NOTE

Emendation of the description of *Blastomonas natatoria* (Sly 1985) Sly and Cahill 1997 as an aerobic photosynthetic bacterium and reclassification of *Erythromonas ursincola* Yurkov *et al.* 1997 as *Blastomonas ursincola* comb. nov.

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Photosynthetic properties of *Blastomonas natatoria* (Sly 1985) Sly and Cahill 1997, which had been recognized as being non-photosynthetic, were examined and compared with those of its close relative, the aerobic photosynthetic bacterium, *Erythromonas ursincola* Yurkov *et al.* 1997. HPLC experiments demonstrated that bacteriochlorophyll *a* was present in a detectable amount in the lipid extract from *B. natatoria* DSM 3183^T as well as that from *E. ursincola* DSM 9006^T. The *puf* genes, encoding the proteins of the photosynthetic reaction centre and core light-harvesting complexes, were detected by PCR from both the organisms. 16S rDNA sequence comparisons and DNA–DNA hybridization studies confirmed that *B. natatoria* and *E. ursincola* were closely related genetically in a single genus. On the basis of phenotypic, chemotaxonomic and phylogenetic data, it is proposed that the description of *B. natatoria* is emended as a species of aerobic photosynthetic bacteria and that *E. ursincola* is reclassified as *Blastomonas ursincola* comb. nov.

Keywords: *Blastomonas natatoria*, *Erythromonas ursincola*, *Blastomonas ursincola*, aerobic photosynthetic bacteria, bacteriochlorophyll

The genus *Blastomonas* (Sly & Cahill, 1997) was created to accommodate the budding aerobic chemo-organotrophic bacterium previously known as ‘*Blastobacter natatorius*’ (Sly, 1985). This genus currently includes only one species, *Blastomonas natatoria*. After proposing creation of the genus *Blastomonas*, Yurkov *et al.* (1997) proposed a new genus of aerobic photosynthetic bacteria, *Erythromonas*, with the type species *Erythromonas ursincola*. Although *E. ursincola* showed a high level of 16S rDNA sequence similarity (99.8%) to *B. natatoria*, Yurkov and colleagues concluded that the two organisms should be placed in different genera

in consideration of the importance of photosynthetic properties in bacterial taxonomy. Whereas *B. natatoria* is recognized as being non-photosynthetic, *E. ursincola* has been shown to have bacteriochlorophyll (BChl) *a* incorporated in photochemically active photosynthetic reaction centre (RC) and core light-harvesting (LH1) complexes (Yurkov *et al.*, 1997, 1998a, 1998b). However, our careful examination has indicated that *B. natatoria* actually produces BChl *a* under aerobic growth conditions and contains *puf* genes, which code for proteins of the L and M subunits of the RC complex and of the LH1 complex. In this study, it is proposed to emend the description of *B. natatoria* as a member of the aerobic photosynthetic bacteria and to reclassify *E. ursincola* as *Blastomonas ursincola* comb. nov. Recently, Yabuuchi *et al.* (1999) proposed the transfer of *Blastomonas* and *Erythromonas* to the genus *Sphingomonas*. However, on the basis of the results of the present study, the name *Blastomonas* has been retained as a separate genus from *Sphingomonas*.

Abbreviations: BChl, bacteriochlorophyll; LH1, light-harvesting complex 1; RC, reaction centre.

The DDBJ accession numbers for the 16S rDNA sequences of *Blastomonas natatoria* DSM 3183^T and *Blastomonas ursincola* DSM 9006^T are AB024288 and AB024289, respectively; the DDBJ accession numbers for the corresponding *puf* genes of each species are AB031015 and AB031016.

Fig. 1. HPLC elution profiles of acetone-methanol extracts from cells of *Erythromonas ursincola* DSM 9006^T (a) and *Blastomonas natatoria* DSM 3183^T (b) grown in 1/10 diluted PBV medium. Absorption spectra of the main elution components at a wavelength range of 500–800 nm are shown in insets. Components were separated with a reverse-phase ODS column [4.6 (internal diameter) × 250 mm] in a column oven at 30 °C and with methanol as the mobile phase at a flow rate of 1 ml min⁻¹.

B. natatoria DSM 3183^T (T=type strain) and *E. ursincola* DSM 9006^T were obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ, Braunschweig, Germany). For comparison, the type strain of *B. natatoria* was also obtained from the Institute for Fermentation (Osaka, Japan) as *B. natatoria* IFO 15649^T. These organisms were grown aerobically at 28 °C in screw-capped test tubes or bottles containing PBV medium [0.5% peptone, 0.3% beef extract and 0.1% yeast extract (all from Difco)] or 1/10 diluted PBV medium. Cells were harvested from cultures in the late exponential phase of growth, washed twice with 50 mM phosphate buffer (pH 7.0) and immediately subjected to photopigment analyses. Lipid components were extracted from washed cells with acetone-methanol (7:2, v/v) and analysed with a Shimadzu BioSpec 1600 spectrophotometer. As expected, the acetone-methanol extract from *E. ursincola* cells showed absorption maxima at 425 (shoulder), 453, 481 and 769 nm, indicating the presence of BChl *a* and carotenoids. On the other hand, although the lipid extracts from *B. natatoria* DSM 3183^T and IFO 15649^T gave similar absorption peaks derived from carotenoid components, it was hard to find the BChl peak by

Fig. 2. Photograph (negative image) showing PCR amplification products from cell extracts of *Erythromonas ursincola* DSM 9006^T and *Blastomonas natatoria* DSM 3183^T and IFO 15649^T. The corresponding 2.1 kb DNA fragments of *puf* genes were amplified with *Taq* DNA polymerase and a pair of primers, B140F (5'-TGGCASTGGCGYCCGTGG-3') and MR (5'-CCATSGTCCAGCGCCAGA-3') (Hiraishi *et al.*, 1998). The cycle profiles were: denaturation at 98 °C for 30 s, annealing at 55 °C for 30 s and extension at 72 °C for 1.5 min in total 30 cycles. PCR products were detected by agarose gel electrophoresis with 1% agarose and staining with ethidium bromide. Lanes: 1, size marker (λ -HindIII digest); 2, *E. ursincola* DSM 9006^T; 3, *B. natatoria* DSM 3183^T; 4, *B. natatoria* IFO 15649^T.

direct spectrophotometric measurement. Therefore, attempts were made to detect BChl *a* in *B. natatoria* by the spectrochromatographic method (HPLC and photodiode array detection) as described previously (Hiraishi *et al.*, 1998). Comparative HPLC elution profiles of the lipid extracts from *E. ursincola* and *B. natatoria* are shown in Fig. 1. The extracts from *B. natatoria* DSM 3183^T and IFO 15649^T gave a very small but detectable amount of a component which had the same retention time as *E. ursincola* BChl *a*. All these components gave an absorption maximum at around 770 nm, thereby ascertaining the presence of BChl *a* in *B. natatoria* as well as in *E. ursincola*. These results indicate that spectrochromatography is necessary for pigment analysis of aerobic photosynthetic bacteria with low BChl contents.

To confirm *B. natatoria* as being potentially photosynthetic, attempts were made to detect the photosynthetic genes from this bacterium. PCR amplification of *puf* genes from cell lysates of *B. natatoria* DSM 3183^T and IFO 15649^T and *E. ursincola* DSM 9006^T was performed with a pair of primers, B140f and MR, according to previously described protocol (Hiraishi *et al.*, 1998). The corresponding 2.1 kb DNA fragments were successfully amplified from all test

Table 1. DNA base composition and DNA–DNA relatedness among *Blastomonas natatoria*, *Erythromonas ursincola* and related organisms

Test organism	DNA G + C content (mol %)	Hybridization (%) to labelled DNA from:*	
		DSM 3183 ^T	DSM 9006 ^T
<i>Blastomonas natatoria</i> DSM 3183 ^T	64.8†	100 (100)	61 (40)
<i>Blastomonas natatoria</i> IFO 15649 ^T	64.9†	103 (100)	54 (31)
<i>Erythromonas ursincola</i> DSM 9006 ^T	65.1†	68 (47)	100 (100)
<i>Erythromicrobium ramosum</i> DSM 8510 ^T	64.1‡	3	4
<i>Porphyrobacter neustonensis</i> DSM 9434 ^T	64.2§	3	5
<i>Sphingomonas paucimobilis</i> IFO 13935 ^T	64.0†	4	2

* Hybridization levels in 50% formamide at 42 °C (data in parentheses are at 44 °C).

† Determined by the HPLC method (Katayama-Fujimura *et al.*, 1984) in this study.

‡ Cited from Yurkov *et al.* (1991).

§ Cited from Fuerst *et al.* (1993).

strains (Fig. 2). Nucleotide sequences of the PCR products and their subcloned DNAs were determined by direct cycle sequencing. The *puf* gene sequences of *B. natatoria* DSM 3183^T and IFO 15649^T were identical and had 96.0 and 95.4% similarities to the sequence of *E. ursincola* in the regions of the L and M subunits, respectively. Recently, T. Hamada reported the *pufL* and *pufM* gene sequences of *B. natatoria* independently (DDBJ/EMBL/GenBank accession number, AB012060). These results and those obtained in this study matched completely.

Nearly complete sequences of the 16S rDNA amplified by PCR from *B. natatoria* DSM 3186^T and *E. ursincola* DSM 9006^T were determined and it was found that the sequences of both the organisms completely matched. Phylogenetic analysis based on 16S rDNA sequences showed that *B. natatoria* and *E. ursincola* formed a cluster within the α -4 group of the α -Proteobacteria with *Rhizomonas suberifaciens* as their nearest phylogenetic neighbour, in accordance with previous studies (Hugenholtz *et al.*, 1994; Sly & Cahill, 1997; Yurkov *et al.*, 1997). Genomic DNA–DNA hybridization studies were further performed by the quantitative dot-blot hybridization method with biotin labelling and colorimetric detection as reported previously (Hiraishi *et al.*, 1991), where *Erythromicrobium ramosum* DSM 8510^T, *Porphyrobacter neustonensis* DSM 9434^T and *Sphingomonas paucimobilis* IFO 13935^T were used as the reference organisms (Table 1). The levels of hybridization between *B. natatoria* strains DSM 3183^T and IFO 15649^T and *E. ursincola* DSM 9006^T were 54–68% at 42 °C and 31–47% at 44 °C (in 50% formamide). The two species showed much lower levels of DNA–DNA relatedness ($\leq 5\%$) to other test organisms. The 54–68% levels of hybridization between *B. natatoria* and *E. ursincola* are somewhat higher than those shown by Yurkov & Beatty (1998) in their review. This difference may result from different methodologies used. Hybridization values obtained

under a more stringent condition (44 °C) were similar to the data shown in the review of Yurkov & Beatty.

B. natatoria and *E. ursincola* are phylogenetically related to members of the genus *Sphingomonas*, a representative genus belonging to the α -4 group of the α -Proteobacteria (Takeuchi *et al.*, 1994). In this context, *B. natatoria* and *E. ursincola* were further studied for phenotypic and chemotaxonomic properties in comparison with members of the genus *Sphingomonas*. Microscopic studies showed that *B. natatoria* DSM 3183^T and *E. ursincola* DSM 9006^T had ovoid to rod-shaped cells reproducing by budding or asymmetric cell division, indicating them to be morphologically distinct from *Sphingomonas* species. As shown in Table 2, *B. natatoria* and *E. ursincola* utilized a wide variety of simple organic compounds as sole carbon sources, but did not grow with aromatic compounds, including benzoate, *p*-cresol, dibenzo-*p*-dioxin, dibenzofuran, dichlorophenol or naphthalene, which support the growth of several species of the genus *Sphingomonas* (Wittich *et al.*, 1992; Balkwill *et al.*, 1997). In these physiological and biochemical tests, major differences were noted between *B. natatoria* and *E. ursincola* in some characteristics including growth with 3% NaCl, aesculin hydrolysis, casein hydrolysis and carbon nutrition. GLC analysis showed that the major cellular fatty acid component of *B. natatoria* DSM 3183^T and *E. ursincola* DSM 9006^T was C18:1(d9) (65–78%). Both the organisms lacked 3-OH fatty acids but contained 2-OH C14:0 as the major hydroxy fatty acid component (60–66% of the total 2-OH acid content). The minor 2-OH acids were C16:0, C16:1 and C15:0 in *B. natatoria* and C16:0 and C15:0 in *E. ursincola*. In these chemotaxonomic traits, *B. natatoria* and *E. ursincola* were similar to members of the genus *Sphingomonas*. However, whereas most species of the genus *Sphingomonas* contained both monosaccharide- and oligosaccharide-type glycosphingolipids, *B. natatoria* and *E. ursincola* had monosaccharide-type

Table 2. Comparative physiological and biochemical characteristics of *Blastomonas natatoria* and *Erythromonas ursincola*

Symbols for physiological and biochemical tests: +, positive reaction; (+), weakly positive reaction; –, negative reaction. Symbols for carbon nutrition tests: ++, good growth ($OD_{660} > 0.5$); +, moderate growth ($OD_{660} = 0.1–0.5$); [+], poor growth ($OD_{660} = 0.05–0.1$); –, no or little growth ($OD_{660} < 0.05$). Reactions positive for all test strains: catalase; oxidase; starch hydrolysis; Tween 80 hydrolysis; utilization of maltose, ++; acetate, +; propionate, +; butyrate, +; pyruvate, ++; succinate, [+]; fumarate, [+]; and glutamate, ++. Reactions negative for all test strains: indole production; H_2S production; nitrate reduction; phenylalanine deaminase; urease; gelatin liquefaction in gelatin tube; acid from glucose in OF test; chitin hydrolysis; and utilization of D-fructose, D-mannose, cellobiose, lactose, methanol, propanol, formate, lactate, citrate, gluconate, phenylacetate, benzoate, *p*-cresol, dichlorophenol, dibenzofuran, dibenzo-*p*-dioxin and naphthalene.

Characteristic	<i>B. natatoria</i> (DSM 3183 ^T /IFO 15649 ^T)	<i>E. ursincola</i> DSM 9006 ^T
Growth with 3 % NaCl	+	–
Hydrolysis of:		
Aesculin	+	–
Casein	–	+
Gelatin (on agar plate)	(+)	–
DNA	(+)	+
Carbon source utilization:		
L-Arabinose	+	–
D-Xylose	++	+
D-Glucose	+	[+]
D-Sorbitol	–	[+]
Malate	–	[+]

glycosphingolipids only. Detailed information on sphingolipids in these bacteria will be reported elsewhere. A concurrent study has revealed that all established species of the genus *Sphingomonas* lack BChl and the photosynthetic genes (A. Hiraishi, unpublished data), unlike *B. natatoria* and *E. ursincola*.

Yurkov *et al.* (1997) considered that the differences in photosynthetic properties between *E. ursincola* and *B. natatoria* provided a basis for classifying them into different genera despite their close phylogenetic relationship. Before the present study, however, *B. natatoria* had been recognized merely as an aerobic chemo-organotroph (Sly, 1985; Sly & Cahill, 1997) without intensive studies on its photosynthetic properties. Our results demonstrate that both *B. natatoria* and *E. ursincola* produce BChl and contain the photosynthetic genes encoding proteins of RC/LH1 complexes and that there are no major physiological and chemotaxonomic differences between the two which warrant different generic allocations. Phylogenetic analyses based on 16S rRNA and *puf* gene sequences also demonstrate that the two organisms are genetically highly related and belong to a single genus.

It is difficult to separate *B. natatoria* and *E. ursincola* on the basis of 16S rDNA sequences. However, DNA–DNA hybridization levels between the two species are lower than 70 %, the lower limit of values indicative of single species status (Wayne *et al.*, 1987).

Also, the two species showed 4–5 % differences in the *pufL* and *pufM* gene sequences. Moreover, they exhibit some phenotypic differences which are useful as diagnostic features for species differentiation, e.g. NaCl tolerance, aesculin and casein hydrolysis, and carbon nutrition (Table 2). Therefore, it is concluded that *B. natatoria* and *E. ursincola* may be classified as different species in a single genus. According to Rule 44 of the International Code of Nomenclature of Bacteria (Lapage *et al.*, 1992), the generic name *Blastomonas* has priority, since *Blastomonas natatoria* was validated earlier than *Erythromonas ursincola*. Thus, it is proposed to emend the description of *B. natatoria* (Sly, 1985) Sly & Cahill 1997 to contain aerobic photosynthetic strains and to transfer *E. ursincola* Yurkov *et al.* 1997 to the genus *Blastomonas* as *B. ursincola* comb. nov.

Finally, phenotypic, chemotaxonomic and phylogenetic data derived in this study confirm that the genus *Blastomonas* is distinct from the genus *Sphingomonas* and other genera of the α -4 group of the α -Proteobacteria. These data turn down a recent proposal for transfer of *B. natatoria* and *E. ursincola* to the genus *Sphingomonas* (Yabuuchi *et al.*, 1999). Unifying the genera *Blastomonas* and *Sphingomonas* in a single genus may bring about taxonomic confusion because of major differences between the two genera in morphology, photosynthetic properties and chemo-

taxonomic traits, including the type of glycosphingolipids. Since the currently defined genus *Sphingomonas* includes genetically diverse species which can be divided into four phylogenetic groups (Yurkov *et al.*, 1997), it is preferable to separate some of these groups from the genus *Sphingomonas* and to transfer them to new genera in the near future.

Emended description of the genus *Blastomonas*

The description of the genus is based on the descriptions reported previously (Sly & Cahill, 1997; Yurkov *et al.*, 1997) and in this study. The chemotaxonomic information is derived from the report of Sittig & Hirsch (1992) and this study. Cells are ovoid or rod-shaped and reproduce by budding or asymmetric cell division. They occur singly or in pairs and may form rosette-like aggregates. No stalks and prosthecae are found. Gram-negative. Non-spore-forming. Motile by means of polar flagella. Strictly aerobic chemo-organotroph and facultative photo-organotroph. No growth occurs under anaerobic conditions in the light. Produces BChl *a*. Colonies and cell suspensions are yellow to orange due to the presence of carotenoids. Mesophilic, neutrophilic and freshwater bacterium. Catalase- and oxidase-positive. Nitrate is not reduced. Acid is not produced in Hugh–Leifson's OF medium. The major whole-cell fatty acid is C18:1(d9). The major hydroxy fatty acid is 2-OH C14:0. 2-OH C15:0 and 2-OH C16:0 are present as minor components. 3-OH fatty acids are absent. Monosaccharide-type glycosphingolipids are present. Ubiquinone-10 is the major respiratory quinone. The genomic DNA G+C content is 64.8–65.2 mol%. The phylogenetic position is in the α -4 group of the α -Proteobacteria. The type species is *Blastomonas natatoria*.

Emended description of *Blastomonas natatoria*

The description of the species is the same as described for the genus. Additional properties are given as follows; the chemotaxonomic information is derived from the report of Sittig & Hirsch (1992) and this study. Cells are ovoid or rod-shaped, 0.6–0.9 by 1.0–2.5 μ m and reproduce by budding or asymmetric cell division. Colonies on complex media containing peptone and beef extract or yeast extract are circular, convex, smooth and opaque and grow to 2 mm within 1 week of incubation. Colour of colonies is yellow, orange or brown, depending upon the composition of growth media. Aerobic chemo-organotrophy is the preferred mode of growth. No chemolithotrophic growth with H₂, sulfide or thiosulfate is found. Optimum temperature for growth is 30–35 °C. Optimum pH is 7.0–7.5. Growth occurs in the presence of 3 % NaCl. No growth factors are required. Hydrolytic activities against aesculin, starch, gelatin, Tween 80 and DNA are present. Chitin, cellulose and casein are not hydrolysed. Urease, phenylalanine deaminase, indole and H₂S are not produced. Good growth occurs

with D-xylose, maltose, pyruvate, glutamate, peptone or yeast extract as sole carbon sources. Other usable carbon sources are L-arabinose, D-glucose, acetate, propionate, butyrate, succinate, fumarate and Casamino acids. No or little growth occurs with D-fructose, D-mannose, cellobiose, lactose, mannitol, sorbitol, lactate, methanol, propanol, formate, citrate, malate, phenylacetate, benzoate, dichlorophenol, dibenzofuran, dibenzo-*p*-dioxin or naphthalene. The major phospholipids are phosphatidylglycerol, phosphatidylethanolamine, phosphatidylmethylethanolamine and phosphatidylcholine. The genomic DNA G+C content is 64.8 mol% (HPLC method). Inhabits freshwater environments. The type strain is DSM 3183^T (= ATCC 35951^T = ACM 2507^T = NCIMB 12085^T = IFO 15649^T).

Description of *Blastomonas ursincola* (Yurkov *et al.* 1997) comb. nov.

Blastomonas ursincola (ur.sin'co.la. M.L. adj. *ursincola* neighbour or compatriot of bears).

The description of *Blastomonas ursincola* is the same as that described for the genus and by Yurkov *et al.* (1997). Additional properties are given as follows. No growth occurs in the presence of 3 % NaCl. Growth factors are not required, but growth is stimulated significantly by vitamins. Hydrolytic activities against starch, casein, Tween 80 and DNA are present. Aesculin, chitin, cellulose and gelatin are not hydrolysed. Urease, phenylalanine deaminase, indole and H₂S are not produced. Good growth occurs with maltose, pyruvate, glutamate, peptone or yeast extract as sole carbon source. Other usable carbon sources are D-xylose, D-glucose, D-sorbitol, acetate, propionate, butyrate, succinate, fumarate, malate and Casamino acids. No or little growth occurs with L-arabinose, D-fructose, D-mannose, cellobiose, lactose, D-mannitol, lactate, methanol, ethanol, propanol, formate, citrate, phenylacetate, benzoate, dichlorophenol, dibenzofuran, dibenzo-*p*-dioxin or naphthalene. The genomic DNA G+C content is 65.1 mol% (HPLC method). Inhabits freshwater environments. The type strain is DSM 9006^T (= V. Yurkov KR-99^T).

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