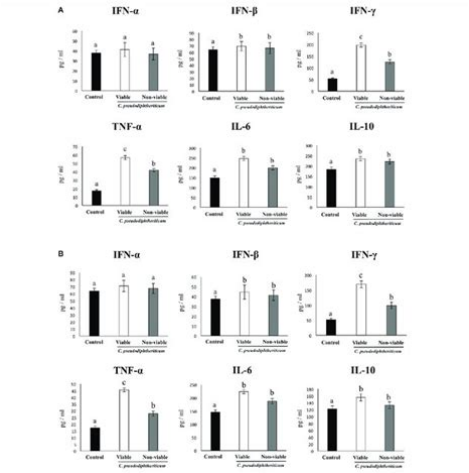
Corynebacterium pseudodiphtheriticum bergey s manual



File Name: Corynebacterium pseudodiphtheriticum bergey s manual.pdf
Size: 4489 KB
Type: PDF, ePub, eBook
Category: Book
Uploaded: 10 May 2019, 12:58 PM
Rating: 4.6/5 from 700 votes.

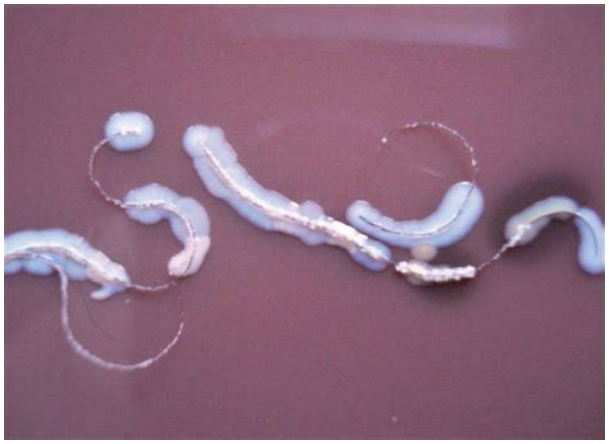
Book Descriptions:

Corynebacterium pseudodiphtheriticum bergey s manual

I have read and accept the Wiley Online Library Terms and Conditions of Use Shareable Link Use the link below to share a fulltext version of this article with your friends and colleagues. Learn more. Copy URL Rods are usually short or of medium length. Clubshaped forms may be observed; sometimes ellipsoidal, ovoid or rarely, “whip handles” see below, Corynebacterium matruchotii or thinner rods with bulges see below, Corynebacterium sundsvallense observed. Snapping division produces angular and palisade arrangements of cells. Gramstainpositive; some cells stain unevenly. Metachromatic synonym being polyphosphate granules may be observed for some species. Nonsporeforming. All species are nonmotile. All species are catalase positive. All species are oxidase negative except for Corynebacterium bovis, Corynebacterium aurimucosum, Corynebacterium doosanense, and Corynebacterium maris below. Many species are facultatively anaerobic and some are aerobic. Chemoorganotrophs. Some species are lipophilic. Many species produce acid from glucose and some other sugars in peptone media. Several species alkalinize citrate as sole carbon sources, but most do not. Rods are usually short or of medium length. Several species alkalinize citrate as sole carbon sources, but most do not.Glycan type of cell walls contains acetyl residues. Major cellwall sugars are arabinose and galactose also referred to as arabinogalactan, but occasionally other sugars detected. Longchained cellular fatty acids are of the straightchain saturated and monounsaturated types, with significant amounts of hexadecanoic palmitic, C 160 , octadecanoic C 180 , and cis 9octadecenoic “oleic”, C 181 9 c acids as major components. Small or moderate amounts of tuberculostearic acid TBSA 10methyl C 180 and other cellular fatty acids may also be present.http://cambariere.com/wallpapers/first-health-network-provider-manual.xml

- **corynebacterium pseudodiphtheriticum bergey s manual, corynebacterium pseudodiphtheriticum bergey s manual pdf, corynebacterium pseudodiphtheriticum bergey s manual download, corynebacterium pseudodiphtheriticum bergey s manual**

diagram, corynebacterium pseudodiphtheriticum bergey s manual test.



Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium pseudotuberculosis, and Corynebacterium vitaeruminis are the only species where significant amounts of the 161 isomer, C 161 7 c, are observed and corynemycolates may be observed to coelute with cellular fatty acids Bernard et al., 1991 . Branchedchain or hydroxylated fatty acids are absent or found only in trace amounts. In addition, MK7H 2 has been detected for Corynebacterium glaucum and Corynebacterium lubricantis; small amounts of MK10H 2 have also been found for Corynebacterium thomssenii below. Phospholipids include simple, phosphatidylinositol, phosphatidylinositol dimannosides, phosphatidylglycerol trehalose dimycolates, and other glycolipids Collins and Cummins, 1986; Yague et al., 1997 . Phosphatidyethanolamine is absent except for Corynebacterium bovis and Corynebacterium urealyticum Kampfer et al., 1999 .Phylogenetic relatedness among Corynebacterium species was first inferred by nearly full 16S rRNA gene sequence relationship studies in 1995 Pascual et al., 1995; Ruimy et al., 1995 Figure 1 . Since the 1st edition of the Manual, members of this genus have been restricted to species most closely related by 16S rRNA gene sequencing to the type species, Corynebacterium diphtheriae. The genus Corynebacterium and the closely related genus, Turicella, are sole genera in the family Corynebacteriaceae Ludwig et al., 2009a; Zhi et al., 2009 . In addition to a close relationship by 16S rRNA or rpoB gene sequence analyses described below, Corynebacterium species share phenotypic, chemotaxonomic, and other commonalities, and so taxa from the 1st edition of this Manual which do not fit this description have now been reassigned to other genera and families outlined below.Bar represents % substitutions. Alignment was done using CLUSTAL W software with MEGA 4 software Kumar et al., 2008 . Numbers represent neighbor joining NJ distances, with robustness estimated after 1000 bootstraps.http://andrelandberg.com/userfiles/first-manual.xml

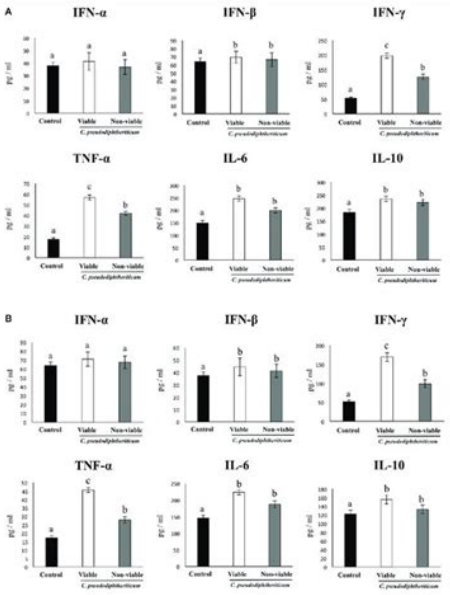
NCIMB, National Collections of Industrial Food and Marine Bacteria incorporating the NCFB, Aberdeen Scotland and NCTC, National Collection of Type Cultures, London UK, both are part of the United Kingdom National Culture Collection UKNCC.One widely used method is that of rpoB gene sequencing, as an adjunct to or in lieu of, 16S rRNA gene sequencing. Sequencing of a gene associated with cell division, div IVA, has been applied to discern Corynebacterium amycolatum from closely related species Letek et al., 2006 . A PCRbased assay to detect dtxR, a chromosomal irondependent repressor gene associated with Corynebacterium diphtheriae strains, has been used as a method to screen for these organisms Pimenta et al., 2008 . A number of other approaches have been used to try to separate closely related Corynebacterium species. Although still in its infancy, comparative analysis of these entire genomes has provided insight into common or different protein expressions found among these taxa including a set of conserved, DNAbinding transcriptional regulators consisting of 28 proteins that is involved with the regulation of cell division, septation, SOS and stress response, carbohydrate metabolism, and macroelement and metal homeostasis Brune et al., 2005 .Concerted efforts to track a large diphtheria outbreak in former Soviet Union FSU states, spearheaded by the European laboratory working group on diphtheria DIPNET, have been studied by various methods, particularly rRNA gene restriction pattern determination ribotyping. With this information, movement of clonal strains to other countries could be tracked Mokrousov et al., 2005 . Four molecular methods ribotyping, AFLP, PFGE, and RAPD for typing Corynebacterium diphtheriae strains have been compared.Thirtytwo strains of Corynebacterium urealyticum from humans or animals, recovered over several years, were extensively characterized by ribotyping.

The resultant disease, diphtheria, has historically been associated with significant morbidity and mortality in humans and animals, prior to universal use of an efficacious vaccine in countries around the world with higher socioeconomic means Funke et al., 1997f . In diphtheria, DT contributes to the formation of a pseudomembrane in the nasopharynx of the patient; although the organism is rarely found outside the infected area, the toxin, once absorbed by the circulatory system, can cause systemic complications, such as myocarditis and neuritis. Therefore, early administration of diphtheria antitoxin DAT, a commercial immunoglobulin which neutralizes circulating DT, is critical for patient care, but local stockpiles of DAT may not exist or be in limited supply in countries where diphtheria has low prevalence Wagner et al., 2009 . Diphtheria is still endemic in some subtropical and tropical countries as well as among individuals of certain ethnic groups e.g. indigenous peoples in the Americas and Australia. At population level, endemic geographicallyspecific variants of Corynebacterium diphtheriae are influenced by human host factors, public health control efforts i.e. universal vaccination, and socioeconomic conditions. Importation of toxigenic strains, or

lysogenization by a bacteriophage also called corynephage of local strains, may instigate an outbreak Mokrousov, 2009 .The biology, structure, and molecular epidemiology of DT and the tox gene have been comprehensively reviewed Holmes, 2000; Yates et al., 2006 . Fragment A of the tox gene contains ADPribosyltransferase activity; fragment B contains the receptorbinding and membraneassociating domains, with the structural tox gene being under the control of the chromosomal irondependant repressor, dtxR, and a promoteroperator region Nakao et al., 1996 .However, some strains contain detectable tox genes but do not express DT.

It has been suggested that these strains have one or more of a variety dysfunctional genetic mechanisms which preclude DT production von Graevenitz and Bernard, 2003 ; such isolates are considered as nontoxigenic with respect to public health response Efstratiou et al., 1998; Efstratiou and George, 1999 . The dtxR gene has been demonstrated to be heterogeneous, but all subtypes of this gene, if functional in strains lyosogenized by corynephage, could theoretically produce DT, and the possibility exists that nontoxigenic strains could revert to toxigenic status De Zoysa et al., 2005.Features of the attachment site in Corynebacterium ulcerans have been reviewed Seto et al., 2008 .This analysis revealed that “lipophila” in Corynebacterium jeikeium, but probably in all other lipophilic species described in this section, is expression of a fatty acid auxotrophy due to the absence of fatty acid synthase Tauch et al., 2005 . This phenomenon was also observed from complete genome analysis of the lipophile Corynebacterium kroppenstedtii which, as a species which lacks mycolates, was also found to lack a mycolate reductase gene Tauch et al., 2008a .The complete genome of an unusual blackpigmented strain of Corynebacterium aurimucosum ATCC 700975, designated the type strain of Corynebacterium nigricans, CN1 T that was associated with the female genital tract of a woman who experienced a spontaneous abortion during month 6 of her pregnancy, was described. A 29,037 bp plasmid designated pET44827 was found to code for a nonribosomal peptide synthetase, which appeared to play a key role in the synthesis of the black pigment; this pigment was conjectured to play a role in both protecting the bacterium from the high hydrogen peroxide concentration of the vagina and play a role in causing complications in pregnancy Trost et al., 2010 .

In addition, there was no consensus on standardized protocols and breakpoint interpretation for many years, so a wide variety of methods were independently used for clinically relevant isolates. Application of the broth microdilution method and specific MIC breakpoints were formally recommended by the CLSI in 2006 Clinical Laboratory Standards Institute, 2006 . A lack of precise species assignments and a lack of published historical data have made it difficult to compare older data to contemporary data to see if significant changes in resistance for specific taxa have occurred over time.The ermX gene, believed to be borne on plasmids or transposons, adds one or two methyl groups to a single adenine in the 23S rRNA moiety and confers high level resistance to macrolides, lincosamides, and streptogramin B MLS phenotype, as evidenced by resistance to at least erythromycin and clindamycin but often to other drug classes Roberts, 2008 .Most are deemed to be rare opportunistic pathogens. Some species thought to be part of the common skin flora, such as Corynebacterium amycolatum, Corynebacterium jeikeium, and some of the other lipophilic species, have been found to be resistant to multiple drug classes and can cause significant and occasionally fatal disease, particularly in immunocompromised patients or nosocomially in hospitals or nursing homes Funke and Bernard, 2007 . However, many of the medically relevant species can also be recovered as commensals or contaminants from a variety of clinical specimens.Virulence factors and mechanisms of pathogenicity remain understudied.These infections have been found to have occurred by occupationally related handling of the animals, by animal bites, or by unknown means.Growth for some species is enhanced by the addition of lipids or by using an extended incubation period detailed below, Corynebacterium urealyticum when recovered from urine.



No species described to date will grow on MacConkey agar except Corynebacterium lubricantis described below. Isolation of Corynebacterium diphtheriae, Corynebacterium ulcerans, or Corynebacterium pseudotuberculosis from nonsterile sites is outlined below.Shortterm weeks or months storage has historically been done using enriched media such as PAIs, Loefflers, or blood agar slants von Graevenitz and Bernard, 2003 .Rapid identification panels such as the API Coryne strip BioMerieux have been described for characterization of many of these species and are especially useful for those which grow well within the allotted 48 h incubation period and are reactive with the slate of substrates. Users are cautioned that the underlying database is only infrequently updated and does not provide enough discrimination to delineate among newly described species outlined here. A webbased query to decode API data exists; it provides possible adjunct tests to assist with identification . Ancillary strips such as BioMerieuxs API ZYM enzyme strip, API CH50 with API 20 E and panels manufactured by other companies, are also frequently used. The automated Biolog system has been used to provide phenotypic characteristics for various Corynebacterium species including the screening of nutritional and other physiological properties FernandezNatal et al., 2009 . Enzyme testing has been done as single test assays, such as described for pyrazinamidase or phosphatase synonym of alkaline phosphatase in a previous version of this chapter Collins and Cummins, 1986 . The characterization of species with no medical relevance that were derived from the environment has been carried out, either manually or by automated means e.g.

by use of the Biolog system by testing the ability of the organism to utilize different carbon compounds, by defining optimal or preferred salinity, temperature, atmosphere, and pH, and by considering chemotaxonomic and genetic features; this has been outlined recently for Corynebacterium lubricantis below Kampfer et al., 2009.Staining for the presence of metachromatic granules is now almost never described.Specific 16S rRNA signature nucleotides for these bacteria have been outlined Zhi et al., 2009 .Additional identification approaches, such as the use of 16S rRNA and rpoB gene sequencing, are being used more routinely as a significant adjunct to characterization. However, assignment of species nova to this genus requires testing for as many genetic and chemotaxonomic properties as are available to researchers, and, increasingly, full genome sequencing is highly recommended.These species can be lyogenized by the bacteriophage that confers ability to produce diphtheria toxin.All Corynebacterium species previously attributed to causing disease in plants have been reassigned, and none of the species described here have been documented to be phytopathogens.Brevibacterium liquefaciens strain ATCC 14929 was subsequently reassigned to Arthrobacter nicotianae GiovannozziSermanni 1959 by Gelsomino et al. 2004 .Colonies on blood tellurite with 0.04% potassium tellurite are gray to black, with appearance dependant on

type. Although less frequently used now, growth on Loefflers medium is abundant, with grayish to cream colored colonies and no liquefaction. The use of historical descriptions of colonies such as gravis being large, radially striated brittle colonies and mitis being smooth, shiny, and butyrous or Gram stain details gravis having short regular rods, intermedius with long rods with marked crossstriations, mitis with long curved irregular rods as a means to subdivide strains into gravis, intermedius, and mitis are now rarely used.

All contain corynemycolates, the polar lipids phosphatidylglycerol, phosphatidylinositol, and monoacylated phosphatidylinositol dimannoside, and MK8 H2 as major menaquinone. Cell wall contains meso diaminopimelic acid and the sugars arabinose and galactose. Straightchain saturated fatty acids are mainly palmitic and stearic acids with minimal branched saturated fatty acids; significant quantities of C 161 7 c isomer is characteristically detected Bernard et al., 1991 . All produce propionic as a product of fermentation Bernard et al., 2002 .All biovars of Corynebacterium diphtheriae may produce diphtheria toxin which clinically should be tested for as described elsewhere in this chapter. Nontoxigenic strains otherwise have typical features. Full genome sequence of Corynebacterium diphtheriae strain NCTC 13129 has been published containing 2,488,635 bp CerdenoTarraga et al., 2003 .Facultatively anaerobic. Fermentation of sucrose is variable. Acid is not produced from lactose, D xylose, trehalose, L arabinose, raffinose, L rhamnose, dextrin, mannitol, dulcitol, D sorbitol, glycerol, myo inositol, salicin, and inulin. Esculin, urea, gelatin, casein, and starch are not hydrolyzed. No production of indol, H 2 S, acetoin, and lipase. The methyl red test is negative. CAMP reaction negative. Cellular fatty acids are as described for the genus. Menaquinone or polar lipid types not extant. Does not produce propionic acid as metabolic product Bernard et al., 2002 .Cells are arranged in typical Vshaped forms or palisades. Nonlipophilic. Good growth under aerobic conditions, and very slight growth under anaerobic conditions. Smooth, grayishwhite colonies with entire margins. Acid is not produced from glucose, glycogen, lactose, sucrose, ribose, D xylose, D mannose, D galactose, trehalose, and D mannitol. Cells utilize acetate and lactate.

Propionate, D glucose, L arabinose, D mannose, D mannitol, N acetylglucosamine, maltose, gluconate, caprate, adipate, malate, citrate, and phenylacetate are not utilized. Nitrate is not reduced. Urea and esculin not hydrolyzed. Tyrosine, gelatin, DNA, and starch are not degraded. The methyl red test is negative, and acetoin, indole, and H 2 S on triplesugar iron agar are not produced. Hydrolysis of hippurate is variable. Growth is visible in 6.5% NaCl. Alkaline phosphatase, esterase, lipase, and acid phosphatase are produced. Galactosidase, galactosidase, glucuronidase, glucosidase, and glucosidase are not produced. All strains are resistant to fosfomycin. CAMP reaction variable Funke and Bernard, 2007 .Cellular fatty acids are consistent with those described for the genus. Corynemycolates are present with C 300, C 301, C 321, C 331, C 342, and C 362 predominating. Does not produce propionic acid as metabolic product Bernard et al., 2002 .In a recent study, the following reactions were found for ATCC 6871 T glucose, ribose, and fructose were slowly fermented, but xylose, mannitol, lactose, maltose, galactose, glycerol, glycogen, raffionse, salicin, trehalose, and mannose were not. Nitrate reduced to nitrite. Urease is produced. Hippurate and tyrosine are hydrolyzed. Gelatin, casein, DNase, and starch are not hydrolyzed. Citrate is alkalinized. CAMP and reverse CAMP reactions are negative.Cell wall contains arabinogalactan polymer. Corynomycolic acids are present. Longchain fatty acids are of the saturated, monounsaturated, and 10methylbranched types with hexadecanoic, octadecanoic, octadecenoic, and 10methyloctadecanoic acids predominating. TBSA detected but does not produce propionic acid as metabolic product Bernard et al., 2010 . The major phospholipids are diphosphatidylglycerol,

phosphatidylglycerol, phosphatidylinositol, and phosphatidylinositol dimannoside. The major menaquinone is MK9H 2 .Colonies are whitishgrayish, dry, rough, and with uneven edges.

Facultatively anaerobic. Acid is usually produced from D fructose, D glucose, glycerol, D mannose, and ribose. Acid production from maltose, sucrose, galactose Wauters et al., 1996 , and trehalose is variable. Nitrate reduction and urea hydrolysis are variable. Esculin, arginine, casein, cellulose, gelatin, ornithine, tyrosine, and xanthine are not hydrolyzed. Starch is hydrolyzed Funke et al., 1996a . Some strains hydrolyze hippurate.Arabinose and galactose are wall sugars. Mycolic acids are not present. The cellular fatty acids are consistent with those described for the genus. The principle menaquinone is MK9H 2 with significant quantities of MK8H 2 . Polar lipid types include acyl phosphatidylglycerol, phosphatidylinositol, phosphatidylinositol dimannoside, and several unknown phospholipids Collins et al., 1988a; Yague et al., 1997 . Strains produce propionic acid as a product of fermentation Funke et al., 1996a .When identification is done based solely on the use of phenotypic methods, Corynebacterium amycolatum isolates have been misidentified as Corynebacterium xerosis, Corynebacterium minutissimum, Corynebacterium striatum, and other closely related taxa Funke et al., 1996a; Wauters et al., 1996; Zinkernagel et al., 1996 . Most strains identified as Corynebacterium amycolatum using a polyphasic approach are MDR due in part to the presence of the ermX gene and other mechanisms as yet not fully elaborated Yague et al., 1997 . Older publications where identification of Corynebacterium xerosis and Corynebacterium minutissimum was based on biochemical, not genetic, traits should be interpreted with caution, as strains described as being multidrug resistant may, in fact, be misidentified Corynebacterium amycolatum isolates.

The Corynebacterium amycolatum type strain CCUG 35685 T and at least one other reference strain, CIP 100836 " Corynebacterium asperum ", differ from most clinical isolates as they are fully sensitive to all drug classes tested by microbroth dilution K. Bernard, personal communication. Strains formerly designated CDC group I2 or CDC group F2 have been assigned to Corynebacterium amycolatum Wauters et al., 1996 .Acetoin production is positive, but indole production is negative. Produces lactate, but not propionate, as the major product of glucose fermentation.Type PI phospholipids pattern with no nitrogencontaining compounds.Oxidase negative. Nonlipophilic. CAMP reaction is negative. Esculin, urea, and gelatin are not hydrolyzed. Alkaline and acid phosphatases, esterase, esterase lipase, leucine arylamidase, chymotrypsin, and phosphoamidase activities are detected.They grow on blood agar as circular acuminated creamy colonies which are not hemolytic. Nonlipophilic. Nitrate is not reduced. Esculin, urea, gelatin, tyrosine, and DNA are not hydrolyzed or degraded. Hydrolyses of starch and hippurate occur variably. Acid is produced from D glucose and fructose but not from sucrose, maltose, lactose, galactose, D xylose, trehalose, glycogen, or D mannitol. Acidification from ribose occurs variably. Pyrazinamidase, esterase lipase, cystine arylamidase, and, characteristically, chymotrypsin are present. Production of esterase, leucine arylamidase, and acid phosphatase is variable, and alkaline phosphatase is usually not produced. Pyrrolidonyl arylamidase, glucuronidase, galactosidase, glucosidase, and N acetyl glucosaminidase are not produced.Strains produce propionic acid as a metabolic product Bernard et al., 2002 .Facultatively anaerobic. Nonlipophilic. Growth occurs in broth containing 7.5% NaCl but not in 10% NaCl. Nitrate is not reduced to nitrite. Esculin, urea, gelatin, and starch are not hydrolyzed.

Acid is produced from D glucose, maltose, ribose, and sucrose but not from lactose, mannitol, glycogen, or D xylose. Activity is detected for glucuronidase, cystine arylamidase, leucine arylamidase, and valine arylamidase. Acetoin is not produced.Mycolic acids are not detected.On trypticase soy agar, they appear colorless or charcoal black and slimy. On brain heart infusion agar supplemented with 1% Tween 80, some strains are able to form a corraloid precipitin in agar when grown in the presence of CO 2. Oxidase very rarely positive. Acid is produced from fructose, D

glucose, maltose, sucrose, and occasionally D mannitol but not from adonitol, amygdalin, arabinose, cellobiose, glycerol, glycogen, inulin, lactose, mannose, melezitose, raffinose, rhamnose, ribose, salicin, sorbitol, trehalose, or xylose. Hydrolyzes hippurate and occasionally gelatin and urea but not starch. Esculin hydrolysis is variable, and nitrate reductase is rare. Acetoin positive and indole negative. Lactate, not propionate, is the major end product of glucose fermentation.Shortchain corynomycolic acids are present. The fatty acid profile contains saturated, unsaturated, and tuberculostearic acids. It has type PI phospholopid pattern with no nitrogencontaining compounds.CP001601 Trost et al., 2010 . By 16S rRNA gene sequencing alone, this species can not be readily discerned from Corynebacterium minutissimum and Corynebacterium singulare, but these species can be resolved using rpoB gene sequencing Khamis et al., 2004 .Colonies are circular, convex, and dry, becoming slightly yellowish with time; slightly adhere to agar. Weakly adherent if subcultured on agar plates. Nonlipophilic. Oxidative metabolism. Acid is not produced from glucose, maltose, sucrose, mannitol, xylose, ribose, lactose, and glycogen. The following substrates are utilized hydroxybutyric acid, L malic acid, pyruvic acid, succinamic acid, N acetyl L glutamic acid, L asparagine, L glutamic acid, glycyl.

L glutamic acid, and L pyroglutamic acid. Nitrate is not reduced. Urea and esculin are not hydrolyzed. The CAMP reaction is positive. Pyrazinamidase, alkaline and acid phosphatases, esterase, esterase lipase, lipase, leucine arylamidase, and phosphoamidase are produced.Propionic acid not detected as metabolic product Bernard et al., 2002 .Corynebacterium auris was originally described as Coryneform CDC group ANF1 like.Obligately aerobic. Nonlipophilic. CAMP reaction negative. Hippurate is hydrolyzed. Esculin hydrolysis is variable. Urea, gelatin, and starch are not hydrolyzed. Alkaline and acid phosphatases, esterase weak reaction, ester lipase weak reaction, leucine arylamidase, phosphoamidase, and pyrrolidonyl arylamidase activities are detected. Lipase activity variable.Xylose, rhamose, lactose, mannitol, mannose, sucrose, raffinose, salicin, and starch not utilized. Esculin, starch, and casein not hydrolyzed. Hippurate hydrolyzed; phosphatase and pyrazinamidase positive, but variable for galactosidase. Nitrate not reduced; urease not produced Collins and Cummins, 1986; Hollis and Weaver, 1981 .MK9 H2 detected. Cellular fatty acids are consistent with those described for the genus Bernard et al., 1991 , with TBSA being detected. Propionic acid not detected as metabolic product Bernard et al., 2002 .Moderate growth on nutrient agar. Glucose, fructose, mannose, maltose, sucrose, trehalose, salicin, and methyl red positive. Hippurate hydrolyzed and urease produced. Negative for arabinose, xylose, rhamnose, galactose, lactose, raffinose, dextrin, and starch fermentation. Esculin, casein, and gelatin hydrolysis negative, and nitrate not reduced.Mycolates are present. Cellular fatty acids are consistent with those of the genus. Menaquinone is MK9H 2 .Facultatively anaerobic. Nonlipophilic. CAMP reaction is strongly positive. Acetoin and indole are not produced.

Acid is produced from glucose, but not from ribose, xylose, mannitol, lactose, maltose, sucrose, and glycogen. Pyrazinamidase, alkaline phosphatase, esterase, esterase lipase, lipase, leucine arylamidase, valine arylamidase, and cystine arylamidase are produced.Facultatively anaerobic. Activities of urease, pyrrolidonyl arylamidase, gelatinase, lipase, cystine arylamidase, chymotrypsin, galactosidase, galactosidase, glucuronidase, N acetylglucosaminidase, mannosidase, and fucosidase are not detected. The CAMP reaction is negative.Cellular fatty acids are consistent with those described for the genus.Colonies are circular, entire, convex, nonhemolytic, and lemonpigmented. Facultatively anaerobic. Nonlipophilic. Acid is produced from glucose but not from lactose, maltose, mannitol, ribose, sucrose, and D xylose. Nitrate is not reduced. Activity for alkaline and acid phosphatases, esterase weak, esterase lipase, lipase weak, and leucine arylamidase is detected.Tuberculostearic acid is not present.Facultatively anaerobic. Nitrate is reduced to nitrite. Esculin, urea, gelatin, tyrosine, and ONPG are not hydrolyzed. CAMP reaction is negative. The isolates do not produce lipase, trypsin, chymotrypsin, galactosidase, mannosidase, galactosidase, glucuronidase, glucosidase, glucosidase, and N acetylglucosaminidase.Nonlipophilic. Colonies are

circular, convex, entire, opaque, dull, nonhemolytic and can be moved across the plate while retaining their integrity. Acid is produced from D glucose and D ribose, but not from glycogen, lactose, maltose, mannitol, sucrose, or D xylose. Urea is hydrolyzed but esculin and gelatin are not. Activity is detected for esterase, esterase lipase, pyrazinamidase, and trypsin.Cellular fatty acids are consistent with those described for the genus; tuberculostearic acid is not present.Facultatively anaerobic.