

Short Communication

Polyamine distribution profiles of new members of the phylum Bacteroidetes

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Cellular polyamine profiles as a phenotypic chemotaxonomic marker within the phylum Bacteroidetes, which is divided into the three classes (orders) Bacteroidetes (Bacteroidales), Flavobacteria (Flavobacteriales) and Sphingobacteria (Sphingobacteriales) have been studied (Hamana and Matsuzaki, 1990, 1991; Hamana and Nakagawa, 2001a, b; Hamana and Nii-tsu, 2001; Hamana et al., 1995; Hosoya and Hamana, 2003, 2004). Our previous analyses revealed that most of the strains examined in the classes Bacteroidetes and Flavobacteria contained two triamines, spermidine and homospermidine, respectively, as major polyamine components; however, the polyamine profiles over the two classes remain to be elucidated with sizable number of species. On the other hand, the polyamine profiles in the class Sphingobacteria are variable depend on genera or families. In the present study, 105 new strains belonging to the phylum Bacteroidetes were analyzed to survey the distribution of spermidine, homospermidine and other polyamines to evaluate their chemotaxonomic significance.

The strains examined were cultured anaerobically at optimum growth temperature (30–37°C) in GAM Broth (Nissui Pharmaceutical Co., Tokyo, Japan), using An-

aerobic Jar KJ-1 (Tomy Seiko, Tokyo) (Hamana et al., 1995), or aerobically at 25–30°C in Marine Broth (DIFCO, MI, USA), Marine Agar, Trypticase Soy Broth (BBL, MD, USA), polyamine-free Synthetic 199 Medium dissolved in seawater (199-SW) and various media listed in ATCC, JCM and NBRC (ATCC website, 2008; JCM website, 2008; NBRC website, 2008). Cells in the stationary growing phase were harvested from a 50–100 ml liquid culture by centrifugation at 3,000×*g* and washed with an isotonic saline or PBS (Nissui Pharmaceutical Co.). The anaerobic strains grown on blood-agar plates were raked from the plates. The cell pellets were homogenized in equal volumes of cold 1.0 M perchloric acid (PCA). Polyamines extracted into 0.5 M PCA were analyzed by high performance liquid chromatography (HPLC) on a Hitachi L6000 high-speed liquid chromatograph using a column of cation-exchange resin (Hamana, 2002; Hamana et al., 1995). When a low polyamine level was detected in the PCA extracts, the PCA extracts from a large-scale culture (1 L) were subjected to a cation-exchange Dowex-50W column (Hamana, 2002), and then the concentrated polyamine fractions were analyzed by HPLC.

Class Bacteroidetes (Order Bacteroidales): The class Bacteroidetes is phylogenetically divided into four families, Bacteroidaceae, Porphyromonadaceae, Prevotellaceae and Rikenellaceae (Boone and Castenholz, 2001; Sakamoto, 2007; NCBI website, 2008). Spermidine has been detected as the major polyamine

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in the six genera, *Bacteroides*, *Dysgonomonas*, *Prevotella*, *Porphyomonas*, *Tannerella* and *Marinilabilia* (Hosoya and Hamana, 2004). In the present study on the family Bacteroidaceae, spermidine was found ubiquitously in the new 12 species of the genus *Bacteroides* and an anaerobe, *Anaerorhabdus furcosa* (Table 1), in addition to the authentic 11 *Bacteroides* species previously analyzed (Hosoya and Hamana, 2004). *Megamonas hypermegae*, transferred recently in the phylum Firmicutes (Morotomi et al., 2007), contained cadaverine as a major polyamine (Table 1). 2-Phenylethylamine was found in *B. coprophiles* (Table 1); however, the chemotaxonomic significance of the occurrence of the aromatic amine is not clear. In the family Porphyromonadaceae, the *Barnesiella*, *Dysgonomonas*, *Parabacteroides*, *Paludibacter*, *Porphyomonas* and *Tannerella* species analyzed here, contained spermidine as the major triamine (Table 1). The major polyamine of the other five *Porphyomonas* species was spermidine (Hosoya and Hamana, 2004). A species of the genus *Hallella* and 14 new species of the genus *Prevotella* belonging to the family Prevotellaceae, analyzed in the present study, ubiquitously contained spermidine (Table 1). Spermidine has been detected in 13 other species of *Prevotella* reported in our previous study (Hosoya and Hamana, 2004). *Alistipes putredinis* (formerly *Bacteroides putredinis*) and *Marinilabilia salmonicolor* contained spermidine (Hosoya and Hamana, 2004). *Rikenella microfus* containing homospermidine, located in the fourth family, Rikenellaceae, was unique in the polyamine profiles within the class Bacteroidetes (Hosoya and Hamana, 2004).

Class Flavobacteria (Order Flavobacteriales): *Crocinitomix catalastica* and *Owenweeksia hongkongensis*, which are located in the family Cryomorphaceae (Bernardet et al., 2002; Nakagawa, 2004; NCBI website, 2008), contained homospermidine as the major triamine (Table 1). Homospermidine has been found as the major polyamine in various genera located in the family Flavobacteriaceae (Hamana and Matsuzaki, 1990, 1991; Hamana and Nakagawa, 2001a, b). The mesophilic, slightly halophilic 42 flavobacteria belonging to the recently validated 18 new genera of the family, analyzed in the present study, ubiquitously contained homospermidine (Table 1). Spermidine detected in some species is a minor contaminant from polyamine-containing media used for their cultures. Cadaverine, agmatine, and 2-phenylethylamine have been found sporadically (Hamana and Niitsu, 2001;

Hosoya and Hamana, 2003, 2004). In the previous studies, homospermidine was the major polyamine in 9 other genera, *Bergeyella*, *Empedobacter*, *Gelidibacter*, *Myroides*, *Ornithobacterium*, *Polaribacter*, *Psychroserpens*, *Riemerella*, and *Weeksella* of this family (Hamana and Nakagawa, 2001a, b).

Class Sphingobacteria (Order Sphingobacteriales): In our previous studies, no significant amount of triamines was detected in *Flammeovirga aprica* or *Flammeovirga arenaria* (formerly *Microscilla arenaria*) (Hosoya and Hamana, 2003; Nakagawa et al., 1997). The polyamine analysis of the three new species, *F. yaeyamensis*, *F. kamogawensis* and *Flammeovirga* sp. (Hosoya and Yokota, 2007; Takahashi et al., 2006) and *Sediminitomix flava* (Khan et al., 2007), belonging to the family Flammeovirgaceae, grown in MA, MB and/or polyamine-free 199-SW media, showed a novel triamine-absent profile (Table 1). Low spermidine levels observed in the MA and MB cultures may be derived from the spermidine-containing media. The cellular levels of putrescine, cadaverine and agmatine as a minor polyamine component might be changed by their growth conditions. The absence of triamines in these organisms is unique within this family, and furthermore, within the class Sphingobacteria and the phylum Bacteroidetes. *Rapidithrix* and *Perexilibacter* analyzed here (Table 1) and *Flexithrix* and *Persicobacter* analyzed previously (Hamana and Nakagawa, 2001a, b; Hamana et al., 1995; Nakagawa et al., 1997), belonging to this family, contained spermidine as the major triamine. Slightly/moderately thermophilic *Thermomonema lapsum* containing homospermidine (Hamana et al., 1992) is unique in this family. Spermine (a tetra-amine) and thermopentamine (a penta-amine) found in moderately thermophilic *Acetomicrobium flavidum* (grown at 60°C) of the class Bacteroidetes (Hamana, 1999) were not detected in the slight/moderate thermophile grown at 60°C. Two types of cellular triamine component were observed in the family Flexibacteraceae, suggesting that the family is a chemotaxonomically heterogeneous group. *Algoriphagus*, *Cyclobacterium*, *Flexibacter* and *Hongiella* contained homospermidine, whereas *Dyadobacter*, *Flectobacillus*, *Microscilla*, *Persicitalea* and *Reichenbachella* contained spermidine (Table 1). In the family Saprospiraceae, *Haliscomenobacter* and *Lewinella* species (Hamana and Nakagawa, 2001a) and *Aureispira marina* analyzed in the present study (Table 1), contained spermidine. *Saprospira grandis* containing agmatine as the

Table 1. Cellular polyamine concentrations within the phylum Bacteroidetes.

Organism		Polyamines (μ mol/g wet weight)						
		Put	Cad	Spd	HSpd	Spm	Agm	Pea
Class Bacteroidetes								
Order Bacteroidales								
Family Bacteroidaceae								
<i>Acetomicrobium flavidum</i> ATCC 43122 ^T	(a)	—	—	0.11	—	0.93	—	—
<i>Anaerorhabdus furcosa</i> ATCC 25662 ^T		—	0.25	0.50	—	0.05	—	—
<i>(Anaerorhabdus furcosus, Bacteroides furcosus)</i>								
<i>Bacteroides barnesiiae</i> JCM 13652 ^T		—	—	0.56	—	—	—	—
<i>Bacteroides coagulans</i> JCM 12528 ^T		0.01	—	0.75	—	—	0.04	—
<i>Bacteroides coprocola</i> JCM 12979 ^T		—	0.04	0.40	—	0.02	0.04	—
<i>Bacteroids coprophilus</i> JCM 13818 ^T		—	—	0.77	—	—	0.03	—
<i>Bacteroides coprosuis</i> JCM 13475 ^T		—	0.03	0.60	—	0.02	0.05	0.30
<i>Bacteroides dorei</i> JCM 13471 ^T		—	—	0.85	—	0.02	0.08	—
<i>Bacteroides finegoldii</i> JCM 13345 ^T		—	—	0.67	—	—	0.15	—
<i>Bacteroides gallinarum</i> JCM 13658 ^T		—	—	0.50	—	—	—	—
<i>Bacteroides helcogenes</i> JCM 6297 ^T		0.01	—	0.55	—	—	0.01	—
<i>Bacteroides intestinalis</i> JCM 13265 ^T		—	—	1.15	—	0.01	0.05	—
<i>Bacteroides plebeius</i> JCM 12973 ^T		—	—	0.80	—	0.02	0.02	—
<i>Bacteroides salanitronis</i> JCM 13657 ^T		0.01	—	0.44	—	0.02	—	—
<i>Megamonas hypermegale</i> ATCC 25560 ^T		—	0.40	0.05	—	—	—	—
(Recently placed in the lineage of Firmicutes; Clostridia; Clostririales; “Acidaminococcaceae”; <i>Megamonas</i>)								
Family Porphyromonadaceae								
<i>Barnesiella viscericola</i> JCM 13660 ^T		—	—	0.50	—	—	—	—
<i>Dysgonomonas gadei</i> ATCC BAA-286 ^T	(b)	—	—	0.45	—	—	—	—
<i>Parabacteroides distasonis</i> JCM 5825 ^T	(c)	0.03	—	0.82	—	0.05	0.20	—
<i>Parabacteroides goldsteinii</i> JCM 13446 ^T		—	—	1.10	—	0.01	0.25	—
<i>Parabacteroides merdae</i> JCM 9497 ^T	(b)	—	—	0.55	—	—	0.04	—
<i>Parabacteroides johnsonii</i> JCM 13406 ^T		—	—	0.60	—	—	—	—
<i>Paludibacter propionigenes</i> JCM 13257 ^T		—	—	0.51	—	—	—	—
<i>Porphylomonas canoris</i> JCM 11138 ^T		—	—	0.62	—	—	—	—
<i>Tannerella forsythensis</i> ATCC 43037 ^T	(b)	—	0.10	1.10	—	—	—	—
Family Prevotellaceae								
<i>Hallella seregens</i> ATCC 51272 ^T		—	—	0.45	—	—	—	—
<i>Prevotella albensis</i> JCM 12258 ^T		0.04	—	0.10	—	—	—	—
<i>Prevotella baroniae</i> JCM 13447 ^T		0.04	—	0.50	—	0.01	—	—
<i>Prevotella buccae</i> JCM 12245 ^T		—	0.02	0.05	—	—	—	—
<i>Prevotella buccalis</i> JCM 12246 ^T		0.02	0.01	0.20	—	—	—	—
<i>Prevotella copri</i> JCM 13464 ^T		—	0.01	0.45	—	0.05	—	—
<i>Prevotella denticola</i> JCM 13449 ^T		0.01	0.01	0.20	—	—	—	—
<i>Prevotella marshii</i> JCM 13450 ^T		0.01	—	0.35	—	—	—	—
<i>Prevotella multiformis</i> JCM 12541 ^T		0.04	—	0.27	—	—	—	—
<i>Prevotella multisaccharivorax</i> JCM 12954 ^T		0.01	—	0.33	—	—	—	—
<i>Prevotella paludivivens</i> JCM 13650 ^T		—	—	0.40	—	—	—	—
<i>Prevotella pleuritidis</i> JCM 14110 ^T		—	—	0.37	—	—	—	—
<i>Prevotella salivae</i> JCM 12084 ^T		0.01	—	0.21	—	—	—	—
<i>Prevotella shahii</i> JCM 12083 ^T		0.05	0.01	0.18	—	0.03	—	—
<i>Prevotella stercorea</i> JCM 13469 ^T		—	—	0.85	—	0.03	—	—
Family Rikenellaceae								
<i>Alistipes putredinis</i> ATCC 29800 ^T	(b)	—	—	1.40	—	0.02	—	—
<i>(Bacteroides putredinis)</i>								
<i>Marinilabilia salmonicolor</i> IFO 14957 ^T	(c)	0.01	—	0.70	—	—	—	—

Table 1. Continued.

Organism		Polyamines (μ mol/g wet weight)						
		Put	Cad	Spd	HSpd	Spm	Agm	Pea
<i>biovar agarovorans</i>								
<i>Marinilabilia salmonicolor</i> NCIMB 2216 ^T	(c)	0.05	—	1.25	—	—	—	—
<i>biovar salmonicolor</i>								
<i>Rikenella microfus</i> JCM 2053 ^T	(c)	0.04	—	0.02	2.25	0.05	—	—
Class Flavobacteria								
Order Flavobacteriales								
Family Blattabacteriaceae								
Family Cryomorphaceae								
<i>Crocinitomix catalastica</i> NCIMB 1418 ^T	(i)	—	—	—	1.00	—	—	—
(<i>Flexibacter aggregans</i> subsp. <i>catalaticus</i>)								
<i>Owenweeksia hongkongensis</i> JCM 12287 ^T		0.02	—	—	1.24	—	0.08	—
Family Flavobacteriaceae								
<i>Aquimarina latercula</i> IAM 14305 ^T	(b)	—	0.95	—	0.54	—	1.51	0.64
(<i>Cytophaga latercula</i>)								
<i>Aquimarina intermedica</i> JCM 13506 ^T		—	—	—	0.80	—	—	—
<i>Arenibacter certesii</i> JCM 13507 ^T		—	—	—	0.95	—	0.08	—
<i>Arenibacter palladensis</i> JCM 13509 ^T		—	—	—	1.02	—	0.20	—
<i>Arenibacter troitsensis</i> JCM 11736 ^T		—	—	—	1.26	—	0.33	—
<i>Capnocytophaga haemolytica</i> JCM 8565 ^T	(d)	—	0.18	—	0.80	—	—	—
<i>Capnocytophaga granulosa</i> JCM 8566 ^T	(d)	—	—	—	0.55	—	—	—
<i>Cellulophaga lytica</i> IFO 15985	(b)	—	—	—	1.75	—	0.25	0.06
<i>Cellulophaga pacifica</i> JCM 11735 ^T		—	—	—	1.10	—	—	—
<i>Chimaericella boritolerans</i> NBRC 101277 ^T		—	—	—	0.85	—	—	—
<i>Chryseobacterium daecheungense</i> NBRC 102008 ^T		—	—	—	0.81	—	—	—
<i>Chryseobacterium hispanicum</i> JCM 13554		—	—	—	1.35	—	—	—
<i>Elizabethkingia miricola</i> JCM 11413 ^T		—	—	—	1.30	—	—	—
<i>Flavobacterium glaciei</i> JCM 13953 ^T		—	—	—	1.48	—	—	—
<i>Flavobacterium granuli</i> IAM 15099 ^T		—	—	—	1.25	—	0.04	—
<i>Flavobacterium antarcticum</i> JCM 12383 ^T		—	—	—	0.82	—	—	—
<i>Flavobacterium frigidimar</i> JCM 12218 ^T		—	—	—	0.90	—	—	—
<i>Flavobacterium segetis</i> JCM 12385 ^T		—	—	—	0.95	—	—	—
<i>Flavobacterium weaverense</i> JCM 12384 ^T		—	—	—	0.91	—	—	—
<i>Flavobacterium xinjiangense</i> JCM 11314 ^T		—	—	—	0.50	—	—	—
<i>Galbibacter mesophilus</i> NBRC 101624 ^T		—	—	—	0.97	—	—	—
<i>Gilvibacter sediminis</i> NBRC 10626 ^T		—	—	0.15	0.85	—	—	—
<i>Gramella echinicola</i> JCM 13510 ^T		—	—	—	0.80	—	0.10	—
<i>Gramella portivictoriae</i> JCM 13192 ^T		—	—	—	1.40	—	0.20	—
<i>Kaistella korensis</i> IAM 15050 ^T		—	—	—	0.88	—	—	0.05
<i>Lutibacter litoralis</i> JCM 13034 ^T		—	—	—	0.90	—	0.02	—
<i>Lutimonas vermicola</i> NBRC 102041 ^T		—	—	—	0.87	—	0.10	—
<i>Marixanthomonas ophiuræ</i> JCM 14121 ^T		—	0.01	—	0.66	—	0.07	—
<i>Muricauda aquimarina</i> JCM 11811 ^T		—	—	—	0.62	—	0.03	—
<i>Muricauda flavescens</i> JCM 11812 ^T		—	—	—	0.60	—	0.05	—
<i>Nonlabens tegetincola</i> JCM 12886 ^T		—	—	—	1.10	—	0.23	—
<i>Psychroflexus torquis</i> ATCC 700755 ^T	(h)	0.02	0.01	0.10	1.20	0.01	0.45	0.36
<i>Psychroflexus gondwanensis</i> ATCC 51287 ^T	(h)	—	—	0.10	1.07	0.01	0.01	—
<i>Salegentibacter salegens</i> NCIMB 13461 ^T	(i)	—	—	—	0.80	—	0.88	—
<i>Salegentibacter catena</i> JCM 14015 ^T		—	—	—	1.15	—	—	—
<i>Salegentibacter mishustinæ</i> NBRC 100592 ^T		—	—	—	0.90	—	0.06	—
<i>Salegentibacter halothuriorum</i> NBRC 100249 ^T		—	—	—	0.59	—	0.06	—

Table 1. Continued.

Organism		Polyamines (μ mol/g wet weight)						
		Put	Cad	Spd	HSpd	Spm	Agm	Pea
<i>Sediminibacter furfurosus</i> NBRC 101622 ^T		—	—	—	0.96	—	0.10	—
<i>Sejongia antarctica</i> JCM 12381 ^T		—	—	—	0.87	—	—	—
<i>Sejongia jeonii</i> JCM 12382 ^T		—	—	—	1.15	—	—	—
<i>Stenothermobacter spongiae</i> JCM 13191 ^T		0.02	0.10	—	0.97	—	0.20	—
<i>Tamlana crocina</i> JCM 14021 ^T		—	—	—	1.05	—	0.25	—
<i>Tenacibaculum amylolyticum</i> IFO 16310 ^T	(b)	—	0.05	—	1.00	—	0.69	0.90
<i>Tenacibaculum maritimum</i> IFO 15946 ^T	(b)	0.04	0.10	0.01	0.59	—	0.31	0.07
<i>Tenacibaculum mesophilum</i> IFO 16307 ^T	(b)	—	0.05	—	1.40	—	0.45	0.45
<i>Tenacibaculum ovolyticum</i> IAM 14318 ^T	(b)	—	—	—	1.10	—	0.19	—
<i>Tenacibaculum aesturarii</i> JCM 13491 ^T		0.04	—	—	0.95	—	0.25	—
<i>Tenacibaculum litoreum</i> JCM 13039 ^T		—	0.02	—	1.20	—	0.10	—
<i>Vitellibacter vladivostokensis</i> JCM 11732 ^T		0.02	—	—	0.75	—	—	—
<i>Winogradskyella poriferorum</i> JCM 12885 ^T		—	—	—	0.80	—	0.22	—
<i>Yeosuana aromativorans</i> JCM 12862 ^T		—	—	—	1.15	—	0.05	—
<i>Zeaxanthimibacter enoshimensis</i> NBRC 101990 ^T		—	—	—	1.20	—	0.05	—
<i>Zhouria amylolytica</i> JCM 14016 ^T		—	—	—	1.25	—	0.30	—
<i>Zobellia uliginosa</i> IAM 14312 ^T	(b)	0.05	—	—	0.90	—	—	—
Class Sphingobacteria								
Order Sphingobacteriales								
Family Flammeovirgaceae								
<i>Flammeovirga aprica</i> IAM 14298 ^T	(e)	—	0.03	—	—	—	—	—
<i>Flammeovirga arenaria</i> IFO 15982 ^T	(e)	0.12	0.08	—	—	—	—	—
(<i>Microscilla arenaria</i>)								
<i>Flammeovirga kamogawensis</i> JCM 23196 ^T	(MA)	—	—	0.03	—	—	0.01	—
	(MB)	—	—	0.07	—	—	0.03	—
	(199-SW)	—	0.11	—	—	—	0.05	—
<i>Flammeovirga yaeyamensis</i> NBRC 100898 ^T	(MB)	—	—	0.03	—	—	—	—
	(199-SW)	—	—	—	—	—	—	—
<i>Flammeovirga</i> sp. NBRC 100889	(MB)	—	—	—	—	—	—	—
<i>Rapidithrix thailandica</i> JCM 23209 ^T	(MB)	—	—	1.30	—	—	0.60	—
	(199-SW)	—	—	1.10	—	—	0.06	—
<i>Flexithrix dorotheae</i> IFO 15987 ^T	(d)	0.01	—	0.56	—	—	0.95	—
<i>Flexithrix dorotheae</i> IAM 14894	(i)	—	—	1.25	—	—	—	—
(<i>Flexibacter aggregans</i> NCIMB 1443)								
<i>Perexilbacter aurantiacus</i> JCM 23194 ^T		—	—	0.54	—	—	0.10	—
<i>Persicobacter diffuens</i> NCIMB 1402 ^T	(c)	0.20	—	2.30	—	—	—	—
<i>Sediminitomix flava</i> NBRC 101625 ^T		—	0.03	0.08	—	—	0.01	—
<i>Thermonema lapsus</i> ATCC 43542 ^T	(f)	—	—	—	0.45	—	—	—
Family Flexibacteraceae								
<i>Algoriphagus locialis</i> JCM 12597 ^T		—	—	—	1.07	—	0.05	—
<i>Algoriphagus winogradskyi</i> JCM 13505 ^T		—	—	—	1.70	—	0.25	—
<i>Algoriphagus yeomjeoni</i> JCM 12598 ^T		—	—	—	1.03	—	—	—
<i>Cyclobacterium lianum</i> JCM 14011 ^T		—	—	—	1.25	—	0.05	—
<i>Cyclobacterium marinum</i> NCIMB 1802 ^T	(d)	—	—	—	1.05	—	0.05	—
<i>Dyadobacter fermentans</i> ATCC 700827 ^T	(b)	0.02	0.01	0.72	—	0.08	—	—
<i>Dyadobacter hamtensis</i> JCM 12919 ^T		0.90	—	0.71	—	—	—	—
<i>Dyadobacter beijingensis</i> JCM 14200 ^T		—	—	0.62	—	—	—	—
<i>Dyadobacter koreensis</i> NBRC 101116 ^T		—	—	0.70	—	—	—	—
<i>Flectobacillus lacus</i> JCM 13398 ^T		—	—	0.90	—	—	—	—
<i>Flexibacter flexilis</i> IFO 16026	(c)	0.01	—	—	1.14	—	—	—

Table 1. Continued.

Organism		Polyamines (μ mol/g wet weight)						
		Put	Cad	Spd	HSpd	Spm	Agm	Pea
<i>Hongiella marincola</i> JCM 12319 ^T		—	—	—	0.49	—	—	—
<i>Microscilla marina</i> IFO 16042 ^T	(b)	0.16	0.50	0.30	—	—	0.02	0.08
<i>Persicitalea jodogahamensis</i> JCM 23159 ^T		—	—	0.35	—	—	0.09	—
<i>Reichenbachella agariperforans</i> JCM 11238 ^T		—	—	0.78	—	—	0.20	—
Family Saprospiraceae								
<i>Aureispira marina</i> JCM 23197 ^T		—	—	1.22	—	—	—	—
<i>Haliscomenobacter hydrossis</i> ATCC 27775 ^T	(d)	—	—	0.95	—	—	—	—
<i>Lewinella cohaerens</i> ATCC 23123 ^T	(d)	—	—	1.02	—	0.04	—	—
<i>Lewinella nigricans</i> ATCC 23147 ^T	(d)	—	—	1.35	—	0.15	—	—
<i>Lewinella persicus</i> ATCC 23167 ^T	(d)	—	—	0.89	—	0.09	—	—
<i>Saprospira grandis</i> NCIMB 1363 ^T	(e)	0.03	—	—	—	0.01	0.75	—
Family Sphingobacteriaceae								
<i>Pedobacter aquatilis</i> JCM 13454 ^T		—	—	—	1.10	—	—	—
<i>Pedobacter himalayensis</i> JCM 12171 ^T		—	—	—	0.80	—	—	—
<i>Pedobacter lentus</i> JCM 14593 ^T		—	—	—	0.77	—	—	—
<i>Pedobacter roseus</i> JCM 13399 ^T		—	0.15	—	1.20	—	—	—
<i>Pedobacter saltans</i> JCM 21818 ^T		—	—	—	0.80	—	—	—
<i>Pedobacter terricola</i> JCM 14594 ^T		—	—	—	0.75	—	—	—
<i>Roseivirga ehrenbergii</i> JCM 13514 ^T		—	—	0.75	0.17	—	0.20	—
<i>Roseivirga seohaensis</i> JCM 12600 ^T		—	—	0.42	0.12	—	0.05	—
<i>Roseivirga spongicola</i> JCM 13337 ^T		0.02	—	0.68	0.10	—	0.20	—
Sphingobacteriales genera incertae sedis (Family "Crenotrichaceae")								
<i>Chitinophaga pinensis</i> IFO 15968 ^T	(d)	—	—	—	0.88	—	—	—
<i>Rhodothermus marinus</i> ATCC 43821 ^T	(f)	0.02	0.02	1.05	—	0.60	—	—
<i>Rhodothermus marinus</i> JCM 9785	(g)	—	—	0.40	—	0.46	—	—
(<i>Rhodothermus obamensis</i>)		—	—	—	—	—	—	—
<i>Salinibacter ruber</i> ATCC BAA-605 ^T		—	0.01	0.05	0.05	—	—	—

Put, putrescine; Cad, cadaverine; Spd, spermidine; HSpd, homospermidine; Spm, spermine; Agm, agmatine; Pea, 2-phenylethylamine; ATCC, American Type Culture Collection, Manassas, Virginia, USA; IAM, IAM Culture Collection, Institute of Molecular and Cellular Biosciences, The University of Tokyo, Tokyo, Japan; IFO, Institute for Fermentation, Osaka, Japan; JCM, Japan Collection of Microorganisms, RIKEN, Saitama, Japan; NBRC, Biological Resource Center, National Institute of Technology and Evaluation, Kisarazu, Japan; NCIMB, The National Collection of Industrial, Marine and Food Bacteria, Aberdeen, Scotland, UK; ^T, type strain; —, not detected (<0.005). Data were obtained from single samples. Former names are shown in parentheses. Double quotation marks show that the scientific name has not been validated. (MA), (MB) and (199-SW), cultured in Marine Agar, Marine Broth, and polyamine-free Synthetic 199 Medium dissolved in seawater, respectively. (a) Cited from Hamana, 1999. (b) Hosoya and Hamana, 2004. (c) Hamana et al., 1995. (d) Hamana and Nakagawa, 2001a. (e) Hosoya and Hamana, 2003. (f) Hamana et al., 1992. (g) Hamana et al., 1998. (h) Hamana and Niitsu, 2001. (i) Hamana and Nakagawa, 2001b. Penta-amines and hexa-amines found in the thermophiles, *Acetomicrobium flavidum* and *Rhodothermus marinus*, previously reported, were omitted in the table.

major polyamine, lacks tiamine synthetic ability (Hamana and Nakagawa, 2001a) and is unique within the phylum Bacteroidetes. The polyamine distribution pattern of the new genus *Roseivirga* of the family Sphingobacteriaceae shows a novel profile containing spermidine and homospermidine (Table 1). Six new species of *Pedobacter* (Table 1) and *P. heparinus*, *P. piscium* and 6 species of *Sphingobacterium* analyzed previously (Hamana and Nakagawa, 2001b), contained ho-

mospermidine. In the tentative family "Crenotrichaceae" (Anton et al., 2002; Mongodin et al., 2005; Pena et al., 2005; Soria-Carrasco et al., 2007), homospermidine has been known as the major polyamine of *Chitinophaga* species (Hamana and Nakagawa, 2001a). The low spermidine and homospermidine concentrations in a novel mesophilic, extremely halophilic *Salinibacter ruber*, are agreement with another report on the cellular polyamines of this organism (Pena et al., 2005).

The polyamine catalogue differ from the observations for extremely halophilic archaeobacteria consisting the order Halobacteriales (Tanaka et al., 2002) and the moderately halophilic eubacterial order Halanaerobiales of the phylum Firmicutes (Hosoya et al., 2006). Homospermidine was not found whereas low spermidine and/or spermine levels were detected in the orders Halobacteriales and Halanaerobiales. The rRNA sequences of *S. ruber* most closely related to the slightly halophilic, extremely thermophilic genus *Rhodothermus*, but the polyamine profile was markedly differentiated between *S. ruber* and *R. marinus* (Hamana et al., 1992, 1998). *R. marinus* grown at 70°C contained spermidine, spermine, thermopentamine and branched *N*⁴-bis(aminopropyl)spermidine, indicating that the occurrence of the tetra-amine and penta-amines correlate to its extremely thermophily (Hamana et al., 1992, 1998).

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