Aeromonas rivuli sp. nov., isolated from the upstream region of a karst water rivulet

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Two freshwater isolates (WB4.1-19T and WB4.4-101), sharing 99.9 % 16S rRNA gene sequence similarity, were highly related to Aeromonas sobria (99.7 % similarity; 6 bp differences). A phylogenetic tree derived from a multi-locus phylogenetic analysis (MLPA) of the concatenated sequences of five housekeeping genes (gyrB, rpoD, recA, dnaJ and gyrA; 3684 bp) revealed that both strains clustered as an independent phylogenetic line next to members of Aeromonas molluscorum and Aeromonas bivalvium. The DNA–DNA reassociation value between the two new isolates was 89.3 %. Strain WB4.1-19T had a DNA–DNA relatedness value of <70 % with the type strains of the other species tested. Phenotypic characterization differentiated the two novel strains from all other type strains of species of the genus Aeromonas. It is concluded that the two new strains represent a novel species of the genus Aeromonas, for which the name Aeromonas rivuli sp. nov. is proposed, with the type strain WB4.1-19T (=CECT 7518T=DSM 22539T=MDC 2511T).

The genus Aeromonas (family Aeromonadaceae, class Gammaproteobacteria), includes bacteria that are considered autochthonous of aquatic environments and are often associated with fish and human diseases (Martin-Carnahan & Joseph, 2005; Figueras, 2005; Janda & Abbott, 2010). At the time of writing, the genus includes more than 20 recognized species (Martin-Carnahan & Joseph, 2005; Saavedra et al., 2006; Miñana-Galbis et al., 2007; Demarta et al., 2008; Martínez-Murcia et al., 2008; Beaz-Hidalgo et al., 2009; Alperi et al., 2010b). Aeromonas group 501 has been recently described and named as Aeromonas diversa (Miñana-Galbis et al., 2010) and two further species, Aeromonas taiwanensis and Aeromonas sanarellii, have also been described recently (Alperi et al., 2010a). The taxonomy of the genus Aeromonas is considered complex when using either classical identification tools, such as phenotypic characteristics, or the 16S rRNA gene (Martínez-Murcia et al., 2005; Ørmen et al., 2005). 16S rRNA gene sequence analysis is considered to be a robust tool that is widely used in bacterial taxonomy. A threshold value for sequence similarity of about 97 % was proposed for the latter gene, below which strains exhibit sufficiently low DNA–DNA reassociation values (i.e. <70 %) to be considered as representing separate species (Stackebrandt & Ebers, 2006, and references therein). Recently, based on a broader dataset, the threshold value was increased to 98.7–99.0 % in order to facilitate taxonomic studies without sacrificing the quality and precision of a ‘species’ description (Stackebrandt & Ebers, 2006). In the genus Aeromonas, only one species (Aeromonas simiae) shows 16S rRNA gene sequence similarities below 97 % (96.8 %), while many of the others show values greater than 99.0 %. Strains of Aeromonas bestiarum, Aeromonas salmonicida and Aeromonas piscicola possess an identical sequence for this gene (Martínez-Murcia et al., 2005; Beaz-Hidalgo et al., 2009; Alperi et al., 2010a, b). These high 16S rRNA gene sequence similarities and the microheterogeneities found in this gene hamper its utility for analysis of this genus (Alperi et al., 2008, 2010a, b).

The use of housekeeping genes has been recommended as part of a polyphasic approach for the genomic circum- scription of species and as a means of differentiating taxa from neighbouring species detected by, for example, 16S rRNA gene sequences (Stackebrandt et al., 2002). We have

Abbreviations: MLPA, multi-locus phylogenetic analysis; VP, Voges–Proskauer.


Supplementary figures and tables are available with the online version of this paper.
introduced sequence analyses of housekeeping genes (gyrB and rpoD) for studies on the phylogenetic relationships between members of the genus Aeromonas (Yáñez et al., 2003; Soler et al., 2004). This approach turned out to constitute a turning point in the taxonomy of aeromonads as these genes, in common with other genes investigated recently (rpoB, dnaJ, recA and cpn60) by other authors (Küffer et al., 2006; Nhung et al., 2007; Sepe et al., 2008; Miñana-Galbis et al., 2009), show a much higher resolution than 16S rRNA gene sequences. The analysis of housekeeping genes has not only led to some proposals for the reclassification of existing taxa (Martínez-Murcia et al., 2009), but has also enabled the recognition of novel species of the genus Aeromonas, e.g. Aeromonas aquariorum and Aeromonas tecta (Martínez-Murcia et al., 2008; Demarta et al., 2008) and, more recently, A. piscicola, A. fluvialis, A. taiwanensis and A. sanarellii (Beaz-Hidalgo et al., 2009; Alperi et al., 2010a, b).

In a recent environmental study, the taxonomic diversity of aerobic bacteria (n=681) in a karst water rivulet in northern Germany (Westerhöfer Bach) was evaluated and 40 different genera and about 60 novel phylospecies were identified (Cousin et al., 2008). Fifteen of the recovered isolates, belonging to the genus Aeromonas on the basis of partial 16S rRNA gene sequences (432 bp), were sent to our laboratory for further molecular characterization. The present communication describes the polyphasic approach adopted for the classification of a novel species of the genus Aeromonas.

All 15 isolates were cultured on sheep blood agar at 30 °C and DNA was extracted from single colonies using InstaGene Matrix (Bio-Rad Laboratories). The conditions for rpoD (820 bp) and 16S rRNA gene (1503 bp) sequence analysis, including primers, amplification conditions and sequencing, were as previously described (Martínez-Murcia et al., 1992; Soler et al., 2004). The sequences obtained were aligned independently with the sequences of the type and reference strains of all the members of the genus Aeromonas taken from our in-house database (constructed with our own sequences) and those that are available in GenBank, using the CLUSTAL_X program version 1.8 (Thompson et al., 1997). Genetic distances were obtained using Kimura’s two-parameter model (Kimura, 1980). Evolutionary trees were constructed by the neighbour-joining method (Saitou & Nei, 1987) using the MEGA4 program (Tamura et al., 2007) and maximum-parsimony method (for the 16S rRNA gene) using PAUP* version 4.0b10 (Swofford, 2002). The stability of the relationships was assessed by bootstrapping (1000 replicates).

The phylogenetic analysis based on the rpoD gene revealed that 13 of the 15 strains belonged to recognized species of the genus Aeromonas, while two strains (WB4.1-19T and WB4.4-101) grouped as an individual lineage within the A. molluscorum/A. bivalvium cluster (data not shown). The two novel isolates shared 98.6 % rpoD gene sequence similarity (9 bp differences between their sequences). Sequence similarity with the closest species, A. molluscum, was 94.3 % for strain WB4.1-19T and 94.5 % for strain WB4.1-101. These values are below the minimum intra-species similarity of 97.4 % previously established for the rpoD gene in the genus Aeromonas (Soler et al., 2004).

The almost complete 16S rRNA gene (1503 bp) was sequenced from both novel strains and revealed that the strains were highly related to each other (99.9 % similarity; 2 bp differences) sharing a very high gene sequence similarity (99.7 %) with Aeromonas sobria NCIMB 12065T. These results were in agreement with those obtained at the DSMZ laboratory (Braunschweig, Germany) using partial sequences (432 bp) of the 16S rRNA gene. The similarities found for the two novel strains were in line with those shown by other species and indicated that the 16S rRNA gene threshold value for delineation of species of the genus Aeromonas (without considering those that show 100 % similarity) should be 99.5–99.7 %, which is higher than the new values of 98.7–99.0 % recently proposed by Stackebrandt & Ebers (2006).

In the phylogenetic trees constructed using the 16S rRNA gene sequences, the two new isolates clustered next to A. sobria NCIMB 12065T. This association was only supported by low bootstrap values (<50 %) no matter whether the neighbour-joining (Fig. 1) or maximum-parsimony algorithms (see Supplementary Fig. S1 in IJSEM Online) were used to determine phylogeny. Chromatogram analysis of the 16S rRNA gene sequences of both strains showed microheterogeneities in two positions (1011 and 1018) for strain WB4.1-19T and in four positions (258, 469, 1355, 1357) for strain WB4.4-101 (see Supplementary Table S1). Microheterogeneities have been described for other species of the genus Aeromonas (Alperi et al., 2008, 2010a, b).

The multi-locus phylogenetic analysis (MLPA) involved sequencing the gyrB (923 bp), rpoD (652 bp), recA (600 bp), dnaJ (800 bp) and gyrA (709 bp) genes. A phylogenetic tree was constructed with the concatenated sequences of these five genes (3684 bp). This analysis was performed at the Molecular Diagnostic Center (MDC), Orihuela, Spain, as described by Alperi et al. (2010a).

The MLPA tree revealed, in agreement with all five single-gene phylogenies and in contrast to that of the 16S rRNA gene, that strains WB4.1-19T and WB4.4-101 were not phylogenetically related to A. sobria, but appeared as an independent branch in a cluster that included A. molluscum and A. bivalvium (Fig. 2). Species delineation based on the analysis of five housekeeping genes was recommended by the ad-hoc committee (Stackebrandt et al., 2002), but only the papers that described the species A. fluvialis (Alperi et al., 2010b) and A. taiwanensis and A. sanarellii from clinical isolates (Alperi et al., 2010a), have complied with this recommendation.

DNA–DNA reassociation experiments were performed between the two novel isolates and between strain
WB4.1-19<sup>T</sup> and the type strains of the closest species, *A. sobria*, *A. molluscorum* and *A. bivalvium*, as well as with *A. bestiarum*, *A. encheleia*, *A. eucrenophila*, *A. piscicola*, *A. popoffii*, *A. salmonicida* and *A. tecta*. DNA extraction and DNA–DNA reassociation experiments were conducted as previously described (Alperi et al., 2010b). The DNA–DNA reassociation value between strains WB4.1-19<sup>T</sup> and WB4.4-101 was 89.5 % (± 6.5 %), while the type strains of the other species of the genus *Aeromonas* showed values below the 70 % threshold established for species delineation (Stackebrandt et al., 2002; see Supplementary Table S2). Optimal growth temperature and pH were determined in tryptic soy broth (TSB, Difco) after 24 h by optical density. Cell sizes, morphologies and the presence of flagella were determined by electron microscopy using previously described methods (Collado et al., 2009). Both strains were straight, non-spore-forming, non-encapsulated rods that were motile by means of polar flagella (see Supplementary Fig. S2).

The cultural characteristics of strains WB4.1-19<sup>T</sup> and WB4.4-101, i.e. the size and colour of colonies and production of a brown diffusible pigment, were determined on tryptic soy agar (TSA, Difco) at 30 °C for 24 h. Sheep blood agar (Biomedics) was used to evaluate haemolysis under the same conditions. Twenty eight phenotypic tests selected from Abbott et al. (2003) and also performed in a previous study (Alperi et al., 2010b) were used for the characterization of strains WB4.1-19<sup>T</sup> and WB4.4-101. In addition, tests were performed to determine the utilization of L-arabinose, L-histidine, L-proline, DL-lactate and salicin as carbon sources and for the hydrolysis of starch. All tests were conducted in triplicate at 30 °C. Some tests were further confirmed using commercial identification kits (API 20NE and API 20E; bioMérieux). Additional tests included in the latter kits, together with the assimilation/oxidation reactions of 49 carbohydrates using the API 50CH kit (bioMérieux) were also considered. Phenotypic characteristics that differentiated both new isolates from other species of the genus *Aeromonas* are presented in Table 1. All type strains of recognized species of the genus *Aeromonas*, including the recently described members, were tested (Table 1) under identical conditions to those used for strains WB4.1-19<sup>T</sup> and WB4.4-101. Interestingly the two novel isolates showed phenotypic similarity with *A. molluscorum* as they were the only taxa
that all gave a negative result in tests for indole, Voges–
Proskauer (VP) reaction, gas from glucose and for
ornithine- and lysine decarboxylase. The characteristics
that differentiated the novel isolates from
*A. molluscorum*
were their ability to hydrolyse starch, but not to use or
produce acid from L-arabinose. Other useful tests to
differentiate the two novel strains from other species of
the genus *Aeromonas* include their inability to produce
indole, gas from D-glucose, VP, lysine decarboxylase and
\(\beta\)-haemolysis from sheep blood agar (Table 1).

Based on molecular and phenotypic evidence, it is
concluded that strains WB4.1-19\(^T\) and WB4.4-101 repre-
sent a novel species of the genus *Aeromonas*, for which the
name *Aeromonas rivuli* sp. nov. is proposed.

**Description of *Aeromonas rivuli* sp. nov.**

*Aeromonas rivuli* (ri’vu.li. L. gen. masc. n. rivuli of/from a
rivulet, a small creek).

Cells are Gram-negative, non-spore-forming motile rods
with a polar flagellum and are 2.0–2.5 \(\mu\)m long and 0.5–
0.7 \(\mu\)m wide. Oxidase and catalase-positive, reduces
nitrates to nitrites and is resistant to the vibriostatic agent
O/129 (150 \(\mu\)g). Colonies on TSA are opaque, beige in
colour and 2.0–2.5 mm in diameter after 48 h incubation
at 30 °C and 1.0–2.0 mm at 37 °C. No brown diffusible
pigment is produced on TSA at 25 °C or 30 °C. No
haemolysis is observed on sheep blood agar at 30 °C.
Growth occurs at 7–37 °C and at 0–3 % NaCl (w/v).
Optimal growth is at 30 °C and at pH 8.7–9.0 after 24 h
on TSB. Positive for the \(\beta\)-galactosidase test, ADH, hydrolysis
of aesculin, gelatin, starch, arbutin, Tween 80 and DNA.

Negative result in tests for ornithine- and lysine decarbo-
xylase, VP, production of indole from tryptophan, gas from
glucose, hydrogen sulphide from cysteine and hydrolysis of
elastin. Utilization of citrate is variable. Able to utilize
glycerol, D-galactose, maltose, starch, glycogen, sucrose,
L-histidine, L-proline, salicin and D-mannitol, but not DL-
lactate, L-arabinose, potassium gluconate, potassium 2-
keto-gluconate or potassium 5-ketogluconate. Acid is
produced from glycerol (only with API 50CH), D-ribose,
D-galactose, D-glucose, D-fructose, D-mannose, D-mannitol,
N-acetylglucosamine, salicin, maltose, sucrose and trehalose.

Does not produce acid from erythritol, D-arabinose, L-
arabinose, D-xylose, L-xylose, D-adonitol, methyl \(\beta\)-D-xylo-
pyranoside, L-sorbose, L-rhamnose, dulcitol, inositol,
D-sorbitol, methyl \(\alpha\)-D-mannopyranoside, methyl \(\alpha\)-D-gluco-
pyranoside, amygdalin, lactose, melibiose, inulin, melezitose,
Table 1. Key phenotypic characteristics that differentiate strains WB4.1-19\textsuperscript{†} and WB4.4-101 from other species of the genus Aeromonas

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*Result from Demarta et al. (2008), performed at 30 °C.
†VP negative result was taken from the species description of Martínez-Murcia et al. (2008) and not from the table where there was an later erratum, (+).
‡Result from Miñana Galbis et al. (2002), performed at 25 °C.
§Result from Allen et al. (1983), performed at 22 °C.
¶Result from Esteve et al. (1995), test performed at 28 °C.
‖Result from Huys et al. (1997), test performed at 28 °C.
#Acid production from glycerol was negative when determined in tube but positive when tested by API 50CH.
\*Result from Valera & Esteve (2002), tests performed at 28 °C.
raffinose, xylitol, gentiobiose, turanose, d-lyxose, d-tagatose, d-fucose, L-fucose, d-arabitol or L-arabitol. Production of acid from cellobiose is variable. The API 20NE and API 20E profiles for strains WB4.1-19T and WB4.1-101 were 5576354 and 3006167, respectively.

The type strain, WB4.1-19T (=CECT 7518 = DSM 225395 = MDC 2511T), was isolated from a karst hard water creek, Westerhöfer Bach, located at the north-western slope of the Harz Mountain, Lower Saxony, Germany. The isolation site was 350 m downstream from the discharge site.

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**References**


