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Cedecea davisae gen. nov., sp. nov. and *Cedecea lapagei* sp. nov., New *Enterobacteriaceae* from Clinical Specimens

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We propose the name *Cedecea* gen. nov. for a group of organisms in the *Enterobacteriaceae* that were isolated from clinical sources in North America (the clinical significance of these organisms is unknown). This name was coined by two of us (P.A.D.G. and F.G.) from the letters CDC, the abbreviation for the Centers for Disease Control, where the organisms were originally discovered. Phenotypically, *Cedecea* resembles no other group of *Enterobacteriaceae*; the members of this genus are lipase positive, resistant to colistin and cephalothin, and negative for deoxyribonuclease, gelatin liquefaction, and utilization of L-arabinose and L-rhamnose. Deoxyribonucleic acid relatedness studies showed that *Cedecea* strains were 32 to 100% related to each other and less than 23% related to other members of the *Enterobacteriaceae*. We found five deoxyribonucleic acid hybridization groups among 17 *Cedecea* strains, but three of these groups contained only 1 strain (strains 001, 002, and 012). Two deoxyribonucleic acid hybridization groups were named. *Cedecea davisae* sp. nov. (nine strains), the type species of the genus, fermented sucrose and D-xylose and was positive in the ornithine decarboxylase and ascorbate tests. *C. davisae* grew in a mineral salts medium with glucose as the carbon source only if the medium was supplemented with 0.1 μg of thiamine per ml. The type strain of *C. davisae* is strain 005 (= ATCC 33431 = CDC 3278-77 = CIP 80.34) *Cedecea lapagei* sp. nov. (five strains) did not ferment sucrose and D-xylose and was negative in the ornithine decarboxylase and ascorbate tests. This species grew on glucose as the role source of carbon and energy with no growth factor requirement. The type strain of *C. lapagei* is strain 004 (= ATCC 33432 = CDC 0485-76 = CIP 80.35). Within species, deoxyribonucleic acid relatedness was 80 to 100% at 60°C (S1 nuclease method), and *C. davisae* and *C. lapagei* were much more closely related to each other (32 to 52%) than to members of any other group within the family *Enterobacteriaceae* (1 to 21%).

Despite the progress made in bacterial taxonomy in the last 20 years, reference laboratories frequently encounter unidentified strains. These strains are often kept in a collection which can be analyzed to detect possible groups of similar unidentified bacteria. In 1977, workers at the Centers for Disease Control gave the vernacular name "Enteric Group 15" to a group of 17 unidentified *Enterobacteriaceae* strains which were lipase (corn oil) positive. In 1980, we proposed a new genus, *Cedecea*, containing two species (*Cedecea davisae* and *Cedecea lapagei*) and three unspecified strains (*Cedecea* sp.) (J. J. Farmer, III, P. A. D. Grimont, F. Grimont, and M. A. Asbury, Abst. Annu. Meet. Am. Soc. Microbiol. 1980, C123, p. 295). However, that proposal did not constitute effective and valid publication of the scientific names.

In this paper we propose the names *Cedecea* gen. nov., *Cedecea davisae* sp. nov., and *Cedecea lapagei* sp. nov. for these organisms on the basis of their deoxyribonucleic acid (DNA)-DNA hybridization and phenotypic characteristics. *Cedecea* is an arbitrarily constructed name derived from the abbreviation CDC (Centers for Disease Control).

MATERIALS AND METHODS

Bacterial strains. The *Cedecea* strains used in this study are listed in Table 1. The origins of the non-*Cedecea* reference strains used in the DNA relatedness study have been reported previously (3, 4, 11).

Methods. A suspension of strain 005 in distilled water (about 0.02 ml) was deposited on a carbon-coated specimen grid, negatively stained with 2% (wt/vol) phosphotungstic acid, and examined with a Siemens Elmiskop electron microscope.

Growth factor requirements were determined by the method of Clowes and Hayes (5). Growth on various compounds as carbon and energy sources was determined by multiple inoculation (9) onto M70 minimal medium (14) supplemented with 0.01 μg of thiamine per ml, 100 μg of cysteine per ml, 0.5 μg of *para-*

TABLE 1. *Origins of the Cedecea strains studied*

Species	Strain designations		Origin[a]	
	This paper	Centers for Disease Control	Source	Location
C. davisae	005	CDC 3278-77	Stool	New Jersey
	006	CDC 0512-78	Eye	New York
	008	CDC 2205-78	Sputum	United States
	010	CDC 1395-75	Gall bladder	Alabama
	015	CDC 2295-78	Sputum	United States
	016	CDC 2296-78	Wound	United States
	018	CDC 2932-78	Urine	United States
	019	CDC 1868-79	Sputum	New York
	020	CDC 1790-78	Wound	California
C. lapagei	004	CDC 0485-76	Throat	Canada
	003	CDC 0818-75	Sputum	Kentucky
	007	CDC 0817-78	Sputum	New York
	009	CDC 1554-75	Sputum	Georgia
	017	CDC 2488-78	Sputum	Virginia
Cedecea sp.	001	CDC 4853-73	Sputum	New Jersey
	002	CDC 0621-75	Foot wound	California
	012	CDC 3699-73	Toe	Canada

[a] All strains were from human clinical specimens.

aminobenzoic acid per ml, and 0.1 to 0.2% carbon source. We used previously described procedures (9) for the following tests: Voges-Proskauer test (Richard modification), hydrolysis of gelatin (plate method), anaerobic growth in the presence of potassium chlorate, reduction of tetrathionate in peptone water, hydrolysis of tributyrin, Tween 40, Tween 60, Tween 80, DNA, chitin, and starch, *o*-nitrophenyl-β-D-galactopyranoside test, β-xylosidase test with *para*-nitrophenyl-β-xyloside (Sigma Chemical Co.), pigment and odor production, growth with 0, 2, 4, 6, and 8% NaCl, and growth at 5, 15, 20, 37, 40, and 42°C. The ascorbate test was performed with ascorbate medium (Enteric fermentation base [Difco] 18 g; bromothymol blue, 0.04 g; sodium L-ascorbate, 10 g; distilled water to 1,000 ml; pH 7.5) This medium was dispensed in 10-ml quantities into tubes (16 by 100 mm) and autoclaved for 10 min at 121°C; 4 ml of mineral oil was then added, and the medium was stored at 4°C. Tubes were discarded if the pH fell below 7.0. All other biochemical tests were performed as described by Edwards and Ewing (7). In addition, the Voges-Proskauer test was performed at the Centers for Disease Control by adding 0.5 ml of API reagent 1 (40% [vol/vol] KOH solution) and 0.5 ml of API reagent 2 (6% alpha-naphthol in absolute ethanol) to 1 ml of a 48-h culture in MR-VP broth (Difco). This method (listed in Table 5 as Voges-Proskauer—special) was a more sensitive method for detecting the acetoin pathway in *Cedecea*.

Susceptibilities to antimicrobial agents were determined by disk diffusion on Mueller-Hinton agar (Institut Pasteur Production), as recommended by an international study group (8). Susceptibility to the vibriostatic compound 0/129 was determined on Mueller-Hinton agar with disks impregnated with 0.5 mg of 2,4-diamino-6,7-diisopropylpteridine phosphate (synonym, compound 0/129; Institut Pasteur Production) per disk.

We used previously described procedures to label DNA with [^{3}H]thymidine (10) to extract and purify radioactive DNAs (1), to extract and purify unlabeled DNAs, and to shear both labeled and unlabeled DNAs (2). Sheared DNAs were dialyzed overnight against 0.042 M NaCl and then stored at 4°C over a layer of chloroform.

In the hybridization experiments, we used the S1 nuclease method (6), slightly modified (10). S1 nuclease was prepared by the method of Sutton (13). The DNA duplexes remaining after S1 nuclease treatment for 40 min at 60°C were precipitated by adding 0.25 ml of ice-cold 25% (wt/vol) trichloroacetic acid and then collected on membrane filters (Sartorius, Göttingen, Germany). The filters were washed with three 5-ml volumes of ice-cold 5% trichloroacetic acid, dried, and put into vials containing 10 ml of scintillant (4 g of Koch-Light "Butyl PBD" per liter of toluene), and the radioactivity was measured with an Intertechnique model SL 4000 liquid scintillation spectrometer. The degree of polynucleotide sequence homology was calculated by determining the ratio between the average counts in the nuclease-treated samples and the average counts in the untreated samples. Results were normalized to the untreated samples and to the homologous reaction, after the percentage of S1-resistant material in the control tube (containing only denatured radioactive DNA) was subtracted. The temperature at which 50% of the reassociated DNA became hydrolyzable by S1 nuclease was determined by the method of Crosa et al. (6). The percent divergence (ΔT_m) (3) was calculated from the difference in such temperatures between the heterologous DNA reaction and the homologous DNA reaction.

The melting temperatures of 50-μg/ml DNA solutions in 0.1× SSC buffer (1×SSC is 0.15 M NaCl plus 0.015 M trisodium citrate) were measured by M. Popoff, using a Gilford spectrophotometer. The guanine-plus-cytosine contents of DNAs were determined from melting temperatures by the equation of Owen et al. (12).

RESULTS

Phenotypic characterization. Figure 1 shows an electron micrograph of a representative strain of *C. davisae* (strain 005). Cells from semisolid nutrient agar were 0.6 to 0.7 by 1.3 to 1.9 μm and peritrichous, with five to nine flagella.

All *C. lapagei* and *Cedecea* sp. strains could grow on glucose as the sole source of carbon and energy. However, *C. lapagei* 009 required cysteine to produce normal-sized colonies. All *C. davisae* strains required thiamine for growth. *C. davisae* 010 required *para*-aminobenzoic acid in addition to thiamine.

The characteristics of *Cedecea* strains that were neither 100 nor 0% positive are shown in Table 2. The characteristics which did not vary in the collection of 17 strains tested are described.

All 17 *Cedecea* strains were gram-negative, peritrichous (when motile), nonsporeforming, straight rods. They grew on nutrient agar at 37°C, producing convex colonies about 1.5 mm in diameter. They were facultatively anaerobic. All 17 strains grew at 15, 20, 37°C at pH 7 and 9 in tryptic soy broth and in peptone water containing 0, 2, and 4% NaCl. All strains produced catalase, reduced nitrates to nitrites, blackened esculin iron agar, and produced acid from D-arabitol, cellobiose, maltose, D-mannitol, D-mannose, salicin, and trehalose.

All *Cedecea* strains utilized the following substrates as sole carbon and energy sources: *N*-acetylglucosamine, D-arabitol, D-cellobiose, 2-ketogluconate, citrate, D-fructose, fumarate, D-galactose, D-galacturonate, β-gentiobiose, D-gluconate, D-glucosamine, D-glucose, D-glucuronate, DL-glycerate, glycerol, DL-lactate, L-malate, D-mannitol, D-mannose, pyruvate, D-ribose, salicin, and trehalose.

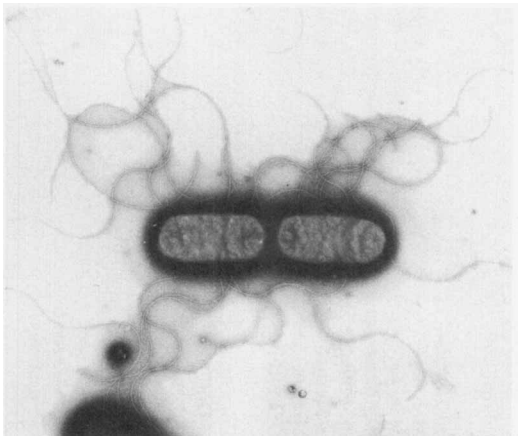

FIG. 1. *Electron micrograph of C. davisae 005. Cell size, 1.5 by 0.7 μm.*

None of the 17 *Cedecea* strains produced pigments, oxidase, indole from peptone water, H_2S from triple sugar iron agar, urease, phenylalanine deaminase, lysine decarboxylase, gelatinase (tube and plate method), deoxyribonuclease, chitinase, polygalacturonase, or amylase. There was no anaerobic growth in the presence of chlorate, and these strains did not produce acid from glucose in the presence of iodoacetate or acid in peptone water containing adonitol, L-arabinose, dulcitol, erythritol, *myo*-inositol, mucate, or L-rhamnose. The tartrate test (Jordan) was negative.

No *Cedecea* strain could use any of the following substrates as a sole carbon and energy source: acetamide, aconitate, adipate, adonitol, β-alanine, DL-3-aminobutyrate, L-arabinose, L-ascorbate, azelate, benzoate, benzylamine, betaine, 2,3-butanediol, butanol, butylamine, butyrate, DL-carnitine, L-cysteine, L-citrulline, dulcitol, *m*-erythritol, ethanol, D-fucose, L-fucose, glutarate, glycine, glycolate, heptanoate, histamine, 2-hydroxybenzoate, 3-hydroxybenzoate, 4-hydroxybenzoate, isobutanol, isobutyrate, L-isoleucine, isopropanol, isovalerate, DL-kynurenine, lactose, L-leucine, L-lysine, D-malate, maleate, D-mandelate, L-mandelate, methanol, L-methionine, nicotinate, L-norleucine, norvaline, oxalate, pelargonate, L-phenylalanine, pimelate, propanol, propionate, quinate, raffinose, L-rhamnose, sarcosine, L-sorbose, suberate, D-tartrate, L-tartrate, L-threonine, trigonelline, tryptamine, D-tryptophane, L-tryptophane, L-tyrosine, *n*-valerate, L-valine, and D-xylitol. All strains were susceptible to carbenicillin, sulfonamide, trimethoprim, streptomycin, kanamycin, tobramycin, gentamicin, amikacin, chloramphenicol, tetracycline, minocycline, nalidixic acid, and furantoin, and all strains were resistant to ampicillin, cephalothin, colistin, and polymyxin (except *C. davisae* strain 010, which was susceptible to colistin and polymyxin); *Cedecea* strains 003, 004, 007, 009, 017, 006, 008, and 002 showed a double zone of inhibition around polymyxin and colistin disks.

Of the 17 strains tested, 15 were resistant to the vibriostatic compound 0/129; strains 016 and 002 showed intermediate susceptibility (inhibition zone, 15 mm).

DNA-DNA hybridization. The DNA relatedness data suggested that *Cedecea* is a new genus in the family *Enterobacteriaceae* and that it has at least five species. The DNA-DNA hybridization results with labeled reference DNA from *C. lapagei* 004 and *C. davisae* 005 are shown in Table 3. The S1 nuclease-resistant cores (in the incubated control tubes containing only labeled DNA) were calculated to be 4.8 ± 1.5% (mean ± standard deviation) for *C. lapagei*

TABLE 2. *Variable characteristics among Cedecea strains*[a]

Characteristic	*C. davisae* (9 strains)				*C. lapagei* (5 strains)				*Cedecea* sp. 001	*Cedecea* sp. 002	*Cedecea* sp. 012
	Reaction of most strains	No. of positive reactions[b]	No. of delayed positive reactions	Strain(s) showing opposite reaction[c]	Reaction of most strains	No. of positive reactions[b]	No. of delayed positive reactions	Strain(s) showing opposite reaction[c]			
Growth on minimal agar containing glucose but not thiamine	−[d]	0			+	5			+	+	+
Utilization of:											
Acetate	(+)		8	020	+	4		009	+	+	+
D-Alanine	+	8		006	+	5			+	+	+
L-Alanine	+	8		006	+	5			+	+	+
DL-4-Amino-butyrate	(+)	1	5	010, 016, 020	+	5			+	−	−
L-Arginine	−		4	(008, 016, 018, 019)[e]	+		4	009	−	(+)	−
L-Aspartate	(+)	1	7	010	+	5			(+)	(+)	(+)
Caprate	−		2	(010, 018)	(+)		3	007, 009	−	−	−
Caproate	−	0			(+)		4	009	−	−	−
Caprylate	−	0			−		1	(017)	−	−	−
L-Glutamate	+	8		010	+	5			+	+	−
L-Histidine	−		3	(008, 018, 019)	−		2	(009, 017)	−	−	−
myo-Inositol	+	6	1	016, 020	(+)	1	4		+	+	+
Malonate	(+)		7	010, 020	(+)		4	009	−	(+)	−
Maltose	+	9			+	4	1		+	+	+
D-Melezitose	−	0			−	0			−	−	+
D-Melibiose	−	0			−	0			+	−	+
α-Methyl-D-glucoside	(+)	3	6		−	0			(+)	(+)	−
Mucate	−	0			+	3	1	007	−	−	−
L-Ornithine	−	0			(+)	2	3		−	(+)	−
L-Proline	+	8		010	+	5			+	+	+
Putrescine	−	0			−	0			+	+	+
D-Raffinose	−	0			−	0			+	−	+
L-Serine	(+)	1	8		(+)	5			(+)	(+)	(+)
D-Sorbitol	−	0			−	0			−	+	+
Succinate	+		7	010, 020	+	5			+	+	+
Sucrose	+	9			−	0			+	+	+
D-Tagatose	−	0			−	0			+	−	−
meso-Tartrate	+	5	1	010, 016, 020	+	5			+	+	(+)
D-Turanose	+	8	1		−	0			+	+	−

D-Xylose	+	9			−	0			+	+	+
Odor of *Serratia odorifera*	−	1		016	−	0			−	−	−
Motility	+	9			+	4		009	+	+	+
Growth at 5°C	+	8	1(w)		−	0			−	−	−
Growth at 40°C	−		4(w)	(006, 009, 018, 019)	+	3		003, 009	+	−	−
Growth at 42°C	−	0			−	2		004, 007	−	−	−
Growth with 6% NaCl	+	6		006, 010, 015	+	5			+	+	+
Growth with 8% NaCl	−		1(w)	(019)	−		1	003	(+)	−	−
KCN test	+	7		010, 015	+	3		004, 009	+	−	+
Tetrathionate reduced	−	1		006	−	0			−	−	−
Citrate (Simmons)	(+)		6(3?)		+	3	2		+	+	+
Acetate	−	0			+	3		007, 009	(+)	(+)	+
Malonate test	+	9		010	+	5			−	+	−
Arginine decarboxylase	+	5	3(?)	010	+	2	2(?)	009	?	+	?
Ornithine decarboxylase	+	9			−	0			−	−	?
Egg yolk reaction	+	7		016, 020	+	5			+	+	−
Tributyrin hydrolyzed	+	7		016, 020	+	5			+	+	+
Corn oil hydrolyzed	+	7		016, 020	+	5			+	+	+
Tween 40 hydrolyzed	+	7		016, 020	+	5			+	+	w
Tween 60 hydrolyzed	+	7		016, 020	+	5			+	w	−
Tween 80 hydrolyzed	+	7		016, 020	+	5			+	w	−
ONPG test[f]	+	7		006, 020	+	5			+	+	+
PNPX (β-xylosidase)[g]	+	6		006, 016, 020	−	0			−	−	−
Glucuronate test (30°C)	+	8	1(w)		+	5			−	+	w
Methyl red test	+	9			−	2		004, 009	+	−	+
Voges-Proskauer test (CDC)[h]	+	7		010, 019	+	5			−	+	+
Voges-Proskauer test (Richard) at:											
20°C	+	6		005, 010, 015	+	5			−	+	+
30°C	+	7		005, 015	+	5			−	+	+
37°C	−	3		018, 019, 020	+	5			+	+	+
Gas from glucose	+	8		010	+	5			+	+	+
Acid from:											
Glycerol	?		5(?)	008, 015, 016, 020[i]	?		5(?)		?	?	−
Lactose	−		4	(005, 010, 015, 018)	(+)	2	2	004	(+)	+	(+)
Melibiose	−	0			−	0			(+)	−	−
α-Methyl-D-glucoside	?		9(?)		−	0			?	−	−
Raffinose	−	0			−	0			+	−	+
D-Sorbitol	−	0			−	0			−	+	+
Sucrose	+	9			−		1	(007)	+	+	+
D-Xylose	+	9			−	0			+	+	+

TABLE 2—*Continued*

[a] Institut Pasteur data. The results of the carbon source utilization tests were determined after 10 and 20 days; the results of the other tests were determined after 2 and 7 days.
[b] Number of positive reactions (excluding delayed or weak positive reactions) observed after 10 days (carbon source utilization) or 2 days (other tests).
[c] Strains that gave a reaction different from the reaction indicated for the species.
[d] Symbols: +, positive reaction; (+), delayed positive reaction; −, negative reaction; w, weak reaction; ?, doubtful reaction.
[e] Strains in parentheses gave delayed positive reactions.
[f] ONPG, *o*-Nitrophenyl-β-D-galactopyranoside.
[g] PNPX, *p*-Nitrophenyl-β-D-xylopyranoside.
[h] CDC, Centers for Disease Control.
[i] These strains gave negative reactions.

004 and 3.8 ± 0.7% for *C. davisae* 005. At 60°C *C. lapagei* strains were 88 ± 8 and 45 ± 4% related to strains 004 and 005, respectively, and *C. davisae* strains were 36 ± 4 and 92 ± 10% related to strains 004 and 005, respectively. Strains 001, 002, and 012 were 36 to 51% related to *C. lapagei* 004 and *C. davisae* 005 at 60°C. The relatedness values for all other species of *Enterobacteriaceae* and *C. lapagei* 004 and *C. davisae* 005 did not exceed 23% at 60°C.

At 75°C, *C. davisae* strains were 24 ± 5% related to strain 004 and 84 ± 17% related to strain 005, and *C. lapagei* strains were 88 ± 11% related to strain 004 and 24 ± 9% related to strain 005.

The ΔT_m values between *C. lapagei* strains and strain 004 were less than 3.3%, and the ΔT_m values between *C. lapagei* strains and strain 005 were 9.5 to 13.3%. The ΔT_m values between *C. davisae* strains and strain 005 were less than 4.2%; the ΔT_m values between *C. davisae* strains and strain 004 were 9.7 to 12.7%.

Table 4 shows the results of the DNA relatedness studies obtained with labeled reference DNAs from *Cedecea* sp. 001 and *Cedecea* sp. 012. The S1 nuclease-resistant core was 5.2 ± 0.8% for strain 001 and 5.6 ± 0.3% for strain 012. No relative binding ratio exceeded 56% at 60°C.

DNA base composition. The guanine-plus-cytosine contents of the DNAs of the *C. davisae* strains were 49 to 50 mol% (strain 005, 48.8 ± 0.8 mol%; strain 018, 49.6 ± 0.4 mol%), and those of the *C. lapagei* strains were 48 to 52 mol% (strain 004, 48.1 ± 0.9 mol%; strain 017, 51.9 ± 0.9 mol%). The DNA of *Escherichia coli* K-12 was tested simultaneously and contained 51.2 ± 0.1 mol% guanine plus cytosine.

DISCUSSION

The DNA relatedness experiments showed that there were five DNA hybridization groups in *Cedecea* (represented by strains 004, 005, 001, 002, and 012), two of which contained more than one strain (*C. davisae* and *C. lapagei*). We found that these hybridization groups are more closely related to each other than to any known genus in the family *Enterobacteriaceae*.

Phenotypically, the 17 strains which we studied do not belong in the genera *Escherichia*, *Shigella*, *Salmonella*, *Citrobacter*, *Proteus*, and *Providencia* because they are positive for the Voges-Proskauer test, the *o*-nitrophenyl-β-D-galactopyranoside test, mannitol, esculin, and lipase and negative for urease, phenylalanine deaminase, H_2S, indole, and lysine decarboxylase. They do not belong in the genera *Klebsiella*, *Enterobacter*, *Erwinia* (including *Pectobacter-*

TABLE 3. *Reassociation of DNAs from C. lapagei 004 and C. davisae 005*[a]

Source of unlabeled DNA	*C. lapagei* 004			*C. davisae* 005		
	% Relative binding at:		ΔT_m at 60°C	% Relative binding at:		ΔT_m at 60°C
	60°C	75°C		60°C	75°C	
C. lapagei 004	100	100	0	46	26	10.5
C. lapagei 003	94	82	1.3	52	22	11.6
C. lapagei 007	84	92	0.8	40	19	11.5
C. lapagei 009	80	77	3.3	45	14	13.3
C. lapagei 017	96	101	0.6	43	37	9.5
C. davisae 005	34	24	10.2	100	100	0
C. davisae 006	36	24	10.3	81	97	2.4
C. davisae 008	38	27	12.7	96	105	2.1
C. davisae 010	32	22	9.7	80	65	3.0
C. davisae 015	36	20	12.3	95	67	3.9
C. davisae 016	32	16	10.3	95	75	4.2
C. davisae 018	45	32	11.0	106	98	1.9
Cedecae sp. 001	48	50		51	29	
Cedecae sp. 002	50	35	8.8	50	27	12.5
Cedecae sp. 012	43	37		36	25	
Citrobacter diversus 1066-71	16			18		
Citrobacter freundii 460-61	12			17		
Edwardsiella tarda 10396	7			12		
Enterobacter aerogenes A1	14			18		
Enterobacter agglomerans E20	9			13		
Enterobacter agglomerans 3123-70	10			5		
Enterobacter agglomerans 1429-71	12			11		
Enterobacter agglomerans 1417-71	9			7		
Enterobacter agglomerans 3482-71	11			14		
Enterobacter agglomerans 6070-69	8			10		
Enterobacter agglomerans 6003-71	14			13		
Enterobacter agglomerans 5422-69	9			7		
Enterobacter agglomerans 4388-71	23			17		
Enterobacter agglomerans 1600-71	19	10		21	14	
Enterobacter agglomerans 5378-71	14			13		
Enterobacter agglomerans 219-71	14			19		
Enterobacter agglomerans 1645-71	6			4		
Enterobacter cloacae C1	11			15		
Enterobacter gergoviae 2-78	18	2		18	4	
Enterobacter sakazakii 4562-70	14	9		17	11	
Enterobacter sp. 2898-73	17			18		
Erwinia amylovora EA 178	7			10		
Erwinia carotovora 495	10			11		
Erwinia carnegieana EC 186	5			4		
Erwinia chrysanthemi SR 32	7			8		
Erwinia cypripedi EC 155	9			12		
Erwinia mallotivora 2851	5			2		
Erwinia nigrifluens EN 104	7			6		
Erwinia nimipressuralis E62	14			16		
Erwinia quercina EQ 102	7			13		
Erwinia rhapontici ER 106	8			14		
Erwinia rubrifaciens ER 105	5			6		
Erwinia salicis ES 102	7			6		
Escherichia blattae 11-78	11			15		
Escherichia coli K-12	10			14		
Hafnia alvei 5632-72	8			6		
Hafnia alvei 4510-75	7			8		
Hafnia alvei 329-73	17	8		20	9	
Klebseilla pneumoniae 2	11			15		
Klebsiella oxytoca 13182	12			12		
Klebsiella sp. 4241-72	12			14		
Levinea amalonatica 25406	13			16		
Morganella morganii 25830	6			5		

TABLE 3—*Continued*

Source of unlabeled DNA	*C. lapagei* 004			*C. davisae* 005		
	% Relative binding at:		ΔT_m at 60°C	% Relative binding at:		ΔT_m at 60°C
	60°C	75°C		60°C	75°C	
Obesumbacterium proteus 4302-74	11			11		
Proteus mirabilis PM1	1			1		
Proteus myxofaciens 19692	2			2		
Providencia rettgeri 1163	2			1		
Providencia alcalifaciens 3370-67	2			2		
P. alcalifaciens 26240	1			2		
Providencia stuartii 2896-68	1			2		
Rahnella aquatilis CUEM 77-115	7			6		
Salmonella typhimurium LT2	10			15		
Serratia fonticola 4556-71	9			9		
Serratia liquefaciens 503	6			10		
Serratia marcescens 504	10			13		
Serratia marinorubra (*S. rubidaea*) 288	7			11		
Serratia odorifera 1073	8			11		
Serratia plymuthica 510	7			10		
Yersinia enterocolitica 614	5			6		
Yersinia pseudotuberculosis P 105	6			4		
Yersinia ruckeri 4535-69	4			3		

[a] Institut Pasteur data.

TABLE 4. *Reassociation of DNAs from Cedecea sp. 001 and Cedecea sp. 012*

Source of unlabeled DNA	*Cedecea* sp. 001			*Cedecea* sp. 012		
	% Relative binding at:		ΔT_m at 60°C	% Relative binding at:		ΔT_m at 60°C
	60°C	75°C		60°C	75°C	
Cedecea sp. 001	100	100	0	55	43	9.2
Cedecea sp. 012	47	23	10.9	100	100	0
Cedecea sp. 002	56	49	6.6	54	53	6.8
C. lapagei 003	47	20	10.4	44	39	5.9
C. lapagei 004	43	32	7.0	43	41	5.4
C. lapagei 007	42	24		44	39	
C. lapagei 009	43	22		41	36	
C. lapagei 017	50	40	8.9	53	40	10.1
C. davisae 005	29	21	7.9	29	22	9.0
C. davisae 006	36	25		35	25	
C. davisae 008	39	24		34	29	
C. davisae 010	29	24		29	24	
C. davisae 015	36	19		30	25	
C. davisae 016	29	16		27	17	
C. davisae 018	39	19	7.9	34	30	9.0
Enterobacter sakazakii 4562-70	17	10		12	7	
Enterobacter gergoviae 2-78	11	5		8	8	
Enterobacter agglomerans 1600-71	17	11		16	7	
Hafnia alvei 329-73	15	9		16	9	

ium), and *Serratia* because they are positive for lipase and D-arabitol and negative for lysine decarboxylase, gelatinase, deoxyribonuclease, chitinase, polygalacturonase, L-rhamnose, and L-arabinose. For these reasons we propose a new genus for the 17 strains described in this study. *Cedecea* gen. nov. is an arbitrarily constructed name derived from the abbreviation CDC (Centers for Disease Control) and is treated as a Medieval Latin feminine substantive. The two hybridization groups containing more than one strain are named as follows: *Cedecea davisae* sp. nov., type species of the genus *Cedecea*, with strain 005 (= ATCC 3343 = CDC 3278-77 = CIP 80.34) as the type strain; and *Cedecea lapagei* sp. nov., with strain 004 (= ATCC 33432 = CDC

0485-76 = CIP 80.35) as the type strain. The specific epithet of *C. davisae* is a Medieval Latin, genitive, feminine form of Davis, in honor of Betty R. Davis, American bacteriologist. The specific epithet of *C. lapagei* is a Medieval Latin, genitive, masculine form of Lapage, in honor of Stephen P. Lapage, British bacteriologist.

Description of the genus *Cedecea*. The

TABLE 5. *Summary of the reactions of Cedecea in biochemical tests which are normally used in enteric bacteriology for identification*[a]

Test	*C. davisae* (nine strains)	*C. lapagei* (five strains)	*Cedecea* sp. 001	*Cedecea* sp. 002	*Cedecea* sp. 012
Indole	−	−	−	−	−
Methyl red	+	V	+	+	+
Voges-Proskauer—normal	−	(+)	−	−	−
Voges-Proskauer—special	(+)	+	−	+	+
Citrate	(+)	+	+	+	+
H_2S (triple sugar iron)	−	−	−	−	−
Urea	−	−	−	−	−
Phenylalanine	−	−	−	−	−
Lysine (Moller)	−	−	−	−	−
Arginine (Moller)	(+)	(+)	+	+	+
Ornithine (Moller)	(+)	−	−	−	+
Motility	+	(+)	+	+	+
Gelatin (22°C)	−	−	−	−	−
KCN	(+)	+	+	−	+
Malonate	(+)	+	−	+	−
D-Glucose (acid)	+	+	+	+	+
D-Glucose (gas)	V	+	+	+	+
Lactose	(−)	(+)	−	+	−
Sucrose	+	−	+	+	+
D-Mannitol	+	+	+	+	+
Dulcitol	−	−	−	−	−
Salicin	+	+	+	+	+
Adonitol	−	−	−	−	−
i-Inositol	−	−	−	−	−
D-Sorbitol	−	−	−	+	+
L-Arabinose	−	−	−	−	−
Raffinose	−	−	+	−	+
L-Rhamnose	−	−	−	−	−
Maltose	+	(+)	+	+	+
D-Xylose	+	−	+	+	+
Trehalose	+	+	+	+	+
Cellobiose	+	+	+	+	+
α-CH_3-glucoside	(−)	−	+	+	−
Erythritol	−	−	−	−	−
Esculin	V	+	+	+	+
Melibiose	−	−	+	−	+
D-Arabitol	+	+	+	+	+
Glycerol	−	−	−	−	−
Mucate	−	−	−	−	−
Jordan tartrate	−	−	−	−	−
Acetate	−	V	+	−	−
Lipase (corn oil)	(+)	+	+	+	−
Deoxyribonuclease (25°C)	−	−	−	−	−
$NO_3^- \rightarrow NO_2^-$	+	+	+	+	+
Oxidase	−	−	−	−	−
ONPG[c]	+	+	+	+	+
Pigment	−	−	−	−	−
D-Mannose	+	+	+	+	+
Tyrosine clearing	−	−	−	−	−

[a] Centers for Disease Control data (48 h, 36°C).

[b] +, 90 to 100% positive; (+), 75 to 89% positive; V, 26 to 74% positive; (−), 11 to 25% positive; −, 0 to 10% positive.

[c] ONPG, *o*-Nitrophenyl-β-D-galactopyranoside.

genus *Cedecea* is composed of motile, non-encapsulated, gram-negative rods that conform to the definition of the family *Enterobacteriaceae*.

The Voges-Proskauer and *o*-nitrophenyl-β-D-galactopyranoside tests are positive. Lysine is not decarboxylated, and indole, H_2S, urease, and phenylalanine deaminase are not produced. Lipase is produced, but gelatinase, deoxyribonuclease, chitinase, amylase, and polygalacturonase are not. Gas is formed from the fermentation of glucose. Acid is produced from D-arabitol, D-cellobiose, maltose, D-mannitol, mannose, salicin, and trehalose but not from adonitol, L-arabinose, dulcitol, or L-rhamnose. Esculin is hydrolyzed. Resistance to colistin, polymyxin, and cephalothin is common. The guanine-plus-cytosine content to the DNA is about 48 to 52 mol%. The type species is *C. davisae*.

C. davisae and *C. lapagei* can be differentiated easily by ornithine decarboxylase and ascorbate tests and by acid production from D-xylose and sucrose (positive for *C. davisae*), production of β-xylosidase (positive for most *C. davisae* strains), and the specific thiamine requirement for growth of *C. davisae*. Further descriptions of the *Cedecea* species are given above and in Table 2. Table 5 provides a summary of the biochemical characteristics which are useful in the identification of *C. davisae* and *C. lapagei* strains in clinical bacteriology laboratories. The clinical significance of *Cedecea* spp. is not yet known.

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REPRINT REQUESTS

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