Classification of avian haemolytic *Actinobacillus*-like organisms (Bisgaard taxon 26) associated with anseriforme birds as *Actinobacillus anseriformium* sp. nov.

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Avian haemolytic *Actinobacillus*-like organisms have tentatively been named Bisgaard taxon 26. Phenotypic information has been published on 65 strains of this taxon. In the current study, 31 isolates were selected for genotypic characterization. Thirty strains had the same *rpoB* sequence and only one strain diverged in 1 nt. The highest *rpoB* similarity to members of other taxa was 89.7 % to the type strain of *Actinobacillus equuli* subsp. *haemolyticus* and the similarity to the type strain of the type species, *Actinobacillus lignieresii*, was 88.2 %. The lowest 16S rRNA gene sequence similarity between strains of the group was determined in previous investigations to be 99.6 % and the highest similarities of 96.4 and 96.2 % outside the group were obtained to the reference strain of *Actinobacillus* genomospecies 2 and to the type strain of *A. equuli* subsp. *equuli*, respectively; 95.8–95.3 % similarity was obtained with the type strain of *A. lignieresii*. *recN* gene sequence similarities within the group were from 99.5 % (strains F66^T and F64) to 99.8 % (strains F66^T and F67) corresponding to genome similarities of 93.9–94.6 %, which are near the upper limit for species compared with other members of the *Pasteurellaceae*. The highest *recN* similarity outside the group (83.4 %) was observed to the type strain of *Actinobacillus capsulatus*, whereas the similarity to the type strain of *A. lignieresii* was 80.9 %, corresponding to genome similarities of 57.7 and 52.0 %, respectively. All isolates meet the phenotypic characters outlined for *Actinobacillus* (urease-, phosphatase- and porphyrin-positive, indole-negative, acid production from fructose, sucrose, maltose and dextrin). β -Haemolysis of bovine blood is observed and isolates may demonstrate *in vitro* satellitic growth, referred to as V-factor or NAD requirement. Isolates have been obtained from the upper respiratory tract of web-footed birds in which they may cause sinusitis, conjunctivitis and septicaemia. Based on the characterization reported, it is proposed that the isolates belong to a novel species, *Actinobacillus anseriformium* sp. nov., which includes taxon 26 and a V-factor-dependent strain. The major fatty acids of the type strain are C_{16:1} ω 7c, C_{14:0}, C_{16:0} and C_{14:0} 3-OH and/or iso-C_{16:1} I, corresponding to the profile observed for the type strain of *A. lignieresii*. Five to 12 characters separate *A. anseriformium* from other taxa of *Actinobacillus*, with *Actinobacillus ureae* being most closely related; *A. anseriformium* can be differentiated from *A. ureae* based on haemolysis, β -glucosidase, and production of acid from (–)-D-sorbitol, trehalose and glycosides. The type strain of *A. anseriformium* is F66^T (=CCUG 60324^T=CCM 7846^T), which was isolated from conjunctivitis in a White Pekin duck.

Christensen & Bisgaard (2010) briefly reviewed the molecular classification of selected members of the *Pasteurellaceae*

The GenBank/EMBL/DDBJ accession numbers for the partial *rpoB* sequences of strains F66^T and 20834/6 are HQ257237 and HQ257238, respectively, and for the partial *recN* sequences of strains F66^T and F64 are HQ257239 and HQ257240, respectively.

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

of veterinary importance and its impact on diagnostics and understanding the phylogeny and epidemiology of these taxa. These organisms are mainly to be found within the genera *Actinobacillus*, *Avibacterium*, *Bibersteinia*, *Gallibacterium*, *Histophilus*, *Mannheimia* and *Pasteurella*. However, several unclassified taxa of veterinary importance exist that remain to be classified. In addition, many taxa have been reported that impose major diagnostic problems (<http://www.the-icsp.org/taxa/PasteurellaceaeList.htm>) (Christensen & Bisgaard,

2008). Avian haemolytic *Actinobacillus* sp. associated with the mucosa of the respiratory tract of apparently normal White Pekin ducks was first reported by Bisgaard (1982). DNA–DNA hybridizations between (–)-D-sorbitol-negative (F64; biovar 3) and -positive (F66^T; biovar 1) isolates demonstrated 82 % DNA binding. These isolates, however, only clustered with a (–)-D-mannitol-negative isolate (F97) with 65 % DNA binding, whereas around 50 % DNA binding was observed with the type strain of *Actinobacillus ureae* (Piechulla *et al.*, 1985). Blindness from conjunctivitis in a Canada goose (*Branta canadensis*) caused by *Actinobacillus suis* was reported by Maddux *et al.* (1987). These bacteria have subsequently been shown to be phenotypically similar to avian haemolytic *Actinobacillus*-like organisms (M. Bisgaard, unpublished data), later tentatively named taxon 26 (Bisgaard, 1993). DNA–DNA hybridization results reported by Piechulla *et al.* (1985) and Mutters *et al.* (1989) located taxon 26 in the vicinity of *Actinobacillus*.

Subsequent studies on inter- and intrafamilial similarities of rRNA cistrons of the *Pasteurellaceae* placed taxon 26 (NCTC 11410; see Supplementary Table S1, available in IJSEM Online) at the common root of the rRNA branches for *Pasteurella multocida*, *Actinobacillus lignieresii* and *Haemophilus influenzae* (De Ley *et al.*, 1990). The classification of the genus dates back to Brumpt (1910). Attempts have been made to reclassify *Actinobacillus sensu stricto* to include the type species *A. lignieresii* and the seven species *Actinobacillus equuli*, *Actinobacillus capsulatus*, *A. suis*, *Actinobacillus pleuropneumoniae*, *Actinobacillus hominis*, *A. ureae* and *Actinobacillus arthritidis*, whereas the eight species [*Actinobacillus*] *seminis*, [*Actinobacillus*] *rossii*, [*Actinobacillus*] *minor*, [*Actinobacillus*] *indolicus*, [*Actinobacillus*] *porcinus*, [*Actinobacillus*] *delphinicola*, [*Actinobacillus*] *scotiae* and [*Actinobacillus*] *succinogenes* need reclassification (Christensen & Bisgaard, 2008). This proposal has mainly been based on phylogenetic 16S rRNA gene sequence comparisons, DNA–DNA reassociation data, phylogenetic comparisons of additional conserved gene sequences and phenotypic data (Christensen *et al.*, 2007). *A. capsulatus* was found to be polyphyletic with *Actinobacillus sensu stricto* by 16S rRNA gene sequence comparison, whereas all other data pointed to classification with *Actinobacillus sensu stricto* (Kuhnert *et al.*, 2007).

According to Busse *et al.* (1997), polyamine patterns are useful for discrimination within the family *Pasteurellaceae*. Members of the genus *Actinobacillus sensu stricto* have been characterized by the presence of 1,3-diaminopropane as the predominant compound, which makes up some 90 % of the total polyamines of taxon 26 (MCCM 01376=F64) and thus corresponds well with the type strain of *A. lignieresii*, the type species of the genus *Actinobacillus*. However, [*Pasteurella*] *langaaensis* demonstrated a polyamine pattern close to taxon 26 (Busse *et al.*, 1997) (square brackets around genus names indicate species that possibly should be excluded from the genera *Pasteurella*, *Actinobacillus* or *Haemophilus*, in accordance with the terminology of Mutters *et al.*, 1989). Comparison of 16S rRNA gene sequences between strains F66^T (biovar 1) and F97 (biovar 2) demonstrated 99.8 %

similarity, whereas the similarity to strain F64 (biovar 3) was 99.6 % (Christensen *et al.*, 2003). A single isolate, 20948/1, obtained from sinusitis in a goose, demonstrated 99.8 % 16S rRNA gene sequence similarity to F66^T and represents a V-factor-dependent isolate of taxon 26 (Christensen *et al.*, 2009). Maximum-likelihood analysis of 16S rRNA gene sequences of taxa of *Pasteurellaceae* included taxon 26 with the monophyletic group of *Actinobacillus sensu stricto* (Christensen *et al.*, 2003; Christensen & Bisgaard, 2004). Delineation of the genus *Actinobacillus* by comparison of partial *infB* sequences showed that [*Pasteurella*] *pneumotropica* P421^T and taxa 26 (CCUG 28015) and 8 (P1572) of Bisgaard were more remotely related with core species of *Actinobacillus* and should not be classified with *Actinobacillus sensu stricto* if an 85 % similarity demarcation line is used for delineation of *Actinobacillus sensu stricto* (Nørskov-Lauritsen *et al.*, 2004).

A new and simplified procedure to identify species of *Actinobacillus*, *Avibacterium*, *Gallibacterium*, *Haemophilus*, *Mannheimia*, *Nicoletella* and *Pasteurella*, which are most commonly isolated from clinical samples of diseased animals in veterinary diagnostic laboratories, was presented recently (Dousse *et al.*, 2008). The procedure enabled identification of 240 out of 267 field isolates investigated. According to this method, taxon 26 would be classified with *Actinobacillus equuli* subsp. *haemolyticus*, undermining our present understanding of the biology and significance of taxa of *Pasteurellaceae*. For the same reasons, the aims of the present investigation were to further characterize, classify and name organisms tentatively named taxon 26.

A total of 65 strains were included in the investigation, including all biovars of taxon 26 that have been characterized phenotypically according to Bisgaard *et al.* (1991) and Christensen *et al.* (2007) as reported previously (Christensen *et al.*, 2003, 2009). Out of the 65 strains, only 31 isolates have been kept/survived and are available for genotypic characterization. The partial *rpoB* sequences of all isolates investigated (Supplementary Table S1, available in IJSEM Online) were determined according to Mollet *et al.* (1997) covering the region 509–680 (*Escherichia coli* numbering) of the deduced protein sequence, as reported previously (Angen *et al.*, 2003; Korczak *et al.*, 2004). *recN* gene sequences were used as a representative target for determining whole-genome sequence similarity as described by Kuhnert & Korczak (2006), with 1283 bp of the gene being sequenced in three strains. Whole genome similarity values were calculated according to Zeigler (2003).

A BLAST search (Altschul *et al.*, 1997) was performed in GenBank (Benson *et al.*, 2010). Pairwise comparisons of similarity were performed by the program WATER included in EMBOSS (Rice *et al.*, 2000). Multiple alignments were performed with CLUSTAL_X (Thompson *et al.*, 1997). Sequences in multiple alignments were trimmed to the same length in BioEdit (Hall, 1999) by removal of all columns with gaps in the 5' and 3' ends of sequences. Phylogenetic trees were drawn from MEGA4 (Tamura *et al.*,

2007). Maximum-likelihood analysis including bootstrap analysis was performed by fastDNAm1 (Felsenstein, 1995; Olsen *et al.*, 1994) on a Linux-compatible server. The analysis was run with transition/transversion ratios of 2.6 and 2.3 for *rpoB* and *recN*, respectively.

The phenotypic results available for the 65 isolates from anserine birds have all been reported previously (Bisgaard, 1982; Christensen *et al.*, 2003, 2009). Forty-nine isolates belonged to biovar 1, whereas 11 isolates belonged to biovar 2 and three belonged to biovar 3. In addition, one V-factor-requiring strain was included that was originally published by Christensen *et al.* (2009). Two isolates originally classified with taxon 26 (biovars 3 and 4) could not be confirmed by genotypic analysis and were excluded from the investigation. Results reported are in accordance with those reported for *Actinobacillus sensu stricto* (Christensen & Bisgaard, 2004; Olsen & Møller, 2005; Kuhnert *et al.*, 2007). Characters separating taxon 26 from other species of *Actinobacillus sensu stricto* are in Table 1. Five to 12 characters separate taxon 26 from other taxa of *Actinobacillus*, with *A. ureae* demonstrating the closest relationship; taxon 26 can be differentiated from *A. ureae* based on differences in haemolysis, β -glucosidase and acid production from (–)-D-sorbitol, trehalose and glycosides. Twelve characters separate taxon 26 and the V-factor-requiring strain from *A. lignieresii* (Table 1).

Twenty-nine strains representing biovars 1 to 3 had the same *rpoB* sequence as a representative strain (F66^T; biovar 1). Strain 20834/6 diverged in 1 nt (99.6 % similarity). Highest *rpoB* similarity outside the group of strains investigated (89.7 %) was obtained with the type strain of *A. equuli* subsp. *haemolyticus*, whereas the similarity to the type strain of *A. lignieresii* was slightly lower (88.2 %). Phylogenetic analysis of taxon 26 and type and reference strains of *Actinobacillus* showed that it was a distantly related member of *Actinobacillus sensu stricto*. The apparent relationship with *[A.] minor* was unsupported by bootstrap analysis (Supplementary Fig. S1, available in IJSEM Online) and not confirmed by 16S rRNA or *recN* phylogenetic analysis (see below). One reason for this could be that only a partial region was analysed. The *rpoB* sequence-based phylogeny was included to evaluate the genotypic coherence of strains of taxon 26 studied and not to investigate phylogenetic relationships at the genus level.

Christensen & Bisgaard (2004) reanalysed sequences with a minimum length of 1346 nt from 83 strains representing 58 named and 25 unnamed taxa of the *Pasteurellaceae* which contained fewer than 10 ambiguous bases and showed that taxon 26 should be classified with *Actinobacillus sensu stricto*. 16S rRNA gene sequence similarities of strains representing biovars 1–3 were 99.6–99.8 % (Christensen *et al.*, 2003, 2009) indicating that taxon 26 seems to represent a single species. 16S rRNA gene sequence similarities between taxon 26 and the type strains of named taxa of *Actinobacillus sensu stricto*, genomospecies 1 and 2, and Bisgaard taxon 8 varied between 93.9 % (*A. capsulatus*) and 96.4 % (*Actinobacillus*

genomospecies 2) with 95.3–95.8 % similarity to the type strain of *A. lignieresii*, indicating that DNA–DNA reassociation experiments are not mandatory for establishing and naming taxon 26 as a novel species of *Actinobacillus* (Tindall *et al.*, 2010).

recN similarities within taxon 26 varied from 99.5 % (F66^T and F64) to 99.8 % (F66^T and F67), corresponding to genome similarities of 93.9–94.6 %, which is clearly at the upper limit for species compared to other members of the *Pasteurellaceae* (Christensen *et al.*, 2011; Kuhnert & Korczak, 2006). The highest *recN* similarity outside taxon 26 (83.4 %) was observed with the type strain of *A. capsulatus*, whereas similarity to the type strain of *A. lignieresii* was 80.9 % corresponding to genome similarities of 57.7 % and 52.0 %, respectively, for *A. capsulatus* and *A. lignieresii*, clearly confirming the distant relationship of taxon 26 to other species of *Actinobacillus*. Phylogenetic analysis of *recN* gene sequences of taxon 26 and type and reference strains of *Actinobacillus* gave similar results to the 16S rRNA analysis in Fig. 1, in that it was the most distantly related member of *Actinobacillus sensu stricto*, with *[A.] minor* being the most closely related outgroup (Supplementary Fig. S2, available in IJSEM Online). The 16S rRNA gene sequence phylogeny shown on Fig. 1, including *Actinobacillus sensu stricto*, and *[A.] minor* and *Mannheimia haemolytica* as outgroup, documented monophyly of the isolates studied with *Actinobacillus sensu stricto*, including *A. lignieresii*. Multiple alignments and phylogenetic trees were constructed as described above for *rpoB*- and *recN*-derived phylogenies. In the current 16S rRNA gene sequence-based phylogeny, a transition/transversion ratio of 1.1 optimized the multiple likelihood.

DNA–DNA hybridizations between F66^T (biovar 1) and F64 (biovar 3) demonstrated 82 % DNA binding according to Piechulla *et al.* (1985). Strain F64 only clustered at 65 % DNA binding with biovar 2 (F97). Considering the standard deviation of 7.3 % stated in the paper, the usual threshold of 70 % DNA reassociation seems to be included with the estimate. Only 51 % DNA binding was observed between F66^T and F97. These results clearly suggest that biovar 2 represents a separate species, contradicting *rpoB*, *infB* and 16S rRNA gene results. However, DNA–DNA hybridizations have previously generated conflicting results as discussed by Kuhnert & Korczak (2006), Christensen *et al.* (2007) and Bisgaard *et al.* (2009). Based upon the work of Zeigler (2003), Kuhnert & Korczak (2006) proposed that sequence comparison of *recN* might replace DNA–DNA hybridization experiments.

Based on previous investigations of phenotypic characteristics and 16S rRNA analysis, as well as *rpoB* and *recN* gene sequence comparisons presented in this investigation, a novel species, *Actinobacillus anseriformium* sp. nov., is proposed to accommodate Bisgaard taxon 26. Previously published 16S rRNA gene sequence phylogenies (Christensen *et al.*, 2003; Christensen & Bisgaard, 2004; Olsen *et al.*, 2005) all documented that taxon 26 was a member of *Actinobacillus sensu stricto*.

Table 1. Phenotypic characters separating *Actinobacillus anseriformium* from other taxa of *Actinobacillus sensu stricto*

Taxa: 1, *Actinobacillus anseriformium* sp. nov.; 2, *Actinobacillus lignieresii*; 3, *Actinobacillus pleuropneumoniae*; 4, *Actinobacillus equuli* subsp. *equuli*; 5, *Actinobacillus equuli* subsp. *haemolyticus*; 6, *Actinobacillus* genomospecies 2; 7, *Actinobacillus arthritidis*; 8, *Actinobacillus suis*; 9, *Actinobacillus ureae*; 10, *Actinobacillus hominis*; 11, *Actinobacillus capsulatus*; 12, Bisgaard taxon 8. +, 90 % or more are positive within 1–2 days; (+), 90 % or more are positive within 3–14 days; –, 10 % or less are positive within 14 days; w, weak reaction; d, 11–89 % are positive within 14 days. Data for 6 are from Christensen *et al.* (2002), data for 11 are from Kuhnert *et al.* (2007) and data for 2–5, 7–10 and 12 are from Christensen & Bisgaard (2004). All species were investigated by the same methods and under the same cultural conditions.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12
Symbiotic growth	–	–	d*	–	–	–	–	–	–	–	–	–
β -Haemolysis	+	–	+	–	+ /w	–	–	+	–	–	–	–
Pigment	–	–	–	–	–	–	–	w	–	–	–	–
Acid from:												
(+) -L-Arabinose	–	–	–	d	–	–	d	+	–	–	d	–
(-) -D-Arabinose	–	+ /(+)	d	–	–	d	d	–	–	–	–	–
(+) -D-Xylose	–	+	+	+	+	+	+	+	–	+	+	+
(-) -D-Mannitol	d*	+	+	+	d*	+	+	–	+	+	+	+
(-) -D-Sorbitol	+*	–	–	–	–	–	+ /(+)	–	–	–	+	–
(-) -L-Fucose	–	+	(+)	–	–	d	d	–	–	–	–	–
(+) -D-Galactose	–	+	+	+	+	+ /(+)	+ /(+)	+	–	+	+ /(+)	(+)
(+) -Melibiose	–	–	–	+ /(+)	+	d	+ /(+)	+	–	+ /(+)	+ /(+)	(+)
Trehalose	+	–	–	+	+	–	–	+	–	+	+	–
Raffinose	–	d	d	+	+	+	+	+	–	+	+	+
Inulin	–	–	–	–	–	–	–	–	–	+	–	–
Other glycosides†	+ /(+)	–	–	–	d*	–	–	+ /(+)	–	d	+	–
ONPG	–	+	+	+	+	+	+	+	–	+	+	+
α -Galactosidase	–	–	–	+	+	+	+	+	–	+	+	+
α -Glucosidase (<i>p</i> -nitrophenyl α -D-glucopyranoside)	d	–	–	d	d	–	–	+	–	d	d	–
β -Glucosidase (<i>p</i> -nitrophenyl β -D-glucopyranoside)	+	–	–	–	+	–	–	+	–	+	+	–
β -Xylosidase (2-nitrophenyl β -D-xylopyranoside)	–	–	–	+	d	d	–	+	–	–	–	+
Hosts	Anseriforme birds	Cattle, sheep, horses‡	Pigs	Horses, pigs	Horses	Horses	Horses	Pigs	Humans	Humans	Leporidae	Guinea pigs

*Biovars reported.

†Includes salicin, amygdalin, arbutin and gentiobiose.

‡Separate genomospecies 1.

Fig. 1. Phylogenetic relationships between *Actinobacillus anseriformium* and existing members of *Actinobacillus sensu stricto* based on maximum-likelihood analysis of nearly full-length 16S rRNA gene sequences; strains of [*A.*] *minor* and *Mannheimia haemolytica* were used as the outgroup. Support values (%) for monophyletic groups by bootstrap analysis are indicated. Accession numbers are given after strain numbers. Bar, sequence variation considering the models for nucleotide substitution and tree-shape used in the maximum-likelihood analysis.

Compared to *rpoB*- and *recN*-derived phylogenies, a minor difference observed in the 16S rRNA phylogeny was that taxon 26 formed an in-group to *Actinobacillus* genomospecies 1 that was the most distantly related member of *Actinobacillus sensu stricto* with [*A.*] *minor* being the closest related outgroup (Fig. 1). This was also shown by Christensen *et al.* (2003). The unusual location of *A. capsulatus* was described and explained by Kuhnert *et al.* (2007). The type strain, F66^T, was selected from biovar 1 since this biovar is the most frequently reported. The fatty acid profile of the type strain was determined by the CCUG (Culture Collection, University of Göteborg, Göteborg, Sweden). Isolates were cultivated aerobically on Columbia II agar base (BBL 4397596) with 5 % horse blood, for 16 h at 37 °C. Cells were carefully removed from the plate to avoid getting medium in the sample; 50–100 mg cells were further analysed according to Sasser (2001), Eerola & Lehtonen (1988) and Viallard *et al.* (1998) as described in detail at http://www.ccug.se/pages/CFA_method_2008.pdf?CFID=659629&CFTOKEN=43544734.

The main fatty acid was C_{16:1}ω7c with C_{14:0}, C_{16:0} and C_{14:0} 3-OH and/or iso-C_{16:1} I as other major components (Supplementary Table S2, available in IJSEM Online). The profile corresponded well with that of the type strain of *A. lignieresii*, thus confirming the relationship of the novel species with the genus *Actinobacillus*. The DNA G+C content of strain F64 has previously been reported as 41.1 mol% and the genome size is 2.0 GDa (Piechulla *et al.*, 1985). The DNA G+C content is very close to that of

other members of *Actinobacillus sensu stricto* (Olsen *et al.*, 2005).

There is an urgent need to reclassify the eight species [*A.*] *seminis*, [*A.*] *rossii*, [*A.*] *minor*, [*A.*] *indolicus*, [*A.*] *porcinus*, [*A.*] *delphinicola*, [*A.*] *scotiae* and [*A.*] *succinogenes* in either new genera or within existing genera of the *Pasteurellaceae*. This is an ongoing process that recently led to the description of a new genus, *Aggregatibacter* (Nørskov-Lauritsen & Kilian, 2006).

Description of *Actinobacillus anseriformium* sp. nov.

Actinobacillus anseriformium (an.se.ri.for'mi.um. N.L. pl. n. *Anseriformes* scientific name of an order which encompasses ducks, geese, swans and other web-footed birds; N.L. gen. pl. n. *anseriformium* of/from *Anseriformes*).

Isolates on blood agar form smooth and shiny, regular, circular, greyish-white colonies demonstrating slight transparency at the periphery. β-Haemolysis of bovine blood is observed, just as adherence to the agar is often noticed. After 24 h aerobic incubation at 37 °C, colonies are 0.5–1.0 mm, increasing in size to 1.5 mm after 48 h incubation. Isolates may demonstrate *in vitro* satellitic growth, referred to as V-factor or NAD requirement. All isolates investigated are Gram-negative, small coccoid or pleomorphic rods, which are non-motile at 22 and 37 °C, and fermentative in Hugh and Leifson's medium with glucose. Most isolates, including the type strain, are positive for catalase and oxidase. All

isolates meet the phenotypic characters outlined for *Actinobacillus* (Olsen & Møller, 2005). All isolates are positive for acid formation from (+)-D-mannose, cellobiose and other glycosides and trehalose, and β -glucosidase, whereas negative reactions are observed for acid formation from (+)-L-arabinose, (-)-D-arabinose, (+)-D-xylose, (-)-L-fucose, (+)-D-galactose, lactose, (+)-melibiose, raffinose and inulin. In addition, positive ONPG, α -galactosidase and β -xylosidase reactions are observed. Different reactions have been observed for acid formation from (-)-D-mannitol and (-)-D-sorbitol as well as for the α -glucosidase test; the two former reactions form the basis for the establishment of biovars. The type strain (F66^T) belongs to biovar 1 and is positive for (-)-D-mannitol, (-)-D-sorbitol and α -glucosidase. The major fatty acids are C_{16:1} ω 7c, C_{14:0}, C_{16:0}, and C_{14:0} 3-OH and/or iso-C_{16:1} I with C_{12:0}, C_{18:2} ω 6,9c and/or ante-C_{18:0}, C_{18:1} ω 9c and C_{18:0} as minor components (Supplementary Table S2, available in IJSEM Online). Isolates have been obtained from the upper respiratory tract of web-footed birds in which they may cause sinusitis or conjunctivitis, and they may cause septicæmia.

The type strain is F66^T (=CCUG 60324^T=CCM 7846^T), isolated from conjunctivitis in a White Pekin duck.

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