Jeotgalicoccus coquinae sp. nov. and *Jeotgalicoccus aerolatus* sp. nov., isolated from poultry houses

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Two Gram-stain-positive, non-motile, non-spore-forming cocci (strains MK-7^T and MPA-33^T) were isolated from poultry houses. Strain MK-7^T was isolated on marine broth agar from coquina, a food supplement for female ducks used in a duck-fattening farm. Strain MPA-33^T was isolated from the air of a turkey house on TSA after filter sampling. On the basis of 16S rRNA gene sequence similarity studies, both strains were shown to belong to the genus *Jeotgalicoccus*; MK-7^T was most closely related to *Jeotgalicoccus psychrophilus* YKJ-115^T (99.3 % similarity) and MPA-33^T was most closely related to *Jeotgalicoccus halotolerans* YKJ-101^T (98.8 %). The quinone system of MK-7^T was composed of equal amounts of menaquinones MK-7 and MK-6 and that of MPA-33^T contained 76 % MK-7 and 24 % MK-6. The polar lipid profile of strain MK-7^T consisted of the major compounds diphosphatidylglycerol and phosphatidylglycerol and six unidentified lipids present in minor to moderate amounts. In strain MPA-33^T, diphosphatidylglycerol was the single predominant lipid, whereas phosphatidylglycerol was detected in moderate amounts. In addition, one unidentified phospholipid and four unidentified lipids were detected. Fatty acid profiles with iso-15:0 and anteiso-15:0 as major fatty acids supported the affiliation of the strains to the genus *Jeotgalicoccus*. The results of physiological and biochemical tests as well as DNA–DNA hybridizations allowed clear phenotypic differentiation of strains MK-7^T and MPA-33^T from the most closely related species. Strains MK-7^T and MPA-33^T therefore represent novel species, for which the names *Jeotgalicoccus coquinae* sp. nov. (type strain MK-7^T = DSM 22419^T = CCM 7682^T = CCUG 57956^T) and *Jeotgalicoccus aerolatus* sp. nov. (type strain MPA-33^T = DSM 22420^T = CCM 7679^T = CCUG 57953^T) are proposed.

The genus *Jeotgalicoccus* was proposed by Yoon *et al.* (2003) to accommodate Gram-positive, non-motile, catalase- and oxidase-positive, coccus-shaped organisms. Two species of the genus, *Jeotgalicoccus halotolerans* and *Jeotgalicoccus psychrophilus*, were isolated from a traditional Korean fermented seafood called jeotgal (Yoon *et al.*, 2003). Later, Hoyles *et al.* (2004) isolated a third species, *Jeotgalicoccus pinnipedialis*, from a southern elephant seal. *Jeotgalicoccus marinus* was described by Chen *et al.* (2009) and was isolated from a sea urchin, and Guo *et al.* (2010) isolated *Jeotgalicoccus huakuui* from a seaside soil in China.

Generally, it can be assumed that *Jeotgalicoccus* strains are widely distributed. For example, Gill *et al.* (2006) showed *Jeotgalicoccus* strains as an inhabitant of the bovine teat canal. Di Giacomo *et al.* (2007) isolated a strain closely related to *J. halotolerans* during their analyses of microbial community structure in a dark fire-cured tobacco fermentation in Italy. Watanabe *et al.* (2008) recorded, by molecular analyses of the bacterial community in fed-batch composting reactors, that 50 % of the sequences in a clone library could be assigned to *J. pinnipedialis*. By a cultivation approach, Oppong *et al.* (2006) showed *J. psychrophilus* to be a bacterial contaminant of fresh hides, and Callon *et al.* (2007) found *J. psychrophilus* during microbial community analyses of goat's milk.

The genus *Jeotgalicoccus* is phylogenetically closely related to the genus *Salinicoccus* and to other coccus-shaped, catalase-positive organisms such as the members of the

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains MK-7^T and MPA-33^T are GU295938 and GU295939.

Two supplementary figures are available with the online version of this paper.

genera *Macrococcus* and *Nosocomiicoccus* in the family *Staphylococcaceae*. However, *Jeotgalicoccus* represents a separate phylogenetic lineage (Yoon *et al.*, 2003). The species of the genus *Jeotgalicoccus* are characterized by having menaquinone MK-7 as the predominant isoprenoid quinone, a cell-wall peptidoglycan of the A3 α type based on L-Lys-L-Gly₃₋₄-L-Ala(Gly) and DNA G + C contents of 36–42 mol% (Yoon *et al.*, 2003; Hoyles *et al.*, 2004; Chen *et al.*, 2009; Guo *et al.*, 2010).

The polyphasic taxonomic study reported here revealed that strains MK-7^T and MPA-33^T, isolated from environments associated with the poultry-fattening industry, represent two novel species of the genus *Jeotgalicoccus*.

Strain MK-7^T was isolated from coquina, a food supplement for female ducks used in a duck-fattening farm. Initially, bacteria were detached from coquina by shaking 0.5 g coquina in 10 ml sterile isotonic NaCl solution. A serial dilution in cell-free isotonic NaCl up to 10⁻¹⁰ followed, and marine broth agar (Becton Dickinson) and tryptone soy agar (TSA; Becton Dickinson) were inoculated with 0.1 ml of each dilution in triplicate (incubated at 26 and 37 °C). Strain MK-7^T grew aerobically at 37 °C on marine broth agar and was isolated from a plate inoculated with fluid from the first decimal dilution. Presumptive counts (i.e. enumeration of colonies with the same appearance at one dilution) found MK-7^T to be present at $\sim 2 \times 10^3$ c.f.u. (g coquina)⁻¹.

Strain MPA-33^T was isolated from bioaerosol samples obtained from a turkey house. Bioaerosol samples were collected according to VDI 4252-Blatt 2 by filtering 500 l turkey house air on gelatin filters at a rate of 30 l min⁻¹. Subsequently, filters were dissolved and the samples were serially diluted in isotonic NaCl. For cultivation, TSA plates were inoculated with 0.1 ml of each dilution in triplicate. Strain MPA-33^T was isolated from a plate inoculated with fluid from the second decimal dilution and incubated at 37 °C. Presumptive counts found MPA-33^T to be present at $\sim 10^4$ c.f.u. (m³ air)⁻¹.

Morphological properties, Gram-staining and cell morphology were observed by phase-contrast microscopy as described by Kämpfer & Kroppenstedt (2004). The 16S rRNA gene sequence was analysed as described previously (Kämpfer *et al.*, 2003). Multiple sequence alignment and analysis of the data were performed using the software package MEGA version 4 (Tamura *et al.*, 2007). For phylogenetic analyses, genetic distances were calculated using the Kimura-2 correction model and phylogenetic trees were constructed using the neighbour-joining (Fig. 1) and maximum-likelihood (Supplementary Fig. S1, available in IJSEM Online) methods.

The 16S rRNA gene sequences of strains MK-7^T and MPA-33^T were continuous stretches of 1325 and 1326 bp, respectively. Sequence similarity calculations after a neighbour-joining analysis indicated that the closest relatives were *J. psychrophilus* YKJ-115^T (99.3 %) for strain MK-7^T and

J. halotolerans YKJ-101^T (98.8 %) for strain MPA-33^T. The sequence similarity of MK-7^T to *J. pinnipedialis* CCUG 42722^T was 94.1 % and the similarity to both *J. marinus* JSM 076033^T and *J. huakuii* NY-2^T was 96.1 %. The sequence similarity of MPA-33^T to *J. pinnipedialis* CCUG 42722^T was 93.8 % and the similarity to both *J. marinus* JSM 076033^T and *J. huakuii* NY-2^T was 96.9 %. Maximum-likelihood analysis was performed using the ARB software package (version December, 2007; Ludwig *et al.*, 2004) and the corresponding SILVA SSURF 100 database (release August 2009; Pruesse *et al.*, 2007). The maximum-likelihood tree was reconstructed with fastDNaml (Olsen *et al.*, 1994) without filters. Similar results were obtained with the neighbour-joining and maximum-likelihood methods (Fig. 1 and Supplementary Fig. S1).

Characteristic nucleotide signatures (Alves *et al.*, 2008) at positions 418–419 and 1270–1273 described for *J. halotolerans* and *J. psychrophilus* were identical in the 16S rRNA gene sequences of strains MPA-33^T and MK-7^T. Additionally, MK-7^T contains signatures at positions 193–194.

For quinone and polar lipid analyses, cells were grown in PYE medium (Busse *et al.*, 2005). Quinone and polar lipid extraction and analyses were carried out as described by Tindall (1990a, b) and Altenburger *et al.* (1996). The HPLC equipment was described by Stolz *et al.* (2007). Analysis of the quinones revealed equal amounts of MK-7 and MK-6 in strain MK-7^T whereas, in MPA-33^T, MK-7 (76 %) was predominant and MK-6 (24 %) was found in moderate amounts. These quinone systems are similar to those reported for *J. halotolerans*, *J. psychrophilus*, *J. pinnipedialis* and *J. marinus* (Hoyles *et al.*, 2004; Chen *et al.*, 2009; Yoon *et al.*, 2003). In contrast, MK-7 was described as the sole quinone of *J. huakuii* (Guo *et al.*, 2010). The polar lipid profile of strain MK-7^T (Supplementary Fig. S2a) consisted of the major compounds diphosphatidylglycerol and phosphatidylglycerol and seven unidentified lipids, not stainable with any of the specific spray reagents applied, present in minor to moderate amounts. Diphosphatidylglycerol was the major compound in strain MPA-33^T, and phosphatidylglycerol and an unidentified phospholipid (PL1) were detected in moderate amounts. In addition, four unidentified polar lipids were detected (Supplementary Fig. S2b). These data suggest that the two isolates can be distinguished from each other based on the relative amount of phosphatidylglycerol and the absence/presence of the unidentified phospholipid PL1 and lipids L1, L2, L5 and L7. Polar lipids of *J. halotolerans* DSM 17274^T and *J. pinnipedialis* CCUG 42722^T were also analysed. Both *J. halotolerans* DSM 17274^T (Supplementary Fig. S2c) and *J. pinnipedialis* CCUG 42722^T (Supplementary Fig. S2d) showed polar lipid profiles in which diphosphatidylglycerol and phosphatidylglycerol predominated and several unidentified lipids were also detected. The profile of *J. halotolerans* DSM 17274^T was most similar to that of strain MK-7^T, differing only in the absence of lipid L2. On the other hand, similar lipid profiles were detected for *J. pinnipedialis* CCUG 42722^T and strain MPA-33^T. The

Fig. 1. Phylogenetic analysis based on 16S rRNA gene sequences available from the EMBL database (accession numbers in parentheses). The tree was constructed using the neighbour-joining method. Bootstrap values based on 1000 replications are listed as percentages at branching points. Bar, 0.01 substitutions per nucleotide position.

presence of lipid L1 and absence of L7 distinguished *J. pinnipedialis* CCUG 42722^T from MPA-33^T. The presence of phosphatidylinositol reported for *J. pinnipedialis* (Hoyle *et al.*, 2004) could not be confirmed, but other characteristics were in agreement with data from this report. Also, the two unidentified phospholipids reported for *J. halotolerans* could not be detected. These differences might result from different cultivation conditions during the production of biomass, but the reported presence of phosphatidylinositol is surprising, since this lipid is more common in actinobacteria.

Fatty acid analysis was performed according to Kämpfer & Kroppenstedt (1996). The fatty acid profiles of strains MK-7^T and MPA-33^T were similar to those obtained from strains of closely related *Jeotgalicoccus* species (Table 1). The major fatty acids detected in strains MK-7^T and MPA-33^T were iso-15:0 and anteiso-15:0.

The results of comparative physiological characterization, using identical test conditions throughout, are given in Table 2 and the species descriptions, obtained using methods described previously (Kämpfer, 1990; Kämpfer *et al.*, 1991). DNA–DNA hybridization experiments were performed with MK-7^T and MPA-33^T and reference type strains *J. psychrophilus* DSM 19085^T, *J. halotolerans* DSM 17274^T and *J. pinnipedialis* CCUG 42722^T. DNA–DNA reassociation values of MK-7^T to these type strains were 28.7, 23.2 and 24.5 %, respectively. DNA–DNA reassociation values of MPA-33^T to *J. psychrophilus* DSM 19085^T, *J. halotolerans* DSM 17274^T and *J. pinnipedialis* CCUG 42722^T were respectively 17.1, 21.2 and 13.5 %. The two strains showed 54.4 % DNA–DNA relatedness to each other.

The observed phenotypic differences and the genotypic differences in 16S rRNA gene sequences and DNA–DNA

pairing clearly warrant the creation of two separate species to accommodate strains MK-7^T and MPA-33^T.

Table 1. Long-chain fatty acid compositions of type strains of *Jeotgalicoccus* species

Strains: 1, MK-7^T; 2, MPA-33^T; 3, *J. marinus* JSM 076033^T (data from Chen *et al.*, 2009); 4, *J. halotolerans* DSM 17274^T; 5, *J. psychrophilus* DSM 19085^T; 6, *J. pinnipedialis* CCUG 42722^T; 7, *J. huakuii* NY-2^T (data from Guo *et al.*, 2010). Data were obtained in this study unless indicated. Values are percentages of total fatty acids. *J. marinus* JSM 076033^T also contained 9.7 % summed feature 4 (iso-17:1 I and/or anteiso-17:1 B) (Chen *et al.*, 2009).

Fatty acid	1	2	3	4	5	6	7
iso-13:0						1.9	0.1
iso-14:0	3.8	3.7		2.8	2.0	1.8	0.8
14:0	1.4	1.3				5.8	1.6
iso-15:0	30.4	37.7	25.9	23.5	12.0	26.1	49.0
anteiso-15:0	36.4	29.0	37.3	36.6	39.7	35.6	19.6
16:1 ω 7c	0.8			3.5	2.7		
iso-16:0	2.3	4.7	6.8	5.2	10.8	2.0	3.3
Unknown 15.669*	3.3	2.7		3.1	1.4	1.0	1.7
16:1 ω 11c	2.6	1.0		2.6	1.0		
16:0	6.8	6.5	1.9	4.1	1.9	8.2	4.3
iso-17:1 ω 10c	1.5	1.2	1.2	3.6	5.8	1.2	0.8
iso-17:0	5.8	6.6	6.2	6.0	4.9	3.8	9.7
anteiso-17:0	2.2	2.8	11.1	8.9	15.0	4.4	4.1
18:0	0.9	1.1				2.0	1.0
iso-19:0	1.8	1.8			1.6	0.7	1.3
anteiso-19:0					1.0		
20:0						5.7	

*Fatty acid that could not be identified by GC using the Microbial Identification System (Microbial ID) software.

Table 2. Physiological characters and quinone systems that differentiate type strains of *Jeotgalicoccus* species

Strains: 1, MK-7^T; 2, MPA-33^T; 3, *J. marinus* JSM 076033^T (data from Chen *et al.*, 2009); 4, *J. halotolerans* DSM 17274^T; 5, *J. psychrophilus* DSM 19085^T; 6, *J. pinnipedialis* CCUG 42722^T; 7, *J. huakuii* NY-2^T (data from Guo *et al.*, 2010). Data were obtained in this study unless indicated. +, Positive; −, negative; (+), weakly positive; ND, no data available.

Characteristic	1	2	3	4	5	6	7
Growth at:							
4 °C	−	−	−	+	+	−	−
37 and 42 °C	+	+	+	+	−	+	+
14 % (w/v) salts	+	+	+	+	+	−	+
20 % (w/v) salts	−	−	+	+	−	−	+
25 % (w/v) salts	−	−	+	−	−	−	−
Acid production from:							
D-Arabinose	−	−	+	+	−	−	+
Cellobiose	−	−	+	−	−	−	−
D-Glucose	(+)	(+)	+	−	−	−	−
D-Mannitol	+	−	+	+	−	−	−
Tyrosine hydrolysis	+	−	−	+	−	+	+
Nitrate reduction to nitrite	−	−	−	−	−	+	−
Menaquinones (%)							
MK-6	49.8	24.0	39.3	2.4	ND	5.1	0
MK-7	50.2	75.4	60.7	90.2	80.0*	94.9	100.0
MK-8	0	0.6	0	7.4	ND	0	0

*Data from Yoon *et al.* (2003).

Description of *Jeotgalicoccus coquinae* sp. nov.

Jeotgalicoccus coquinae [co.qui'nae. N.L. gen. n. *coquinae* of coquina (a limestone composed chiefly of shell fragments), referring to the source of isolation of the type strain].

Coccoid cells, 1.5–2.0 µm in diameter. Gram-stain-positive, oxidase-positive and catalase-positive, showing an aerobic respiratory metabolism. Good growth occurs after 2 days of incubation on TSA and on R2A agar at 30 °C. Colonies are white, circular and low-convex. Good growth also occurs on Chapman agar (*Staphylococcus* medium 110; Becton Dickinson) at 26 °C. The quinone system contains almost identical amounts of MK-7 and MK-6. The polar lipid profile consists of the major lipids diphosphatidylglycerol and phosphatidylglycerol and six unidentified lipids present in moderate to minor amounts. Major fatty acids are iso-15:0 and anteiso-15:0. Grows at 37 and 42 °C, but not at 4 °C. Grows in the presence of 0 and 14 % NaCl, but not >20 % NaCl. Acid is produced weakly from D-glucose, L-rhamnose, D-xylose and D-mannitol. Positive reaction in the Voges–Proskauer test. No acid is produced from sucrose, D-adonitol or *myo*-inositol. Tests for arginine dihydrolase, ornithine decarboxylase, lysine decarboxylase, urease and *o*-nitrophenyl β-galactopyranoside (ONPG) hydrolysis (β-galactosidase) are negative. No production of

indole or H₂S is observed. Does not reduce nitrate to nitrite.

The type strain is MK-7^T (=DSM 22419^T =CCM 7682^T =CCUG 57956^T), isolated from coquina after a cultivation approach.

Description of *Jeotgalicoccus aerolatus* sp. nov.

Jeotgalicoccus aerolatus (ae.ro.la'tus. Gr. n. *aer* air; L. masc. part. adj. *latus* carried; N.L. masc. part. adj. *aerolatus* airborne).

Coccoid cells, about 1.5–2.0 µm in diameter. Gram-stain-positive, oxidase-positive and catalase-positive, showing an aerobic respiratory metabolism. Good growth occurs after 2 days of incubation on TSA and R2A agar at 30 °C. Colonies are white, circular and low-convex. Good growth also occurs on Chapman agar (*Staphylococcus* medium 110; Becton Dickinson) at 26 °C. The quinone system contains predominantly menaquinone MK-7, with moderate amounts of MK-6. The polar lipid profile consists of the major lipid diphosphatidylglycerol, moderate amounts of phosphatidylglycerol and an unidentified phospholipid (PL1) and minor amounts of four unidentified polar lipids. Major fatty acids are iso-15:0 and anteiso-15:0. Produces acid only weakly from D-glucose, L-rhamnose and D-xylose. Positive reaction in the Voges–Proskauer test. No acid is produced from sucrose, D-adonitol or *myo*-inositol. Tests for arginine dihydrolase, ornithine decarboxylase, lysine decarboxylase, urease and ONPG hydrolysis (β-galactosidase) are negative. No production of indole or H₂S is observed. Grows at 37 and 42 °C, but not at 4 °C. Grows in the presence of 0 and 14 % NaCl, but not >20 % NaCl. Does not reduce nitrate to nitrite.

The type strain is MPA-33^T (=DSM 22420^T =CCM 7679^T =CCUG 57953^T), isolated from air sampled in a turkey house.

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References

- Altenburger, P., Kämpfer, P., Makristathis, A., Lubitz, W. & Busse, H.-J. (1996). Classification of bacteria isolated from a medieval wall painting. *J Biotechnol* **47**, 39–52.
- Alves, M., Nogueira, C., de Magalhães-Sant'ana, A., Chung, A. P., Morais, P. V. & da Costa, M. S. (2008). *Nosocomiicoccus ampullae* gen. nov., sp. nov., isolated from the surface of bottles of saline solution used in wound cleansing. *Int J Syst Evol Microbiol* **58**, 2939–2944.
- Busse, H.-J., Hauser, E. & Kämpfer, P. (2005). Description of two novel species, *Sphingomonas abaci* sp. nov. and *Sphingomonas panni* sp. nov. *Int J Syst Evol Microbiol* **55**, 2565–2569.
- Callon, C., Duthoit, F., Delbès, C., Ferrand, M., Le Frileux, Y., De Crémoux, R. & Montel, M.-C. (2007). Stability of microbial communities in goat milk during a lactation year: molecular approaches. *Syst Appl Microbiol* **30**, 547–560.

- Chen, Y.-G., Zhang, Y.-Q., Shi, J.-X., Xiao, H.-D., Tang, S.-K., Liu, Z.-X., Huang, K., Cui, X.-L. & Li, W.-J. (2009). *Jeotgalicoccus marinus* sp. nov., a marine bacterium isolated from a sea urchin. *Int J Syst Evol Microbiol* **59**, 1625–1629.
- Di Giacomo, M., Paolino, M., Silvestro, D., Vigliotta, G., Imperi, F., Visca, P., Alifano, P. & Parente, D. (2007). Microbial community structure and dynamics of dark fire-cured tobacco fermentation. *Appl Environ Microbiol* **73**, 825–837.
- Gill, J. J., Sabour, P. M., Gong, J., Yu, H., Leslie, K. E. & Griffiths, M. W. (2006). Characterization of bacterial populations recovered from the teat canals of lactating dairy and beef cattle by 16S rRNA gene sequence analysis. *FEMS Microbiol Ecol* **56**, 471–481.
- Guo, X.-Q., Li, R., Zheng, L.-Q., Lin, D.-Q., Sun, J.-Q., Li, S.-P., Li, W.-J. & Jiang, J.-D. (2010). *Jeotgalicoccus huakuui* sp. nov., a halotolerant bacterium isolated from seaside soil. *Int J Syst Evol Microbiol* **60**, 1307–1310.
- Hoyles, L., Collins, M. D., Foster, G., Falsen, E. & Schumann, P. (2004). *Jeotgalicoccus pinnipedialis* sp. nov., from a southern elephant seal (*Mirounga leonina*). *Int J Syst Evol Microbiol* **54**, 745–748.
- Kämpfer, P. (1990). Evaluation of the Titertek-Enterobac-Automated System (TTE-AS) for identification of members of the family Enterobacteriaceae. *Zentralbl Bakteriol* **273**, 164–172.
- Kämpfer, P. & Kroppenstedt, R. M. (1996). Numerical analysis of fatty acid patterns of coryneform bacteria and related taxa. *Can J Microbiol* **42**, 989–1005.
- Kämpfer, P. & Kroppenstedt, R. M. (2004). *Dietzia benzenivorans* sp. nov. *Int J Syst Evol Microbiol* **54**, 749–751.
- Kämpfer, P., Steiof, M. & Dott, W. (1991). Microbiological characterization of a fuel-oil contaminated site including numerical identification of heterotrophic water and soil bacteria. *Microb Ecol* **21**, 227–251.
- Kämpfer, P., Dreyer, U., Neef, A., Dott, W. & Busse, H.-J. (2003). *Chryseobacterium defluvii* sp. nov., isolated from wastewater. *Int J Syst Evol Microbiol* **53**, 93–97.
- Ludwig, W., Strunk, O., Westram, R., Richter, L., Meier, H., Yadhukumar, Buchner, A., Lai, T., Steppi, S. & other authors (2004). ARB: a software environment for sequence data. *Nucleic Acids Res* **32**, 1363–1371.
- Olsen, G. J., Matsuda, H., Hagström, R. & Overbeek, R. (1994). fastDNAm1: a tool for construction of phylogenetic trees of DNA sequences using maximum likelihood. *Comput Appl Biosci* **10**, 41–48.
- Oppong, D., Bryant, S. D., Rangarajan, R., Steele, S., Radwell, D., Hyllengren, L., Bailey, D. G., Dudley, R. & Rabinovich, D. (2006). Application of molecular techniques to identify bacteria isolated from the leather industry. *J Am Leather Chem Assoc* **101**, 140–145.
- Pruesse, E., Quast, C., Knittel, K., Fuchs, B. M., Ludwig, W., Peplies, J. & Glöckner, F. O. (2007). SILVA: a comprehensive online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB. *Nucleic Acids Res* **35**, 7188–7196.
- Stolz, A., Busse, H.-J. & Kämpfer, P. (2007). *Pseudomonas knackmussii* sp. nov. *Int J Syst Evol Microbiol* **57**, 572–576.
- Tamura, K., Dudley, J., Nei, M. & Kumar, S. (2007). MEGA4: molecular evolutionary genetics analysis (MEGA) software version 4.0. *Mol Biol Evol* **24**, 1596–1599.
- Tindall, B. J. (1990a). Lipid composition of *Halobacterium lacusprofundi*. *FEMS Microbiol Lett* **66**, 199–202.
- Tindall, B. J. (1990b). A comparative study of the lipid composition of *Halobacterium saccharovororum* from various sources. *Syst Appl Microbiol* **13**, 128–130.
- Watanabe, K., Nagao, N., Toda, T. & Kurosawa, N. (2008). Changes in bacterial communities accompanied by aggregation in fed-batch composting reactor. *Curr Microbiol* **56**, 458–467.
- Yoon, J. H., Lee, K. C., Weiss, N., Kang, K. H. & Park, Y. H. (2003). *Jeotgalicoccus halotolerans* gen. nov., sp. nov. and *Jeotgalicoccus psychrophilus* sp. nov., isolated from the traditional Korean fermented seafood jeotgal. *Int J Syst Evol Microbiol* **53**, 595–602.