Phylogenetic and phenotypic evidence for the transfer of *Eubacterium aerofaciens* to the genus *Collinsella* as *Collinsella aerofaciens* gen. nov., comb. nov.

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Three strains of *Eubacterium aerofaciens*, JCM 10188^T, JCM 7790 and JCM 7791, and 178 freshly isolated strains of the *Eubacterium aerofaciens* group from human faeces were characterized by biochemical tests, cell wall peptidoglycan type and 16S rRNA analysis. The *Eubacterium aerofaciens* group was divided into four groups by fermentation patterns of sucrose and cellobiose, and were further divided into 16 sub-groups by fermentation patterns of aesculin, salicin and amygdalin. All of the strains of the *Eubacterium aerofaciens* group were shown to be phylogenetically distantly related to *Eubacterium limosum*, which is the type species of genus *Eubacterium*. *Eubacterium aerofaciens* was shown to have a specific phylogenetic association with *Coriobacterium glomerans*. All the strains belonging to *Eubacterium aerofaciens* resembled *Coriobacterium glomerans* in possessing a high G+C content (60 mol%). Cell wall analysis, however, revealed the presence of different A4 β (L-Ala)-D-Glu-L-Orn-L-Asp peptidoglycan types. Based on a 16S rRNA sequence divergence of greater than 9% with *Coriobacterium glomerans* and the presence of a unique peptidoglycan type, a new genus, *Collinsella*, is proposed for *Eubacterium aerofaciens*, with one species, *Collinsella aerofaciens*. The type strain of *Collinsella aerofaciens* is JCM 10188^T.

Keywords: *Collinsella aerofaciens* gen. nov., comb. nov., *Eubacterium aerofaciens*, 16S rDNA, cell wall

INTRODUCTION

Intestinal microflora in humans and animals consists of many micro-organisms, both anaerobic and aerobic. Species of the genus *Eubacterium*, anaerobic Gram-positive non-sporing rods, belong to the predominant micro-organisms of the intestinal microflora. The number and incidence of *Eubacterium aerofaciens*, in particular, are the highest in human intestine compared with other species of genus *Eubacterium*.

The genus *Eubacterium* contains uniform or pleomorphic non-sporing Gram-positive bacilli which are obligately anaerobic, they produce organic acids from carbohydrates or peptone, often including large amounts of butyric, acetic or formic acids. These

micro-organisms do not produce propionic, lactic or succinic acids as a major acid product. This definition, by differentiation from other anaerobic genera on the basis of negative fermentation characteristics, provided a convenient, pragmatic classification when little or no phylogenetic data were available (Moore & Holdeman-Moore, 1986). Because of its broad definition, this genus has over the years acted as a repository for a large number of phenotypically diverse species (Andreesen, 1992). In addition to this marked phenotypic heterogeneity, it is recognized that eubacteria are not phylogenetically homologous, with species dispersed among many of the different groups. In particular, the wide range of genomic DNA G+C contents indicates that the genus includes organisms that are not related phylogenetically.

In this paper we report on the phenotypic and phylogenetic characterization of 181 strains of the *Eubacterium aerofaciens* group isolated from human

The GenBank/EMBL/DDBJ accession numbers for the sequences determined in this paper are AB011814 (*Eubacterium aerofaciens* JCM 7790), AB011815 (JCM 7791) and AB011816 (JCM 10188^T).

Table 1. List of *Eubacterium aerofaciens*-like strains isolated from human faeces and their sources

Group	n	Strain name	Source*	Year
I-A	16	JCM 7791	American	
		RCA55-47, RCA55-95	Healthy adults	1986
		RCA57-8, RCA57-76	Healthy adults	1986
		RCA58-61	Healthy adult	1987
		A2-231	Canadian	1982
		A7-5, A7-10, A7-30, A7-48	Healthy adults	1978
		A11-212, A11-250, A11-263, A11-264, A11-267	CC patients	1981
I-B	15	RCA56-50	Healthy adult	1986
		RCA57-62	Healthy adult	1986
		RCA58-8	Healthy adult	1987
		A2-156	UC patient	1978
		A5-13	Japanese	1983
		A7-15, A7-32, A7-58	Healthy adults	1978
		A11-185, A11-194, A11-196, A11-197, A11-200, A11-254, A11-261	CC patients	1981
I-C	1	A11-239	CC patient	1976
I-D	2	RCA55-19, RCA55-68	Japanese	1983
I-E	19	RCA56-51, RCA56-52, RCA56-56, RCA56-61	Healthy adults	1986
		RCA57-7, RCA57-21	Healthy adults	1986
		A2-70, A2-71	Japanese	1981
		A7-4, A7-53, A7-54	Healthy adults	1978
		A9-8	Japanese	1981
		A11-195, A11-208, A11-210, A11-231, A11-237, A11-251, A11-262	CD patients	1983
		RCA55-86	Healthy adult	1986
I-F	12	RCA56-76, RCA56-83	Healthy adults	1986
		RCA57-63	Healthy adult	1986
		A1-75, A1-78	Japanese	1983
		A2-44, A2-147	UC patients	1978
		A7-3, A7-57	Healthy adults	1978
		A11-191, A11-233	UC patients	1976
		RCA2-45, RCA2-49	Japanese	1981
II-A	44	RCA55-16, RCA55-18, RCA55-21, RCA55-24, RCA55-25, RCA55-30, RCA55-44, RCA55-51, RCA55-53, RCA55-57, RCA55-61, RCA55-93, RCA55-97	Healthy adults	1986
		RCA57-59, RCA57-60, RCA57-66, RCA57-67, RCA57-68, RCA57-70, RCA57-71, RCA57-72, RCA57-81, RCA57-83, RCA57-89	Healthy adults	1986
		RCA58-7, RCA58-11, RCA58-14, RCA58-15	Healthy adults	1987
		A1-25	Japanese	1983
		A2-227	Canadian	1982
		A3-65, A3-89, A3-122, A3-215, A3-231, A3-232, A3-264	Healthy adults	1981
		A7-20, A7-34, A7-35, A7-51	Healthy adults	1978
		A11-269	CD patient	1983
		RCA55-23, RCA55-59, RCA74	Healthy adults	1986
		RCA58-60	Healthy adult	1987
		A3-84, A3-85, A3-88, A3-90, A3-96, A3-124, A3-174, A3-175, A3-218, A3-227, A3-229, A3-230, A3-238, A3-239, A3-242	Japanese	1981
II-B	19			
II-C	5	A1-51	Japanese	1983
		A3-51	CC patient	1976
		A7-2, A7-43, A7-56	Healthy adults	1978
II-D	14	RCA2-35	Japanese	1981
		RCA55-3, RCA55-6, RCA55-20, RCA55-29, RCA55-36, RCA55-45, RCA55-46, RCA55-52, RCA55-80, RCA55-87, RCA55-94	Healthy adults	1986
		RCA58-59	Healthy adult	1987
		A1-102	Japanese	1983
II-E	4	RCA55-2, RCA55-22, RCA55-67, RCA55-88	Healthy adults	1986

Table 1. (cont.)

Group	n	Strain name	Source*	Year
II-F	13	RCA57-78	Healthy adult	1986
		A1-45	Japanese	1983
		A3-53, A3-72	CC patients	1976
		A7-1, A7-16, A7-40, A7-41, A7-44, A7-50, A7-52, A7-55	Healthy adults	1978
		A11-186	Stomach cancer	1981
			UC patients	1976
II-G	2	A11-226, A11-228		
III-A	8	JCM 10188 ^T , JCM 7790	American	
		RCA1-29	Healthy adult	1982
		RCA57-32	Healthy adult	1986
IV-A	6	A7-8, A7-11, A7-28, A7-31	Healthy adults	1978
		RCA1-28, RCA1-30	Healthy adults	1981
		RCA55-85	Healthy adult	1986
		RCA57-11	Healthy adult	1986
		A7-6, A7-12	Healthy adults	1978
IV-B	1	A11-209	UC patient	1976

* CC, Colon cancer; CD, Crohn's disease; UC, ulcerative colitis.

faeces, including three deposited strains, JCM 10188^T, JCM 7790 and JCM 7791. On the basis of the results presented, we propose that these organisms be classified as *Collinsella aerofaciens* gen. nov., comb. nov.

METHODS

Bacterial strains studied and cultivation. The bacterial strains used in this study were 178 strains isolated from human faeces from 1977 to 1987 and three strains of *Eubacterium aerofaciens* JCM 10188^T (= ATCC 25986^T), JCM 7790 and JCM 7791, as shown in Table 1. All strains were cultivated for 2 d at 37 °C on EG agar [pre-mixed EG agar (Eiken Chemical) supplied with 5% horse blood that contains 3 g beef extract, 5 g yeast extract, 10 g peptone, 1.5 g glucose, 0.5 g L-cysteine.HCl, 0.2 g L-cystine, 4 g Na₂HPO₄, 0.5 g soluble starch, 0.5 g Tween 80, 0.5 g silicone and 15 g agar in 1000 ml, pH 7.7] in an anaerobic chamber.

Phenotypic characteristics. Acid production from carbohydrates, assimilation of organic acids, nitrate reduction and hydrolysis of starch and gelatin were tested as described previously (Holdeman *et al.*, 1977; Kaneuchi *et al.*, 1976).

Chemotaxonomy. Freeze-dried cells for chemotaxonomic analyses were obtained from cultures grown in EGF broth [containing 2.4 g Lab-Lemco powder (Oxoid), 10 g Proteose peptone No. 3 (Difco), 5 g yeast extract (Difco), 4 g Na₂HPO₄, 40 ml sterilized horse blood, 5 g glucose, 0.5 g soluble starch (Sigma) and 0.5 g L-cysteine.HCl in 960 ml distilled water; pH 7.6] in an anaerobic chamber at 37 °C.

Cell wall peptidoglycan was prepared and hydrolysed by the methods of Kawamoto *et al.* (1981), and the amino acid composition was analysed with an automatic amino acid analyser (model 835; Hitachi). The neutral amino acid fraction was reacted with a chiral reagent [(+)-1-(9-fluorenyl)ethyl chloroformate] and used for HPLC as described by Einarsson & Josefsson (1987).

DNA studies. DNA was isolated as described by Saito & Miura (1983). DNA base composition was estimated by HPLC (Fujimura, 1986; Tamaoka & Komagata, 1984).

Levels of DNA–DNA relatedness were determined by the method of Ezaki *et al.* (1989) by using photobiotin and microplates.

16S rDNA sequencing. The 16S rRNA gene was amplified using the PCR method and prokaryotic 16S rDNA universal primers 27F (5' AGAGTTTGATCCTGGCTCAG 3') and 1492R (5' GGTTACCTTGTTACGACTT 3'). PCR was performed with a DNA thermal cycler (Perkin-Elmer Cetus) using 30 cycles consisting of denaturation at 94 °C for 60 s, primer annealing at 55 °C for 150 s, and primer extension at 72 °C for 150 s (with 30 s per cycle added). Ligation was performed using plasmid pT7 Blue T-Vector (Novagen) and a ligation kit (Takara Shuzo) as recommended by the manufacturers. Transformation provided *Escherichia coli* MJ1190 competent cells and select colonies for analysis. Plasmids were prepared for sequencing using the alkaline lysis method.

Sequencing was performed using the ALFred AutoCycle Sequencing kit with an ALFexpress DNA sequencer (both from Pharmacia Biotech). These sequences were aligned with previously published sequences obtain from GenBank, including all species of the genus *Eubacterium* and related micro-organisms. Nucleotide substitution rates (K_{nuc} values) were calculated (Kimura & Ohta, 1972), and phylogenetic trees were constructed by the neighbour-joining method (Saitou & Nei, 1987). The topology of the trees was evaluated by performing a bootstrap analysis of the sequence data with the CLUSTAL W software (Thompson *et al.*, 1994) (Fig. 2). The DNAML program in the PHYLIP 3.5c package (Felsenstein, 1985) was used for the maximum-likelihood analysis, with the default transition/transversion ratio of 2.000000 (Fig. 3).

RESULTS

Morphological characteristics

All of the strains which we studied were Gram-positive, non-sporing, anaerobic rods. Colonies were white in the centre with clear surroundings and protuberant on EG agar. Cells were 0.3–0.7 × 1.2–4.3 µm long and occurred in chains of 6–120 coccid cells.

Table 2. Physiological and biochemical characteristics of strains of *Eubacterium aerofaciens*

Data are based on the reaction of our 178 isolated strains and *Eubacterium aerofaciens* JCM 10188^T, JCM 7790 and JCM 7791. +, Positive; −, negative; d+, > 80% positive; d−, > 80% negative; w+, > 60–70% positive; w−, > 60–70% negative. All isolates produced acid from glucose, mannose, galactose, fructose, maltose and lactose. None produced acid from arabinose, xylose, melezitose, soluble starch, glycogen, mannitol, sorbitol, inositol or erythritol.

Acid from:	Type strain	Other strains
Arabinose	−	−
Xylose	−	−
Rhamnose	−	d−
Ribose	−	d−
Sucrose	+	w+
Maltose	+	+
Cellobiose	−	d+
Trehalose	−	d−
Raffinose	−	d−
Aesculin	−	w−
Salicin	−	w−
Amygdalin	−	d−

Biochemical and physiological tests

A total of 181 strains of the *Eubacterium aerofaciens* group isolated from human faeces and three strains of *Eubacterium aerofaciens*, JCM 10188^T, JCM 7790 and JCM 7791, were characterized. All isolates produced acid from glucose, mannose, galactose, fructose, maltose and lactose. No isolates produced acid from arabinose, xylose, melezitose, soluble starch, glycogen, mannitol, sorbitol, inositol or erythritol (Table 2). Moore & Holdeman (1974) recognized three phenotypic groups (I–III) of *Eubacterium aerofaciens* isolated

Fig. 1. Fragment of the primary structure of cell wall peptidoglycan of *Eubacterium aerofaciens* JCM 10188^T.

from human faeces. In this study, seven strains which did not produce acid from sucrose or cellobiose were recognized and distinguished as group IV. These four groups were further divided into 16 sub-groups by their ability to ferment aesculin, salicin and amygdalin as shown in Table 3. Of the *Eubacterium aerofaciens* groups tested, group II was isolated at the highest incidence (55.2%) and group I also occurred at high levels (36.6%).

Chemotaxonomic characteristics

The structure of the cell wall peptidoglycan of *Eubacterium aerofaciens* JCM 10188^T was determined. The peptidoglycan contained, in addition to muramic acid and glucosamine, the amino acids glutamic acid,

Table 3. Grouping of the *Eubacterium aerofaciens* group by fermentation of five sugars

Data are based on the reactions of 178 *Eubacterium aerofaciens*-like strains and *Eubacterium aerofaciens* JCM 10188^T, JCM 7790 and JCM 7791.

Group* ...	I						II							III	IV	
Sub-group† ...	A	B	C	D	E	F	A	B	C	D	E	F	G	A	A	B
n ...	16	15	1	2	19	12	44	19	5	14	4	13	2	8	6	1
Sucrose	+	+	+	+	+	+	−	−	−	−	−	−	−	+	−	−
Cellobiose	+	+	+	+	+	+	+	+	+	+	+	+	+	−	−	−
Aesculin	−	−	−	+	+	+	−	+	−	−	+	+	+	−	−	+
Salicin	−	+	+	−	+	+	−	−	+	−	−	+	+	−	−	−
Amygdalin	−	−	+	+	−	+	−	−	−	+	+	−	+	−	−	−

* Groups are divided by fermentation pattern of sucrose and cellobiose.

† Groups are divided into 16 sub-groups by fermentation patterns of five sugars.

Table 4. DNA base composition and levels of DNA–DNA relatedness among *Eubacterium aerofaciens* strains

Strain	G + C content (mol %)	Percentage DNA–DNA reassociation with:		
		JCM 10188 ^T	JMC 7790	JCM 7791
<i>Eubacterium aerofaciens</i> JCM 10188 ^T	61	100	84	75
<i>Eubacterium aerofaciens</i> JCM 7790	60	82	100	74
<i>Eubacterium aerofaciens</i> JCM 7791	61	75	73	100

aspartic acid, ornithine and alanine at a molar ratio of 1:1:1:2, respectively. Both ornithine and aspartic acid occur in the L configuration; to determine the composition of the isomers, the neutral amino acid fraction was reacted with a chiral reagent [(+)-1-(9-fluorenyl)ethyl chloroformate] and analysed by HPLC. Until recently, only D-aspartic acid has been found in bacterial cell walls, but in this study of *Eubacterium aerofaciens* L-aspartic acid was found. This indicated that the structural type was a previously unknown A4 β -type, (L-Ala)-D-Glu-L-Orn-L-Asp (Fig. 1). However, Willems *et al.* (1997) found that *Holdemania filiformis*, whose phenotypic and phylogenetic characters are similar to the genus *Eubacterium*, has L-aspartic acid in its cell wall.

DNA base composition and DNA–DNA relatedness

The DNA base composition of *Eubacterium aerofaciens* JCM 10188^T, JCM 7790 and JCM 7791 was 59.8–61.1 mol% G + C by the HPLC nucleoside method (Table 4). The levels of DNA–DNA relatedness among three *Eubacterium aerofaciens* strains ranged from 73 to 84% (Table 4). The results show that these three strains are the same species.

16S rDNA sequence analysis

More than 1400 bases of the 16S rDNA sequences (positions 28–1492; *Escherichia coli* numbering system) of *Eubacterium aerofaciens* JCM 10188^T, JCM 7790 and JCM 7791 were determined, and these sequences have been deposited in the DDBJ database. Fig. 2 shows a phylogenetic tree based on calculated K_{nuc} values created by using our sequences and those obtained from public databases. Fig. 3 shows a phylogenetic tree based on maximum-likelihood analysis. A database search demonstrated that *Eubacterium aerofaciens* belongs to the family *Coriobacteriaceae*, which contains the genera *Coriobacterium* and *Atopobium* (Hass & König, 1988). A phylogenetic analysis showed that three strains of *Eubacterium aerofaciens*, JCM 10188^T, JCM 7790 and JCM 7791, had different characteristic fermentation patterns but that they created one cluster which was distant from other *Eubacterium* species and closest to *Coriobacterium glomerans* (Lewis & Sutter, 1981). The sequence similarity values were: JCM 10188^T vs JCM

7790, 96.6%; JCM 10188^T vs JCM 7791, 97.6%; JCM 7790 vs JCM 7791, 97.8%.

DISCUSSION

Of all members of the genus *Eubacterium*, one of the predominant micro-organisms in the intestinal microflora, *Eubacterium aerofaciens* is found at the highest levels and most frequently in the human intestine (Benno *et al.*, 1986; Finegold & Sutter, 1978; Moore & Holdeman, 1974). Some characteristics and the phylogenetic position, however, are not clear. The definition of the genus *Eubacterium* was unclear and all species which were anaerobic, Gram-positive, non-spore, rod-shaped bacteria which were not members of the genera *Propionibacterium* or *Bifidobacterium* were included in genus *Eubacterium* (Lewis & Sutter, 1981; Moore & Holdeman, 1986). Therefore, this genus contained many species with different characteristics and a broad range of G + C contents, which caused considerable confusion (Nakazawa & Hoshino, 1994).

Moore & Holdeman (1974) reported that *Eubacterium aerofaciens* isolated from human intestine was mainly divided into three groups (I–III) by fermentation patterns of sucrose and cellobiose: group I uniformly produced acid from sucrose and cellobiose; group II uniformly produced acid from cellobiose but not from sucrose; and group III uniformly produced acid from sucrose but not from cellobiose. In the present study, 181 strains of the *Eubacterium aerofaciens* group were characterized using the fermentation patterns of sucrose and cellobiose and divided into four groups. Three groups were the same as in the previous study, but group IV which uniformly produced no acid from sucrose and cellobiose was different. Previously, none of the strains of the *Eubacterium aerofaciens* group tested produced acid from aesculin, salicin or amygdalin, but in the present study, some strains fermented these glycosides. They were divided into 16 sub-groups (I–A–F, II–A–G, III–A and IV–A and –B) according to fermentation patterns of aesculin, salicin and amygdalin (Table 3). These results showed that the *Eubacterium aerofaciens* group has very variable characters.

The genus *Eubacterium* was heterogeneous with respect to, for example, the G + C content of DNA and the wide range of the phylogenetic positions

Fig. 2. Unrooted phylogenetic tree derived from 16S rDNA sequences. The tree was created using the neighbour-joining method and K_{nuc} values. The numbers on the tree indicate bootstrap values for the branch points. Only values above 50% significance are indicated. The sequence data for species other than *Collinsella aerofaciens* were obtained from the GenBank database. *E.*, *Eubacterium*; *C.*, *Collinsella*.

Fig. 3. Unrooted phylogenetic tree derived from 16S rDNA sequence. The tree was created using maximum-likelihood analysis. The sequence data for species other than *Collinsella aerofaciens* were obtained from the GenBank database. *E.*, *Eubacterium*; *C.*, *Collinsella*.

(Nakazawa & Hoshino, 1994). In the present study, the phylogenetic positions of the *Eubacterium aerofaciens* group were demonstrated using 16S rRNA

sequences. A database search revealed that three strains of *Eubacterium aerofaciens* belonged to the actinomycetes line of descent. A new hierarchic classi-

fication structure for the taxa between the taxonomic levels of genus and class is proposed for the actinomycete line of descent as defined by analysis of small-subunit (16S) rRNA and genes encoding this molecule (rDNA). A new class, *Actinobacteria*, which contains the orders *Acidimicrobiales*, *Rubrobacterales*, *Coriobacterales*, *Sphaerobacterales*, *Actinomycetales* and *Bifidobacterales*, was proposed by Stackebrandt *et al.* (1997). The *Eubacterium aerofaciens* group belongs to class *Coriobacterales*, family *Coriobacteriaceae*, and this family contains the genera *Coriobacterium* and *Atopobium* as a new classification.

To elucidate the topology of *Eubacterium aerofaciens*, two different phylogenetic analyses (neighbour-joining and maximum likelihood; Figs 2 and 3) were performed that included all species of the genus *Eubacterium* and all other taxa from the family *Coriobacteriaceae* – the genus *Eubacterium* is confused, because so many other genera, for example *Clostridium*, are close to it – thus genera outside the *Coriobacteriaceae* were omitted as the tree would have been too complex. Both our analyses showed that three strains of the *Eubacterium aerofaciens* group formed one cluster near *Coriobacterium glomerans* (Hass & König, 1988). The genus *Eubacterium* was very heterogeneous, so a few different topologies occurred between the two analyses. However, the topology of family *Coriobacteriaceae*, which contains *Eubacterium aerofaciens* strains, was the same. The sequence similarity values were 96.6–97.8%, which is not very high, and three strains of the *Eubacterium aerofaciens* group showed different sugar fermentations. Therefore, we checked the similarity of three strains based on DNA–DNA homology. The result showed that the three strains were the same species (Table 4).

The type species of genus *Eubacterium* is *Eubacterium limosum*. It is evident from recent studies that *Eubacterium limosum*, *Eubacterium barkeri* and *Eubacterium callanderi* (Mountfort *et al.*, 1988) can form the nucleus of a redefined genus *Eubacterium*. On the basis of the characteristics of this group, a preliminary working definition of *Eubacterium sensu stricto* should be as follows: Gram-positive rod-shaped organisms that are non-motile and obligately anaerobic, may form endospores and are saccharolytic. The main end products from glucose fermentation are butyrate, acetate, lactate and H₂. Formate or CO₂ may also be produced by three species. The cell walls contain a type B peptidoglycan. The G + C content of the DNA is 45–47 mol% (Willems & Collins, 1996).

Phylogenetic analysis of the *Eubacterium aerofaciens* group showed they varied widely from *Eubacterium sensu stricto*. The G + C content of *Eubacterium aerofaciens* was much higher than that of *Eubacterium sensu stricto* and the cell wall contained A4 β -type peptidoglycan. On the other hand, *Coriobacterium glomerans* was anaerobic, Gram-positive and formed long chains of irregular pear-shaped cells with large spherical involutions. This species was isolated from

the intestinal tract of red soldier bugs. This species also had a high DNA G + C content of 60–61 mol% and the peptidoglycan was Lys–Asp type. *Coriobacterium glomerans* produced acetic acid, lactic acid, ethanol, CO₂ and H₂ from glucose as end products (Hass & König, 1988).

From peptidoglycan amino acid analysis and the 16S rRNA gene sequence composition, it is evident that this bacterium has a close phylogenetic relationship with *Coriobacterium glomerans*. Although the association between these taxa is statistically significant, a sequence divergence of >9% suggests that this relationship is that of two phylogenetically closely related, but nevertheless different, genera.

Based on 16S rRNA sequence analysis and the unique A4 β -type peptidoglycan, we propose that *Eubacterium aerofaciens* be reclassified as the first species of a new genus, *Collinsella* gen. nov., comb. nov.

Description of *Collinsella* gen. nov.

Collinsella (Col.lin.sel'la. M.L. fem. dim. ending -ella, M.L. fem. n. *Collinsella* named to honour Matthew D. Collins, a contemporary English microbiologist, for his outstanding contribution to microbial taxonomy and phylogeny).

Cells occur in chains of coccid cells. Gram-positive and obligately anaerobic. Spores and flagella are absent. Fermentation products of glucose are H₂, ethanol, formate and lactate. Cell wall contains a A4 β -type peptidoglycan with an (L-Ala)-D-Glu-L-Orn-L-Asp peptide subunit whose interpeptide bridge consists only of L-Asp. DNA G + C content is 60–61 mol%. Type species is *Collinsella aerofaciens*. The genus *Collinsella* is a member of the *Coriobacteriaceae* and exhibits a close phylogenetic association with the genus *Coriobacterium*.

Description of *Collinsella aerofaciens* [*Eubacterium aerofaciens* (Eggerth) Prévot 1938] comb. nov.

Collinsella aerofaciens (ae.ro.fa'ci.ens. Gr. n. *aer* gas; L. v. *facere* to make, to produce; M.L. part. adj. *aerofaciens* gas-producing).

Cells are 0.3–0.7 $\times$ 1.2–4.3 μ m long and occur in chains of 6–120 coccid cells. Gram-positive and obligately anaerobic. Spores and flagella are absent. Colonies are white in the centre with clear surroundings and protuberant on EG agar. Can be cultivated for 2 d at 37 °C on EG agar in an anaerobic jar with 100% CO₂. Cells produce acid from glucose, mannose, galactose, fructose, maltose and lactose but not from arabinose, xylose, melezitose, soluble starch, glycogen, mannitol, sorbitol, inositol or erythritol. Cell wall contains a A4 β -type peptidoglycan with an (L-Ala)-D-Glu-L-Orn-L-Asp peptide subunit and interpeptide bridge consists only of L-Asp. DNA G + C content is 61 mol%. Type strain of *Collinsella aerofaciens* is strain

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