

Polyamine Profiles of Some Members of the Alpha Subclass of the Class *Proteobacteria*: Polyamine Analysis of Twenty Recently Described Genera

Koei Hamana^{1)*}, Azusa Sakamoto¹⁾, Satomi Tachiyanagi¹⁾,
Eri Terauchi¹⁾ and Mariko Takeuchi²⁾

¹⁾ Department of Laboratory Sciences, School of Health Sciences, Faculty of Medicine, Gunma University, 39-15 Showa-machi 3-chome, Maebashi, Gunma 371-8514, Japan

²⁾ Institute for Fermentation, Osaka, 17-85, Juso-honmachi 2-chome, Yodogawa-ku, Osaka, 532-8686, Japan

Cellular polyamines of 41 newly validated or reclassified alpha proteobacteria belonging to 20 genera were analyzed by HPLC. Acetic acid bacteria belonging to the new genus *Asaia* and the genera *Gluconobacter*, *Gluconacetobacter*, *Acetobacter* and *Acidomonas* of the alpha-1 subgroup ubiquitously contained spermidine as the major polyamine. Aerobic bacteriochlorophyll *a*-containing *Acidisphaera*, *Craurococcus* and *Paracraurococcus* (alpha-1) and *Roseibium* (alpha-2) contained spermidine and lacked homospermidine. New *Rhizobium* species, including some species transferred from the genera *Agrobacterium* and *Allorhizobium*, and new *Sinorhizobium* and *Mesorhizobium* species of the alpha-2 subgroup contained homospermidine as a major polyamine. Homospermidine was the major polyamine in the genera *Oligotropha*, *Carbophilus*, *Zavarzinia*, *Blastobacter*, *Starkeya* and *Rhodoblastus* of the alpha-2 subgroup. *Rhodobaca bogoriensis* of the alpha-3 subgroup contained spermidine. Within the alpha-4 subgroup, the genus *Sphingomonas* has been divided into four clusters, and species of the emended *Sphingomonas* (cluster I) contained homospermidine whereas those of the three newly described genera *Sphingobium*, *Novosphingobium* and *Sphingopyxis* (corresponding to clusters II, III and IV of the former *Sphingomonas*) ubiquitously contained spermidine. The distribution of the triamines, spermidine and homospermidine, serves as a phenotypic chemotaxonomic marker within the alpha subclass of *Proteobacteria*.

Key words : polyamine, spermidine, homospermidine, proteobacteria

INTRODUCTION

Cellular polyamine compositions have been shown to serve as chemotaxonomic markers within the alpha, beta, gamma, delta and epsilon subclasses of the class *Proteobacteria* (2, 7-18). The distribution of the two triamines, spermidine and homospermidine, within alpha proteobacteria which are phylo-

genetically composed of four subgroups, correlated with their phylogenetic classifications (17, 18). Another triamine, norspermidine, which is the major polyamine in some gamma proteobacteria, has never been detected in the alpha subclass of *Proteobacteria*. The absence of homospermidine within the alpha-3 subgroup was suggested by the previous analyses of seven genera of this subgroup (17, 18). The distribution of homospermidine and/or spermidine within

* Correspondence author

15 genera of subgroup-1, 10 genera of subgroup-2 and 8 genera of subgroup-4 were described (17, 18).

Recently, new members of alpha proteobacteria belonging to the 20 genera, *Asaia*, *Gluconobacter*, *Gluconacetobacter*, *Acetobacter*, *Acidomonas*, *Acidosphaera*, *Craurococcus*, *Paracraurococcus* (subgroup-1), *Roseibium*, *Rhizobium*, *Sinorhizobium*, *Mesorhizobium*, *Blastobacter*, *Oligotropha*, *Carbophilus*, *Zavarzinia*, *Starkeya*, *Rhodoblastus* (subgroup-2), *Rhodobaca* (subgroup-3), and *Sphingomonas* (subgroup-4) were described. To establish additional polyamine catalogues of the alpha subclass of *Proteobacteria*, cellular polyamines of the reclassified and newly validated 41 alpha proteobacteria belonging to the 20 genera, have been analyzed in the present study.

MATERIALS AND METHODS

Alpha proteobacteria were cultivated in the media designated in the list of culture collections as shown by Medium No., the organic complex media such as Nutrient broth (NB) (Nissui Pharmaceutical Co., Ltd., Tokyo, Japan), Trypticase soy broth (TSB) (BBL, Bectone Dickinson and Company, Cockeysville, MD, USA) and peptone-yeast extract medium (PY), and the synthetic 199 medium (Nissui Pharmaceutical Co., Ltd., Tokyo, Japan). Stationary growing cells at the optimum growth temperature were harvested by centrifugation. The pellets of organisms were homogenized in 0.5 M perchloric acid (HClO₄) at 2 °C. Polyamines were extracted into HClO₄ and analyzed by high-performance liquid chromatography (HPLC) on an L6000 High-Speed Liquid Chromatograph (Hitachi Ltd., Tokyo, Japan) (17, 18). 2-Hydroxyputrescine, 1,3-diaminopropane, putrescine, cadaverine, spermidine, norspermidine, homospermidine, agmatine and spermine were separately eluted in the HPLC.

RESULTS AND DISCUSSION

Some typical chromatograms of HPLC are shown in Fig. 1. Estimated cellular concentrations of putrescine, cadaverine, spermidine, homospermidine and agmatine are listed in Table 1. Other polyamines such as diaminopropane, norspermidine, spermine

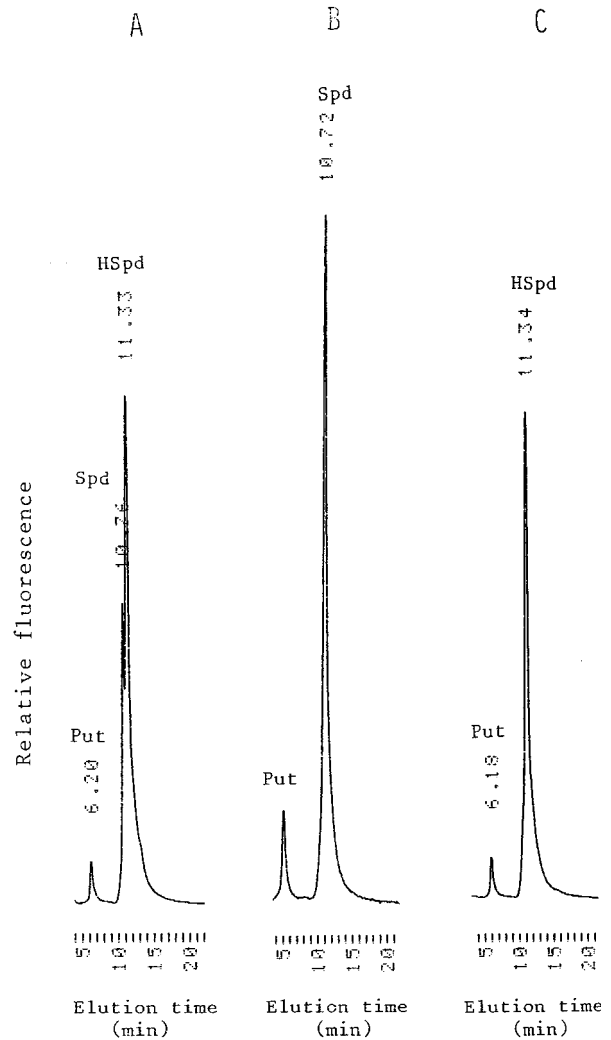


Fig. 1. HPLC analysis of polyamines extracted from *Blastobacter aggregatus* NCIMB 12290(A), *B. capsulatus* NCIMB 12291(B) and *B. denitrificans* NCIMB 12292(C).

Printed numbers on elution peaks indicate the elution time (min) of the peak. Abbreviations for polyamines are shown in Table 1.

and hydroxypolyamines were not found.

Subgroup-1

Phylogenetic analysis of *Asaia bogorensis* and *A. siamensis* indicated that the two species are located in the acetic acid bacteria lineage, but distant from the genera *Acetobacter*, *Gluconobacter*, *Gluconacetobacter* and *Acidomonas* within the alpha-1 subgroup (23, 38). Spermidine was the major polyamine in the

two species of *Asaia* and six new species of *Acetobacter* (27), as well as the other species belonging to *Acetobacter*, *Gluconobacter*, *Gluconacetobacter* and *Acidomonas* (8, 11). The same polyamine patterns were obtained in the 15 strains within 7 species of *Gluconobacter* including the duplicate type strains deposited in IAM and IFO, indicating that polyamine composition is invariable within the genus *Gluconobacter*.

Spermidine was the major polyamine in *Acidisphaera rubrifaciens*, *Craurococcus roseus* and *Paracraurococcus ruber* containing bacteriochlorophyll *a*. *A. rubrifaciens* is the closest relative to an anaerobic phototrophic bacterium, *Rhodospira globiformis* (19), however, *R. globiformis* contains spermidine and homospermidine (18). *C. roseus* and *P. ruber* are phylogenetically related to *Roseococcus thio-sulfatophilus* (30), which is an aerobic bacteriochlorophyll *a*-containing bacterium and contains spermidine as the major polyamine (17).

Subgroup - 2

Two species of *Roseibium*, which is an aerobic bacteriochlorophyll *a*-containing bacterium belonging to the alpha-2 subgroup (32), contained putrescine, cadaverine and spermidine. Although the *Roseibium* species are phylogenetically related to *Stappia stellulata* and *Stappia agregata* (32), the *Stappia* species contain putrescine and spermidine without cadaverine (17).

Three carboxidotrophic alpha-2 proteobacteria, *Oligotropha carboxidovorans*, *Carbophilus carboxidus* and *Zavarzinia compransoris*, were transferred from *Pseudomonas*, *Alcaligenes* and *Pseudomonas*, respectively (28). Homospermidine was the major polyamine in the three species, as shown in the present study and another previous report (28). In contrast, authentic species of the genus *Pseudomonas* (gamma subclass) and the genus *Alcaligenes* (beta subclass) lack homospermidine (18).

Rhizobium and *Sinorhizobium* consisting of the family *Rhizobiaceae*, and *Mesorhizobium* and *Phyllobacterium* belonging to the family *Phyllobacteriaceae*, are located in the alpha-2 subgroup (4, 22, 37). Recently, all species of *Agrobacterium* and

Allorhizobium undicola (3) were reclassified into the genus *Rhizobium* (37). The four genera, *Rhizobium*, *Sinorhizobium*, *Mesorhizobium* and *Phyllobacterium*, as well as the other rhizobia, *Azorhizobium* and *Bradyrhizobium*, are phylogenetically divergent within the alpha-2 subgroup and they contain putrescine and homospermidine as the major polyamine (13, 17, 18). Besides, a significant amount of spermidine was sporadically detected in some species of *Rhizobium* and *Sinorhizobium*.

Blastobacter aggregatus and *Blastobacter capsulatus* are closely related to each other and to *Rhizobium*, and *Blastobacter denitrificans* is closely related to *Bradyrhizobium* (20). *B. aggregatus* contained spermidine and homospermidine, as found in a polyamine profile of some *Rhizobium* species. *B. capsulatus* contained spermidine, and corresponds to another polyamine profile found in *Rhizobium* species. The polyamine profile of *B. denitrificans* containing homospermidine was similar to that of *Bradyrhizobium* species (13). *Starkeya novella* transferred from the genus *Thiobacillus* (24) and *Rhodoplastus acidophilus* transferred from the genus *Rhodopseudomonas* (21) contained homospermidine.

Subgroup - 3

Rhodobaca bogoriensis, an alkaliphilic alpha-3 proteobacterium, was phylogenetically located in *Rhodobacter/Rhodovulum* clade (29). *R. bogoriensis* as well as *Rhodobacter* and *Rhodovulum* species (17) contained putrescine and spermidine.

Subgroup - 4

Former *Sphingomonas* species belonging to the alpha-4 subgroup (the family *Sphingomonadaceae*) were divided into four clusters by rDNA sequence similarity (33). In the previous study, 13 species belonging to the genus *Sphingomonas* sensu stricto (cluster I) ubiquitously contained homospermidine as the major polyamine whereas three species of cluster II (genus *Sphingobium*), six species of cluster III (genus *Novosphingobium*) and three species of cluster IV (genus *Sphingopyxis*) contained spermidine (33). In the present study, *Sphingomonas roseiflava*, *Sphingomonas* sp. MK329, *Sphingomonas* sp.

Table 1. Polyamine concentration within the alpha subclass of *Proteobacteria*

Organism	Medium	Temp (°C)	Polyamines (μ mol/g wet cell)				
			Put	Cad	Spd	HSpd	Agm
Subgroup-1							
<i>Asaia bogorensis</i>	JCM 10569 ^T	97-30	0.03	—	0.75	—	—
<i>Asaia siamensis</i>	JCM 10715 ^T	97-30	0.04	—	1.02	—	—
<i>Gluconobacter asaii</i>	IAM 14721 ^T	B6-30	0.08	—	1.27	—	—
	IFO 3276 ^T	(b)	0.05	—	0.55	—	—
<i>Gluconobacter frateurii</i>	IAM 1816	B6-25	0.08	—	0.86	—	—
	IAM 1830	B6-25	0.04	—	0.80	—	—
	IFO 3264 ^T	(b)	0.05	—	1.55	—	—
<i>Gluconobacter oxydans</i>	IAM 14436 ^T	B6-25	0.15	—	1.75	—	—
	IAM 1829	(a)	0.01	—	0.85	—	—
	IFO 14819 ^T	(a)	0.03	—	0.74	—	—
	IFO 12467	(b)	0.04	—	0.80	—	—
	IFO 3170	(b)	0.04	—	1.20	—	—
<i>Gluconobacter cerinus</i>	IFO 3267 ^T	(a)	0.21	—	1.25	—	—
	IAM 1832	(a)	0.12	—	2.20	—	—
<i>Gluconacetobacter xylinus</i> (<i>Acetobacter xylinum</i>)	IFO 15237 ^T	(b)	0.02	—	0.50	—	—
<i>Gluconacetobacter hansenii</i> (<i>Acetobacter hansenii</i>)	IFO 14820 ^T	(a)	0.05	—	1.10	—	—
<i>Gluconacetobacter liquefaciens</i> (<i>Acetobacter liquefaciens</i>)	IFO 12388 ^T	(a)	0.08	—	0.74	—	—
<i>Acetobacter estunensis</i>	IFO 13751 ^T	804-30	—	—	1.42	—	—
<i>Acetobacter indonesiensis</i>	IFO 16471 ^T	804-30	0.02	—	1.30	—	—
<i>Acetobacter lovaniensis</i>	IFO 13753 ^T	804-30	—	—	1.40	—	—
<i>Acetobacter orleanensis</i>	IFO 13752 ^T	804-30	—	—	1.45	—	—
<i>Acetobacter peroxydans</i>	IFO 13755 ^T	804-30	—	—	1.33	—	—
<i>Acetobacter tropicalis</i>	IFO 16470 ^T	804-30	0.01	—	1.50	—	—
<i>Acetobacter aceti</i>	IFO 14818 ^T	(a)	0.08	—	0.50	—	—
	IAM 1802	(a)	0.21	—	0.90	—	—
<i>Acetobacter pasteurianus</i>	IFO 14814	(a)	0.08	—	1.35	—	—
<i>Acidomonas mthanolica</i>	JCM 6891 ^T	(b)	0.10	—	1.75	—	—
<i>Acidisphaera rubrifaciens</i>	JCM 10600 ^T	270-30	—	—	1.15	—	—
<i>Craurococcus roseus</i>	JCM 9933 ^T	NB-30	0.10	0.05	0.70	—	—
<i>Paracraurococcus ruber</i>	JCM 9931 ^T	NB-30	0.12	0.03	0.80	—	—
Subgroup-2							
<i>Roseibium denhamense</i>	JCM 10543 ^T	41-30	0.91	0.30	0.99	—	—
<i>Roseibium hamelinense</i>	JCM 10544 ^T	41-30	0.90	0.15	1.43	—	—
<i>Oligotropha carboxidovorans</i>	ATCC 49405 ^T	1789-30	0.07	—	—	0.97	—
<i>Carbophilus carboxidus</i>	ATCC 51424 ^T	1932-30	0.75	—	—	0.60	—
<i>Zavarzinia compransoris</i>	ATCC 51430 ^T	1932-30	0.35	—	—	0.85	—
<i>Sinorhizobium sahelense</i> (<i>S. sahelii</i>)	NCIMB 13341 ^T	199-30	0.42	—	—	1.24	—
<i>Sinorhizobium teranga</i> (<i>S. teranga</i>)	NCIMB 13342 ^T	199-30	0.10	—	—	1.05	—
	IAM 13623	(c)	0.13	—	—	1.60	—
<i>Sinorhizobium xinjiangense</i> (<i>S. xinjiangensis</i>)	IAM 14142 ^T	(d)	—	—	0.05	0.60	—
<i>Sinorhizobium fredii</i>	IAM 13625 ^T	(c)	0.03	—	—	1.20	—
<i>Sinorhizobium meliloti</i>	IAM 12611 ^T	(c)	0.15	0.03	0.90	0.55	—
<i>Rhizobium undicola</i> (<i>Allorhizobium undicola</i>)	ATCC 700741 ^T	2122-28	0.03	—	0.95	0.20	—
<i>Rhizobium radiobacter</i> (<i>Agrobacterium radiobacter</i>) (<i>Agrobacterium tumefaciens</i>)	IAM 12048 ^T	(e)	0.08	—	2.65	0.06	—
<i>Rhizobium rhizogenes</i>	IFO 13257 ^T	(e)	0.15	—	—	1.55	—

<i>(Agrobacterium rhizogenes)</i>								
<i>Rhizobium rubi</i>	IFO 13261 ^T	(e)	0.16	–	1.82	0.05	–	
<i>(Agrobacterium rubi)</i>								
<i>Rhizobium vitis</i>	IFO 15140 ^T	(e)	0.05	–	1.07	0.17	–	
<i>(Agrobacterium vitis)</i>								
<i>Rhizobium galegae</i>	IAM 13631 ^T	(c)	0.01	–	–	1.20	–	
<i>Rhizobium tropici</i>	IFO 15247 ^T	(d)	0.04	–	–	0.50	–	
<i>Rhizobium leguminosarum</i>	IAM 12609 ^T	(d)	0.06	0.03	–	1.00	–	
<i>Rhizobium etli</i>	IFO 15573 ^T	(d)	0.10	–	0.08	0.94	–	
<i>Mesorhizobium ciceri</i>	NCIMB 13356 ^T	408–28	0.15	0.02	–	1.35	–	
<i>Mesorhizobium loti</i>	IAM 13588 ^T	(c)	0.08	–	–	2.20	–	
<i>Mesorhizobium huakuii</i>	IFO 15243 ^T	(d)	0.08	0.18	–	0.64	–	
<i>Blastobacter aggregatus</i>	NCIMB 12290 ^T	334–25	0.08	–	0.35	0.92	–	
<i>Blastobacter capsulatus</i>	NCIMB 12291 ^T	334–25	0.18	–	1.20	–	–	
<i>Blastobacter denitrificans</i>	NCIMB 12292 ^T	272–30	0.08	–	–	0.89	–	
<i>Starkeya novella</i>	IAM 12100 ^T	(f)	0.16	–	–	0.12	–	
<i>(Thiobacillus novellus)</i>								
<i>Rhodoblastus acidophilus</i>	NCIMB 11761 ^T	(g)	0.15	–	–	2.40	–	
<i>(Rhodopseudomonas acidophila)</i>								
Subgroup–3								
<i>Rhodobaca bogoriensis</i>	ATCC 700920 ^T	2193–35	0.02	–	1.05	–	–	
Subgroup–4								
<i>(Sphingomonas cluster I)</i>								
<i>Sphingomonas roseiflava</i>	IAM 14823 ^T	B38–25	–	–	–	1.20	–	
<i>Sphingomonas aquatilis</i>	IFO 16141 ^T	PY–30	0.02	–	1.30	–	0.04	
		199–30	0.10	–	2.07	–	0.08	
<i>Sphingomonas koreensis</i>	IFO 16142 ^T	PY–30	0.02	–	0.96	–	0.02	
		199–30	–	–	0.90	–	0.04	
<i>Sphingomonas</i> sp.	IAM 14822 (=MK329)	B38–25	–	–	–	1.37	–	
		IAM 14824 (=MK346)	B38–25	–	–	–	1.57	–
		IAM 14825 (=MK347)	B38–25	–	–	–	1.40	0.02
		IAM 14826 (=MK355)	B38–25	–	–	–	1.40	0.04
<i>(Sphingomonas cluster II)</i>								
“ <i>Sphingomonas abikonensis</i> ”	IFO 16140	PY–30	–	–	1.08	–	–	
(“ <i>Pseudomonas abikonensis</i> ”)		199–30	–	–	1.50	–	0.15	
	IAM 12404	B1–30	–	–	1.14	–	0.04	
<i>Sphingomonas cloacae</i>	IAM 14885 ^T	NB–30	–	–	1.12	–	–	
<i>Sphingomonas wittichii</i>	JCM 10273 ^T	TSB–25	–	0.10	0.75	–	0.10	
<i>(Sphingomonas cluster IV)</i>								
<i>Sphingomonas taejonensis</i>	IFO 16144 ^T	PY–30	0.04	–	1.37	–	0.04	
		199–30	0.02	–	0.97	–	0.04	
<i>Sphingomonas</i> sp.	IFO 15917 (=Cu–D)	PY–30	0.01	–	0.95	–	0.04	

Note : Put, putrescine ; Cad, cadaverine ; Spd, spermidine ; HSpd, homospermidine ; Spm, spermine ; Agm, agmatine ; IAM, IAM Culture Collection, Institute of Molecular and Cellular Biosciences, The University of Tokyo, Tokyo, Japan ; JCM, Japan Collection of Microorganisms, RIKEN, Saitama, Japan ; Institute for Fermentation, Osaka, Japan ; NCIMB, The National Collections of Industrial and Marine Bacteria, Aberdeen, Scotland, UK ; ATCC, American Type Culture Collection, Manassas, Virginia, USA ; ^T, Type strain ; –, not detectable (<0.005). Former names are shown in parentheses. Quotation marks indicate the scientific name has been validly published. a, cited from Hamana and Matsuzaki (11). b, cited from Hamana and Kishimoto (8). c, cited from Hamana et al. (13). d, cited from Hamana and Takeuchi (18). e, cited from Hamana et al. (12). f, cited from Hamana and Matsuzaki (9). g, cited from Hamana et al. (17).

MK346, *Sphingomonas* sp. MK347 and *Sphingomonas* sp. MK355 belonging to cluster I (39) contained homospermidine. However, spermidine was the major polyamine in *S. aquatilis* and *S. koreensis* located in cluster I (26), indicating the first report on the occurrence of spermidine in cluster I. *S. cloacae* (6), *S. wittichi* (36) and “*S. abikonensis*” (1) belonging to cluster II and *S. taejonensis* (26) and *Sphingomonas* sp. Cu-D (33) belonging to cluster IV contained spermidine.

Distribution of spermidine and homospermidine

Three triamine-distribution types: spermidine-type, homospermidine-type, and spermidine and homospermidine-type, have been found in the alpha-1 subgroup. Spermidine was the major polyamine in all eight genera, analyzed in the present study, *Asaia*, *Gluconobacter*, *Gluconacetobacter*, *Acetobacter*, *Acidomonas*, *Acidisphaera*, *Craurococcus* and *Paracraurococcus*. The other 11 genera of this subgroup, *Acidophilum*, *Aquaspirillum*, *Azospirillum*, *Magnetospirillum*, *Phaeospirillum*, *Rhodocista*, *Rhodopila*, *Rhodospirillum*, *Rhodothalassium*, *Rhodovibrio* and *Roseococcus*, are each one of the three types (14, 17, 18).

Within the alpha-2 subgroup analyzed in the present study, the three triamine-distribution types were observed. *Roseibium* contained spermidine alone. *Oligotropha*, *Carbophilus*, *Zavarzinia*, *Starkeya*, *Rhodoblastus* and *Mesorhizobium* contained homospermidine alone. In addition to homospermidine-type, spermidine and homospermidine-type was found in *Sinorhizobium*, *Rhizobium* and *Blastobacter* species. As shown previously, *Azorhizobium*, *Bradyrhizobium*, *Phyllobacterium*, *Caulobacter*, *Maricaulis*, *Ancalomicrobium*, *Nitrobacter*, *Xanthobacter*, and the phototrophs, *Rhodopseudomonas* and *Blastochloris*, are homospermidine-type (13, 17, 18). The 11 genera *Stappia*, *Ahrensia*, *Aquabacter*, *Hypomicrobium*, *Firomicrobium*, *Pedomicrobium*, *Hyphomonas*, *Dicotomicrobium*, *Rhodomicrobium*, *Ochrobacterium* and *Devosia*, are spermidine-type (17, 18). From the viewpoint of the present and previous analyses, single types of the triamine profiles occur in each of the genera within the alpha-2 sub-

group. Exceptionally, however, two triamine types (*i.e.* spermidine-dominant type and homospermidine-dominant type) have been observed in the genera *Rhodobium*, *Brebundimonas* and *Rhodoplanes* (17, 18).

Spermidine-dominant profiles have been found in all seven genera, *Paracoccus*, *Rhodobacter*, *Rhodovulum*, *Roseobacter*, *Rubrimonas*, *Roseivivax* and *Ruegeria*, analyzed in the alpha-3 subgroup (17, 18). In the present analysis, a new *Rhodobaca* species belonging to this subgroup contained spermidine alone, suggesting that the absence of homospermidine is a feature of this subgroup.

Within the alpha-4 subgroup, spermidine was widely distributed in the six genera *Porphyrobacter*, *Erythrobacter*, *Erythromicrobium*, *Blastomonas*, *Rhizomonas* and *Erythromonas* (17, 18, 33, 34) and new genera *Sphingobium*, *Novosphingobium* and *Sphingopyxis* (33). The occurrence of homospermidine was restricted in *Zymomonas* and *Sphingomonas* species within this subgroup (33, 34), although the polyamine type of the latter genus was found to be heterogeneous as shown in this study.

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α サブクラスに属する数種のプロテオバクテリアにおけるポリアミン構成：
近年記載された20属についてのポリアミン分析

浜名康栄¹⁾, 坂本 梓¹⁾, 立柳聡美¹⁾, 寺内恵里¹⁾, 武内真理子²⁾

¹⁾ 群馬大学医学部保健学科検査技術科学専攻

²⁾ 財団法人 発酵研究所

新たに単離されたか、再分類により新規登録された α プロテオバクテリア41種(20属)のポリアミンをHPLCにて分析し、分析済みの同属および近縁属の種と比較し、プロテオバクテリアの α サブクラス内のポリアミン構成に注目した。

α -1サブグループにおいて、*Gluconobacter*属、*Gluconacetobacter*属、*Acetobacter*属、*Acidomonas*属、さらに新属の*Asaia*属に属する17種の酢酸菌はスペルミジンを主ポリアミンとして含有していた。好気性の光合成菌である*Acidisphaera*属、*Craurococcus*属、*Paracraurococcus*属(α -1サブグループ)の各1種と*Roseibium*属2種(α -2サブグループ)では、スペルミジンを含有していた。 α -2サブグループでは、*Agrobacterium*属や*Allorhizobium*属から移された種を含む*Rhizobium*属、*Sinorhizobium*属、*Mesorhizobium*属の15種と*Oligotropha*属、*Carbophilus*属、*Zavarzinia*属、*Blastobacter*属、*Starkeya*属、*Rhodoblastus*属の種が主ポリアミンとしてホモスペルミジンを含有していた。 α -3サブグループの新種*Rhodobaca bogoriensis*はスペルミジンを含んでいた。 α -4サブグループに属する*Sphingomonas*属では、4つのクラスターに区分されるが、クラスターIに属するほとんどの種はホモスペルミジンを主ポリアミンとし、クラスターII, III, IV, に各々対応している新属の*Sphingobium*属、*Novosphingobium*属、*Sphingopyxis*属の種ではスペルミジンを主ポリアミンとしていた。

トリアミンであるスペルミジンとホモスペルミジンの分布が、プロテオバクテリアの α サブクラスにおいて、属レベルの化学分類マーカーとして有用であると考えられる。