Paenibacillus forsythiae sp. nov., a nitrogen-fixing species isolated from rhizosphere soil of *Forsythia mira*

Yu-Chao Ma^{1,2} and San-Feng Chen^{1,3}

Correspondence
San-Feng Chen
chensf@cau.edu.cn

¹National Key Laboratory for Agrobiotechnology, China Agricultural University, Beijing 100094, PR China

²Key Laboratory of Agro-Microbial and Application, China Agricultural University, Beijing 100094, PR China

³College of Biological Sciences, China Agricultural University, Beijing 100094, PR China

A nitrogen-fixing bacterium, designated strain T98^T, was isolated from rhizosphere soil of *Forsythia mira*. Phylogenetic analysis based on a fragment of the *nifH* gene and the full-length 16S rRNA gene sequence revealed that strain T98^T was a member of the genus *Paenibacillus*. High levels of 16S rRNA gene similarity were found between strain T98^T and *Paenibacillus durus* ATCC 35681^T (97.0 %), *Paenibacillus sabinae* DSM 17841^T (98.3 %) and *Paenibacillus zanthoxyli* DSM 18202^T (96.8 %). Levels of 16S rRNA gene sequence similarity between strain T98^T and the type strains of other recognized members of the genus *Paenibacillus* were below 97.0 %. Levels of DNA–DNA relatedness between strain T98^T and *P. durus* ATCC 35681^T, *P. sabinae* DSM 17841^T and *P. zanthoxyli* DSM 18202^T were 27.6, 30.0 and 32.1 %, respectively. The DNA G + C content of strain T98^T was 50.4 mol%. The major fatty acids were anteiso-C_{15:0}, C_{16:0} and iso-C_{16:0}. On the basis of its phenotypic characteristics and levels of DNA–DNA hybridization, strain T98^T is considered to represent a novel species of the genus *Paenibacillus*, for which the name *Paenibacillus forsythiae* sp. nov. is proposed. The type strain is T98^T (=CCBAU 10203^T = DSM 17842^T).

The genus *Paenibacillus* was erected by Ash *et al.* (1993) on the basis of analysis of the 16S rRNA gene sequences of group 3 bacilli. Members of the genus are widely distributed in nature and have physiologically diverse characteristics. Some species consistently show a great capacity to fix atmospheric nitrogen *in vitro* (Berge *et al.*, 2002; Ma *et al.*, 2007a, b; Ding *et al.*, 2005; Elo *et al.*, 2001; Grau & Wilson, 1962; Rodríguez-Díaz *et al.*, 2005; Seldin *et al.*, 1984). Here we show that a bacterial strain, designated T98^T, isolated from rhizosphere soil of *Forsythia mira* represents a novel nitrogen-fixing species of the genus *Paenibacillus*.

Strain T98^T was isolated from rhizosphere soil of *F. mira* by screening on nitrogen-free medium (Ma *et al.*, 2007a). The nitrogen-free medium contained 20 g sucrose, 0.1 g K₂HPO₄, 0.4 g KH₂PO₄, 0.2 g MgSO₄·7H₂O, 0.1 g NaCl,

0.01 g FeCl₃ and 0.002 g Na₂MoO₄ per litre of water. One gram of soil was placed in 9 ml sterile water and stirred for 50 min. Aqueous volumes (100 µl of the mixture) were heated at 80 °C for 10 min and then spread on nitrogen-free medium in triplicate and incubated at 30 °C. After 3 days incubation, strain T98^T was selected for further study.

To confirm the nitrogen-fixing capacity of strain T98^T, an assay for nitrogenase activity and PCR amplification of the *nifH* gene were carried out. For measurement of nitrogenase activity, strain T98^T and several reference strains were grown on solid RCV mineral medium containing 0.5 % glucose, malate, starch and mannitol (Weaver *et al.*, 1975). After 48 h at 30 °C, strains were incubated under 2 % (v/v) acetylene in air for 2 h and then analysed for ethylene production by GC (Berge *et al.*, 2002). As shown in Table 1, strain T98^T exhibited high nitrogenase activity. Whole-cell DNA for PCR amplification was extracted according to standard methods (Sambrook *et al.*, 1989). A 324-bp fragment of the *nifH* gene was amplified by using two degenerate primers for the nitrogenase Fe protein gene and then sequenced as described by Ding *et al.* (2005). A phylogenetic tree was generated by the neighbour-joining method by using the software package TREECON for

The GenBank/EMBL/DDBJ accession numbers for the partial *nifH* gene sequence and 16S rRNA gene sequence of strain T98^T are respectively DQ349124 and DQ338443.

A neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic position of strain T98^T compared with all recognized species of the genus *Paenibacillus* is available as supplementary material with the online version of this paper.

Table 1. Nitrogenase activity of strain T98^T compared with some nitrogen-fixing species of the genus *Paenibacillus*Results are means $\pm$ SD of three determinations.

Strain	Nitrogenase activity [nmol C ₂ H ₂ (mg protein) ⁻¹]
<i>P. durus</i> ATCC 35681 ^T	2256.8 $\pm$ 46.9
<i>P. polymyxa</i> ATCC 842 ^T	3.2 $\pm$ 0.55
<i>P. macerans</i> ATCC 8244 ^T	2.48 $\pm$ 0.2
<i>P. odorifer</i> TOD45 ^T	37.62 $\pm$ 18.9
<i>P. graminis</i> RSA19 ^T	272.9 $\pm$ 7.9
<i>P. sabiniae</i> DSM 17841 ^T	3885.9 $\pm$ 72.9
<i>P. zanthoxyli</i> DSM 18202 ^T	6282.4 $\pm$ 107.97
Strain T98 ^T	1537.0 $\pm$ 10.9

Windows (Van de Peer & de Wachter, 1994). Phylogenetic analysis based on *nifH* gene sequences revealed that strain T98^T clustered together with species of the genus *Paenibacillus* (Fig. 1). Levels of *nifH* gene sequence similarity between strain T98^T and *Paenibacillus zanthoxyli* DSM 18202^T, *Paenibacillus sabiniae* DSM 17841^T, *Paenibacillus durus* ATCC 35681^T, *Paenibacillus polymyxa* DSM 36^T, *Paenibacillus odorifer* TOD45^T, *Paenibacillus graminis* RSA19^T, *Paenibacillus macerans* ATCC 8244^T and *Paenibacillus wynnii* LMG 22176^T were 98.15, 97.0, 96.30, 89.0, 88.07, 80.73, 81.65 and 84.0 %, respectively.

A full-length sequence of the 16S rRNA gene (1500 bp) was obtained from a PCR product amplified from strain T98^T by using the universal forward primer P1 and the universal reverse primer P6. Primer P1 (5'-AGAGTTTGATCCTGGTCAGAACGCT-3') corresponds to positions 8–37 and primer P6 (5'-TACGGCTACCTTGTTACGACTTCACCC-C-3') corresponds to positions 1479–1506 in the *Escherichia coli* 16S rRNA gene (Yanagi & Yamasato, 1993). The amplified 16S rRNA gene was sequenced by using an ABI377 automatic sequencer (Applied Biosystems). The 16S rRNA gene sequence of strain T98^T was aligned with sequences of recognized species of the genus *Paenibacillus* by using the CLUSTAL_X program (Thompson *et al.*, 1997). Phylogenetic analysis revealed

Fig. 2. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain T98^T among species of the genus *Paenibacillus*. *Bacillus subtilis* NCDO 1769^T was used as an outgroup. Bootstrap analyses were made based on 1000 cycles; only values >50 % are shown at branch points. Bar, 0.1 substitutions per nucleotide position. An extended version of this tree including all species of *Paenibacillus* with validly published names is available as Supplementary Fig. S1 in IJSEM Online.

that strain T98^T clustered together with *Paenibacillus* species (Fig. 2; an extended version of this tree is available as Supplementary Fig. S1 in IJSEM Online). Strain T98^T showed highest 16S rRNA gene sequence similarity with *P. sabiniae* DSM 17841^T, *P. durus* ATCC 35681^T, *P. zanthoxyli* DSM 18202^T and *Paenibacillus stellifer* DSM 14472^T (98.3, 97, 96.8 and 96.5 %, respectively). Levels of 16S rRNA gene sequence similarity between strain T98^T and other recognized members of the genus *Paenibacillus* were below 96 %.

Strain T98^T was tested for a range of phenotypic, physiological and biochemical characteristics together with the type strains of closely related *Paenibacillus* species, including *P. durus* ATCC 35681^T, *P. sabiniae* DSM 17841^T, *P. zanthoxyli* DSM 18202^T, *P. polymyxa* ATCC 842^T, *P. macerans* ATCC 8244^T, *P. odorifer* TOD45^T and *P. graminis* RSA19^T, as reference strains. For observation of cell

Fig. 1. Phylogenetic tree based on partial *nifH* gene sequences, showing the position of strain T98^T in relation to other reference bacterial species. Bootstrap analyses were made based on 1000 cycles; only values >50 % are shown at branch points. Bar, 0.1 substitutions per nucleotide position.

morphology, strain T98^T was grown on endospore-forming medium [0.07 % yeast extract, 0.1 % tryptone, 0.1 % glucose, 0.02 % (NH₄)₂SO₄, 0.02 % MgSO₄·7H₂O and 0.1 % K₂HPO₄, pH 7.2] for 72 h, and cells were then examined by light microscopy. Strain T98^T formed ellipsoidal spores, located centrally in swollen sporangia. Colonies on RCV mineral medium agar were circular, convex and glossy with entire margins. Gram-staining demonstrated that cells of strain T98^T were Gram-positive or Gram-variable rods (0.4–0.5 × 2.0–2.6 µm). Cell motility was determined by using two methods, i.e. directly by light microscopy and observation of growth spread of cells in test tubes containing semisolid RCV medium after 3 days incubation. Cells of strain T98^T were motile. To determine aerotactic ability, bacterial cells were inoculated by mixing them with semisolid medium at 40–50 °C in test tubes followed by growth at 30 °C for 3 days. Although cells of strain T98^T grew throughout the medium in test tubes, cells near the surface grew better than those near the bottom, suggesting that strain T98^T was facultatively aerobic.

Most physiological and biochemical tests, including Gram staining, nitrate reduction, production of dextrin, temperature and pH optima for growth, activities of catalase, oxidase and the Voges–Proskauer reaction, growth inhibition by NaCl and lysozyme, were performed according to Gordon *et al.* (1973), Priest *et al.* (1981) and Rhodes-Roberts (1981). Hydrolysis of casein, gelatin and starch was determined as described by Cowan & Steel (1965). Utilization of various substrates as carbon and energy sources was determined as described by Shirling & Gottlieb (1966). The physiological and biochemical characteristics of strain T98^T compared with those of the type strains of closely related *Paenibacillus* species are presented in Table 2. As shown, strain T98^T has physiological properties that allowed its distinction from these recognized *Paenibacillus* species.

The DNA G+C content was determined by using the thermal denaturation protocol (De Ley *et al.*, 1970). The G+C content of strain T98^T was 50.4 mol% (Table 1), which is within the range of values for recognized *Paenibacillus* species (Shida *et al.*, 1997).

For DNA–DNA hybridization experiments, total genomic DNA was extracted and purified according to the method described by Marmur (1961) with some modifications. DNA–DNA hybridization was determined by the initial renaturation rate method (De Ley *et al.*, 1970). Levels of DNA–DNA relatedness between strain T98^T and *P. sabinae* DSM 18741^T, *P. durus* ATCC 35681^T and *P. zanthoxyli* DSM 18202^T were 30.0, 27.6 and 32.1 %, respectively, indicating that strain T98^T represented a species distinct from these three species.

For determination of its cellular fatty acid composition, strain T98^T was grown in RVC mineral medium at 30 °C for 3 days. Analysis was carried out as described by Komagata & Suzuki (1987) by using the Sherlock Identification System (MIDI) (Sasser *et al.*, 2005). Profiles of the major fatty acids of strain T98^T and of

closely related *Paenibacillus* type strains are shown in Table 3. Anteiso-C_{15:0}, the major fatty acid in recognized members of the genus *Paenibacillus*, was also the major fatty acid component of strain T98^T (29.87 %).

In summary, phylogenetic analysis based on the full-length 16S rRNA gene sequence and on a fragment of the *nifH* gene sequence, DNA G+C content, and chemotaxonomic properties revealed that strain T98^T was a member of the genus *Paenibacillus*. Several phenotypic characteristics and levels of DNA–DNA hybridization further demonstrated that strain T98^T represents a novel species of the genus *Paenibacillus*, for which the name *Paenibacillus forsythiae* sp. nov. is proposed.

Description of *Paenibacillus forsythiae* sp. nov.

Paenibacillus forsythiae (for.sy'thi.æ. N.L. gen. n. *forsythiae* of *Forsythia*, referring to the plant *Forsythia mira*, the source of the rhizosphere soil from which the type strain was isolated).

Gram-positive or Gram-variable, facultatively aerobic, motile, straight rods (0.4–0.5 × 2.0–2.6 µm). Ellipsoidal

Table 2. Differential phenotypic characteristics between strain T98^T and the type strains of selected *Paenibacillus*

Strains: 1, strain T98^T; 2, *P. durus* ATCC 35681^T; 3, *P. sabinae* DSM 17841^T; 4, *P. zanthoxyli* DSM 18202^T; 5, *P. polymyxa* ATCC 842^T; 6, *P. macerans* ATCC 8244^T; 7, *P. odorifer* TOD45^T; 8, *P. graminis* RSA19^T. +, Positive; –, negative; ND, not determined. Data for physiological and biochemical characteristics of strain T98^T and reference strains are from the present study. Data for G+C contents of strain T98^T, *P. sabinae* DSM 17841^T and *P. zanthoxyli* DSM 18202^T are from the present study. Data for G+C contents of *P. durus* ATCC 35681^T, *P. polymyxa* ATCC 842^T, *P. macerans* ATCC 8244^T, *P. odorifer* TOD45^T and *P. graminis* RSA19^T are from Seldin *et al.* (1984), Nakamura (1987) and Berge *et al.* (2002).

Characteristic	1	2	3	4	5	6	7	8
Growth with lysozyme (0.001 %)	–	–	–	–	–	+	+	–
Voges–Proskauer reaction	+	+	+	+	+	+	–	–
Production of dextrin	–	–	–	–	–	+	–	–
Hydrolysis of casein	+	–	–	–	–	–	–	–
Acid produced from:								
Sucrose	–	–	–	–	+	+	+	–
Glucose	–	+	–	–	+	+	+	+
Glycerol	–	–	–	–	+	+	–	–
Maltose	–	+	–	–	+	+	+	+
Lactose	–	–	–	–	+	+	ND	ND
D-Sorbitol	–	–	–	–	+	+	–	–
Sodium succinate	+	–	–	–	–	+	–	–
L-Aspartate	–	+	–	–	+	+	+	+
DNA G+C content (mol%)	50.4	50.7	51.9	53.2	45	53	44	52.1

Table 3. Cellular fatty acid profiles of strain T98^T and closely related *Paenibacillus* type strains

Strains: 1, strain T98^T; 2, *P. durus* ATCC 35681^T (data from Yoon *et al.*, 2003); 3, *P. sabinae* DSM 17841^T (Ma *et al.*, 2007a); 4, *P. zanthoxyli* DSM 18202^T (Ma *et al.*, 2007b); 5, *P. stellifer* DSM 14472^T (Suominen *et al.*, 2003); 6, *P. polymyxa* DSM 36^T (Yoon *et al.*, 2003); 7, *P. macerans* ATCC 8244^T (Elo *et al.*, 2001). Data are percentages of the total fatty acids. NR, Not reported. For unsaturated fatty acids, the position of the double bond can be located by counting from the methyl (ω) end of the carbon chain; *cis* isomers are indicated by the suffix *c*.

Fatty acid	1	2	3	4	5	6	7
Saturated straight-chain							
C _{14:0}	4.85	5.0	2.96	4.87	0.7	5.0	3.7
C _{15:0}	1.92	2.2	1.54	2.07	0.5	3.4	0.5
C _{16:0}	18.70	15.5	18.19	12.83	9.1	20.5	17.9
C _{18:0}	5.64	0.3	3.28	6.74	1.1	0.3	NR
Saturated iso-branched							
iso-C _{13:0} 3-OH	3.74	<0.2	1.39	<0.2	<0.2	NR	NR
iso-C _{14:0}	2.64	4.7	3.20	3.99	0.6	4.7	1.8
iso-C _{15:0}	0.97	8.7	1.37	1.51	5.5	8.7	2.6
iso-C _{16:0}	11.48	5.3	14.40	14.85	7.7	NR	17.1
iso-C _{17:0}	0.98	1.1	0.79	0.61	7.0	NR	4.1
Saturated anteiso-branched							
anteiso-C _{15:0}	29.87	45.4	36.59	32.19	49.9	45.5	34.5
anteiso-C _{17:0}	4.52	2.1	6.38	3.89	16.7	2.1	16.1
Unsaturated							
C _{18:1} ω _{9c}	4.87	<0.2	3.88	1.51	<0.2	<0.2	<0.2

spores are located centrally in swollen sporangia. Colonies on RVC mineral medium are circular, convex and glossy with entire margins and measure 2.0–2.5 mm in diameter after 72 h at 30 °C. The temperature range for growth is 10–40 °C, with optimum growth at 30 °C. Grows at pH 4.0–10.0, with optimum growth at pH 7.0–7.2. Grows in the absence of NaCl and in 3% (w/v) NaCl, but is unable to tolerate 5% NaCl. Growth is inhibited by 0.001% (w/v) lysozyme. Catalase-positive and oxidase-negative. Positive for the Voges–Proskauer reaction. Nitrate is reduced to nitrite. Nitrogen is fixed. Able to utilize succinate to produce acid, but not glucose, sucrose, lactose, fructose, glycerol, xylose, maltose, D-sorbitol, sodium citrate, glycine or L-aspartate. Casein is hydrolysed but gelatin and starch are not. The G+C content of the DNA is 50.4 mol% (thermal denaturation method).

The type strain, T98^T (=CCBAU 10203^T =DSM 17842^T), was isolated from rhizosphere soil of the plant *Forsythia mira* in the Beijing region, China.

Acknowledgements

We thank Professor Tian-Shen Tao, Chinese Academy of Agricultural Sciences, for technical help. This work was supported by the Chinese National '973' Project (grant no. 001CB108904).

References

- Ash, C., Priest, F. G. & Collins, M. D. (1993). Molecular identification of rRNA group 3 bacilli (Ash, Farrow, Wallbanks and Collins) using a PCR probe test. Proposal for the creation of a new genus *Paenibacillus*. *Antonie van Leeuwenhoek* **64**, 253–260.
- Berge, O., Guinebretière, M. H., Achouak, W., Normand, P. & Heulin, T. (2002). *Paenibacillus graminis* sp. nov. and *Paenibacillus odorifer* sp. nov., isolated from plant roots, soil and food. *Int J Syst Evol Microbiol* **52**, 607–616.
- Cowan, S. T. & Steel, K. J. (1965). *Manual for the Identification of Medical Bacteria*. London: Cambridge University Press.
- De Ley, J., Cattoir, H. & Reynaerts, A. (1970). The quantitative measurement of DNA hybridization from renaturation rates. *Eur J Biochem* **12**, 133–142.
- Ding, Y., Wang, J., Liu, Y. & Chen, S. (2005). Isolation and identification of nitrogen-fixing bacilli from plant rhizospheres in Beijing region. *J Appl Microbiol* **99**, 1271–1281.
- Elo, S., Suominen, I., Kämpfer, P., Juhanoja, J., Salkinoja-Salonen, M. & Haahtela, K. (2001). *Paenibacillus borealis* sp. nov., a nitrogen-fixing species isolated from spruce forest humus in Finland. *Int J Syst Evol Microbiol* **51**, 535–545.
- Gordon, R. E., Haynes, W. C. & Pang, C. H.-N. (1973). *The Genus Bacillus*. US Department of Agriculture Handbook no. 427. Washington, DC: Agricultural Research Service.
- Grau, F. H. & Wilson, P. W. (1962). Physiology of nitrogen fixation by *Bacillus polymyxa*. *J Bacteriol* **83**, 490–496.
- Komagata, K. & Suzuki, K. (1987). Lipid and cell-wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Ma, Y., Xia, Z., Liu, X. & Chen, S. (2007a). *Paenibacillus sabinae* sp. nov., a nitrogen-fixing species isolated from the rhizosphere soils of shrubs. *Int J Syst Evol Microbiol* **57**, 6–11.
- Ma, Y., Zhang, J. & Chen, S. (2007b). *Paenibacillus zanthoxyli* sp. nov., a novel nitrogen-fixing species isolated from the rhizosphere of *Zanthoxyli similans*. *Int J Syst Evol Microbiol* **57**, 873–877.
- Marmur, J. (1961). A procedure for the isolation of deoxyribonucleic acid from microorganisms. *J Mol Biol* **3**, 208–218.
- Nakamura, L. K. (1987). *Bacillus polymyxa* (Prazmowski) Mace 1889 deoxyribonucleic acid relatedness and base composition. *Int J Syst Bacteriol* **37**, 391–397.
- Priest, F. G., Goodfellow, M. & Todd, C. (1981). The genus *Bacillus*: a numerical analysis. In *The Aerobic Endospore-Forming Bacteria. Classification and Identification*, pp. 91–103. Edited by R. C. W. Berkeley & M. Goodfellow. London: Academic Press.
- Rhodes-Roberts, M. (1981). The taxonomy of some nitrogen-fixing *Bacillus* species with special reference to nitrogen fixation. In *The Aerobic Endospore-Forming Bacteria. Classification and Identification*, pp. 315–335. Edited by R. C. W. Berkeley & M. Goodfellow. London: Academic Press.
- Rodríguez-Díaz, M., Lebbe, L., Rodelas, B., Heyrman, J., De Vos, P. & Logan, N. A. (2005). *Paenibacillus wynnii* sp. nov., a novel species harbouring the *nifH* gene, isolated from Alexander Island, Antarctica. *Int J Syst Evol Microbiol* **55**, 2093–2099.
- Sambrook, J., Fritsch, E. F. & Maniatis, T. (1989). *Molecular Cloning: a Laboratory Manual*, 2nd edn. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press.
- Sasser, M., Kunitsky, C., Jackoway, G., Ezzell, J. W., Teska, J. D., Harper, B., Parker, S., Barden, D., Blair, H. & other authors (2005). Identification of *Bacillus anthracis* from culture using gas chromatographic analysis of fatty acid methyl esters. *J AOAC Int* **88**, 178–181.

- Seldin, L., van Elsas, J. D. & Penido, E. G. C. (1984).** *Bacillus azotofixans* sp. nov., a nitrogen-fixing species from Brazilian soils and grass roots. *Int J Syst Bacteriol* **34**, 451–456.
- Shida, O., Takagi, H., Kadowaki, K., Nakamura, L. K. & Komagata, K. (1997).** Transfer of *Bacillus alginolyticus*, *Bacillus chondroitinus*, *Bacillus curdlanolyticus*, *Bacillus glucanolyticus*, *Bacillus kobensis*, and *Bacillus thiaminolyticus* to the genus *Paenibacillus* and emended description of the genus *Paenibacillus*. *Int J Syst Bacteriol* **47**, 289–298.
- Shirling, E. B. & Gottlieb, D. (1966).** Methods for characterization of *Streptomyces* species. *Int J Syst Bacteriol* **16**, 313–340.
- Suominen, I., Spröer, C., Kämpfer, P., Rainey, F. A., Lounatmaa, K. & Salkinoja-Salonen, M. (2003).** *Paenibacillus stellifer* sp. nov., a cyclodextrin-producing species isolated from paperboard. *Int J Syst Evol Microbiol* **53**, 1369–1374.
- Thompson, J. D., Gibson, T. J., Plewniak, F., Jeanmougin, F. & Higgins, D. G. (1997).** The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* **25**, 4876–4882.
- Van de Peer, Y. & de Wachter, R. (1994).** TREECON for Windows: a software package for construction and drawing of evolutionary trees for the Microsoft Windows environment. *Comput Appl Biosci* **10**, 569–570.
- Weaver, P. F., Wall, J. D. & Gest, H. (1975).** Characterization of *Rhodopseudomonas capsulata*. *Arch Microbiol* **105**, 207–216.
- Yanagi, M. & Yamasato, K. (1993).** Phylogenetic analysis of the family *Rhizobiaceae* and related bacteria by sequencing of 16S rRNA gene using PCR and DNA sequencer. *FEMS Microbiol Lett* **107**, 115–120.
- Yoon, J. H., Oh, H. M., Yoon, B. D., Kang, K. H. & Park, Y. H. (2003).** *Paenibacillus kribbensis* sp. nov. and *Paenibacillus terrae* sp. nov., biofloculants for efficient harvesting of algal cells. *Int J Syst Evol Microbiol* **53**, 295–301.