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Escherichia fergusonii and *Enterobacter taylorae*, Two New Species of *Enterobacteriaceae* Isolated from Clinical Specimens

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Escherichia fergusonii **(formerly known as Enteric Group 10) and** ***Enterobacter taylorae*** **(formerly known as Enteric Group 19) are proposed as new species in the family** ***Enterobacteriaceae*****. By DNA hybridization (^{32}P, 60°C, hydroxyapatite), strains of** ***E. fergusonii*** **were 90 to 97% related to the type strain (holotype) ATCC 35469. They were most closely related to** ***Escherichia coli*** **and more distantly related to species in other genera.** ***E. fergusonii*** **strains are positive for indole production, methyl red, lysine decarboxylase, ornithine decarboxylase, and motility. They ferment D-glucose with gas production and also ferment adonitol, L-arabinose, L-rhamnose, maltose, D-xylose, trehalose, cellobiose, and D-arabitol. They are negative for Voges-Proskauer, citrate utilization (17% positive), urea hydrolysis, phenylalanine deamination, arginine dihydrolase, growth in KCN, and fermentation of lactose, sucrose,** ***myo*****-inositol, D-sorbitol, raffinose, and α-methyl-D-glucoside. By DNA hybridization (^{32}P, 60°C, hydroxyapatite), strains of** ***E. taylorae*** **were 84 to 95% related to the type strain (holotype) ATCC 35317. Their nearest relative was** ***E. cloacae*****, to which they were 61% related. Other named species were more distantly related. Strains of** ***E. taylorae*** **are positive for Voges-Proskauer, citrate utilization, arginine dihydrolase, ornithine decarboxylase, motility, growth in KCN medium, and malonate utilization. They ferment D-glucose with gas production and also ferment D-mannitol, L-arabinose, L-rhamnose, maltose, D-xylose, trehalose, and cellobiose. They are negative for indole production, methyl red, H_2S production on triple sugar-iron agar, urea hydrolysis, phenylalanine deamination, lysine decarboxylase, gelatin hydrolysis, and fermentation of adonitol,** ***i*****-inositol, D-sorbitol, and raffinose. Both new species occur in human clinical specimens. Two strains of** ***E. fergusonii*** **were isolated from blood. Five strains of** ***E. taylorae*** **were isolated from blood, and one was from spinal fluid. These blood and spinal fluid isolates suggest possible clinical significance, but this point requires further study.**

Several years ago, we noticed two groups of strains that were biochemically distinct from all of the named species and biogroups of *Enterobacteriaceae*. Most strains of these two new groups had been isolated from human clinical specimens. The first group, which was indole positive, methyl red positive, Voges-Proskauer negative, and citrate negative, was given the vernacular name Enteric Group 10. The second group, which was indole negative, methyl red negative, Voges-Proskauer positive, and citrate positive, was given the vernacular name Enteric Group 19. These vernacular names were used until the strains could be studied further and a more definitive classification could be proposed. In this article we present the results of these studies and propose scientific names for these two new species of *Enterobacteriaceae*.

MATERIALS AND METHODS

Nomenclature. Only names that have (or will soon have) standing in nomenclature are used. In this paper we propose the new species name *Escherichia fergusonii* for the group of strains previously known as Enteric Group 10 and the new species name *Enterobacter taylorae* for the group of strains previously known as Enteric Group 19. These two new names will have standing in nomenclature as soon as they are validated in the *International Journal of Systematic Bacteriology*.

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Bacterial strains. Table 1 gives the sources of the strains of *Escherichia fergusonii* and *Enterobacter taylorae*. Table 2 gives some additional information for the 10 strains that were deposited in the American Type Culture Collection (ATCC).

Antibiotic susceptibility. Antibiograms were determined on a limited number of strains (13 of *E. fergusonii* and 32 of *E. taylorae*) by agar diffusion on Mueller-Hinton medium by the disk method of Bauer et al. (1). The zone sizes were recorded and interpreted as "susceptible," "intermediate," or "resistant." The percent susceptible is given below.

Media and biochemical tests. The media and biochemical tests are those that have been used for many years by the Enteric Laboratories at the Centers for Disease Control (4, 6). Dehydrated commercial media were used whenever possible. A blank space in Table 4 indicates that the test was not done at that particular time period.

DNA hybridization. The relatedness of strains was determined by DNA-DNA hybridization by the methods of Brenner et al. (2, 3). ^{32}P-labeled DNA was prepared with a commercial nick-translation reagent kit (catalog no. 8160; Bethesda Research Laboratories, Inc., Rockville, Md.). This is essentially the method of Rigby et al. (7). DNA hybridization reactions were done on hydroxyapatite at 60°C and sometimes at 75°C. The relationship of *E. taylorae* to the other named species was done at 75°C rather than at the usual temperature of 60°C; however, those species that were more closely related were then also tested at 60°C. Thermal elution profiles were done on closely related strains to

TABLE 1. Sources of *Escherichia fergusonii* and *Enterobacter taylorae* strains

Source	No. of isolates	
	Escherichia fergusonii	*Enterobacter taylorae*
Human		
Cerebrospinal fluid	0	1
Blood	2	5
Urine	5	6
Wound		
Unspecified	0	15
Face	0	3
Abdomen	1	1
Hand or arm	0	7
Leg	0	7
Foot	0	2
Respiratory tract	0	15
Feces	16	10
Abdominal fluid	0	1
Bone	0	1
Gallbladder	0	3
Knee fluid	0	1
Nose	0	1
Miscellaneous or unknown	1	15
Non-human		
Animal, unspecified	3	2
Cow	1	1
Pig	3	0
Horse	1	0
Turkey	1	0
Water	0	1
Unknown	7	4

determine divergence in nucleotide sequences. All results are for hybridization at 60°C unless otherwise indicated.

RESULTS AND DISCUSSION

***Escherichia fergusonii* (formerly Enteric Group 10).** Table 3 gives the results of the DNA hybridization experiments. The type strain was 90% or more related to eight other strains that had previously been classified in this new group based on biochemical reactons (Table 3). The closest relatives to this new organism were in *Escherichia coli-Shigella*, which were up to 64% related. Other genera were more distantly related. Based on these and biochemical results (Table 4), we propose that the group of strains formerly known as Enteric Group 10 be classified as a new species in the genus *Escherichia*.

Description of the new species *Escherichia fergusonii*. Strains of *Escherichia fergusonii* have the following properties of

TABLE 2. Cultures deposited in the American Type Culture Collection

Species	ATCC no.	CDC no.	Source and additional information
Escherichia fergusonii	35469	0568-73	Human, stool; type strain
	35470	3296-73	(No source stated)
	35471	1016-74	Human, stool
	35472	3014-74	Human, urine
	35473	3458-74	Human, stool
Enterobacter taylorae	35317	2126-81	Human, arm wound; type strain
	35316	1124-78	Human, stool
	35315	0697-81	Human, abdominal fluid
	35318	9252-81	Human, spinal fluid
	35314	0045-82	Human, blood

TABLE 3. Relationship by DNA hybridization of the *Escherichia fergusonii* type strain to strains of *Escherichia fergusonii*, *Escherichia coli*, and other *Enterobacteriaceae*

Source of unlabeled DNA	% Related to *Escherichia fergusonii* type strain ATCC 35469 (labeled strain)		
	60°C	D[a]	75°C
Escherichia fergusonii type strain ATCC 35469	100[b]	0.0	100
2388-74	97	1.0	94
3004-74	95	1.0	93
0488-77	93	0.5	89
1016-74	92	0.5	91
3458-74	92	0.5	90
3014-74	92	1.0	88
3296-73	91	1.0	90
1485-75	90	1.0	86
Escherichia coli 3192-76	59	4.5	44
Escherichia coli 2509-76	63	4.5	48
Escherichia coli 2549-70	49	12.5	20
Escherichia coli (*Escherichia aurescens*) 448-77	63	4.5	
Escherichia coli K-12	60		45
Shigella boydii C-13	59	8.5	
Escherichia hermannii 0980-73	36	14.5	
Edwardsiella tarda 3592-64	19		
Salmonella typhimurium LT2	46	14.5	20
Citrobacter freundii 0460-61	46		
Citrobacter diversus 1066-71	55		
Citrobacter amalonaticus 25406	50		
Klebsiella pneumoniae 2	41		
Enterobacter aerogenes 1627-66	37		
Enterobacter cloacae 1347-71	39		
Enterobacter sakazakii 4562-70	28		
Serratia marcescens 0868-57	27		
Hafnia alvei II 4510-75	28		
H. alvei I 5632-72	39		
Moellerella wisconsensis 0329-73	43	14.3	
Obesumbacterium proteus 4302-74	22		
Escherichia blattae 9005-74	29		
Enterobacter agglomerans 3123-70	30		
1429-71	31		
1741-71	33		
3482-71	19		
6070-69	24		
6003-71	44		
5422-69	30		
4388-71	28		
1600-71	29		
5378-71	41		
0219-71	39		
1645-71	21		
Erwinia amylovora EA178	19		
Erwinia salicis ES102	21		
Erwinia carotovora ATCC 495	19		
Erwinia chrysanthemi SR32	17		
Erwinia cypripedii EC155	18		
Morganella morganii 25830	20		
Proteus mirabilis PR14	7		1
Proteus vulgaris PR1	8		
Proteus alcalifaciens 3370-67	9		
Proteus rettgeri ATCC 1163	7		
Yersinia enterocolitica 497-70	33		
Yersinia pseudotuberculosis P62	17		
Yersinia ruckeri 4535-69	20		

[a] D, Divergence, expressed to the nearest 0.5%. Divergence was calculated on the assumption that 1°C decrease in the thermal stability of a heterologous DNA duplex compared to that of a homologous DNA duplex is caused by each 1% of unpaired bases within the duplex.

[b] Homologous reactions (labeled and unlabeled DNA from the same strain were arbitrarily designated (100%). The actual reassociation obtained in homologous *Escherichia fergusonii* 0568-73 reactions averaged 84% in 60°C reactions and 80% in 75°C reactions. All heterologous reactions were done at least twice.

other species in the family *Enterobacteriaceae*: they are gram-negative rods, oxidase negative, catalase positive, and usually motile, reduce nitrate to nitrite, and ferment D-glucose. Strains of *Escherichia fergusonii* have the following properties of the genus *Escherichia*: they are positive for indole production, methyl red, motility, and acetate utilization and negative for the Voges-Proskauer reaction, H_2S production on triple sugar-iron agar, urea hydrolysis, phenylalanine deaminase, and growth in the presence of KCN. *Escherichia fergusonii* ferments many of the sugars nad polyhydroxyl alcohols used in enteric bacteriology. More details on these biochemical reactions that form the species

TABLE 4. Biochemical reactions of *Escherichia fergusonii* and *Enterobacter taylorae*

Test	*Escherichia fergusonii* (41 strains)				*Enterobacter taylorae* (102 strains)			
	Cumulative % positive on day:			Type strain ATCC 35469[a]	Cumulative % positive on day:			Type strain ATCC 35317[a]
	1	2	7		1	2	7	
Indole production		98		+		0		−
Methyl red		100		+		5		−
Voges-Proskauer		0		−		100		+
Citrate, Simmons	0	17	42	$+^{8}$	79	100	100	+
Hydrogen sulfide on TSI[b]	0	0	2	−	0	0	0	−
Urea, Christensen	0	0	0	−	1	1	1	−
Phenylalanine	0			−	0			−
Lysine, Moeller	95	95	98	+	0	0	0	−
Arginine, Moeller	0	5	32	−	28	94	98	$+^{2}$
Ornithine, Moeller	100	100	100	+	99	99	100	+
Motility at 36°C	93	93	95	+	99	99	99	+
Gelatin hydrolysis at 22°C	0	0	0	−	0	0	0	−
Growth in KCN	0	0	7	−	94	98	98	$+^{2}$
Malonate utilization	12	34	46	−	81	100	100	+
D-Glucose, acid production	100	100	100	+	100	100	100	+
D-Glucose, gas production	93	95	95	+	98	100	100	+
Acid production from:								
D-Adonitol	93	98	100	+	0	0	0	−
L-Arabinose	98	98	98	+	100	100	100	+
D-Arabitol	100	100	100	+	0	0	0	−
Cellobiose	95	98	100	+	100	100	100	+
Dulcitol	50	50	58	−	0	0	1	−
Erythritol	0	0	0	−	0	0	0	−
D-Galactose	100	100	100	+	100	100	100	+
Glycerol	8	13	45	−	0	1	52	−
myo-Inositol	0	0	0	−	0	0	0	−
Lactose	0	0	66	$+^{7}$	3	10	99	$+^{6}$
Maltose	98	98	100	+	99	99	100	+
D-Mannitol	100	100	100	+	100	100	100	+
D-Mannose	100	100	100	+	100	100	100	+
Melibiose	0	0	0	−	0	0	0	−
α-Methyl-D-glucoside	0	0	3	−	0	0	0	−
Raffinose	0	0	0	−	0	0	0	−
L-Rhamnose	88	93	95	+	98	100	100	+
Salicin	20	63	95	$+^{7}$	92	92	100	+
D-Sorbitol	0	0	2	−	0	1	10	−
Sucrose	0	0	0	−	0	0	0	−
Trehalose	98	98	100	+	100	100	100	+
D-Xylose	98	98	100	+	100	100	100	+
Mucate, acid production	0	0	22	−	38	77	98	$+^{2}$
Tartrate, Jordan	88	93	93	+	0	0	2	−
Esculin hydrolysis	10	41	95	$+^{7}$	88	90	96	+
Acetate utilization	73	95	98	+	5	31	72	$+^{3}$
Citrate, Christensen	13	43	80	$+^{2}$	88	100	100	+
Hydrogen sulfide on PIA	0	0	0	−	0	0	0	−
$NO_3^- \rightarrow NO_2^-$	100			+	100			+
Oxidase	0			−	0			−
DNase 25°C	0	0	0	−	0	0	0	−
Lipase (corn oil)	0	0	0	−	0	0	0	−
ONPG test[c]	87	87	90	+	99	100	100	+
Yellow pigment at 25°C	0	0	0	−	0	0	0	−
Tyrosine clearing	0	0	0	−	0	0	0	−

[a] Symbols: −, negative at end of incubation period (see text); +, positive at 24 h; $+^{7}$, the superscript gives the day the reaction became positive; a blank space, not done.

[b] TSI, Triple sugar-iron agar.

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

TABLE 5. Relationship by DNA hybridization of the *Enterobacter taylorae* type strain to strains of *Enterobacter taylorae* and other *Enterobacteriaceae*

Source of unlabeled DNA[a]	% Related to *Enterobacter taylorae* type strain ATCC 35317 (labeled strain)		
	60°C	D[b]	75°C
Enterobacter taylorae type strain ATCC 35317	100[c]	0.0	100[c]
1846-81 (CL^R)	93	0.0	89
3153-78	92	0.0	88
0023-82	91	0.5	87
2679-80 (Sor +5)	90	1.5	81
1524-81	88	0.0	86
2364-81	87	0.0	81
2123-81	86	1.0	87
1124-78	86	1.0	84
0099-82	86	1.0	84
2328-80 (Arg^-)	85	2.0	81
0287-81	84	1.0	84
0697-81 (Sor +3)	84	0.0	80
Enterobacter cloacae 1347-71	61	11.5	38
Erwinia dissolvens ATCC 23373	54	10.0	35
Erwinia nimipressuralis EN1	45	12.5	25
Escherichia coli K-12			11
Shigella boydii C-13			09
Edwardsiella tarda 3592-64			0
Salmonella typhimurium LT2			12
Citrobacter freundii 0460-61			13
Citrobacter diversus 1066-71			18
Citrobacter amalonaticus 25406			16
Klebsiella pneumoniae 2			13
Enterobacter aerogenes 1627-66			16
Enterobacter sakazakii 4562-70			13
Serratia marcescens 0868-57			8
Hafnia alvei II 4510-75			4
Hafnia alvei II 5632-72			3
Moellerella wisconsensis 0329-73			18
Obesumbacterium proteus 4302-74			6
Escherichia blattae 9005-74			6
Enterobacter agglomerans 3123-70			8
1429-71			8
1741-71			6
3482-71			6
6070-69			5
6003-71	44	13.5	24
5422-69			8
4388-71			16
1600-71			8
5378-71	50	13.1	26
Erwinia amylovora EA178			4
Erwinia salicis ES102			3
Erwinia carotovora ATCC 495			4
Erwinia chrysanthemi SR32			4
Erwinia cypripedii EC155			6
Morganella morganii 25830			4
Proteus mirabilis PR14			4
Proteus vulgaris PR1			2
Proteus alcalifaciens 3370-67			2
Proteus rettgeri ATCC 1163			2
Yersinia enterocolitica 497-70			3
Yersinia pseudotuberculosis P62			3
Yersinia ruckeri 4535-69			3
Cedecea davisae 3278-77			10
Cedecea lapagei 0485-76			12
Cedecea neteri 0621-75			10
Escherichia hermannii 980-73			9
Klebsiella oxytoca ATCC 13182			17
Enterobacter amnigenus 1385-73	39	13.5	22
Enterobacter amnigenus 1319-79	44	12.5	26
Enterobacter gergoviae 76.01			15
Serratia liquefaciens 446-68			4
Serratia rubidaea 934-72			3
Serratia fonticola 4556-71			6
Enterobacter agglomerans 2780-70			8
Enterobacter agglomerans 219-71			15
Enterobacter agglomerans 1645-71			6
Escherichia vulneris			16
Erwinia nigrifluens EN104			5
Erwinia quercina EQ102			3
Erwinia rubrifaciens ER105			3
Erwinia mallotivora ATCC 2851			3
Erwinia carnegieana EC186			4
Erwinia rhapontici			5
Proteus myxofaciens			2
Proteus rustigianii ATCC 26240			1
Proteus stuartii 2896-68			2
Yersinia intermedia 48			2
Yersinia frederiksenii 867			2
Yersinia kristensenii 1474			2

[a] Symbols: CL^R, resistant to colistin, Sor +5, ferments D-sorbitol at 5 days, Sor +3, ferments D-sorbitol at 3 days, Arg^-, arginine dihydrolyase negative.
[b] See footnote *a* of Table 3 for definition of D.
[c] Actual binding percentages for homologous *Enterobacter taylorae* 2126-81 reactions averaged 65% at 60°C and 68% at 75°C.

description are given in Table 4. All strains were susceptible to colistin, gentamicin, and chloramphenicol, but were resistant to penicillin. Susceptibility was variable for nalidixic acid (77% susceptible), sulfadiazine (62% susceptible), streptomycin (46% susceptible), tetracycline (62% susceptible), ampicillin (77% susceptible), carbenicillin (77% susceptible), and cephalothin (31% susceptible). A more complete description of *Escherichia fergusonii* based on 26 strains is given in Table 4. The species name "*fergusonii*" (pronunciation [with a classical Latin pronunciation of the ending], fur guh sew´ knee ee) is a neo (modern) Latin substantive (masculine) coined to honor the American microbiologist William H. Ferguson, who made many contributions to enteric bacteriology and was one of the first to show the role of certain strains of *E. coli* in infantile diarrhea. The type strain (holotype) is designated as ATCC 35469, which has biochemical reactions typical of the species (Table 4). Some comments that were sent with cultures include: "multiple abscesses following a gun shot to the abdomen"; "from urinary tract infection in a woman"; "from the cloaca of a hawk"; "isolated from the infusion material of a 58-year-old male with ALS who had post infusion sepsis"; "diarrheal stool from a 66-year-old female with diabetes"; "large intestine of 'Sitatunga' from the National Animal Center, Ames, Iowa."

***Enterobacter taylorae* (formerly Enteric Group 19).** Table 5 gives the results of the DNA hybridization experiments. The type strain was 84 to 93% related to 12 other strains that had been classified in this group based on their biochemical similarity. The closest relative was *Enterobacter cloacae*, the type species for the genus *Enterobacter*, which was 61% related. Based on these and biochemical results (Table 4), we propose that the group of strains formerly known as Enteric Group 19 be classified as a new species in the genus *Enterobacter*.

Description of the new species *Enterobacter taylorae*. Strains of *Enterobacter taylorae* have the following properties typ-

ical of the family *Enterobacteriaceae*: they are gram-negative rods, oxidase negative, catalase positive, and usually motile, reduce nitrate to nitrite, and ferment D-glucose. They have the following properties typical of the genus *Enterobacter*: they are Voges-Proskauer positive, grow in the presence of KCN, are susceptible to colistin, and are resistant to cephalothin. Other biochemical reactions for *Enterobacter taylorae* are given in Table 4 and include the following: positive tests for citrate and malonate utilization, arginine dihydrolase, ornithine decarboxylase, and gas production during fermentation. Negative results were found for indole production, methyl red, H_2S production on triple sugar-iron agar, phenylalanine deaminase, lysine decarboxylase, gelatin hydrolysis, and production of a distinct pigment. *Enterobacter taylorae* ferments many of the sugars and polyhydroxyl alcohols used for the identification of *Enterobacteriaceae*. More details on these biochemical results which form the species description are given in Table 4. Strains were generally susceptible to colistin (94% susceptible), nalidixic acid (100% susceptible), sulfadiazine (97% susceptible), gentamicin (97% susceptible), kanamycin (97% susceptible), chloramphenicol (100% susceptible), and tetracycline (81% susceptible). They were resistant to penicillin (0% susceptible) and cephalothin (3% susceptible). Susceptibility was more variable for streptomycin (50% susceptible), ampicillin (53% susceptible), and carbenicillin (69% susceptible). The type strain (holotype) is designated as ATCC 35317, which has biochemical reactions typical of the species. The species name "taylorae" (pronunciation [with a classical Latin pronunciation of the ending], tay´ lohr eye) is a neo (modern) Latin genitive (feminine) form of taylor to honor the British bacteriologist Joan Taylor, who for many years was chief of the Salmonella Reference Laboratory, Central Public Health Laboratory, Colindale, London, England, and who has made many contributions to our knowledge of the family *Enterobacteriaceae*, particularly on *Salmonella*, *Shigella*, and the role of certain *Escherichia coli* strains in infantile diarrhea. The name also honors Welton Taylor, an American clinical microbiologist who has also made many contributions to our knowledge of the family *Enterobacteriaceae*, particularly the development of XLD agar and the isolation of *Shigella* and other bacterial pathogens from feces.

Differential tables for *Escherichia* and *Enterobacter*. Table 9 in a companion paper in this issue (5) gives the biochemical tests that differentiate *Escherichia fergusonii* from other species of *Escherichia*. Table 8 in this companion paper gives the differential reactions for the genus *Enterobacter* (5).

Clinical significance. Little is known about the clinical significance of these two new organisms. There were two blood isolates of *Escherichia fergusonii* and one spinal fluid and five blood isolates of *Enterobacter taylorae*. These sources suggest possible clinical significance, but this point requires a more systematic study.

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