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Riemerella columbina sp. nov., a bacterium associated with respiratory disease in pigeons

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Thirteen Gram-negative bacterial isolates were recovered from diseased pigeons and were tentatively classified as *Riemerella anatipestifer*-like strains based on conventional phenotypic features and disease symptoms. Phenotypic characteristics that differentiated the pigeon isolates from *R. anatipestifer* included their greyish-white to beige pigment formation on Columbia blood agar and the hydrolysis of aesculin. Furthermore, *R. anatipestifer* strains have thus far not been reported in pigeons. The phenotypic differences together with the unique host range of the new isolates have prompted the inclusion of these strains in a polyphasic taxonomic study. Extensive phenotypic examination, PAGE of total proteins and GC analysis of fatty acid contents revealed that the pigeon isolates constitute a homogeneous cluster, distinct from the *R. anatipestifer* reference strains. The phylogenetic position of representative strains was examined by using DNA–rRNA hybridizations and indicated that this taxon belongs to the genus *Riemerella*. Finally, DNA-binding values confirmed that the strains constitute a separate species for which the name *Riemerella columbina* sp. nov. is proposed. Strain LMG 11607^T was selected as the type strain. Clinical observations suggest that these organisms are involved in pathogenesis of respiratory diseases, similar to those associated with *R. anatipestifer* infections. However, the role of co-factors and the interaction with other agents are unknown.

Keywords: *Riemerella columbina* sp. nov., identification, polyphasic taxonomy

INTRODUCTION

Riemerella anatipestifer strains have been isolated worldwide from domestic and wild birds. The organism causes a disease named exudative septicaemia (Riemer, 1904) which particularly affects ducks, less frequently geese and turkeys, and sporadically chickens and wild birds (Brodgen, 1989; Hinz *et al.*, 1998b). The organism was previously referred to as [*Moraxella*] *anatipestifer* or [*Pasteurella*] *anatipestifer* and considered a species *incertae sedis* in *Bergey's Manual of Systematic Bacteriology* (Bøvre, 1984; Mannheim, 1984). Piechulla and co-workers denoted for the first time the correct affiliation within the *Flavobacterium–Cytophaga* group (Piechulla *et al.*, 1986). In 1991, Rossau and co-workers reported similarities between the latter group and [*M.*] *anatipestifer*, i.e. the lack of flagellation, the low DNA base ratio, the presence of menaquinones as sole respiratory quinones and the presence of branched-chain fatty acids in high percentages, the absence of carbohydrate fermentation and a similar pattern of hydrolytic enzymes (Rossau *et al.*, 1991). Finally, in 1993, the species was reclassified in a newly described genus, *Riemerella*, based not only on its genomic divergence from allied taxa within rRNA superfamily V, but also on a number of unique chemotaxonomic and phenotypic properties, including its capnophilic metabolism, the absence of pigments and its fatty acid and menaquinone content (Segers *et al.*, 1993). 16S rRNA gene sequence analysis confirmed the phylogenetic position of *Riemerella anatipestifer* as a separate branch within the *Flavobacterium–Cytophaga* group (Subramaniam *et al.*, 1997). At present, *R. anatipestifer* is the only validly described species of the genus.

One of us (K.-H. H.) examined 13 strains from diseased pigeons and tentatively identified them as *R. anatipestifer*-like strains. In the present study, we performed

Abbreviation: BSS, buffered single substrate.

a polyphasic taxonomic study to clarify the taxonomic position of these strains. Below, we show that these isolates constitute a novel *Riemerella* species, for which we propose the name *Riemerella columbina* sp. nov.

METHODS

Bacterial strains and growth conditions. Data on the origin of the strains are listed in Table 1. *R. columbina* strains were grown and maintained on Trypticase Soy agar (BBL) and incubated at 36–37 °C in a microaerobic atmosphere containing approximately 5% O_2, 3·5% CO_2, 7·5% H_2 and 84% N_2, unless stated otherwise. Bacteriological purity was checked by plating and examining living and Gram-stained cells.

Fatty acid methyl ester analysis. All strains were grown for 48 h on one or two Petri dishes. A loopful of well-grown cells was harvested; preparation, separation, identification and numerical comparison of the fatty acid methyl esters were performed using the Microbial Identification System (Microbial ID) as described before (Vandamme *et al.*, 1992).

PAGE of whole-cell proteins. After incubation of cells for 48 h, whole-cell protein extracts were prepared, and SDS-PAGE was performed as described by Pot *et al.* (1994). A densitometric analysis, normalization and interpolation of the protein profiles, and a numerical analysis were performed by using the Gelcompar software package version 4.0 (Applied Maths, Kortrijk, Belgium).

Preparation of high-molecular-mass DNA. High-molecular-mass native DNA was prepared as described before (Vandamme *et al.*, 1992).

DNA base compositions. All of the mean mol% G+C values were determined by thermal denaturation and calculated by using the equation of Marmur & Doty (1962), as modified by De Ley (1970).

DNA–DNA hybridization experiments. The degree of DNA–DNA binding, expressed as a percentage, was determined spectrophotometrically by the initial renaturation rate method of De Ley *et al.* (1970). Each value is the mean of at least two hybridization experiments. Values of 30% DNA binding and less do not represent significant DNA homology. The total DNA concentration was about 59·3 μg

Table 1. Strains studied

Type strains are indicated by a superscript T. CCUG, Culture Collection of the University of Göteborg, Department of Clinical Bacteriology, University of Göteborg, Göteborg, Sweden; Hinz, K.-H. Hinz, Clinic for Poultry, School of Veterinary Medicine Hannover, Hannover, Germany; Hommez, J. Hommez, Provinciaal Verbond voor Dierenziektenbestrijding, Torhout, Belgium; Köhler, B. Köhler, Staatliches Veterinär- und Lebensmitteluntersuchungsamt, Potsdam, Germany; LMG, BCCM/LMG Culture Collection Laboratorium voor Microbiologie, University of Ghent, Ghent, Belgium; MCCM, Medical Culture Collection of Microorganisms, Marburg, Germany.

Name	Strain no.	Other strain designation	Source and place of isolation
Riemerella anatipestifer	LMG 10957	Hommez 3-8	Duck, Belgium
Riemerella anatipestifer	LMG 10988	Hommez 5-25	Chicken, Belgium
Riemerella anatipestifer	LMG 11054^T	CCUG 14215^T	Duck blood, USA
Riemerella anatipestifer	LMG 11056	CCUG 25000	Duck, UK, 1966–1969
Riemerella anatipestifer	LMG 11059	CCUG 25005	Duck, UK, 1966–1969
Riemerella anatipestifer	LMG 11060	CCUG 25054	
Riemerella anatipestifer	LMG 11146	CCUG 21370	Duck blood, USA
Riemerella anatipestifer	LMG 11601	MCCM 00762	Duck, Germany, 1985
Riemerella anatipestifer	LMG 11602	MCCM 00771	Goose, Germany, 1985
Riemerella anatipestifer	LMG 11603	MCCM 00772	USA
Riemerella anatipestifer	LMG 11605	MCCM 00793	Duck, Germany, 1981
Riemerella columbina	LMG 11607^T	Hinz x183-89^T	Pigeon palatine cleft, Germany
Riemerella columbina	LMG 11608	Hinz x220-90	Pigeon palatine cleft, Germany
Riemerella columbina	LMG 12983	Hinz x520-82	Pigeon lung, Germany
Riemerella columbina	LMG 12987	Hinz x296-83	Pigeon trachea, Germany
Riemerella columbina	LMG 15723	Hinz x163-90	Pigeon lung, Germany
Riemerella columbina	LMG 15724	Hinz x100-90	Pigeon palatine cleft, Germany
Riemerella columbina	LMG 16900	Köhler G 1844-95	Internal and respiratory organs of pigeon, Germany
Riemerella columbina	LMG 18232	Köhler G 1024-94	Pigeon brain, Germany
Riemerella columbina	LMG 18233	Köhler G 1274-94	Pigeon trachea, Germany
Riemerella columbina	LMG 18234	Köhler G 1844-95	Pigeon trachea, Germany
Riemerella columbina	LMG 18235	Köhler G 704-97	Pigeon airsac fibrin, Germany
Riemerella columbina	LMG 18236	Köhler G 1009-97	Pigeon lung, Germany
Riemerella columbina	LMG 18237	Köhler G 1364-97	Pigeon trachea, Germany

ml^{-1}, and the optimal renaturation temperature in 1 × SSC was 60·8 °C.

DNA–rRNA hybridization experiments. ^{3}H-labelled rRNA of the type strain of *R. anatipestifer* was isolated and purified as reported earlier (Segers *et al.*, 1993). Hybridization between the rRNA probe and single-stranded filter-fixed DNA of *R. columbina* LMG 11607^T and LMG 11608 was carried out as described previously by Van Landschoot & De Ley (1983). Each DNA–rRNA hybrid was characterized by the $T_{m(e)}$ value (the temperature at which half of the DNA–rRNA hybrid is thermally denatured).

Phenotypic tests. Strains were grown on Columbia agar base (Oxoid) supplemented with 7% defibrinated sheep blood unless stated otherwise. Growth was evaluated aerobically and anaerobically at 37 °C and microaerobically at 24, 37 and 42 °C. Growth tests on MacConkey agar and on litmus lactose agar, capsule and flagella staining, and motility were performed as described by Vandamme *et al.* (1998).

Cells used as inocula for conventional biochemical tests were grown for 16–24 h under microaerobic conditions in a moist chamber. Bacteria were suspended in 0·15 M NaCl solution, pH 7·0 ± 1, to a concentration of about 10^8 viable bacterial cells. Growth was recorded daily at least up to 3 d. Oxidation and fermentation of glucose, aesculin and gelatin hydrolysis, determination of oxidase, catalase, urease and arginine dihydrolase activity, nitrate reduction, hyaluronidase and chondroitin sulfatase activity and Voges–Proskauer test were performed as described by Vandamme *et al.* (1998).

The API 20NE, API ZYM and API ID32E microtest systems were used according to the recommendations of the manufacturer (bioMérieux).

The buffered single substrate (BSS) test was used for the detection of a weak acidification of carbohydrates (using conventional phenotypic tests, acid production may be masked by accumulation of alkaline breakdown products of complex medium components as, for example, peptone). The base medium consisted of buffered saline (KH_2PO_4, 0·1%; K_2HPO_4, 0·1%; NaCl, 0·5%; pH 7·6) containing 2% carbohydrate and phenol red in a final concentration of 1:50000 as indicator (Lautrop, 1960). A heavy inoculum (100 µl of a suspension of about 400 mg wet bacterial mass in 2 ml 0·15 M NaCl solution) was added to 0·5 ml of buffered carbohydrate solution in a tube with a diameter of 7 mm. The reactions were read after 6 and 24 h incubation in a water bath at 37 °C. Uninoculated carbohydrate-containing media and inoculated media without carbohydrate were incubated as controls. The reactions were recorded as weak positive if the pH values were 7·1–6·9 (orange-coloured reaction) and positive if the pH decreased to 6·8 or lower (yellow-coloured reaction).

Sensitivity to antimicrobial drugs was tested under standard conditions on D.S.T. agar (Oxoid), supplemented with 5% defibrinated sheep blood, by using the antimicrobial susceptibility test discs from Oxoid. Plates were incubated microaerobically at 37 °C for 16–18 h. A zone of inhibition of more than 1 mm was recorded as a positive test result and was interpreted as '*in vitro* susceptible'.

RESULTS

Isolation procedures and pathology

The 13 strains studied were isolated from the airsac, lung, palatine cleft, trachea or brain of pigeons (Table 1). The birds suffered from airsacculitis, tracheitis, pneumonia, hepatitis and/or other lesions similar to those of the *R. anatipestifer*-associated exudative septicaemia. In some cases, an additional infection with coccidia (LMG 18236), capillaria (LMG 18236), paramyxovirus (LMG 18234, LMG 18236) or *Salmonella* (LMG 18237) was observed.

Phenotypic characterization

From a large set of conventional phenotypic tests, only two features clearly differentiated all *R. columbina* strains examined from *R. anatipestifer* reference strains: pigment formation and aesculin hydrolysis. A further extensive phenotypic characterization using API galleries (API 20NE, API ID32E, API ZYM) and the BSS test did not yield additional characters for distinguishing both taxa unequivocally (see below).

Out of six strains examined, all six were susceptible to 10 µg ampicillin, 15 µg erythromycin and 10 µg penicillin, and four of them were sensitive to 30 µg oxytetracycline. In addition, all strains were resistant to 100 µg nitrofurantoin, 10 µg gentamicin, 10 µg neomycin and sulfonamides.

GC analysis of methylated fatty acids

The cellular fatty acid compositions of *Riemerella* strains are shown in Table 2. Major fatty acids for all strains were the branched-chain fatty acids 13:0 iso, 15:0 iso, 15:0 anteiso, 15:0 iso 3-OH and 17:0 iso 3-OH. Based on the relative amounts of these dominant features, and on the presence of some minor peaks, *R. columbina* strains were easily differentiated from reference strains of *R. anatipestifer*. Strains of the latter taxon were characterized by the presence of significantly lower amounts of 15:0 anteiso (5% versus 22%) and higher amounts of 15:0 iso (52% versus 45%), 15:0 iso 3-OH (8% versus 4%) and 17:0 iso 3-OH (14% versus 7%). Furthermore, only *R. columbina* strains contained appreciable amounts of 13:0 anteiso (2%), 17:0 2-OH (1%) and 'summed feature 4' (3%; for explanation see Table 2).

PAGE of whole-cell proteins

Duplicate protein extracts were prepared to check the reproducibility of the growth conditions and the preparation of the extracts. The correlation level between duplicate protein patterns was $r \geqslant 0{\cdot}95$.

The whole-cell protein profiles of the *R. columbina* strains were analysed together with those of reference strains of *R. anatipestifer*. The whole-cell protein profiles and the corresponding dendrogram obtained after average-linkage cluster analysis are shown in Fig. 1. At a correlation coefficient of 0·71, two clusters (I and II) were delineated. All *R. columbina* strains grouped in cluster I at a level $r \geqslant 0{\cdot}75$, and *R. anatipestifer* strains constituted a second cluster (II) at $r \geqslant 0{\cdot}78$.

Table 2. Fatty acid composition of *Riemerella* species

All strains listed in Table 1 were investigated. Fatty acids that accounted for less than 1·0% of the total fatty acids in all of the strains studied are not shown. TR, Trace (less than 1·0%); ND, not detected.

Species	13:0 iso	13:0 anteiso	UN* 13·566	14:0 iso	15:0 2-OH	15:0 iso	15:0 anteiso	15:0 iso 3-OH	17:0 2-OH	17:0 iso 3-OH	Summed feature 4†
R. anatipestifer	15·1±3·8	TR	1·4±0·5	TR	TR	52·4±4·6	5·4±1·1	8·2±2·4	ND	13·6±3·4	ND
R. columbina	10·1±1·8	2·0±0·7	TR	1·0±0·2	1·0±0·4	45·3±3·3	22·1±3·3	3·9±0·9	1·0±0·1	7·0±1·5	2·9±1·3

* ECL, equivalent chain-length. The identity of the fatty acid is not known.

† Summed feature 4 consisted of one or more of the following fatty acids which could not be separated by the Microbial Identification System: 15:0 iso 2-OH, 16:1ω7*c* and 16:1ω7*t*.

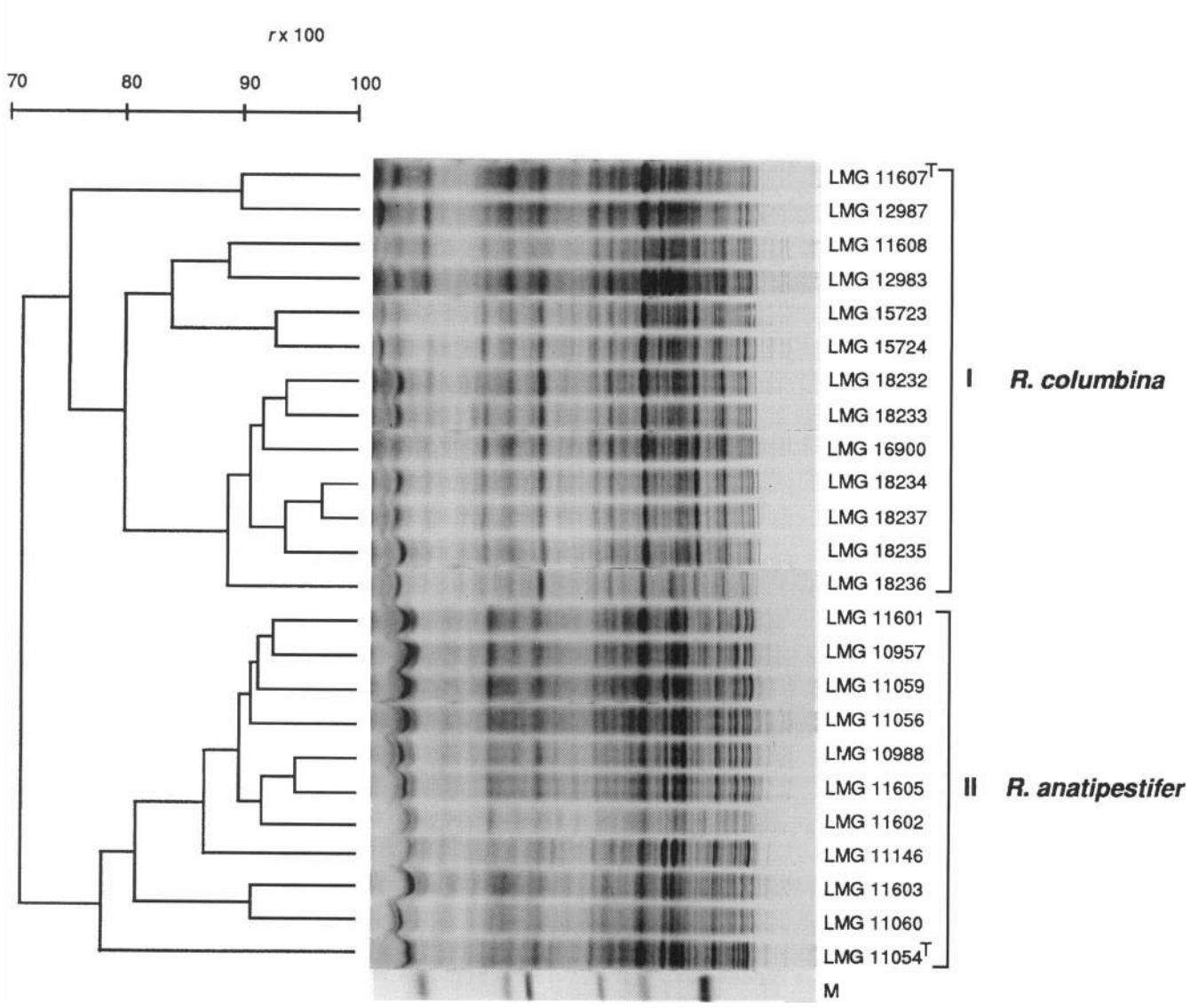

Fig. 1. Protein profiles of *Riemerella* strains listed and corresponding dendrogram derived from the unweighted pair group average linkage of correlation coefficients *r* (expressed for convenience as a percentage value). The positions of the molecular mass markers (track labelled M) are indicated from left to right: trypsin inhibitor, 20100 Da; trypsinogen, 24000 Da; carbonic anhydrase, 29000 Da; glyceraldehyde-3-phosphate dehydrogenase, 36000 Da; egg albumin, 45000 Da; and bovine albumin, 66000 Da.

DNA–DNA hybridizations

DNA–DNA hybridization data revealed that the *R. columbina* strains LMG 11608 and LMG 16900 exhibited DNA-binding values of, respectively, 89 and 100% with the type strain LMG 11607^T. No significant DNA relatedness (12%) was measured between the type strain of *R. columbina* and *R. anatipestifer*.

DNA base compositions

Determination of the DNA base composition yielded G+C contents between 36 and 37 mol% for the three *R. columbina* strains studied (LMG 11607^T, LMG 11608 and LMG 16900). A G+C value of 35 mol% was obtained for the type strain of *R. anatipestifer*.

DNA–rRNA hybridizations

DNA–rRNA hybridization experiments were performed with rRNA from the type strain of *R. anatipestifer* LMG 11054^T and DNA from, respectively, *R. columbina* LMG 11607^T and LMG 11608. Small differences in melting temperatures [$T_{m(e)}$] of 1–2 °C differentiated *R. columbina* from *R. anatipestifer* strains.

DISCUSSION

Thirteen strains isolated from diseased pigeons were investigated using a number of conventional phenotypic tests and were tentatively identified as *R. anatipestifer*-like strains. Only few tests differentiated the latter strains from *R. anatipestifer*. Colonies of all *R. anatipestifer*-like strains showed a greyish-white to beige pigmentation on Columbia blood agar, whereas those of *R. anatipestifer* were nonpigmented. Furthermore, the new isolates differed from the latter species by their ability to hydrolyse aesculin. In addition, the unique source of the isolates (available literature data indicate that *R. anatipestifer* strains were not previously isolated from pigeons) also prompted us to compare these pigeon isolates in a polyphasic approach with *R. anatipestifer* reference strains to determine if both groups of strains represented separate taxonomic units.

The fatty acid compositions of all strains were determined to evaluate the usefulness of this characteristic for differentiation and identification of both taxa (Table 2). A similar overall fatty acid content was observed for all strains. Dominant fatty acids were 13:0 iso, 15:0 iso, 15:0 anteiso, 15:0 iso 3-OH and 17:0 iso 3-OH. *R. anatipestifer* yielded higher amounts of 13:0 iso, 15:0 iso, 15:0 iso 3-OH and 17:0 iso 3-OH and a significantly lower amount of 15:0 anteiso. Characteristic for *R. anatipestifer*-like strains was the presence of small but significant relative amounts of 13:0 anteiso, 17:0 2-OH and 'summed feature 4'.

All strains listed in Table 1 were further compared by using SDS-PAGE of whole-cell proteins (Fig. 1). Two major clusters were identified grouping 13 *R. anatipestifer*-like strains (cluster I; $r \geqslant 0{\cdot}75$) and 11 *R. anatipestifer* reference strains (cluster II; $r \geqslant 0{\cdot}78$), respectively. Based on these data, strains were selected for DNA–DNA hybridization experiments. Among the *R. anatipestifer*-like strains, DNA-binding values of, respectively, 89% and 100% were observed between strain LMG 11607^T and strains LMG 11608 and LMG 16900. No significant DNA relatedness was measured between strains of the latter taxon and the type strain of *R. anatipestifer*.

These phenotypic, chemotaxonomic and genomic data demonstrated that the pigeon strains constitute a homogeneous group and should be allocated to a new species. A further extensive phenotypic study was performed to look for additional features for distinguishing both taxa. As for *R. anatipestifer*, also the new species was characterized by the absence of a large number of biochemical properties (see below).

The phylogenetic affiliations of two representative strains of *R. anatipestifer*-like strains, LMG 11607^T and LMG 11608, were determined by using DNA–rRNA hybridization experiments. These data demonstrated that both strains are highly related to *R. anatipestifer*, differing only in $T_{m(e)}$ values of 1–2 °C and clearly indicating that both species belong to a single genus. DNA base compositions of representative strains were determined and values between 36 and 37 mol% G+C were detected. This DNA base content is slightly higher than the values of 29–35 mol% which were determined for *R. anatipestifer* by Segers *et al.* (1993).

From this polyphasic approach, it is demonstrated that the *R. anatipestifer*-like strains belong to the genus *Riemerella* and constitute a separate species for which the name *R. columbina* is proposed. The species name reflects the narrow host range, pigeons, from which all currently described members of this taxon were isolated. An emended genus description is based on data from Hinz *et al.* (1998a, b), Segers *et al.* (1993), Bernardet *et al.* (1996) and the present study.

Emended description of the genus *Riemerella*

Riemerella cells are Gram-negative, nonsporulating and nonmotile rods 0·2–0·5 μm wide and 1–2·5 μm long. All strains grow microaerobically and most of them aerobically on blood agar. Some strains grow anaerobically at 37 °C. Colonies are smooth, nonpigmented or greyish-white to beige pigmented. Growth on litmus lactose agar is strain-dependent, no growth is obtained on MacConkey's agar. Most strains show a positive Voges–Proskauer reaction. Nitrates are not reduced. Reaction for acid production from glucose is frequently negative in peptone-containing media. Activity of the following enzymes is present: oxidase, catalase, gelatinase, α-glucosidase, α-maltosidase, alkaline and acid phosphatase, esterase lipase C8, esterase C4, naphthol-AS-BI-phosphohydrolase, leucine arylamidase, valine arylamidase, cystine arylamidase and L-aspartic acid arylamidase. The fol-

lowing reactions are strain-dependent: urease, chymotrypsin, trypsin and arginine dihydrolase activity, indole production, haemolysis on blood, aesculin hydrolysis. Depending on the micro-test kit used, the following enzyme reactions give variable results: β-glucosidase, α-galactosidase and lipase activity (these three reactions were all positive in the API ID32E and negative in the API ZYM system) and *N*-acetyl-β-glucosaminidase [negative in API ZYM and API ID32E, positive in LRA-ZYM-OSIDASES (Hinz *et al.*, 1998b); only some representative *R. anatipestifer* strains were tested using the latter system]. Activity of the following enzymes is absent: chondroitin sulfatase, hyaluronidase, β-galactosidase, β-glucuronidase, α-mannosidase, α-fucosidase, trypsin, ornithine and lysine decarboxylase. None of the strains used malonate as a carbon source, or assimilated in the API 20NE system D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, maltose, D-gluconate, caprate, adipate, L-malate, citrate or phenyl acetate. No acid production was detected from D- and L-arabitol, galacturonate, 5-ketogluconate, phenol red, D-mannitol, maltose, adonitol, palatinose, saccharose, L-arabinose, trehalose, rhamnose, inositol, sorbitol or cellobiose in the API ID32E system. Using the BSS test, however, acidification of the following carbohydrates may be detected: D-glucose, maltose, D-mannose and dextrin, and to a lesser extent D-fructose, L-sorbose and trehalose. No acid was produced from lactose, D-galactose, *N*-acetyl-D-glucosamine, lactulose, trehalose, saccharose, D-mannitol, L-arabinose, *myo*-inositol, D-sorbitol, D-xylose, dulcitol, salicin or adonitol. The genus is a member of the family *Flavobacteriaceae*. The closest phylogenetic neighbours are the genera *Chryseobacterium* and *Bergeyella*. Menaquinone-6 is the major respiratory quinone detected in the type species. The dominant fatty acids are the branched-chain fatty acids 13:0 iso, 15:0 iso, 15:0 anteiso, 15:0 iso 3-OH and 17:0 iso 3-OH. Isolated mainly from diseased birds, in a few cases from pigs. The illness caused by the organism is a septicaemic disease in ducks, pigeons and other domestic and wild birds. The type species is *R. anatipestifer*. The DNA G+C composition ranges from 29 to 37 mol%.

Description of *Riemerella columbina* sp. nov.

Riemerella columbina (co.lum.bi'na. L. fem. adj. *columbina* pertaining to pigeons).

The description of *R. columbina* is as for the genus, with the following specifications which allow differentiation of the newly described species from the type species *R. anatipestifer*. On Columbia blood agar, all strains showed good growth when incubated aerobically at 37 °C and microaerobically at 24, 37 and 42 °C and produced a grey–white or beige pigment (*R. anatipestifer* strains are nonpigmented). None of the strains grew anaerobically at 37 °C and no growth was observed on litmus lactose agar (variable features for *R. anatipestifer* strains). All strains tested hydrolysed aesculin (negative for *R. anatipestifer* strains). When using the API ID32E system, all strains showed a positive β-glucosidase activity (negative for *R. anatipestifer* strains; this reaction was, however, negative for *R. columbina* strains in the API ZYM system). None of the strains produced indole and all strains showed chymotrypsin activity (variable reactions for *R. anatipestifer* strains). Using the BSS test, all strains produced acid from D-glucose, maltose, D-mannose and dextrin (variable reactions for *R. anatipestifer*). A variable reaction (negative or weakly positive reaction) was obtained for the acid production of D-fructose and L-sorbose. The dominant fatty acid content consists of the branched-chain fatty acids 13:0 iso, 13:0 anteiso, 15:0 iso, 15:0 anteiso, 15:0 iso 3-OH and 17:0 iso 3-OH and 'summed feature 4'. Isolated from respiratory disease in pigeons. The type strain is LMG 11607^T, which was isolated from a pigeon palatine cleft in Germany. Its G+C content is 36 mol%.

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