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Cellular Fatty Acid Composition and Phenotypic and Cultural Characterization of CDC Fermentative Coryneform Groups 3 and 5

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Seventy strains of fermentative, asporogenous, gram-positive coccobacilli or short rods form two closely related groups which have been designated CDC fermentative coryneform groups 3 (32 strains, xylose fermenters) and 5 (38 strains, xylose nonfermenters). The two taxa are otherwise similar to each other phenotypically and culturally and by a distinctive *Staphylococcus*-like odor and by cellular fatty acid (CFA) composition. CDC group 3 and CDC group 5 strains have been isolated from clinical sources (blood, abscesses, and wounds but not urine or respiratory specimens) in Canada and the United States and among referrals from Belgium, Sweden, and Spain. Coryneform CDC group 3 strains were phenotypically similar to CDC coryneform group A-3 but were distinguishable by their inability to reduce nitrate and by their lack of motility. Coryneform CDC group 5 isolates were phenotypically somewhat similar to *Actinomyces viscosus* and *Rothia dentocariosa*, except that none of this group reduced nitrate. Both CDC groups could be differentiated from these similar bacteria by the ability to decarboxylate lysine and ornithine. The CFA compositions of CDC group 3 and 5 strains were similar to each other, were distinctive from those of other coryneforms, and were of the branched-chain type. API CORYNE codes were consistent for both CDC group 3 and CDC group 5 bacteria, suggesting that this method could be useful as an identification method.

The Special Bacteriology laboratories at the Centers for Disease Control and Prevention (CDC) and the Laboratory Centre for Disease Control (LCDC) have collected 70 strains of asporogenous, fermentative, gram-positive coccobacilli which can be phenotypically differentiated from other described taxa. These bacteria had been isolated from a variety of clinical sources (blood, abscesses, wounds, and ulcers) from all parts of the United States and Canada, as well as from Spain, Sweden, and Belgium. Strains that ferment xylose were designated CDC fermentative coryneform group 3 and xylose nonfermenters were designated CDC fermentative coryneform group 5 by D. Hollis. CDC groups 3 and 5 were found in 1992 to be consistent biochemically and culturally with a collection of unidentifiable gram-positive coccobacilli characterized by LCDC. CDC fermentative coryneform group 3 phenotypically resembled but could be distinguished from CDC fermentative coryneform group A-3 by conventional test methods. CDC fermentative coryneform group 5 strains had been mistaken as possible *Actinomyces viscosus* or *Rothia dentocariosa* strains by submitting laboratories. For the purpose of this paper, the CDC fermentative coryneform groups 3 and 5 will be called CDC groups 3 and 5.

In this study, clinical information, cellular fatty acid (CFA) composition data, and phenotypic and cultural characteristics of CDC group 3 and CDC group 5 strains which had been referred to the CDC and LCDC were compiled. These data should enable other clinical laboratories to recognize and distinguish CDC group 3 and CDC group 5 taxa from other fermentative coryneforms. Two strains each of CDC group 3, LCDC 90-0137 (ATCC 51323) and LCDC 91-0230 (ATCC 51324), and CDC group 5, LCDC 79-0730 (CDC E6535, ATCC 51325) and LCDC 88-0597 (G2904, ATCC 51326), have been deposited with the American Type Culture Collection.

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MATERIALS AND METHODS

Bacterial strains. Seventy isolates were characterized by using conventional cultural and biochemical tests (3, 4). In addition, all LCDC strains were grown at 35°C on Tryp-soy agar (TSA) (lot 9206-166; Quelab Laboratories, Montréal, Québec, Canada). A total of 32 strains of CDC group 3 (20 characterized by CDC and 12 characterized by LCDC) were studied. Thirty-eight strains of CDC group 5 were examined, including 16 characterized by CDC, 18 characterized by LCDC, and 4 strains (with the following LCDC and CDC numbers, respectively: 79-0730, E6535; 88-0597, G2904; 89-0010, G2905; and 89-0184, G2907) characterized by both laboratories. A representative number of isolates of CDC group A-3, *R. dentocariosa* (including the type strain ATCC 17931), and *A. viscosus*, from the collections of CDC and LCDC that had been identified by conventional methods, were analyzed for CFA composition and also were tested in the API CORYNE system for comparison with CDC group 3 and CDC group 5.

Fatty acid analysis. At the LCDC, cells for fatty acid analysis were grown on Columbia blood agar base with 5% sheep blood, saponified, methylated, and analyzed by gas-liquid

TABLE 1. Characteristics of coryneform CDC groups 3 and 5[a]

Test or characteristic[b]	CDC group 3 (n = 32)		CDC group 5 (n = 38)	
	No. of positive strains/total (% positive)	Result[c]	No. of positive strains/total (% positive)	Result
Catalase	32/32 (100)	+	38/38 (100)	+
Oxidase	3/32 (9)	−	2/38 (5)	−
Production of acid from carbohydrate base[d]				
D-Glucose	32/32 (100)	+	38/38 (100)	+
D-Xylose	32/32 (100)	+	0/38 (0)	−
D-Mannitol	0/32 (0)	−	0/38 (0)	−
Lactose	32/32 (100)	+	38/38 (100)	+
Sucrose	32/32 (100)	+	38/38 (100)	+
Maltose	32/32 (100)	+	38/38 (100)	+
Growth in NaCl at concn of:				
0%	32/32 (100)	+	38/38 (100)	+
6%	16/32 (50)	v	23/38 (60)	v
Growth at:				
25°C	26/32 (81)	v	34/38 (90)	+
42°C	23/32 (72)	v	21/38 (55)	v
Production of acid in TSI				
Slant	32/32 (100)	+	38/38 (100)	+
Butt	28/32 (87)	v	38/38 (100)	+
H_2S				
TSI butt	0/32 (0)	−	0/38 (0)	−
Pb acetate paper	23/32 (72)	v	30/38 (79)	v
Nitrate reduction to nitrite	0/32 (0)	−	0/38 (0)	−
Urea hydrolysis	2/32 (6)	−	0/38 (0)	−
Gelatin[e]	9/32 (28)	v	13/38 (34)	v
Lysine decarboxylase	32/32 (100)	+	38/38 (100)	+
Arginine decarboxylase	0/32 (0)	−	0/38 (0)	−
Ornithine decarboxylase	32/32 (100)	+	38/38 (100)	+

[a] Taxa were considered indistinguishable with respect to colonial morphology and Gram reaction. n, number of strains tested. All strains grew well on blood agar at 35°C, in air or 5% CO_2, and on TSA at 35°C (only Canadian strains tested) and were capable of growing anaerobically. All strains were positive for esculin hydrolysis. All strains lacked vegetative hyphae and flagella and were nonmotile. All strains were negative for the following tests: growth on MacConkey agar, Simmons citrate, Voges-Proskauer (called acetoin in text), (Ehrlich's) indole, tyrosine, and DNase hydrolysis. A total of 2 of 32 strains (6%) of CDC group 3 and 0 of 38 CDC group 5 strains (0%) were positive in the methyl red test. Variable reactions were observed for hemolysis on blood agar plates (usually alpha-hemolysis, more rarely no hemolysis or lavender reaction) and litmus milk (acid, indicator reduced, negative).

[b] TSI, triple sugar iron agar; H_2S, hydrogen sulfide; Pb acetate, lead acetate.

[c] +, ≥90% positive; v, variable, 10 to 89% positive; −, negative, 0 to 9% positive.

[d] Strains may exhibit delayed (2 to 6 days) or weak fermentation of carbohydrates; one strain, LCDC 87-0018 (CDC group 3), fermented sugars in 48 h with serum but in 7 days without serum.

[e] Gelatin hydrolysis was delayed, being observed only after 9 to 30 days.

chromatography using the Microbial Identification System and Library Generation System (LGS) software (Microbial ID, Inc. [MIDI], Newark, Del.) as previously described (2). CDC methods used to perform CFA composition analyses after growth on heart infusion agar with 5% rabbit blood base have been previously described (6).

Gas-liquid chromatography of CFAs. At LCDC, tentative peak identifications were made on the basis of a reference standard of fatty acids obtained from MIDI. Chromatographic profiles were created and updated for storage in an in-house library for aerobes and facultative anaerobes called LCDC1 (2), whose method, LCDCAER2, was rooted to the commercial method AEROBE (MIDI) version 3.7 and validated by using LGS software. CFA profiles of all strains were tested against the commercial aerobe library CLIN version 3.7 (MIDI). Reference standards of fatty acids were analyzed and confirmed by using trifluoroacetylation, hydrogenation, and mass spectrometry for strains tested at CDC (6).

API CORYNE. Fifty-six strains (12 group 3, 22 group 5, 14 *R. dentocariosa*, 6 *A. viscosus*, and 2 CDC group A-3) were tested as described by the manufacturer, Biomérieux (API Produits de Laboratoire Ltée, St. Laurent, Québec, Canada), and results were compared with the data compiled in the *API CORYNE Analytical Profile Index* (1).

RESULTS AND DISCUSSION

The cultural and biochemical characteristics of CDC groups 3 and 5 are shown in Table 1. Both taxa could be described as short gram-positive rods, coccobacilli, or coccoidal cells and appeared to be indistinguishable with respect to colonial morphology. Both taxa characteristically were observed to have convex, low, grey-white moist colonies which became slightly yellow-pigmented with age. A distinctive pungent odor, described as *Staphylococcus*-like or "leafy," was consistently detected with CDC group 3 and 5 strains. All strains grew well on blood agar at 35°C, in air or 5% CO_2, and on TSA at 35°C and were capable of growing anaerobically. All bacteria were found to be nonmotile, lacked flagella and vegetative hyphae, were catalase positive, could ferment glucose, lactose, sucrose, and maltose, could hydrolyze esculin, and could decarboxylate lysine and ornithine. All CDC group 3 strains fermented D-xylose, which permitted differentiation from the D-xylose-nonfermenting CDC group 5. It had been observed in both laboratories that fermentation of sucrose and lactose, and more rarely glucose and maltose, may be delayed (2 to 7 days) or only weakly positive. One strain (LCDC 87-0018) required serum to ferment sugars in 48 h.

TABLE 2. CFA composition analysis of CDC groups 3 and 5

Testing laboratory and CDC group or species	% of total fatty acids[a]													
	14:0	i15:0	a15:0	15:0	i16:0	16:0	a17:0	18:2	18:1ω9c	18:1ω7c	18:0	19:1ω12t[b]	20:1ω9t[b]	Unknown[b]
LCDC[c]														
Group 3 (n = 12[d])	1	11	25	tr	14	3	33	4	4	tr	2	tr	1	—
Group 5 (n = 22[e])	1	11	24	tr	13	4	31	4	5	tr	2	1	1	—
Group A-3 (n = 2)	7	4	44	2	5	16	14	2	2	tr	2	—	—	—
R. dentocariosa (n = 33)	tr	3	36	2	16	7	28	2	2	tr	1	—	—	—
CDC[f]														
Group 3 (n = 19)	5	9	25	—	8	9	16	8	6	3	4	—	—	3
Group 5 (n = 12)	2	7	22	—	8	8	23	8	7	2	3	—	—	3
Group A-3 (n = 11)	5	4	47	6	3	14	6	2	4	3	5	—	—	—
R. dentocariosa (n = 6)	1	3	47	tr	9	10	15	5	4	—	1	—	—	—
A. viscosus (n = 7)	4	—	—	—	—	46	—	7	32	—	5	—	—	—

[a] Values shown are arithmetic means rounded off to the nearest whole percent. The number to the left of each colon is the number of carbon atoms, and the number to the right is the number of double bonds; ω, double-bond position from the hydrocarbon end of the chain; c, *cis* isomer; t, *trans* isomer; i, methyl group at the penultimate (iso) carbon atom; a, methyl group at the antepenultimate (anteiso) carbon atom; unknown, unidentified component. The MIDI peak naming table (version 3.7) more commonly refers to 18:2 as part of summed feature 6 and to 18:1ω7c as part of summed feature 7. —, 0 to 0.29%; tr, trace (0.3 to 0.7%). Both LCDC and CDC found trace to small amounts (2%) of i14:0 for all bacteria except for strains of *A. viscosus*; CDC found a small amount (1%) of i13:0 for *R. dentocariosa* strains as well as small amounts (1 to 2%) of 12:0 and 16:1ω9c for *A. viscosus* strains.

[b] With the MIDI system at LCDC, trace to small volumes (1%) of two peaks tentatively identified as 19:1ω12t (equivalent chain length, 18.823) and 20:1ω9t (equivalent chain length, 19.833) were usually observed for strains of CDC groups 3 and 5. However, the CDC suggests that the peak(s) which eluted at this time is probably not correctly identified and should, for the present, be referred to as an unknown component(s) until additional work is done.

[c] Analysis done at LCDC using cells grown on Columbia blood agar base with 5% sheep blood.

[d] With the LGS validation program, 7 of 12 strains were identified as CDC group 3 as first choice, with CDC group 5 as second choice; the remaining five strains were CDC group 5 as first choice and CDC group 3 as second choice.

[e] Of 22 strains, 21 were identified as CDC group 5 as first choice with CDC group 3 as second choice; the remaining strain was identified as CDC group 3 as first choice and CDC group 5 as second choice.

[f] Analysis done at CDC using cells grown on heart infusion agar base with 5% rabbit blood.

No members of either group could reduce nitrate to nitrite or decarboxylate arginine, and all were negative for citrate, indole, acetoin, tyrosine, and DNase hydrolysis. Strains of both taxa gave different results with respect to oxidase, gelatin hydrolysis (which was always delayed 9 to 30 days), litmus milk, growth in 6% NaCl, hemolysis on blood agar, and growth at 42°C.

The CFA compositions for CDC group 3 and CDC group 5 strains, in comparison with those of the phenotypically similar taxa CDC group A-3, *R. dentocariosa*, and *A. viscosus*, are described in Table 2. Data obtained by LCDC and CDC are cited separately, as quantitative differences attributable to the use of different bases of blood agar media had been observed.

CFA compositions of CDC group 3 and CDC group 5 were found to be essentially identical (Table 2) even when studied independently in two laboratories. The majority of the CFAs of CDC group 3 and CDC group 5 were observed to be of the branched-chain type, with significant amounts of isopentadecanoic acid (i15:0), anteisopentadecanoic acid (a15:0), isopalmitic acid (i16:0), and anteisoheptadecanoic acid (a17:0). Qualitatively, these profiles are somewhat similar to those described previously for coryneform CDC group A-3 and *R. dentocariosa* (2). However, it can be seen in Table 2 that significant quantitative differences in the relative amounts of CFAs among these taxa were observed. When the MIDI aerobe peak naming table version 3.7 was used, members of CDC group 3 and CDC group 5 were usually found to have trace or small volumes (1%) of unidentified compounds corresponding to monounsaturated 19-carbon acid (19:1ω12t) and a monounsaturated 20-carbon acid (20:1ω9t), which were not detected among strains of CDC group A-3 and *R. dentocariosa*. However, preliminary work done by one of us (C. W. Moss)

TABLE 3. Useful characteristics for differentiating coryneform CDC groups 3 and 5 from other phenotypically similar bacteria

Organism	Result for characteristic[a]						% a15:0 distinguishing CFA[b]
	Motility	NO_3	Xylose	Lactose	Lysine	Ornithine	
CDC group							
3	−	−	+	+	+	+	25 (LCDC) 25 (CDC)
5	−	−	−	+	+	+	24 (LCDC) 22 (CDC)
A-3	+	+	+	+	−	−	44 (LCDC) 47 (CDC)
A. viscosus	−	+	−	+	−	−	—[c] (CDC)
R. dentocariosa	−	+	−	−	−	−	36 (LCDC) 47 (CDC)

[a] Symbols described in Table 1, footnote *c*. NO_3, nitrate reduction; xylose and lactose, acid fermentation; lysine and ornithine, decarboxylase of lysine and ornithine.

[b] CFA composition data derived from Table 2. Values are percentages of total CFA present; —, CFA not detected. Other qualitative differences among CFAs, including unique CFAs, are discussed in the text. *R. dentocariosa* and CDC group A-3 strains also contain trace to small amounts (6%) of CFA $C_{15:0}$.

[c] CFAs of *A. viscosus* are of the straight-chain saturated and monounsaturated types and so may be readily distinguished from the other taxa listed here.

TABLE 4. Results with API CORYNE

Taxon group or species	API code(s) generated	No. of strains/ code	API identification (confidence level)	No. of strains with variable reactions[a]
CDC group				
3 (n = 12)	4570765	10	Group A (99.6%)	10/12 PAL +
	4470765	2	Group A (99.9%)	2/12 PAL −
5 (n = 22)	4570365	19	No match	19/22 ribose + and sucrose +
	4570165	2	No match	2/22 ribose − and sucrose +
	4570364	1	No match	1/22 ribose + and sucrose −[b]
A-3 (n = 2)	7470765	2	No match	
R. dentocariosa (n = 14)	7050125	12	No match[c]	10/12 gelatin −
	7052125	2	No match	2/12 gelatin +
A. viscosus (n = 6)	3540367	4	No match	
	3550367	2	*Oerskovia* sp. (99.9%)	2/6 α-GLU +

[a] API CORYNE tests which differed among strains within a single taxon group. For example, 10 of 12 CDC group 3 strains were PAL positive, generating a code which differed from those of the 2 of 12 strains which were PAL negative. α-GLU, α-glucosidase.
[b] LCDC 93-0287 fermented sucrose slowly (7 days), using conventional sugars.
[c] *R. dentocariosa* and *A. viscosus* are not included in the first edition of the *API CORYNE Analytical Profile Index* (1).

indicates that these peaks are not fatty acid methyl esters, and they are listed together as unknown in Table 2. Both laboratories also observed trace to small volumes (trace to 6%) of pentadecanoic acid (15:0) in CDC group A-3 and *R. dentocariosa* strains which were not detected among CDC group 3 and CDC group 5 strains. These small qualitative and large quantitative differences among CFAs contributed to the ability of the MIDI system to correctly match with either CDC group 3 or CDC group 5. It was found at LCDC that once specific entries for both taxa were defined in the MIDI system by using the LGS software, CDC group 3 or 5 came up as first choice for 100% of strains (Table 2). LGS-generated similarity indices for either CDC group 3 or 5 LCDC1 entries ranged from 0.30 (for LCDC 93-0287) to 0.93 (data not shown). Each strain of CDC group 3 or group 5 was found to have no match when tested against the commercial library CLIN, which did not contain these organisms.

Key characteristics which can be used to distinguish CDC group 3 and CDC group 5 from other phenotypically similar coryneforms are summarized in Table 3. Many laboratories may not include testing for lysine and ornithine decarboxylases in their identification schemes for coryneforms; however, as shown in Table 3, these tests, in addition to an inability to reduce nitrate and the xylose and lactose fermentation reactions, should assist in differentiating these taxa.

The results for 12 strains of CDC group 3, 22 strains of CDC group 5, 2 strains of CDC group A-3, 6 strains of *A. viscosus*, and 14 strains of *R. dentocariosa* that were evaluated by using API CORYNE are given in Table 4. CDC group 3 isolates generated only two codes, with 2 of 12 strains (LCDC 92-105 and 92-481) not utilizing the enzyme alkaline phosphatase (PAL). As shown in Table 4, all CDC group 3 isolates were identified as CDC group A at high confidence levels, whether or not they were positive for PAL. None of the CDC group 5 strains matched entries in the *API CORYNE Analytical Profile Index*, and they generated only three different codes. Among CDC group 5 bacteria, 2 of 22 strains (LCDC 88-0580 and 89-0184) did not ferment ribose and 1 of 22 (93-0287) did not ferment sucrose. This last strain was found by conventional methods to ferment sucrose very slowly, which possibly could not be detected in the incubation period suggested by the manufacturer; as discussed previously, this strain was also statistically most different from other CDC group 5 strains when the CFA composition was studied by using the LGS. The two strains of CDC group A-3 studied here to compare with the new taxon groups generated identical codes but no matches to entries in the *Analytical Profile Index*. Although the manufacturer's insert does not allude to *A. viscosus* and recommends identifying *R. dentocariosa* by conventional means, the data presented in Table 4 indicate that API CORYNE potentially could be useful for identifying these bacteria. In this study, 12 of 14 strains of *R. dentocariosa* generated the same no-match code number, 7050125. The two remaining strains coded like the other *Rothia* strains tested except that gelatin hydrolysis was detectable, generating the no-match code number 7052125. This was in contrast with the much higher positivity rate of gelatin hydrolysis when tested by conventional methods (4) (Table 1). Similarly, four of six strains of *A. viscosus* generated the same no-match code number, 3540367. The two remaining strains generated code 3550367, as α-glucosidase was detected, and were identified by API CORYNE as an *Oerskovia* sp. at high confidence levels.

It is apparent from this study that coryneform CDC group 3 and group 5 are distinct from other previously described coryneform taxa as determined by conventional phenotypic methods or CFA composition analysis. The two taxa appear to share most characteristics, such as reactions to most biochemical tests (except xylose fermentation), odor produced, colonial and cellular morphologies, Gram reaction (Table 1), and CFA composition (Table 2). They also appear to be recovered from similar types of clinical material from humans, including blood cultures, abscesses, wounds, and other superficial body sites but not expectorated material or urine (Table 5). Of the 32

TABLE 5. Sources of coryneform CDC groups 3 and 5

Source	No. of strains (%)	
	CDC group 3 (n = 32)	CDC group 5 (n = 38)
Blood	18 (56)	20 (53)
Abscess	2 (6)	4 (9)
Wound	3 (9)	3 (8)
Foot	0 (0)	2 (5)
Eye	2 (6)	0 (0)
Other	7[a] (22)	9[b] (24)

[a] One strain each from lung, thoracic wall, skin, sebaceous cyst, pericardial fluid, dialysate bag, and ankle tissue.
[b] One strain each from cerebrospinal fluid, axillary node, peritoneal fluid, liver, breast, toe, ear, and leg ulcer and one from an unknown source.

TABLE 6. CDC group 3 and group 5 blood culture isolates[a]

Group and isolate	Diagnosis or underlying condition of patient	Sex/age of patient (yr)[b]	Geographical source of isolate and yr received
CDC group 3 (n = 18)			
E2863	Renal failure, sepsis, diabetes mellitus	F/19	Michigan, 1978
E5170		F/40	Hawaii, 1979
F3878		M/30	Maryland, 1982
F5058	Premature newborn	F/NB	Hawaii, 1983
F6232	Hypovolemia	F/84	Pennsylvania, 1984
F6362	Septicemia	F/UNK	South Carolina, 1984
F7262	Lymphoma	M/35	Maryland, 1985
F7461	Septicemia	F/84	Florida, 1985
F9056	Septicemia	M/78	New Jersey, 1986
87-0018		M/80	Montreal, Québec, Canada, 1987
G1344	Infected ulcer, stump; diabetes mellitus	M/67	Pennsylvania, 1988
G1918	Fever of unknown origin	F/28	Texas, 1988
90-0378	Fever of unknown origin	M/UNK	Toronto, Ontario, Canada, 1990
91-0230	Renal cell carcinoma	F/61	Timmins, Ontario, Canada, 1991
G7119		UNK/UNK	Belgium, 1992
G8033	Anemia, bacteremia	M/30	Texas, 1992
92-0481	Cerebrovascular accident	F/61	Toronto, Ontario, Canada, 1992
93-0326	Seizures	M/48	Toronto, Ontario, Canada, 1993
CDC group 5 (n = 20)			
79-0730 (=E6535)		M/45	Edmonton, Alberta, Canada, 1979
87-0420	Angina, fever of unknown origin	M/72	Edmonton, Alberta, Canada, 1987
F9707	Sepsis	M/33	Texas, 1987
G850		F/UNK	Oklahoma, 1987
88-0580		M/UNK	Montreal, Québec, Canada, 1988
88-0597 (=G2904)	Fever, infectious mononucleosis	F/19	Vancouver, British Columbia, Canada, 1988
88-0628	Abdominal pain	F/UNK	Montreal, Québec, Canada, 1988
89-0184 (=G2907)		M/67	Vancouver, British Columbia, Canada, 1989
G3197		M/NB	Hawaii, 1989
G3862	Fever of unknown origin	F/69	South Carolina, 1989
89-0471	Renal failure	F/54	Calgary, Alberta, Canada, 1989
90-0080		F/42	Toronto, Ontario, Canada, 1990
91-0303		F/UNK	Calgary, Alberta, Canada, 1991
91-0589		M/65	Moncton, New Brunswick, Canada, 1991
G5864	Septic arthritis	UNK/UNK	Sweden, 1991
G6181	Pneumonia, bronchitis	F/70	Hawaii, 1991
G7506	Subacute bacterial endocarditis	M/29	Hawaii, 1992
G7815	Bacteremia	F/71	South Carolina, 1992
92-0482	Febrile, neutropenia	M/22	Toronto, Ontario, Canada, 1992
92-0566		F/75	Toronto, Ontario, Canada, 1992

[a] All isolates (when this information had been provided by the submitting laboratory) were single blood culture isolates recovered from one patient; no multiple blood culture isolates were documented among these cases.
[b] F, female; M, male; NB, newborn; UNK, age unknown.

group 3 isolates, 56% (18 strains) were from blood, and of the 38 group 5 isolates, 53% (20 strains) were from blood. Clinical information which accompanied CDC group 3 and CDC group 5 referrals was often scanty; however, information pertaining to the 18 CDC group 3 and 20 CDC group 5 blood culture isolates is given in Table 6. These isolates had been referred from five countries (Canada, the United States, Belgium, Sweden, and Spain), from almost equal numbers of females and males ranging from newborn to 84 years old. However, more conclusive evidence associating these bacteria with specific disease processes needs to be accumulated. Additional chemotaxonomic and genetic investigations which will clarify the taxonomic relationship of CDC group 3 and CDC group 5 to each other, as well as to other described coryneform taxa, are required.

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ADDENDUM

During the preparation of the manuscript, we (CDC) obtained and studied the type strain of *Dermabacter hominis*, ATCC 49369 (5). The morphology, biochemical reactions, and CFA composition of this organism were like those of CDC coryneform group 5. Genetic studies will be required to determine the relationship of these taxa.

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