Aeromonas taiwanensis sp. nov. and Aeromonas sanarellii sp. nov., clinical species from Taiwan

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Two clinical Aeromonas strains (A2-50T and A2-67T) recovered from the wounds of two patients in Taiwan could not be assigned to any known species of this genus based on their 16S rRNA gene sequences, which showed similarities of 99.6–99.8 % to those of the type strains of Aeromonas caviae, A. trota and A. aquariorum. The rpoD phylogenetic tree allocated these strains to two novel and independent phylogenetic lineages, the neighbouring species being A. caviae, the type strain of which showed 93.2 % similarity (56 bp differences) to strain A2-50T and 92.2 % (63 bp differences) to strain A2-67T. A multilocus phylogenetic analysis of five housekeeping genes (gyrB, rpoD, recA, dnaJ and gyrA; 3684 bp) confirmed that the two strains formed independent phylogenetic lineages within the genus. These data, together with phenotypic characterization and DNA–DNA reassociation results, revealed that these strains represent novel Aeromonas species, for which the names Aeromonas taiwanensis sp. nov. (type strain A2-50T = CECT 7403T = LMG 24683) and Aeromonas sanarellii sp. nov. (type strain A2-67T = CECT 7402T = LMG 24682) are proposed.

The genus Aeromonas includes facultatively anaerobic, Gram-negative, non-spore-forming bacilli or coccobacilli that are generally motile, usually oxidase- and catalase-positive, able to reduce nitrate to nitrite and generally resistant to the vibriostatic agent O/129 (2,4-diamino-6,7-diisopropylpteridine) (Abbott et al., 2003; Martin-Carnahan & Joseph, 2005). The genus belongs to the family Aeromonadaceae, order Aeromonadales, class Gammaproteobacteria (Martin-Carnahan & Joseph, 2005). At the time of writing, the genus Aeromonas includes 20 recognized species: Aeromonas hydrophila (the type species), A. bestiarum, A. salmonicida, A. caviae, A. media, A. eucrenophila, A. sobria, A. veronii, A. jandaei, A. schuberti, A. trota, A. allosaccharophila, A. encheleia, A. popoffii (Martin-Carnahan & Joseph, 2005), A. simiae (Harf-Monteil et al., 2004), A. molluscorum (Miñana-Galbis et al., 2004), A. bivalvium (Miñana-Galbis et al., 2007), A. aquariorum (Martín-Murcia et al., 2008), A. testa (Demarta et al., 2008) and the recently described A. fluvialis, isolated from river water (Alperi et al., 2010). Furthermore, Aeromonas piscicola, isolated from diseased fish, has been proposed by our group (Beaz-Hidalgo et al., 2009), as well as some reclassifications (Martín-Murcia et al., 2007, 2009). The taxonomy of this genus is complex because, despite each species apparently having specific phenotypic characteristics, biochemical identification is laborious and very imprecise, showing poor correlation with genotypic identification (Borrell et al., 1998; Soler et al., 2008; Figueras, 2005; Ormen et al., 2005). The 16S rRNA gene sequence similarity among species of the genus is very high, ranging from 96.7 to 100 % (Martín-Murcia et al., 1992, 2007; Saavedra et al., 2006). Furthermore, this gene presents microheterogeneities (Figueras et al., 2005; Martín-Murcia et al., 2005; Morandi et al., 2005; Alperi et al., 2008) that reduce its usefulness for identification (Alperi et al., 2008); such was the case for Aeromonas culicicola (Figueras et al., 2005; Alperi et al., 2008), now considered a synonym of A. veronii (Huys et al., 2005). However, several housekeeping genes have proven to have
high discriminatory power for differentiating neighbouring species and have been used to clarify the phylogeny of *Aeromonas* (Yáñez et al., 2003; Soler et al., 2004; Kupfer et al., 2006; Nhung et al., 2007; Sepe et al., 2008).

*Aeromonas* strains are primarily inhabitants of aquatic environments, often associated with fish and human diseases (Figuera, 2005; Martin-Carnahan & Joseph, 2005). The most common clinical presentation of *Aeromonas* is diarrhoea, followed by localized soft-tissue infections and bacteraemia, the prevailing associated species being *A. veronii*, *A. caviae* and *A. hydrophila* (Figuera, 2005). In recent years, numerous cases of *Aeromonas* infection have been described in Taiwan (Huang et al., 2007; Wu et al., 2007 and references therein). The present investigation was initiated to identify genetically a group of extraintestinal *Aeromonas* strains isolated in the National Cheng Kung University Hospital (Tainan, Taiwan) using a previously described 16S rRNA gene RFLP method (Figuera, 2000). Two of these strains, A2-50T and A2-67T, received as *A. hydrophila* and *A. caviae*, respectively, showed atypical RFLP patterns similar to patterns observed for *A. caviae* strains that presented microheterogeneities in the 16S rRNA gene (Alperi et al., 2008). However, the rpoD sequences showed that these strains might constitute novel and independent phylogenetic lines within *Aeromonas*.

In the present study, a polyphasic approach, based on 16S rRNA gene sequence analysis, multilocus phenotypic analysis (MLPA) of five genes (*gyrB, rpoD, recA, dnaJ* and *gyrA*), DNA–DNA reassociation experiments and phenotypic analysis, was adopted to establish the taxonomic position of the clinical isolates A2-50T and A2-67T.

Strain A2-50T, together with strains of *Enterobacter cloacae* and *Enterococcus* sp., was isolated on the tenth day of hospitalization from a burn wound of a 40-year-old male with flame burns involving 52% of the body surface area. The patient also developed a concurrent *Aeromonas* and *Enterococcus* bacteraemia, but unfortunately the *Aeromonas* blood isolate was lost. Both the burn wound infection and the bacteraemia were considered nosocomial. Strain A2-67T was isolated from a 70-year-old female with non-insulin-dependent diabetes mellitus. She had experienced trauma and had abrasion wounds over her right elbow and a right humeral fracture. On admission, a wound culture from her right elbow grew *Aeromonas, Pseudomonas aeruginosa* and *Bacillus* species. No bacteraemia was noted.

To perform the phylogenetic study, strains A2-50T and A2-67T were cultured on sheep-blood agar at 30 °C and DNA was extracted from single colonies using InstaGene Matrix (Bio-Rad) following the manufacturer’s instructions in order to sequence the 16S rRNA (1503 bp) and rpoD (820 bp) genes. Primers and conditions for amplification and sequencing have been described previously (Martínez-Murcia et al., 1992; Soler et al., 2004).

The MLPA was performed on the basis of *gyrB* (923 bp), *rpoD* (652 bp), *recA* (600 bp), *dnaJ* (800 bp) and *gyrA* (709 bp) gene sequences, as described elsewhere (A. J. Martinez-Murcia, A. Monera, R. Oncina, M. Lopez-Alvarez, E. Lara, M. J. Saavedra & M. J. Figueras, unpublished results).

The sequences obtained were aligned with the sequences of type and references strains of all members of the genus *Aeromonas* that were available in GenBank (http://www.ncbi.nlm.nih.gov/sites/entrez?db=nuccore) by using the CLUSTAL W program, version 1.83 (Thompson et al., 1994). Genetic distances and clustering were obtained using Kimura’s two-parameter model (Kimura, 1980) and phylogenetic trees were reconstructed by the neighbour-joining, maximum-parsimony and minimum-evolution methods (Saitou & Nei, 1987) using the MEGA4 program (Tamura et al., 2007). Stability of relationships was assessed by bootstrapping (1000 replicates).

16S rRNA gene phylogenetic trees (Fig. 1 and Supplementary Fig. S1, available in IJSEM Online) showed strains A2-50T and A2-67T as independent phylogenetic lines within the genus *Aeromonas*. The strains clustered in the 16S rRNA gene trees with *A. caviae*, *A. trota* and *A. aquariorum*, with robust bootstrap values of 99% when the phylogeny was inferred with the neighbour-joining algorithm (Fig. 1) and 96% with the maximum-parsimony algorithm (Supplementary Fig. S1). The two strains were highly related to each other, with just three bp differences (99.8%) between their 16S rRNA gene sequences. The nearest type strains to strains A2-50T and A2-67T on the basis of the 16S rRNA gene sequence were those of *A. trota* (99.7 and 99.6% similarity, four and five bp differences, respectively), *A. caviae* (99.6 and 99.7% similarity, five and four bp differences) and the recently described *A. aquariorum* (99.8 and 99.6% similarity, two and five bp differences). Chromatogram analysis of the 16S rRNA gene sequences (1503 bp) of strains A2-50T and A2-67T revealed the existence of microheterogeneities in eight and three positions, respectively (Supplementary Table S1), representing variability of 0.33% and 0.2%, respectively. Microheterogeneities were located within the V3 and V6 regions, which contain signature nucleotides that enable identification of most *Aeromonas* species (Martinez-Murcia et al., 1992; Saavedra et al., 2006), thereby hampering proper identification (Alperi et al., 2008). Strains A2-50T and A2-67T showed 99% similarity to the type strains of *A. caviae*, *A. trota* and *A. aquariorum* using BLAST (http://blast.ncbi.nlm.nih.gov/Blasct.cgi). This high similarity is in agreement with generally observed similarity within this genus. In fact, two type strains, those of *A. salmonicida* and *A. bestiarum*, possess identical 16S rRNA gene sequences (Martinez-Murcia et al., 1992, 2005), and the other type strains possess similarities that range from 96.8% (48 bp differences between *A. simiae* and *A. bestiarum*) to 99.8% (three bp differences between *A. molluscorum* and *A. encheleia* and between *A. hydrophila* and *A. media*). Consequently, the 16S rRNA gene sequence similarity cut-off value of 97% proposed for species differentiation (Stackebrandt & Goebel, 1994; Stackebrandt et al., 2002)
cannot be applied to *Aeromonas*, nor can the new proposed value of 98.7–99% (Stackebrandt & Ebers, 2006). This statement agrees with conclusions derived from an early 16S rRNA gene sequence phylogeny published by Martínez-Murcia et al. (1992), where absolute values for species delineation in bacteria were not recommended because of different rates of sequence divergence.

The *rpoD* phylogenetic tree showed strains A2-50T and A2-67T as two independent phylogenetic lines within *Aeromonas* (Fig. 2), showing 92.7% similarity (59 bp differences) between their sequences. The nearest type strain on the basis of the *rpoD* gene was that of *A. caviae*, showing sequence similarities of 93.2% (56 bp differences) to A2-50T and 92.2% (63 bp differences) to A2-67T. These values are below the mean intraspecies similarity of 97% established previously for the *rpoD* gene in the genus *Aeromonas* (Soler et al., 2004) and confirmed in our laboratory after sequencing this gene in more than 149 strains of different species (not shown).

The MLPA tree showed, in concordance with the *rpoD* phylogeny and in contrast to the 16S rRNA gene, that strains A2-50T and A2-67T were not phylogenetically related to *A. trota* or *A. aquaticum* (Fig. 3 and Supplementary Fig. S2), but appeared in the same cluster that included *A. media* and *A. caviae*, forming independent branches. Species delineation based on the analysis of five housekeeping genes has been recommended (Stackebrandt et al., 2002), although only the recently described *A. fluvialis* (Alperi et al., 2010) and the two species described in this study comply with this recommendation in the genus *Aeromonas*.

To establish DNA–DNA reassociation values, DNA was extracted using Marmur’s method (Marmur, 1961). Reassociation experiments were conducted using the methodology of Ziemke et al. (1998) and Urdiain et al. (2008). Reassociation was performed under optimal conditions at 70°C, reassociation values were determined at least three times (direct and reciprocal reactions, e.g. A × B and B × A) for any given strain pair and results are...
expressed as means ± SD, as described previously (Alperi et al., 2010). The mean DNA–DNA reassociation values between strains A2-50T and A2-67T and A. caviae CECT 838T and A. media CECT 4232T, the most closely related type strains on the basis of MLPA, were 59.9 and 64.7 %, respectively, with A. caviae CECT 838T and 54.5 and 29.4 %, respectively, with A. media CECT 4232T; the two novel strains showed 63.8 % relatedness (Supplementary Table S2). These values were all below the 70 % established for species delineation (Wayne et al., 1987; Stackebrandt & Goebel, 1994; Stackebrandt et al., 2002; Rosselló-Móra, 2006). Although DNA–DNA hybridization values >60 % may be considered borderline, these values are quite common for different Aeromonas species (Nhung et al., 2007; Alperi et al., 2010). This also happens among species of the neighbouring genus Vibrio (Gómez-Gil et al., 2003; Thompson et al., 2003).

The G+C content of the DNA of strains A2-50T and A2-67T was determined by three independent analyses by the HPLC technique at the BCCM/LMG Identification Service (Universiteit Gent, Belgium) following the procedures described by Miñana-Galbis et al. (2004, 2007). The DNA G+C content of strains A2-50T and A2-67T was 62.8 and 63.1 mol%, respectively, within the range described for the genus Aeromonas (57–63 mol%; Martin-Carnahan & Joseph, 2005).

In order to determine colony characteristics, i.e. size, colour and production of brown diffusible pigment, strains A2-50T and A2-67T were grown at 30 °C for 24 h on TSA and on blood agar to determine the existence of haemolysis. Optimal growth temperature and pH were determined on TSB after 24 h by following optical density. Twenty-eight phenotypic tests, selected from Abbott et al. (2003) and listed in a previous study (Alperi et al., 2010), were used for the characterization of strains A2-50T and A2-67T. These tests were performed three times and were incubated at 30 °C and also at 36 °C, due to the clinical origin of the strains. Test results were read every 24 h for up to 7 days. Some tests were confirmed in parallel using commercial identification kits (API 20NE and API 20E; bioMérieux). Additional tests from the latter kits, together with acid production from/hydrolysis of 49 carbohydrates using API 50CH (bioMérieux), were also considered. The type strains of all Aeromonas species were evaluated, under conditions identical to those used for A2-50T and A2-67T, for all differential tests included in Table 1.

Strains A2-50T and A2-67T showed relatively similar biochemical profiles, but they could be differentiated from each other because A2-50T was able to use citrate and to produce acid from raffinose, whereas strain A2-67T was not. In addition, the latter was able to grow at 45 °C on sheep-blood agar, whereas strain A2-50T was not (Table 1). No differences were observed between biochemical profiles at 30 and 36 °C. Strains A2-50T and A2-67T showed distinctive characters that separated them from other species (A. hydrophila, A. veronii bv. Sobia and A. caviae).
Table 1. Key tests for phenotypic differentiation of strains A2-50\textsuperscript{T} (A. taiwanensis sp. nov.) and A2-67\textsuperscript{T} (A. sanarellii sp. nov.) from other Aeromonas species

| Characteristic | A | B | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 |
| VP            | − | − | +(+ | v(+) | v(−) | −(− | −(− | −(− | −(− | +(+ | v(−) | v(−) | −(− | −(− | −(− | +(+ | v(−) | v(−) | −(− | −(− | −(− | v(+) | −(− | |
| LDH           | − | − | +(+ | v(−) | v(+ | −(− | −(− | −(− | +(+ | +(+ | +(+ | v(+) | (+ | +(+ | −(− | +(+ | +(+ | v(+) | −(− | +(+ | +(+ | v(+) | −(− | |
| Gas from glucose | − | − | +(+ | v(+) | v(−) | −(− | −(− | +(+ | +(+ | +(+ | v(+) | (+ | +(+ | −(− | +(+ | +(+ | v(+) | −(− | +(+ | +(+ | v(+) | −(− | |
| Hydrolysis of ascin | + | + | +(+ | v(+) | v(+) | v(+) | v(+) | −(− | −(− | −(− | +(+ | −(− | −(− | v(+) | v(+) | −(− | v(−) | (+ | +(+ | +(+ | v(+) | −(− | |
| Citrate utilization | + | − | +(+ | v(+) | v(+) | −(− | +(+ | v(+ | (+ | +(+ | v(+) | v(+ | (+ | −(− | v(+) | −(− | ND(− | +(+ | (−− | ND (+ | ND (+ | v(+ | +(+ | |
| Growth at 45 °C | − | + | +(+ | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | |
| on sheep-blood agar | Acid from: | Amygdalin | + | + | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | −(− | |
| Cellobiose | − | − | −(− | v(−) | v(+ | +(+ | +(+ | v(+ | v(+) | v(+ | v(+ | +(+ | v(+ | v(+ | v(+ | v(+ | v(+ | v(+ | v(+ | v(+ | v(+ | +(+ | +(+ | +(+ | +(+ | +(+ | |
| Raffinose | − | − | −(− | v(−) | v(+ | +(+ | +(+ | v(+ | v(+) | v(+ | v(+ | +(+ | v(+ | v(+ | v(+ | v(+ | v(+ | v(+ | v(+ | v(+ | v(+ | +(+ | +(+ | +(+ | +(+ | +(+ | |
| L-Arabinose | + | + | +(+ | v(+) | +(+ | +(+ | +(+ | v(+) | v(+) | v(+) | v(+) | +(+ | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | |
| Glycerol | + | + | +(+ | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | +(+ | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | |
| D-Mannose | − | − | +(+ | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | |
| Salcin | + | + | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | v(+) | |
commonly encountered in clinical samples (Table 1). Interestingly, both strains were able to produce acid from amygdalin, a characteristic only described so far in nine *Aeromonas* strains within a study performed by Abbott et al. (2003), who evaluated the atypical phenotypic properties of the genus. In that study, they encountered four *A. caviae* strains that produced acid from amygdalin and from raffinose, which coincides with the profile of A2-50\(^T\) (Table 1). Other traits that differentiated A2-50\(^T\) and A2-67\(^T\) from other species were their capacity to produce acid from D-arabinose, glycerol and salicin as well as to hydrolyse aesculin, and their negative results for the Voges–Proskauer test, lysine decarboxylase activity and production of gas from glucose and acid from cellobiose and D-mannose (Table 1). Interestingly, strain A2-67\(^T\) displayed two colony types of the same size (4–5 mm in diameter). One was opaque, circular and beige in colour, while the other was translucent on TSA after 48 h at 30 °C. These two morphologies were also observed on blood agar. The two colony types responded to the same biochemical responses and showed identical ERIC-PCR profiles (not shown).

Cell sizes and morphologies and the presence of flagella were determined by electron microscopy following procedures described previously (Collado et al., 2009).

The susceptibilities of strains A2-50\(^T\) and A2-67\(^T\) against 27 antibiotics were tested, as described previously (Alperi et al., 2010). Both strains showed resistance to amoxicillin, amoxicillin plus clavulanic acid, ticarcillin, ticarcillin plus clavulanic acid, cephalothin and erythromycin; A2-50\(^T\) was immediately susceptible to streptomycin, while A2-67\(^T\) showed resistance to cefoxitine. Both strains were susceptible to the other antimicrobials tested.

The 16S rRNA gene sequences, MLPA, phenotypic characterization and DNA–DNA reassociation results all clearly separated strain A2-50\(^T\) from A2-67\(^T\) and both strains from the other *Aeromonas* species.

**Description of Aeromonas taiwanensis** sp. nov.

*Aeromonas taiwanensis* (tai.wan.en’sis. N.L. masc. adj. taiwanensis of Taiwan, where the type strain was isolated).

Cells are straight, Gram-negative, non-sporo-forming, non-encapsulated, motile rods, 0.8–1 μm wide and 1.8–2.5 μm long. Oxidase- and catalase-positive, reduces nitrate to nitrite and resistant to vibriostatic agent O/129. Colonies on TSA are 2–5 mm in diameter, opaque, circular and beige in colour after 48 h at 30 °C. No brown diffusible pigment is produced on TSA. Optimal growth occurs at 30 °C. Growth is observed at 36 °C but not at ≥40 or 4 °C after 24 h on sheep-blood agar. No β-haemolysis is observed on sheep-blood agar at 30 or 36 °C. Grows on MacConkey agar and in the absence of NaCl but not at 6% NaCl after 24 h on TSA. Optimal growth occurs at pH 8.5–9.5 after 24 h on TSA; does not grow at pH 4.5. Produces indole from tryptophan and arginine dihydrolase activity, is positive for the ONPG test (β-galactosidase activity) and hydrolysis of aesculin, gelatin, DNA and L-tryptophan and is able to use citrate. Negative for the Voges–Proskauer test, hydrolysis of elastin and urea, production of hydrogen sulfide from cysteine and gas from glucose, swarming and for lysine decarboxylase and ornithine decarboxylase tests. Hydrolyses starch, arbutin and aesculin. Uses D-glucose, L-arabinose, D-mannitol, maltose, N-acetylgalactosamine, potassium gluconate, capric acid, malic acid, glycogen and potassium gluconate as sole carbon and energy sources, but not potassium 2-ketogluconate, potassium 5-ketogluconate, D-mannose, adipic acid, phenylacetic acid or trisodium citrate. Acid is produced from D-glucose, sucrose, L-arabinose, raffinose, D-ribose, amygdalin, salicin, D-galactose, D-fructose, D-mannitol, glycerol, N-acetylgalactosamine, maltose and trehalose, but not from cellobiose, D-arabinose, L-rhamnose, myo-inositol, erythritol, L- or D-xylene, D-adonitol, methyl β-D-xylopyranoside, D-mannose, L-sorbitol, L-rhamnose, dulcitol, inositol, D-sorbitol, methyl α-D-mannopyranoside, methyl z-D-glucopyranoside, lactose, melibiose, inulin, melezitose, xylitol, gentiobiase, turanose, D-lyxose, D-tagatose, L- or D-fucose or L- or D-arabitol. The API 20E and API 20NE codes for the type strain are 3266127 and 7575754, respectively. Resistant to amoxicillin, amoxicillin plus clavulanic acid, ticarcillin, ticarcillin plus clavulanic acid, cephalothin and erythromycin, shows intermediate resistance to streptomycin and is susceptible to piperacillin, piperacillin plus tazobactam, cefotaxime, cefotaxime, cefoperazone, cefazidime, ceftriaxone, ceftazidime, ceftriaxone, cefepime, aztreonam, imipenem, gentamicin, kanamycin, tobramycin, amikacin, tetracycline, ciprofloxacin, nalidixic acid, fosfomycin, trimethoprim-sulfamethoxazole and chloramphenicol.

The type strain, A2-50\(^T\) (=CECT 7403\(^T\) =LMG 24683\(^T\)), was isolated from a wound infection from a patient at Tainan, Taiwan.

**Description of Aeromonas sanarellii** sp. nov.

*Aeromonas sanarellii* [s.a.n.a.rell’i.i. N.L. gen. masc. n. sanarellii of Sanarelli, named in honour of G. Sanarelli, for his contribution to our knowledge of *Aeromonas*, having described the first member of *Aeromonas* as *Bacillus hydrophilus fuscus* in 1891 (Martin-Carnahan & Joseph, 2005)].

Cells are straight, non-sporo-forming, non-encapsulated, motile rods, 0.7 μm wide and 2.5 μm long. Gram-negative, oxidase- and catalase-positive, reduces nitrate to nitrite and resistant to vibriostatic agent O/129. Displays two colony types on TSA and blood agar. Colonies on TSA are 4–5 mm in diameter; one colony type is opaque, circular and beige in colour, while the other is translucent, after 48 h at 30 °C. No brown diffusible pigment is produced on TSA. Optimal growth occurs at 30 °C; growth is observed up to 45 °C but not at 50 °C after 48 h or at 4 °C after 7 days on sheep-blood agar. No β-haemolysis is observed on sheep-blood agar at 30 or 36 °C. Able to grow on MacConkey and in the absence of NaCl but not at 6% NaCl on TSA.
Optimal growth occurs at pH 9 after 24 h on TSA; does not grow at pH 4.5. Produces indole from tryptophan and arginine dihydrolase activity and is positive for the ONPG test (β-galactosidase) and hydrolyses arbutin, starch, aesculin, gelatin, DNA and L-tryptophan. Negative for the Voges–Proskauer test, utilization of citrate, hydrolysis of elastin and urea, production of hydrogen sulfide from cysteine and gas from glucose, swarming and for lysine decarboxylase and ornithine decarboxylase tests. Able to use potassium gluconate, D-glucose, L-arabinose, D-mannitol, maltose, N-acetylglucomamine, potassium gluconate, capric acid and malic acid as sole carbon and energy sources but not potassium 2-ketogluconate, potassium 5-ketogluconate, D-mannose, adipic acid, phenylacetic acid or trisodium citrate. Acid is produced from D-glucose, sucrose, L-arabinose, D-ribose, amygdalin, salicin, D-galactose, D-fructose, D-mannitol, glycerol, N-acetylglucomamine, maltose, trehalose and glycogen but not from cellulobiose, raffinose, D-arabinose, L-rhamnose, myo-inositol, erythritol, L- or D-xylene, D-adonitol, methyl β-D-xlyopyranoside, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, D-sorbitol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, lactose, melibiose, inulin, melezitose, xyitol, gentiose, turanose, D-lyxose, D-tartrate, L- or D-fucose or L- or D-arabitol. The API 20E and API 20NE codes for the type strain are 3066127 and 7575754, respectively. Resistant to amoxicillin, amoxicillin and clavulanic acid, ticarcillin, ticarcillin plus clavulanic acid, cefalothin, cefoxitin, ceftazidime, ceftriaxone, cefepime, aztreonam, imipenem, gentamicin, kanamycin, tobramycin, amikacin, streptomycin, tetracycline, ciprofloxacin, nalidixic acid, fosfomycin, trimethoprim-sulfamethoxazole and chloramphenicol.

The type strain, A2-67T (=CECT 7402T =LMG 24682T), was isolated from a wound culture from a patient at Tainan, Taiwan.

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References
Two novel clinical Aeromonas species from Taiwan


