Ochrobactrum anthropi gen. nov., sp. nov. from Human Clinical Specimens and Previously Known as Group Vd

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In this study we examined the taxonomic relationships of strains variously labeled Achromobacter species biotypes 1 and 2, Achromobacter group A, and Centers for Disease Control (CDC) groups Vd-1 and Vd-2. Previous studies of ribosomal ribonucleic acid cistron similarities placed these organisms on the Brucella ribosomal ribonucleic acid branch of ribosomal ribonucleic acid superfamily IV; their closest neighbors were Brucella, Phyllobacterium, and the Agrobacterium-Rhizobium complex. We performed a numerical taxonomic analysis of 284 phenotypic features (69 conventional tests, 147 API assimilation tests, 68 API ZYM tests) carried out on 95 strains. These organisms comprised 56 strains thought to correspond to CDC group Vd (including 3 strains originally labeled “Pseudomonas arsenoxydans”) and 39 strains (included for reference purposes) representing the genera Achromobacter, Agrobacterium, Alcaligenes, Brucella, Mycoplana, Phyllobacterium, and Rhizobium. A phenotypic analysis showed that group Vd bacteria are most similar to Phyllobacterium. However, strains of Group Vd were shown to be distinct by deoxyribonucleic acid (DNA)-DNA hybridization and by several phenotypic tests from Phyllobacterium and other related taxa. The CDC group Vd strains formed essentially a single taxon in the numerical taxonomic analysis of phenotypic characters and as determined by DNA-DNA hybridization. This taxon could be subdivided into three biotypes (biotypes A, C, and D), but none of these corresponded to the two biotypes originally described among the group Vd strains. For CDC group Vd we propose a new genus and new species, Ochrobactrum anthropi; the type strain is strain CIP 82.115 (= CIP 14970 = NCTC 12168 = LMG 3331). O. anthropi strains are rod shaped, aerobic, gram negative, nonpigmented, and motile by means of peritrichous flagella, produce acid from several carbohydrates, and reduce both nitrate and nitrite. The guanine-plus-cytosine contents of the DNAs of 29 strains ranged from 56 to 59 mol%. Almost all 56 group Vd strains were originally isolated from various human clinical specimens, commonly from blood cultures.

Tatum et al. (25) stated that the genus Achromobacter should comprise gram-negative rod-shaped organisms that had peritrichous flagella, were strictly aerobic, showed oxidative metabolism of carbohydrates, produced oxidase, and failed to produce 3-ketolactose. These authors found the species biotypes 1 and 2, which all fell into their group A. Similarly, Chester and Cooper (3) could not demonstrate production of acid from maltose, mannitol, and sucrose in their reference strains of Achromobacter species biotype 2. Dees and Moss (6) were also unable to distinguish between the two biotypes by cellular fatty acid analysis. The distinction into two biotypes is no longer recognized, and the taxon is referred to as group Vd (4). As determined by deoxyribonucleic acid (DNA)-ribosomal ribonucleic acid (rRNA) hybridization (7, 17), guanine-plus-cytosine (G+C) content, type of respiratory quinone, and major fatty acid types (N. Ohishi, K. Yamasato, T. Kaneko, and H. Kuraishi, Abstr. XIV Int. Congr. Microbiol., p. 44, 1986), the strains of group Vd have been shown to be closely related but distinct from Agrobacterium, Brucella, Mycoplana, Phyllobacterium, and Rhizobium.

The purpose of this study was to examine the within-taxon homogeneity of group Vd organisms and to show how this taxon is differentiated from its closest relatives (as well as the phenotypically similar genera Achromobacter and Alcaligenes) by G+C content, DNA-DNA hybridization levels, and phenotypic characters. We propose a new genus and new species, Ochrobactrum anthropi, with strain CIP 14970 (= NCTC 12168 = LMG 3331) as the type strain.

MATERIALS AND METHODS

Bacterial strains. The strains examined in the numerical phenotypic study and their sources are listed in Table 1. Selected strains were also studied for G+C content and levels of DNA-DNA hybridization. Brucella suis NCTC 10095 was included in these studies only and hence is not listed in Table 1.

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### TABLE 1. Strains used

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<th>Name as received</th>
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<th>Source</th>
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### Table 1—Continued

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* API, Appareils et Procédés d’Identification, La Balme-les-Grottes, France; ATCC, American Type Culture Collection, Rockville, Md.; BBL, Baltimore Biological Laboratories, Cockeysville, Md.; CIP, Collection de l’Institut Pasteur, Paris, France; CDC, Centers for Disease Control, Atlanta, Ga.; DSM, Deutsche Sammlung von Mikroorganismen, Göttingen, Federal Republic of Germany; ICPB, International Collection of Phytopathogenic Bacteria, Davis, Calif.; NCIB, National Collection of Industrial Bacteria, Torry Research Station, Aberdeen, Scotland, now NCIMB, National Collections of Industrial and Marine Bacteria Ltd., Torry Research Station, Aberdeen, Scotland; NCTC, National Collection of Type Cultures, Central Public Health Laboratory, London, England; USDA, United States Department of Agriculture, Washington, D.C.; strains prefixed by the letters AB were received from H. Laustrup, Statens Serum Institut, Copenhagen, Denmark; strains prefixed by the letters CL are strains received for identification by the Computer Identification Laboratory, National Collection of Type Cultures, Central Public Health laboratory, London, England; strains prefixed by the letters CNS are strains received by the Centre National des Salmonella, Paris, France; strains prefixed by the letters EF were received from E. Falken, Universität Göteborg, Göteborg, Sweden; strains prefixed by the letters LMG were received from D. Knüsel, Hamburg, Federal Republic of Germany.

**Bacteriological investigations.** The following tests were performed at the National Collection of Type Cultures by using methods which have been described previously: 68 API ZYM tests (12) and 69 conventional tests performed by the methods of Holmes et al. (15), except that the changes or additions described below were made. Indole production was tested for with Kovacs reagent and with Ehrlich reagent, the latter by using method 3 of Cowan (5). Tributyrin hydrolysis was tested for on nutrient agar containing 1% (vol/vol) glycerol tributyrate, as described by Hayes (11). Phosphatase production was determined by method 1 of Cowan (5). The 147 API assimilation tests were performed mainly at the Laboratorium voor Microbiologie en Microbiële Genetica by using methods described previously (8); the Brucella cultures were tested by the same methods in the containment facility at the National Collection of Type Cultures.

**Numerical analysis of phenotypic features.** Of the 284 characters determined, 42 were deleted because the results obtained were variable for all of the strains. The majority of tests were treated as two-state characters, and the results were coded as 0 (negative or doubtful positive) or 1 (positive or weak positive). For two-state related tests, implied negative results were treated as no comparison (24). The Hugh-Leifson oxidation-fermentation test was treated as a qualitative (unordered) multistate character. The results for gelatin hydrolysis (stab and plate methods) were combined to give a single quantitative (ordered) multistate character. The API ZYM tests the color grade (0 to 7 days) of incubation at 30°C), 2 (weak growth after 4 to 7 days), 3 (growth positive 7 days), 4 (growth positive after 4 days), 5 (growth positive after 48 h), or 6 (growth positive after 24 h). The between-
strain similarities were calculated by using the Gower (10) general similarity coefficient, and negative matches were included for the two-state characters. The strains were clustered by using the method of unweighted pair group average linkage and by single-linkage cluster analysis (24). All calculations were carried out on a VAX computer at Leicester University (Leicester, United Kingdom) with a program developed by M. J. Sackin and R. P. Key of the Department of Microbiology, University of Leicester. The within- and between-taxon average levels of similarity were calculated as arithmetic means of the relevant levels of similarity.

**G+C content and DNA-DNA hybridization.** The methods used to determine G+C contents (19) and for DNA-DNA hybridization (7) at the Institut Pasteur and the Laboratoire pour Microbiologie en Microbiéle Genética have been described previously. G+C contents were determined by the thermal denaturation method. DNA from Escherichia coli K-12 was used as the control (melting temperature, 75.7°C; G+C content, 51.67 mol% according to the formula of Owen et al. [22]).

**RESULTS**

The similarities among the strains studied are shown in the dendrogram in Fig. 1, which was derived by unweighted pair group average linkage. At a similarity level of 84% the 56 group Vd-like strains formed a single cluster, although 5 strains formed two separate subclusters while the remaining 51 cultures joined at the 87% similarity level; thus, three biotypes were recognizable. At the 84% similarity level other clusters or single strains formed which corresponded to *Phyllobacterium* (3 strains), *Agrobacterium tumefaciens* (including *Agrobacterium radiobacter*, 6 strains), *Agrobacterium rhizogenes* (1 strain), *Rhizobium melliloti* (1 strain), *Rhizobium loti* (1 strain), *Rhizobium leguminosarum* (1 strain), *Mycoplana* (2 strains), *Brucella* (5 strains), high-G+C-content *Alcaligenes* species (11 strains), and low-G+C-content *Alcaligenes* species (8 strains). Within the high-G+C-content *Alcaligenes* cluster a subcluster was formed at the 91% similarity level, which contained all of the strains of *Alcaligenes xylosoxidans* together with the type strain of *Alcaligenes ruhlandii*. The low-G+C-content *Alcaligenes* cluster comprised reference strains of both *Alcaligenes faecalis* and *Alcaligenes odorans* including the respective type strains.

The G+C contents were determined for representative strains (Table 2); the values determined for 35 group Vd strains ranged from 56 to 59 mol%. Table 2 also shows the results of DNA-DNA hybridization experiments. Two DNA hybridization groups were apparent among the group Vd strains. Most strains tested (32 strains) grouped around the proposed type strain of *O. anthropi*, strain CIP 14970, with an average relative binding ratio of 80.5 ± 7.2%. A second group (five strains) formed around strain CNS 2-75 with an average relative binding ratio of 87 ± 11%. Two strains (CDC A9521 and EF 1821) occupied a somewhat separate position. The two DNA hybridization groups hybridized at an average degree of relative binding of 45 ± 4%.

**DISCUSSION**

A previous study of rRNA cistron similarities (7) included 14 group Vd strains which were included in the present study; labeled DNA from 2 of these strains was used in our DNA-DNA hybridization studies described. DNAs from the 14 strains were hybridized with labeled rRNA probes of *Brucella abortus* ATCC 23448 (T. = type strain) and *Agrobacterium tumefaciens* ICPB TT1111 (7), both of which were also included in the present study. The DNA-rRNA hybridization data clearly showed that the nearest neighbors of group Vd were *Brucella, Phyllobacterium, Agrobacterium, Mycoplana,* and *Rhizobium;* all of these organisms belong in rRNA superfamily IV. There was no relationship whatsoever at the suprageneric level to the *Alcaligenes* species (including *Achromobacter xylosoxidans*), which belong to rRNA superfamily III (7, 8). The close relationship of group Vd to *Agrobacterium* and *Rhizobium* was independently confirmed by Ohishi et al. (Abstr. XIV Int. Congr. Microbiol., 1986), who demonstrated similarities in G+C content (58 to 63 mol%), types of major fatty acids (C18:1 [70 to 90%] and 30H-C14), and type of respiratory quinone (ubiquinone 10): *Achromobacter xylosoxidans* was clearly different on the basis of these criteria (67 to 70 mol% G+C; C16:0, C16: 1, 2OH-C12, 2OH-C14, 30H-C14; ubiquinone 8).

Therefore, representative strains of all of the taxa described above were included in the numerical analysis of phenotypic features (Fig. 1). The dendrogram showed a very close correlation with the DNA-rRNA hybridization results, although whereas *Brucella* was the nearest rRNA neighbor to group Vd, with *Phyllobacterium* the next nearest, *Phyllobacterium* was closest to group Vd phenotypically but *Brucella* showed the lowest level of similarity.

The DNA-DNA hybridization study (Table 2) showed two DNA hybridization groups, both of which exhibited less than 30% hybridization with *Brucella* strains. The major group of 32 strains comprised strains of the *Achromobacter* groups A and D of Holmes and Dawson (13). These organisms are separable phenotypically (Table 3), as we confirmed in the present study (Fig. 1) (the group D strains are strains CL447/80, CL448/80, and CL449/80). The DNA-DNA hybridization data clearly show that these three group D strains, despite the phenotypic differences, show a high degree of DNA relatedness (≥90%) to the strains of *Achromobacter* group A (13). The second DNA hybridization group (five strains) contains two strains which represent *Achromobacter* group C of Holmes and Dawson (13). These strains are also separable phenotypically (Table 3), as we confirmed in the present study (Fig. 1) (the group C strains are strains CL634/77 and CL52/78). However, the other three strains of the second DNA hybridization group (strains CDC A6140, CNS 2-75, and CNS 23-76) are contained in the major subcluster of 51 strains (as are strains CDC A9521 and EF 1821, which occupy an intermediate position).

Group Vd clearly represents a new genus quite distinct from *Achromobacter*, a genus with which it has long been associated. (Although it did not appear on the Approved Lists of Bacterial Names [23], the genus *Achromobacter* was subsequently revived with the single species *Achromobacter xylosoxidans* [27]; the latter taxon was subsequently transferred to the genus *Alcaligenes* [18], leaving no species in *Achromobacter*.) Group Vd is homogeneous phenotypically except for five strains; three of these represent a separate biotype but are genotypically indistinguishable from the major group of strains. The taxon is also homogeneous genotypically except for seven strains, but only two of these can be distinguished phenotypically from the major group of strains. Thus, there seems to be no advantage at present to do other than recognize group Vd as a single species in a new genus. (We consider it inappropriate to place group Vd in *Achromobacter* [for the reasons given above] or to consider reviving the epithet *arsenoxydans* for the species name.)
FIG. 1. Dendrogram based on unweighted pair group average linkage. Percentages of similarity were calculated by using the general similarity coefficient of Gower, with negative matches included.
Alcaligenes xylosoxidans
Agrobacterium radiobacter
Agrobacterium tumefaciens
Brucella abortus
Brucella suis
Brucella suis
Brucella suis
Alcaligenes ruhlandii
Alcaligenes piechaudii
Rhizobium meliloti
Agrobacterium tumefaciens
Phyllobacterium rubiacearum
Phyllobacterium myrsinacearum
Brucella melitensis
Rhizobium leguminosarum
Mycoplana dimorpha
Mycoplana bullata
Phyllobacterium myrsinacearum
determinations were done at least in duplicate.
caused by 1% unpaired bases within the duplex.
The assumption that each 1°C decrease in the thermal stability of a heterologous DNA compared with the thermal stability of the homologous DNA duplex is

Data from reference 9.

The relative binding ratio was calculated as follows: (percentage of heterologous DNA bound/percentage of homologous DNA bound) × 100. All determinations were done at least in duplicate.

Percentages of divergence were calculated from the differences between the thermal denaturation values of the homologous and heterologous reactions, on the assumption that each 1°C decrease in the thermal stability of a heterologous DNA compared with the thermal stability of the homologous DNA duplex is caused by 1% unpaired bases within the duplex.

Data from reference 19.

Data from reference 2.

Unlabeled DNAs were used. The degree of DNA binding was measured by using the initial renaturation rate method.

Data from reference 9.

Data from reference 8.

### TABLE 2. DNA base compositions and degrees of DNA relatedness at 65°C of *O. anthropl strains*

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<th>Source of unlabeled DNA</th>
<th>Species</th>
<th>Strain</th>
<th>G+C content (mol%)</th>
<th>Relative binding ratio (%)</th>
<th>% Divergence (%)</th>
<th>Relative binding ratio (%)</th>
<th>% Divergence (%)</th>
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* Data from reference 7.

* Data from reference 8.

* Data from reference 9.

* Data from reference 10.

* Data from reference 11.

* Data from reference 12.

* Data from reference 13.

* Data from reference 14.
Acid produced from
ASS
Adonitol + * + + −
Lactose − − + + −
Sucrose + + + − −
Nitrite reduction + + − + −
Utilization of L-arabitol − − − + −
Hydrolysis of: β-D-Galactopyranoside − + + + −
β-D-Fucopyranoside − + + + −

* O. anthropi biotypes A, C, and D correspond to Achromobacter groups A, C, and D of Holmes and Dawson (13), respectively.
+ ASS, Ammonium salt sugars.
+ *, All strains positive; −, all strains negative.

For this new genus we propose the name Ochrobactrum (O.chro. bac’ trum. Gr. adj. ochros, pale, colorless; Gr. neu. n. baktron, a staff or stick; M.L. neu. n. Ochrobactrum, a colorless rod). Phenotypic and genotypic analyses (7) do not unequivocally indicate whether the new genus should be included in the family Rhizobiaceae.

Ochrobactrum gen. nov. The characteristics of Ochrobac- trum gen. nov. are given below. The cells are rod-shaped with parallel sides and rounded ends and usually occur singly. Resting stages are not known. The cells are gram negative and motile by means of peritrichous flagella. These organisms are obligately aerobic, possessing a strictly respiratory type of metabolism with oxygen as the terminal electron acceptor. The optimum growth temperature is in the range from 20 to 37°C. Colonies on nutrient agar are nonpigmented. The cells are oxidase positive and catalase positive. Indole is not produced. Esculin, gelatin, and DNA are not hydrolyzed. Cells are chemoorganotrophic, using a variety of amino acids, organic acids, and carbohydrates as carbon sources. They occur in human clinical specimens. The G+C content of the DNA is 56 to 59 mol%. Parameters of DNA-rRNA hybrids indicate that Ochrobactrum belongs to the Brucella rRNA branch within rRNA superfamily IV (7). At the suprageneric level Ochrobactrum is related to Brucella, Phyllobacterium, Rhizobium, and Agrobacterium. The type species is Ochrobactrum anthropi.

Ochrobactrum anthropi sp. nov. The characteristics of Ochrobactrum anthropi (an. thro’pi. Gr. n. anthropos, a human being; N.L. gen. n. anthropi, of a human being, since virtually all strains thus far recovered are from human clinical specimens) are given below. The cells are motile in hanging-drop preparations after overnight growth in nutrient broth incubated at either 37°C or room temperature (18 to 22°C); they are motile by means of peritrichous flagella (Fig. 2). After growth on nutrient agar for 24 h, colonies are typically circular, low convex, about 1 mm in diameter, smooth, shining, and entire.

A total of 163 characteristics are common to all strains (either all positive or all negative). There are 121 characteristics in which one or more of the strains differ (Table 4). All strains have the following positive characteristics in common: growth at 37°C; growth at room temperature (18 to 22°C); growth on MacConkey agar; catalase production; oxidase production; production of acid in ammonium salt medium under aerobic conditions from glucose, arabinose, ethanol, fructose, rhamnose, and xylose; and growth on β-hydroxybutyrate.

All strains have the following negative characteristics in common: pigment production; gluconate oxidation; lysine decarboxylase and ornithine decarboxylase production; acid and gas produced in glucose peptone water medium; reduction of 0.4% (wt/vol) selenite; casein digestion; production of extracellular deoxyribonuclease; production of acid in ammonium salt medium under aerobic conditions from raffinose; indole production (Kovacs and Ehrlich reagents); arginine desimidase production; hydrolysis of Tween 20 and Tween 80; production of a brown melaninlike pigment on tyrosine agar; accumulation of lipids after growth on β-hydroxybutyrate; fluorescence on King medium B; growth at 5°C; production of 3-ketolactose and lecithinase; hydrolysis of starch; and production of acid from 10% (wt/vol) lactose.

All strains utilize the following substrates (tests done with API 50AA, API 50AO, and API 50CH galleries): glycine, D-alanine, L-alanine, L-leucine, L-isoleucine, L-valine, L-serine, L-threonine, L-histidine, L-aspartate, L-glutamate, L-ornithine, L-lysine, L-citrulline, L-arginine, L-proline, betaine, D,L-3-aminoxybutyrate, D,L-4-aminoxybutyrate, sarcosine, glucosamine, acetate, propionate, isobutyrate, N-valerate, succinate, fumarate, glutarate, D,L-lactate, D,L-glycerate, D,L-3-hydroxybutyrate, D-malate, L-malate, 2-ketogluconate, erythritol, D-arabinose, L-arabinose, ribose, adonitol, galac-
tose, D-glucose, D-fructose, D-mannose, rhamnose, dulcitol, inositol, mannitol, sorbitol, N-acetylglucosamine, D-lyxose.
TABLE 4. Characteristics in which the 56 strains of O. anthropi differed

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<th>No. of strains positive</th>
<th>Result for type strain CIP 14970</th>
<th>Characteristic</th>
<th>No. of strains positive</th>
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* ASS, Ammonium salt sugars.

b ONPG, o-Nitrophenyl-β-D-galactopyranosidase.
TABLE 5. Differentiation of *O. anthropi* from closely related and phenotypically similar genera

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<tr>
<td>β-D-Glucoyranoside</td>
<td>-</td>
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<td>2/3</td>
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<tr>
<td>L-Isoleucyl-β-naphthylamide</td>
<td>-</td>
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<tr>
<td>L-Prolyl-β-naphthylamide hydrochloride</td>
<td>+</td>
<td>+</td>
<td>4/7</td>
<td>+</td>
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</table>

<sup>a</sup> , All strains positive; - , all strains negative.

<sup>b</sup> Number of strains positive/number of strains tested.

<sup>c</sup> Room temperature was 18 to 22°C.

<sup>d</sup> ASS, Ammonium salt sugars.
D-tagatose, D-fucose, L-fucose, D-arabitol, glucuronate, and 2-ketogluconate.

No strain utilizes the following substrates (tests done with API 50AA, API 50AO, and API 50CH galleries): D-tryptophan, L-tryptophan, trigonelline, DL-kyurenine, 3-amino- benzoate, 4-aminobenzoate, urea, acetamide, ethylamine, butyramine, amylamine, benzylamine, diaminobutane, spermine, histamine, tryptamine, heptanoate, caprylate, pimelate, L-tartrate, levulinate, itaconate, mesaconate, 2-hydroxybenzoate, D-mandelate, phthalate, isophthalate, terephthalate, methyl-xyloside, D-melibiose, inulin, D-raffinose, and glycochen.

All strains hydrolyze the following substrates (tests done with API ZYM galleries): L-prolyl-β-naphthylamide hydrochloride and L-γ-ε-β-d-naphthylamide.


The G+C contents of the DNAs of 35 strains of *O. anthropi* are between 56 and 59 mol%, with a mean of 57.0 mol% and a standard deviation of ± 0.7 mol%; the G+C content of the DNA of the type strain is 57 mol% (as estimated by the thermal denaturation method). The type strain is strain CIP 14970 (= CIP 82.115 = NCTC 12168 = LMG 3331). Thus, our results agree well with those of Ohishi et al. (57.6 to 60.5 mol% G+C; 9 strains) (Ohishi et al., Abstr. XIV Int. Congr. Microbiol., 1986) and with those of De Ley et al. (57.3 to 59.2 mol% G+C; 14 strains) (7).

Group Vd strains have been isolated predominantly from blood, respiratory tracts, urogenital tracts, and urine, with only a few isolates from feces and wounds (25). Our isolates (Table 1) were obtained from blood (17 strains), wounds (10 strains), urogenital tracts or urine (7 strains), respiratory tracts (6 strains), ears (3 strains), feces (3 strains), an eye (1 strain), and spinal fluid (1 strain); 2 strains were isolated from hospital apparatus, four strains were isolated from environmental sources, and the sources of 2 strains were unknown. Although group Vd strains are widely distributed in clinical specimens, the clinical significance of group Vd remains largely unknown. One strain was reported to be a cause of bacteremia in an immunocompromised host (20), but other workers believed that the characteristics presented by the authors were insufficient for unequivocal identification of the strain as a member of group Vd (G. L. Gilardi and M. J. Pickett, Letter, J. Clin. Microbiol. 22:139, 1985). However, one strain has been reported in association with a pancreatic abscess (1), and another has been associated with puncture wound osteochondritis of a foot (2). Group Vd strains are susceptible to aminoglycosides, carbenicillin, nalidixic acid, tetracycline, and trimethoprim-sulfamethoxazole but are resistant to other antimicrobial agents (26). *O. anthropi* appears to be widely distributed as our study included (Table 1) 22 strains from the United States, 18 strains from France, 7 strains from the United Kingdom, 3 strains from Denmark, 2 strains from Sweden, and 1 strain from Australia; the geographical sources of three strains were unknown.

Characteristics for the differentiation of *O. anthropi* from phylogenetically closely related taxa and from phenotypically similar taxa are given in Table 5. Almost all of the strains of *O. anthropi* (which included two reference strains of *Achromobacter* species biotype 2) tested produced acid from maltose, mannitol, and sucrose so our results differ from those of Chester and Cooper (3), who found that their reference strains of *Achromobacter* species biotype 2 (and almost all of their field strains) were unable to acidify these carbohydrates. The results of Oberhofer et al. (21) are in accord with our results, as these authors found that one-half of their strains were able to acidify these carbohydrates, and their strains also fell into more than two biotypes. Although these organisms are peritrichously flagellated, the flagella are generally small in number (one flagellum is common) and are laterally attached; apparent polar flagella are occasionally seen as also noted by Chester and Cooper (3).

The numerical phenotypic analysis confirmed previous observations that the following pairs of species are synonyms: *Agrobacterium radiobacter* and *Agrobacterium tumefaciens* (14), *Alcaligenes xylosoxidans* and *Alcaligenes rublandii* (13, 19, 28), and *Alcaligenes faeicillus* and *Alcaligenes odorans* (13). Our analysis also confirmed the distinction as separate taxa of *Agrobacterium* rhizogenes from *Agrobacterium tumefaciens* (14) and of *Alcaligenes denitrificans* and *Alcaligenes piechaudii* from each other and from *Alcaligenes faeicillus* (13, 19).

The following additional strains of *O. anthropi* have been deposited in the National Collection of Type Cultures: strains CDC A8409 (= NCTC 12169 = LMG 394), CL44780 (= NCTC 12170 = LMG 5429), CNS 2-75 (= NCTC 12171 = LMG 3301), and CL634/77 (= NCTC 12172 = LMG 5426).

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