibited fatty acid compositions, when grown on both propionate and lactate, which were dominated by odd numbered straight chain fatty acids, 83% and 55% of the total fatty acids, respectively. However, *Desulfobulbus* sp. grown on H₂/CO₂ and assimilating carbon through acetate showed an abundance of even straight chain fatty acids (79%). Interestingly, *Desulfobulbus* with all the growth substrates used always contained significant amounts of C_{15:0} and C_{17:1ω8} and on growth with propionate and lactate these two fatty acids alone accounted for 75% and 46%, respectively, of the total cellular fatty acids. In marked contrast to the other two genera of sulphate reducers studied, the cellular fatty acids of *Desulfovibrio desulfuricans* grown on H₂/CO₂ or lactate was dominated in each case by branched iso and anteiso fatty acids 75% and 85%, respectively, with iso-C_{15:0} and iso-C_{17:1ω7} dominating. Unlike *Desulfobulbus* sp., growth of *Desulfovibrio desulfuricans* on H₂/CO₂ produced only a minor increase in the even normal straight chain fatty acids (from 15% to 26%), compared with growth on lactate.

In general, *Desulfobacter* sp. contained lower molecular weight fatty acids in the range C₁₂-C₁₆, which accounted for approximately 80% of the total acids of this species (Table 1). The proportion of longer chain fatty acids C₁₇-C₁₉ was much higher in both *Desulfobulbus* sp. and *Desulfovibrio desulfuricans*, ranging from 40% to 62% and 69% to 75%, respectively (Table 1). In all three species low molecular weight fatty acids in the C₁₂-C₁₆ range were predominantly saturated (85-95%) while the higher molecular weight acids were almost invariably unsaturated (72-92%).

Desulfobacter sp. contained quantities of 10 Me-C_{16:0} (11%) and ∇C_{17:0} (3%) fatty acids and in this respect differed from the other two sulphate-reducing species studied. The unusual fatty acid, 10 Me-C_{16:0} was identified from gas chromatography retention times, which were similar to those reported by Boon & de Leeuw (1978) and from its mass spectrum which exhibited a molecular ion peak at *m/e* 284 and characteristic ion peaks (Apon & Nicolaides, 1975) at *m/e* 129, 130, 149, 167, 171, 172, 173 and 199.

The distribution of fatty acids in the sulphate-reducing bacteria with respect to their chain initiators for fatty acid biosynthesis is shown in Table 2. *Desulfobacter* sp. grown on acetate was dominated by fatty acids (93%, Table 2) biosynthesized from acetyl-coenzyme A as a chain initiator. In *Desulfobulbus* sp. the dominant chain initiator for fatty acid biosynthesis was dependent on growth substrate. When grown on propionate, 83% of the cellular fatty acids were initiated by propionyl-coenzyme A. Growth on lactate used two major chain initiators for fatty

acid biosynthesis, acetyl-coenzyme A (44%) and propionyl-coenzyme A (55%). Growth on H_2/CO_2 , with assimilation of carbon via acetate, was dominated by cellular fatty acids biosynthesized by acetyl-coenzyme A initiation. In contrast, in *Desulfovibrio desulfuricans* the dominant chain initiator for fatty acid biosynthesis varied little with growth substrate, with isovaleryl-coenzyme A accounting for 75% and 64% of the cellular fatty acids of this bacterium when grown on lactate and H_2/CO_2 , respectively.

DISCUSSION

Desulfobacter sp., *Desulfobulbus* sp. and *Desulfovibrio desulfuricans* exhibit markedly different cellular fatty acid distributions (Tables 1 and 2). The dominance of even numbered straight chain acids in *Desulfobacter* sp. grown on acetate and odd numbered straight chain acids in *Desulfobulbus* sp. grown on propionate can be explained in terms of the readily available supply of acetate and propionate in their respective growth media. Both these substrates can act as precursors of the chain initiators involved in fatty acid biosynthesis, acetate leading to even straight chain acids and propionate to odd straight chain acids. In contrast, the branched chain fatty acids of *Desulfovibrio desulfuricans*, grown on a lactate medium, must involve *de novo* synthesis of the appropriate initiators (e.g. isovaleryl-CoA) for their biosynthesis, since lactate itself cannot be used directly as a chain initiator for fatty acid biosynthesis (Kates, 1964; Kaneda, 1977). The presence of substantial amounts of 10 Me- $C_{16:0}$ in *Desulfobacter* sp. is unusual, such 10-methyl acids having been previously found only in actinomycetes (Lechevalier, 1977) and *Agrobacterium tumefaciens* (Kaneshino & Thomas, 1969), although it has been widely reported in marine sediments (Parkes & Taylor, 1983; Boon & de Leeuw, 1978; Volkman *et al.*, 1980).

The effect of chain initiators, in the growth medium, on cellular fatty acid distribution was studied by Cerniglia & Perry (1975) who observed a change in the major fatty acids from even to odd in *Mycobacterium convolutum*, as a result of a change in substrate from acetate to propionate. However, researchers using other organisms have shown little or no effect on fatty acid distributions as a result of changing or adding substrates (Thoen *et al.*, 1971; Weerkamp & Heinen, 1972). Normally the influence of chain initiators on the cellular fatty acid distributions of different bacterial types is overcome by growing the organisms on identical medium (Shaw, 1974; Lechevalier, 1982). In the present case, however, with nutritionally limited sulphate-reducing bacteria the situation is complex since they will not all grow on the same substrate, and in the case of *Desulfobacter* sp. grown on acetate and *Desulfobulbus* sp. grown on propionate the growth substrate and fatty acid chain initiator are one and the same. This raises the question as to whether the fatty acid compositions observed for the sulphate-reducing bacteria studied are characteristic of the bacteria or merely a reflection of the substrate used for growth.

In an attempt to address this question, the fatty acid profile was obtained for *Desulfobulbus* sp. grown on lactate and H_2/CO_2 , and for *Desulfovibrio desulfuricans* grown on H_2/CO_2 . This enabled a comparison of the fatty acid profiles of the three sulphate-reducing bacteria grown under conditions which, as far as their limited nutrition allowed, minimized variability due to growth substrate. The results obtained (Tables 1 and 2) enabled characteristic features in the fatty acid profiles of the three sulphate-reducing bacteria to be distinguished. The fatty acid distribution of *Desulfovibrio desulfuricans* showed little variation when grown on lactate or H_2/CO_2 , being dominated in each case by characteristic branched chain fatty acids, in particular iso- $C_{15:0}$ and iso- $C_{17:1\omega7}$. The fatty acid distribution of *Desulfovibrio desulfuricans* also seems to be independent of growth phase, as the fatty acid distribution reported here for batch growth of this organism is almost identical to that previously reported for the same organism in continuous culture (Parkes & Taylor, 1983).

In contrast, the fatty acid distribution of *Desulfobulbus* sp. varied in the relative abundance of odd and even straight chain acids when grown on different substrates. But even when grown on lactate or H_2/CO_2 , which allowed a direct comparison with the fatty acid profile of *Desulfovibrio desulfuricans*, the branched chain fatty acid component of *Desulfobulbus* sp. remained low (Table 2). The dominance of odd straight chain acids (83%, Table 2) when *Desulfobulbus* sp. was grown on propionate changed to a majority of even straight chain acids (79%) when grown on

H₂/CO₂, in which case carbon assimilation occurs through acetate. This probably reflects the availability in the growth media of the appropriate chain initiator substrates, propionate and acetate, respectively. However, even when accumulating carbon via acetate when grown on H₂/CO₂ or synthesizing the chain initiator *de novo* as with lactate, *Desulfobulbus* sp. still exhibited relatively high abundances of C_{15:0} and C_{17:1ω8} fatty acids. The latter was the most dominant fatty acid when *Desulfobulbus* sp. was grown on propionate and lactate and appears to be characteristic of this bacterium.

The cellular fatty acids of both *Desulfobacter* sp. and *Desulfobulbus* sp. were dominated by straight chain acids (94–99%, Table 2) whilst that of *Desulfovibrio desulfuricans* was composed mainly of branched chain iso and anteiso fatty acids (76–85%, Table 2). Thus, regardless of the substrate used for growth, the three sulphate-reducers studied could be grouped into two types, on the basis of their observed fatty acid compositions, and hence the biosynthetic pathways operative (Uchida & Mogi, 1972; Kaneda, 1977). Type 1, *Desulfobacter* sp. and *Desulfobulbus* sp., exhibited fatty acid distributions consistent with a biosynthetic pathway involving palmitic acid synthetase with specificity towards C₂ and C₃ chain initiators (Kaneda, 1977). In contrast, Type 2, *Desulfovibrio desulfuricans*, has a high proportion of branched fatty acids, indicating fatty acid biosynthesis involving branched chain fatty acid synthetase, with specificity towards branched C₄ and C₅ chain initiators.

Kaneda (1977) using a similar classification for the genus *Bacillus*, proposed that bacteria whose cellular fatty acids were predominantly branched, and hence involved branched fatty acid synthetase for their *de novo* fatty acid synthesis, were evolutionarily more primitive than bacteria using palmitic acid synthetase. On this basis *Desulfovibrio desulfuricans* could be classified as evolutionarily more primitive than either *Desulfobacter* or *Desulfobulbus*, a view consistent with the findings of Gottschalk (1968), who considered *Desulfovibrio desulfuricans* to be a primitive sulphate-reducing bacterium due to the presence of the unusual (R)-citrate synthase.

The dominance of iso-C_{17:1ω7} in the fatty acid profile of *Desulfovibrio desulfuricans* has also been reported by Boon *et al.* (1977), who proposed that this fatty acid could be used as a biomarker for this organism within marine sediments. The results of the fatty acid profiles of *Desulfobulbus* sp. and *Desulfobacter* sp. demonstrate that this biomarker cannot be extended to cover sulphate-reducing bacteria in general. The characteristic fatty acids of *Desulfobulbus* sp. and *Desulfovibrio desulfuricans*, C_{17:1ω8} and iso-C_{17:1ω7}, respectively, were present in only trace amounts in the zone of sulphate reduction in a recent marine sediment (Parkes & Taylor, 1983), whereas the fatty acids found for *Desulfobacter* sp. growing on acetate were similar to those within the sediment, both being dominated by saturated and monounsaturated even chain acids C₁₂, C₁₄, C₁₆ and C₁₈. This data tends to support recent work which emphasizes the important role of acetate in sulphate reduction within marine sediments (Sørensen *et al.*, 1981; Balba & Nedwell, 1982), but how far fatty acid profiles of laboratory grown organisms can be used to interpret the fatty acid distributions within the complex sediment environment, requires further investigation before any firm conclusions can be drawn.

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