Avibacterium endocarditidis sp. nov., isolated from valvular endocarditis in chickens

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A novel species of the Pasteurellaceae, Avibacterium endocarditidis sp. nov., is proposed based upon characterization of 27 isolates from valvular endocarditis in adult broiler parents. All isolates shared the same PFGE type after digestion of DNA with Smal and XbaI. In addition, all isolates meet the phenotypic characters for the genus Avibacterium. Separation of the novel species from other species of Avibacterium was possible by means of tests for catalase, symbiotic growth, aerobic growth on agar, acid production from glycerol, xylitol, (+)-L-arabinose, (−)-d-mannitol, (−)-d-sorbitol, (−)-L-fucose, (+)-d-galactose, maltose, trehalose, raffinose and dextrin in addition to reactions with ONPG (β-galactosidase) and PNPG (α-glucosidase). The closest relationship was observed with Avibacterium gallinarum which, however, can be separated from Avibacterium endocarditidis in acid production from (−)-d-mannitol, (−)-d-sorbitol and (−)-L-fucose. The highest 16S rRNA gene sequence similarity (98.4 %) was found to strain Modesto, belonging to serogroup C of Avibacterium paragallinarum. recN gene DNA sequence similarities corrected by the formula of Zeigler (2003) (Int J Syst Evol Microbiol 53, 1893–1900) documented 85 % or less DNA sequence similarity between the type strain of Avibacterium endocarditidis and species of Avibacterium, confirming the separate species status of this taxon according to the multilocus sequence analysis method of Kuhnert & Korczak (2006) (Microbiology 152, 2537–2548). The type strain of Avibacterium endocarditidis sp. nov., strain 20186H4H1T (=CCUG 52860T =DSM 18224T), was isolated from valvular endocarditis of a chicken in Denmark in 2004.

Within the Pasteurellaceae, two new genera Gallibacterium (Christensen et al., 2003a) and Volucribacter (Christensen et al., 2004) have recently been established within the avian 16S rRNA cluster 18 of Olsen et al. (2005). Four named species as well as an unnamed taxon were subsequently transferred to a new genus Avibacterium as Avibacterium gallinarum gen. nov., comb. nov., Avibacterium paragallinarum comb. nov., Avibacterium avium comb. nov., Avibacterium volantium comb. nov. and Avibacterium species A (Blackall et al., 2005). While all of the named species of Avibacterium are routinely encountered in the investigation of upper respiratory tract diseases in birds, only Avibacterium paragallinarum is regarded as a primary pathogen, being the causative agent of infectious coryza of chickens (Blackall, 1999). Avibacterium avium, Avibacterium volantium and Avibacterium sp. A are normally regarded as part of the commensal microbiota of the upper respiratory tract of chickens and other birds, but are occasionally implicated in various pathologies (Hinz, 1980; Hinz & Kunjara, 1977; Mutters et al., 1985; Bisgaard, 1993). The only species of Avibacterium involved in systemic infections in addition to upper respiratory tract infections seems to be Avibacterium gallinarum, affecting gallinaceous birds (Christensen et al., 2002a; Bisgaard et al., 2005). In one report, Avibacterium paragallinarum has been isolated from lung, kidney and liver, probably related to systemic infection (Sandoval et al., 1994). A novel non-V-factor-requiring group of the Pasteurellaceae showing phenotypic characters similar to those of Avibacterium and tentatively named taxon 50 was recently isolated from valvular endocarditis and septicaemia in broiler parents (M. Bisgaard, unpublished data). Based on phenotypic and genotypic data including PFGE and sequencing of 16S rRNA and recN genes, we propose to accommodate taxon 50 within the genus Avibacterium as a separate species.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain 20186H4H1T is DQ465412, and those for the recN sequences of strain 20186H4H1T, A. volantium NCTC 3438T, A. paragallinarum NCTC 11296T and Avibacterium sp. A strain CCUG 18782 are DQ899746–DQ899749, respectively.

PFGE results and a recN sequence-based maximum-likelihood tree are available as supplementary material with the online version of this paper.
Bacterial strains and growth conditions

A total of 27 isolates from 22 adult broiler parents of the same flock were sampled over a period of 10 weeks and characterized. Twenty isolates were obtained from valvular endocarditis. Eighteen were recorded during production, while two cases were recorded among dead hens left in the house after collection of birds for slaughtering. Two birds with endocarditis allowed two isolates from the liver and two isolates from the spleen to be investigated. Finally, two isolates were obtained from degenerative arthritis and a single isolate originated from chronic adhesive pericarditis (M. Bisgaard, unpublished data). All isolates were grown aerobically on 5% bovine blood agar (blood agar base, CM 55; Oxoid) at 37 °C unless otherwise stated.

Phenotypic characterization

Classical phenotypic tests were performed as reported previously (Bisgaard et al., 1991). Additional characterization included API 20NE tests, which were carried out according to the recommendations of the manufacturer (bioMérieux).

All 27 isolates tentatively classified as taxon 50 were Gram-negative, non-motile, pleomorphic rods that were catalase- and oxidase-positive and produced acid from glucose without gas in Hugh & Leifson’s medium. Haemolysis of bovine red-blood cells was negative and symbiotic growth without gas in Hugh & Leifson’s medium. Phenotypic characters that separate the genus Avibacterium from other genera of the Pasteurellaceae were recently published by Blackall et al. (2005).

Pulsed field gel electrophoresis (PFGE)

PFGE using Smal and Xbal for digestion of DNA was performed as reported previously (Ojeniyi et al., 1991; Christensen et al., 2003a; Chadfield et al., 2007). The size marker N0350S (New England Biolabs) was used for comparison. All isolates of taxon 50 shared the same PFGE type (Supplementary Fig. S1 available in IJSEM Online), indicative of a clonal outbreak of valvular endocarditis. However, since the isolates reported represent the first and only isolates described, additional isolates are needed to allow comments on the genetic diversity of this novel taxon of the Pasteurellaceae. The type strain of Avibacterium gallinarum showed a divergent Xbal profile, sharing only two bands with taxon 50 (Supplementary Fig. S1).

All 27 isolates were isolated from the same flock over a period of 10 weeks and shared a common phenotype and genotype. To describe a novel species, greater diversity would have been desirable (Christensen et al., 2007). However, the minimal standards for description of novel taxa of the Pasteurellaceae recommend naming of species of particular pathogenic importance irrespective of whether they cover geographical and ecological diversity (Christensen et al., 2007). By doing so, type strains are also made available to the public for further characterization, including investigations of mechanisms of pathogenicity.

16S rRNA gene sequencing

16S rRNA gene sequencing of strain 20186H4H1T was performed as reported previously (Angen et al., 2003; Christensen et al., 2002b). BLAST searching (Altschul et al., 1997) in GenBank (Benson et al., 2006) showed that no other sequences had been deposited with high similarity to strain 20186H4H1T. Pairwise comparisons for similarity were performed by the program WATER included in EMBOSS (Rice et al., 2000). The 16S rRNA gene sequence for strain 20186H4H1T was obtained in the region covering Escherichia coli positions 194–1412.
The highest 16S rRNA gene sequence similarity between this strain and other taxa of the Pasteurellaceae was obtained to species of Avibacterium. The highest similarity (98.4%) was obtained to strain Modesto, belonging to serogroup C of Avibacterium paragallinarum (GenBank accession no. AY498870). Similarities to other members of Avibacterium ranged between 96.5%, to the type strain of Avibacterium gallinarum (GenBank accession no. M75059), and 97.9%, to strain SA7177 of biovar 2 of Avibacterium paragallinarum (accession no. AY498871) as well as strain CCUG 18782 of Avibacterium sp. A (accession no. M75055). Similarities to strains Wuthe DS 1801/91 (GenBank accession no. AF224311) and CCUG 19808 (accession no. AF224312), closely related to Avibacterium, were 93.6 and 92.1%, respectively. Outside Avibacterium, similarities to the type strains of Volucribacter psittaciidica and Volucribacter amazoneae were 94 and 93.5%, respectively, and the highest similarity to the taxon 2 and 3 complex of Bisgaard was 93.8%, as observed to the reference strain NCTC 11412 of taxon 3 (GenBank accession no. L06079), while 93.1% similarity was observed to the type strain of Gallibacterium anatis (accession no. AF228001).

The highest similarity outside the avian 16S rRNA cluster (Olsen et al., 2005) was obtained to the type strain of [Pasteurella] caballi, at 95.4% (GenBank accession no. AF224291) [brackets around genus names indicate species suggested to be excluded from the respective genera in accordance with the terminology of Mutters et al. (1989)].

A multiple alignment was constructed by CLUSTAL_X (Thompson et al., 1997) and included the region between E. coli positions 194 and 1391 of the rrrB gene, with 1175 positions left after removal of gapped columns and 196 data patterns analysed. Maximum-likelihood analysis including bootstrap analysis was performed by fastDNAml (Olsen et al., 1994; Felsenstein, 1995) run on a Linux 7.2-compatible server. The analysis was run with a transition/transversion ratio of 1.5.

The phylogenetic analysis shown in Fig. 1 was obtained with 22 sequences selected to include all Avibacterium type strains within the avian 16S rRNA cluster of the Pasteurellaceae (Olsen et al., 2005) and type species of other genera within the Pasteurellaceae. The novel species was found to belong to the monophyletic group including taxa of Avibacterium, confirming the 16S rRNA gene sequence similarities. Monophyly for Avibacterium was confirmed in accordance with Christensen et al. (2003b) and Blackall et al. (2005). The low bootstrap value of the group of only 57% and the lack of documentation of the avian 16S rRNA group (Olsen et al., 2005) was probably related to an
unbalanced representation of members of the *Pasteurellaceae* with a focus on only the type strains of type species of genera.

**recN sequencing and analysis**

16S rRNA gene sequence analysis is insufficient to separate taxa within *Avibacterium* (Blackall et al., 2005) and, since the species status of taxon 50 could not be documented unequivocally through 16S rRNA gene sequence comparison, comparison of the recN sequence of 20186H4H1T to those of the type strains of the species of *Avibacterium* and strain CCUG 18782 of *Avibacterium* sp. A was performed. Sequencing of strain 20186H4H1T (*Avibacterium endocarditidis* sp. nov.), *Avibacterium paragallinarum* NCTC 11296T, *Avibacterium volantium* NCTC 3438T and *Avibacterium* sp. A strain CCUG 18782 was carried out as reported by Kuhnert & Korczak (2006). In addition to the primers listed by Kuhnert & Korczak (2006), the sequencing primers 5'-AAAATGCGCAAGCTTTGAGT and 5'-ACACGGCGTAAAATACAG were used to determine the 3' and 5' regions, respectively, of the recN sequence. DNA sequences were obtained of the region 94–1255 of the recN gene (numbered according to annotation of the genomic sequence of *Pasteurella multocida* strain Pm70 deposited under GenBank accession no. AE004439). The type strain of *Avibacterium avium* did not generate a PCR product with the recN primers stated above, indicating significant differences from the other species of *Avibacterium*, and this species was not included in the analysis. The published sequences of the type strains of *Avibacterium gallinarum* and *Pasteurella multocida* and of *Volucracter psittaciæida* strain 101 were also included in the comparison. The phylogenetic analysis was performed as reported for 16S rRNA gene sequences, including 1255 positions and the use of a transition/transversion ratio of 1.1, which was found to maximize the likelihood. The phylogenetic tree shown in Supplementary Fig. S2 shows the unique position of taxon 50 within *Avibacterium*.

Similarities of 41, 84 and 85% were calculated using the formula for conversion given by Zeigler, (2003) between strain 20186H4H1T and the type strains of *Avibacterium paragallinarum*, *Avibacterium gallinarum* and *Avibacterium volantium*, respectively, whereas the similarity to *Avibacterium* sp. A was 83%. DNA sequence similarity values calculated from recN sequences of 17 strains of *Actinobacillus capsulatus* representing seven different countries and four continents showed similarities between 94 and 95% (Kuhnert et al., 2007), while similarity values between different serovars of *Actinobacillus pleuropneumoniae* varied between 91 and 95% (Kuhnert & Korczak, 2006). Comparison of recN in the present study therefore clearly confirmed the species status of taxon 50 (*Avibacterium endocarditidis* sp. nov.).

**Description of Avibacterium endocarditidis sp. nov.**

*Avibacterium endocarditidis* (en.do.car.di’ti.dis. N.L. n. *endocarditis* endocarditis, the medical term for an infection of the inner heart; N.L. gen. n. *endocarditidis* of endocarditis).

Growth on blood agar is non-symbiotic, isolates forming regular, circular, slightly raised, non-phaemolytic colonies with an entire margin. The surface of the colonies is smooth, shiny and opaque with a greyish tinge. Colonies have a diameter of 1.0–1.5 mm after aerobic incubation for 24 h at 37°C. The consistency of the colonies is unguent-like and colonies do not adhere to the agar surface. All
isolates meet the phenotypic characters for the genus *Avibacterium* reported previously (Blackall et al., 2005). Catalase is produced. Acid is produced from glyceral, (-)-d-mannitol, (-)-d-sorbitol, (+)-d-galactose, maltose, trehalose, raffinose and dextrin but not from xylitol, (+)-l-arabinose or (-)-l-fucose. ONPG and PNPG tests are positive. The characters stated allow separation from other species of *Avibacterium*. Detailed phenotypic characters for all isolates including the type strain are given under phenotypic characterization.

The type strain, 2018H4H1* T* (=CCUG 52860* T* =DSM 18224* T*), was isolated from valvular endocarditis of a chicken in Denmark in 2004.

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**References**


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