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Classification, Identification, and Clinical Significance of *Proteus*, *Providencia*, and *Morganella*

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INTRODUCTION

The taxonomy of *Proteus*, *Providencia*, and *Morganella* is a fascinating story that is enmeshed throughout the early history of the evolving science of microbiology. Species within these genera are not considered frank pathogens, unlike some of the other members of the *Enterobacteriaceae*, and are commonly isolated in clinical laboratories. As with other opportunistic pathogens, they may also cause morbidity and mortality. It is clear that while the more pathogenic members of the *Enterobacteriaceae*, such as *Salmonella*, *Shigella*, and *Escherichia coli*, may exact more urgent attention, the presence of any one of these less pathogenic genera in body fluids and in some deep or superficial lesions would lead one to suspect their potential etiologic nature.

In this review, the evolution of the "family tree" of *Proteus*, *Providencia*, and *Morganella* will be discussed within each genus, along with the current methods for the identification of each species of the genus, incorporating both conventional biochemical and commercial methods. Their clinical significance will also be discussed. While all of these organisms are ubiquitous in the environment, individual case reports and nosocomial-outbreak reports indicate that they are capable of causing major infectious disease problems. Lastly, anticipated antimicrobial susceptibility patterns will be considered. Many of these organisms are easily controlled, but some problems have arisen with the advent of newer and more powerful antimicrobial agents.

PROTEUS, *PROVIDENCIA*, AND *MORGANELLA*

To discuss the taxonomy of *Proteus*, *Providencia*, and *Morganella* independently of each other is very difficult. Their taxonomic development is as intertwined as the flagella that are characteristic of some of the individual species and illustrates the evolution of the science of taxonomy as well as the nomenclature of these genera. Because the eight species within the *Proteus*, *Providencia*, and *Morganella* have often been classified in different genera over time, one might find their taxonomic evolution confusing. Tables 1, 2, and 3 summarize the major

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TABLE 1. Timeline of the genus *Proteus*

Date	Author	Event	Reference
1885	Hauser	Described the genus *Proteus* and species *P. mirabilis*, *P. vulgaris*, and *P. zenkeri*	42
1919	Wenner and Rettger	Separated *P. vulgaris* and *P. mirabilis* on the basis of sugar fermentations	108
1966	Cosenza and Podgwaite	Described *P. myxofaciens*	19
1978	Brenner et al.	Defined *P. vulgaris* biogroup 1	9
1982	Hickman et al.	Described *P. penneri*; established two additional biogroups of *P. vulgaris*	46
1993	Costas et al.	Used SDS-PAGE to separate *P. vulgaris* biogroup 2 and further subdivide *P. vulgaris* biogroup 3 into two separate "taxa"	20
1995	Brenner et al.	Requested replacement of *P. vulgaris* type strain NCTC 4175 with ATCC 29905	10
1999	Trüper	Replacement of *P. vulgaris* type strain with ATCC 29905 granted	103

changes within each genus, and each species is addressed in the genus in which it now is classified. Historically, these three genera were placed in the tribe *Proteeae*. The tribe designation is not often used; however, as a matter of convenience, this term will be used in this review.

TABLE 2. Timeline of the genus *Providencia*

Date	Author	Event	Reference
1918	Hadley et al.	Described *Bacterium rettgerei*	41
1920	Ornstein	Described *Bacillus inconstans*	75
1923	St. John-Brooks and Rhodes	Renamed *B. rettgerei* as *Bacillus rettgeri*	97
1943	Rustigian and Stuart	Redescribed *B. rettgeri* as *Proteus rettgeri*	84
1943	Stuart et al.	Described "anaerogenic paracolon 29911"	98
1944	Gomes	Described *Eberthella alcalifaciens*	38
1951	Kauffmann	Anaerogenic paracolon 29911 designated Providence group	53
1952	Kauffmann and Edwards	Providence group named *Providencia providenciae*	56
1954	Buttiaux et al.	Providence group renamed *Proteus stuartii*	13
1955	Shaw and Clarke	*Bacillus inconstans* renamed *Proteus inconstans*	88
1962	Ewing	*E. alcalifaciens* redescribed as *Providencia alcalifaciens* with second subgroup named *P. stuartii*	26
1978	Brenner et al.	*Proteus rettgeri* becomes *Providencia rettgeri*	9
1983	Hickman-Brenner et al.	Described *Providencia rustigianii*	48
1983	Müller	Described *Providencia fredericiana*	67
1986	Müller et al.	Described *Providencia heimbachae*	69
1986	Hickman-Brenner et al.	*P. rustigianii* has priority over *P. fredericiana*	47

TABLE 3. Timeline of the genus *Morganella*

Date	Author	Event	Reference
1906	Morgan	Described Morgan's bacillus	66
1914	Castellani	Described *Bacterium columbense*	14
1919	Winslow et al.	Named Morgan's bacillus *Bacillus morganii*	111
1936	Rauss	Renamed *B. morganii* as *Proteus morganii*	80
1943	Fulton	Showed that *B. columbensis* and *P. morganii* were the same; defined the genus *Morganella* with species *M. morganii* and *M. columbensis*	35
1962	Ewing	*Bacterium columbense* Castellani 1914 reidentified as *Escherichia coli*	26
1976	Siboni	*P. morganii* divided into two biogroups	89
1978	Brenner et al.	Described *Morganella morganii*	9
1992	Jensen et al.	Described two subspecies of *Morganella morganii* as subsp. *morganii* and subsp. *sibonii*	50

Phenotypic Differentiation of the Genera

Table 4 shows the conventional biochemical tests necessary for the differentiation of *Proteus*, *Providencia*, and *Morganella* (29). All three genera are positive for phenylalanine deaminase and negative for arginine decarboxylase, malonate utilization, and acid production from dulcitol, D-sorbitol, and L-arabinose.

THE GENUS *PROTEUS*

Current Classification

The genus *Proteus* currently consists of five named species (*P. mirabilis*, *P. penneri*, *P. vulgaris*, *P. myxofaciens*, and *P. hauseri*) and three unnamed genomospecies (*Proteus* genomospecies 4, 5, and 6).

The literature abounds with studies on the taxonomy of the genus *Proteus* since the original publication by Hauser, who first described the genus (Table 1) (42). The term *Proteus* means "changeability of form, as personified in the Homeric poems in Proteus . . . and has the gift of endless transformation" (108).

The genus originally had two species: *P. mirabilis* and *P. vulgaris*, both first described by Hauser in 1885 (42). He noted

TABLE 4. Differentiation among the genera *Proteus*, *Providencia*, and *Morganella*[a]

Biochemical test or property	*Proteus*[b]	*Providencia*[b]	*Morganella*[b]
Citrate utilization	v	+	−
D-Mannose fermentation	−	+	+
Gelatin liquefaction (22°C)	+	−	−
H_2S production (TSI)[c]	+	−	v
myo-Inositol fermentation	−	v	−
Lipase (corn oil)	+	−	−
Ornithine decarboxylase	v	−	(+)
Swarming	+	−	−
Urea hydrolysis	+	v	+

[a] Data from reference 28a.
[b] Symbols (all data are reactions at 48 h unless otherwise specified): +, 90 to 100% positive; (+), 75 to 89.9% positive; v, 25.1 to 74.9% positive; (−), 10.1 to 25% positive; −, 0 to 10% positive.
[c] TSI, triple sugar iron.

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the swarming nature of the organisms and divided the strains into the two species based on the speed of their ability to liquify gelatin: *P. vulgaris* liquefies gelatin "rapidly," and *P. mirabilis* does so "more slowly". Hauser also described "*Proteus zenkeri*," which neither swarmed nor liquefied gelatin, but he rescinded this particular finding 7 years later (43).

In 1894, Theobald Smith reported the fermentative characteristics of the two species using glucose, sucrose, and lactose and their greatly diminished or complete loss of the ability to liquefy gelatin as the culture aged (93). The previous year, he had demonstrated the unusually small amount of gas produced from glucose by *P. vulgaris* compared to other then-known enteric organisms.

In 1919, Wenner and Rettger in Connecticut were studying the biochemical characteristics of a larger group of *Proteus* strains (108). Consistent with Hauser's work of 1885, their strains also swarmed and liquefied gelatin. All of these strains also produced hydrogen sulfide and were lactose nonfermenters. The ability to ferment glucose, sucrose, and maltose served as a means to further subdivide the strains into two groups, as Hauser had done. *P. vulgaris* fermented glucose, sucrose, and maltose readily, while *P. mirabilis* fermented glucose readily and sucrose slowly and did not ferment maltose.

It should be noted that in 1952 Kauffmann and Edwards published a taxonomic table listing "*Proteus hauseri*" var. *vulgaris* and var. *mirabilis*, an alternative classification that was not long-lived (56).

In 1966, Cosenza and Podgwaite described another new species, *Proteus myxofaciens*, that they isolated from the larvae of the gypsy moth (19). It produces slime and is not known to have been isolated from a human. The name derives from "myxo" (Greek for slime) and "faciens" (Latin for producing).

Until the early 1960s, bacterial classification had been based primarily on cultural observations and phenotypic analysis. In 1961, Marmur described a procedure for isolating stable, biologically active, highly polymerized DNA from bacteria that was relatively free from protein and RNA (62). This was to become the first step toward molecular genetic characterization of bacteria. In 1965, Britten and Kohne developed a technique of DNA hybridization that would become the tool to resolve many of the problems in bacterial taxonomy (10a). This technique used hydroxyapatite binding for the fractionation of DNA. This process used the fact that double-stranded DNA can be cleaved to single strands and that the single strands seek to reanneal with their complementary strands. The more closely related the organisms, the more efficient the DNA-reannealing process.

After the advent of techniques such as DNA-DNA hybridization and guanine-plus-cytosine (G+C) determination, which enabled scientists to place new species into their correct genera, biochemical testing remained important but only secondarily to the results of experiments in genetic relationships. It has become clear after years of experience in determining the current taxonomic stature of human isolates that recognizing the correct classification is often a key to ascribing appropriate etiologic relationships to these strains.

In a 1978 study of 122 strains, Brenner et al., utilizing this technology, showed for the first time the genetic heterogeneity of *P. vulgaris* (9). One group of strains was indole, salicin, and esculin negative and was designated *P. vulgaris* biogroup 1. In 1982, Hickman et al. proposed that this group be renamed *Proteus penneri* in honor of John Penner, the Canadian microbiologist who made many contributions to studies of the three genera of *Proteeae* (46).

The mid-1980s saw the advent of high-resolution polyacrylamide gel electrophoresis of proteins with computerized analysis of patterns as another taxonomic tool to identify and type bacteria (59). In 1993, Costas et al. in England used this technique to further subdivide *P. vulgaris* into biogroups 2, 3a, and 3b, with the type strain (NCTC 4175/ATCC 13315) being included in biogroup 3a with only one other strain (20). During the same time, O'Hara et al. in the United States, in collaboration with Grimont in France, studied many of the same strains by DNA-DNA hybridization, phenotypic characterization, and carbon source utilization. Their results paralleled those of Costas et al. and revealed that the type strain of *P. vulgaris* was genetically uncharacteristic of the hundreds of strains considered typical members of *P. vulgaris* (C. M. O'Hara, F. W. Hickman-Brenner, A. G. Steigerwalt et al., Abstr. 94th Gen. Meet. Am. Soc. Microbiol. 1994, abstr. C-253, p. 535, 1994). In 1995, Brenner et al. requested that a neotype strain be designated for *P. vulgaris* (10). In 1999, this request was approved by the Judicial Commission (103). The name did not change, but a new phenotypically accurate type strain, ATCC 29905, was designated.

The studies of O'Hara et al. cited above confirmed the existence of four genomospecies within biogroup 3, which were called *Proteus* genomospecies 3, 4, 5, and 6. Genomospecies 3 contains only the original type strain of *P. vulgaris* (ATCC 13315) and one other strain. These authors have proposed that genomospecies 3 be named *Proteus hauseri* and that genomospecies 4, 5, and 6 remain unnamed as *Proteus* genomospecies 4, 5, and 6, respectively (71). *Proteus hauseri* would honor Gustav Hauser, the German microbiologist, who first described the genus. The respective *Proteus* type strains are listed in Table 5.

16S rRNA Classification

In the early 1980s, sequencing of 16S rRNA genes with subsequent comparison of these sequences and phylogenetic analysis became another promising taxonomic tool. The 16S rRNA gene of three strains of *P. vulgaris* (GenBank file names PVU233425 [95], PRMRRD [13a], and PVRN16S [direct submission]) have been completely sequenced, but extensive studies have not been completed that would prove other taxonomic relationships.

Phenotypic Identification of the Species

Conventional methods. Table 6 shows the biochemical test results for the four species of *Proteus*. Pompei et al. reported a methyl green-phenolphthalein phosphatase test which would accurately and simply separate members of the tribe *Proteeae* (78a).

Commercial methods. With the ever-increasing cost of commercial identification methods (73, 74), spot testing is both rapid and cost-effective (64) and can be helpful in many instances. If the colonies on a sheep blood agar plate swarm and are oxidase negative and if a spot indole test using *para*-dimethylaminocinnemaldehyde reagent is negative, the probability of the culture being either *P. mirabilis* or *P. penneri* is very high. To separate these two species, a positive test for ornithine decarboxylase will be obtained with *P. mirabilis*. If the spot indole test is positive, the culture is most likely to be *P. vulgaris. P. penneri* is often described as indole-negative *P. vulgaris*. In most instances, identifications by rapid spot tests need not be confirmed by conventional or commercial methods.

Table 7 shows the database entries for nine manual, semiautomated, or automated commercial bacterial identification products now available. The two Vitek products and the Biolog system combine the identification of *P. vulgaris* and *P. penneri*

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TABLE 5. Type strains for *Proteus*, *Providencia* and *Morganella*

Species	Type strain[a]						
	ATCC	CCUG	CDC	CIP	DSM	JCM	NCTC
Morganella morganii ssp. *morganii*	25830	6328	4567-84	A231	30164	1672	235
Morganella morganii ssp. *sibonii*	49948	30886	8103-85	103648			12357
Proteus hauseri	700826	35386	1732-80				
Proteus mirabilis	29906	26767	PR 14; 9165-79	103181	4479	1669	11938
Proteus myxofaciens	19692	18769	9338-76		4482	1670	
Proteus penneri	33519	15722	1808-73	103030	4544	3948	12737
Proteus vulgaris	29905	35382	9166-79	104989			13145
Providencia alcalifaciens	9886	6325	9014-82	82.90	30120	1673	10286
Providencia heimbachae	35613	16446	8025-83	103031	3591		12003
Providencia rettgeri	29944	14804	1163; 9167-79	103182	4542	1675	11801
Providencia rustigianii	33673	15723	132-68	103032	4541	3953	11802
Providencia stuartii	29914	14805	2896-68	104687	4539		11800

[a] ATCC, American Type Culture Collection; CCUG, Culture Collection, University of Göteberg, Göteborg, Sweden; CDC, Centers for Disease Control and Prevention, Atlanta, Ga.; CIP, Collection d'Institut Pasteur, Paris, France; DSM, Deutsche Sämmlung von Mikroorganismem und Zellkulturen GmbH, Braunschweig, Germany; JCM, Japan Collection of Microorganisms; NCTC, National Collection of Type Cultures, London, United Kingdom.

and require that an off-line spot indole be performed to complete the identification.

When the three species of *Proteus* are inoculated into these identification systems, reported accuracies are 100% for the Crystal ID-E/NF (Becton Dickinson Microbiology Systems, Sparks, Md.), GNI, GNI+, and API 20E (bioMérieux Inc., Hazelwood, Mo.), and Rapid Neg ID3 (Dade Behring, Inc., MicroScan, Inc., W. Sacramento, California) (73, 74, 81). Other authors report 95% accuracy for the Rapid Neg ID3 (2), 97% for the Vitek GNI cards, and 97% for the Vitek GNI+ cards (8). Because many of these systems now incorporate enzymatic substrates which cannot be easily reproduced in the laboratory, it is usually impossible to pinpoint exactly why an identification is in error.

Typing Systems

Typing systems for the *Proteeae* include phage, bacteriocin, protein profile, serological, restriction fragment length polymorphisms, and PCR. Because these systems are not routinely used in clinical laboratory work, they will not be discussed in this review. Senior reviewed all of these systems for the three genera in 1998 (87).

Clinical Significance

Proteeae are widespread in the environment and make up part of the normal flora of the human gastrointestinal tract. Although *Escherichia coli* accounts for the largest percentage of cases of uncomplicated cystitis, pyelonephritis, and prostatitis, *Proteus* ranks third as the cause of these infections, particularly in hospital-acquired cases (96). *P. mirabilis* accounts for approximately 3% of nosocomial infections in the United States (15) and is commonly isolated in clinical microbiology laboratories.

In a study by Müller, *P. mirabilis* and *P. penneri* were isolated significantly more often from stools of patients with diarrheal disease than from healthy patients, leading him to speculate that these species may play a role in some diarrheal disease (68). Their true role, however, remains unsubstantiated.

P. mirabilis has been implicated in bacteremia (3, 106), neonatal meningoencephalitis (39), empyema (49), and osteomyelitis (63). *P. penneri* has been implicated in a case of bacteremia and concomitant subcutaneous thigh abscess in a neutropenic patient with acute lymphocytic leukemia (23) and in nosocomial urosepsis in a diabetic patient from whom the organism was also subsequently isolated from bronchoalveolar lavage fluid and a pulmonary artery catheter tip (60). The urease enzyme of *P. penneri* is also believed to be a leading cause of kidney stone formation (40); indeed, the organism has been isolated from the center of a stone removed from a patient with persistent *P. penneri* bacteriuria (57). *P. penneri* has also been isolated from stool and infected conjunctiva.

Nosocomial transmission, while uncommon, has been reported. In 1983, Williams et al. reported on five patients in a cardiac surgery unit with septicemia caused by either *P. mirabilis*, *Morganella morganii*, or both organisms (109). No environmental source was identified, although O serotyping confirmed cross-infection of patients by both species. Other reports have included an outbreak of neonatal meningoencephalitis (92), infections in a hospital newborn nursery traced to a single nurse (12), and an outbreak in a surgical intensive care unit spread either by autoinfection or gastrointestinal colonization prior to cross-infection (16). In a review of 27 cases in Toronto, Canada, in 1987, Krajden et al. reported the isolation of *P. penneri* from urine, abdominal, neck, groin, and hip wounds, conjunctiva, sacral decubitus, and sputum (58). All of these infections were hospital-acquired infections. The report by Burke et al. also reviewed other cases where *P. mirabilis* was incriminated as the cause of hospital-acquired infections (12).

In a very unusual case reported by Engstrand et al., a patient with *P. mirabilis* bacteremia was shown to have contaminated a unit of platelet concentrate (24). This is in direct contrast to the chain of events which normally occurs in which blood or platelet concentrate is contaminated and the patient suffers a transfusion-transmitted bacteremia. Arbitrarily primed PCR typing was used to confirm identical patterns in strains from both the patient and the platelet concentrate.

In the last 10 years, there has been a report in the literature to suggest that *P. mirabilis* may play an etiopathogenic role in rheumatoid arthritis (110). This study showed that patients with rheumatoid arthritis have higher levels of urinary *Proteus* than do comparable healthy controls of either sex or women with non-rheumatoid-arthritis arthritic conditions, findings which are disputed by another group (63b), perhaps due to a difference in the methods used in their studies.

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TABLE 6. Differentiation of *Proteus* species[a]

Test	% Positive at 48 h[b] for:				
	P. mirabilis	*P. myxofaciens*[c]	*P. penneri*	*P. vulgaris*	
				Biogroup 2	Biogroup 3[d]
Indole production	**2**	**0**	**0**	**100**	**100**
Methyl red	97	100	100	86	100
Voges-Proskauer	**50**	**100**	**0**	**0**	**0**
Citrate, Simmons'	65	100	0	29	0
Hydrogen sulfide (on TSI[e] agar)	**98**	**0**	**30**	**57**	**83**
Urea, Christensen	98	100	100	86	100
Phenylalanine deaminase	98	100	99	100	100
Lysine decarboxylase	0	0	0	0	0
Arginine dihydrolase	0	0	0	0	0
Ornithine decarboxylase	**99**	**0**	**0**	**0**	**0**
Motility (36°C)	95	100	85	57	97
Gelatin hydrolysis (22°C)	90	100	50	57	100
Growth in KCN	98	100	99	99	97
Malonate utilization	2	0	0	0	0
D-Glucose					
Acid production	100	100	100	100	100
Gas production	96	100	45	86	81
Acid production from:					
D-Adonitol	0	0	0	0	0
L-Arabinose	0	0	0	0	0
D-Arabitol	0	0	0	0	0
Cellobiose	1	0	0	0	0
Dulcitol	0	0	0	0	0
Erythritol	0	0	0	0	0
Glycerol	70	100	40	29	0
i(*myo*)-Inositol	0	0	0	0	0
Lactose	2	0	1	0	0
Maltose	**0**	**100**	**96**	**100**	**100**
D-Mannitol	0	0	0	0	0
D-Mannose	0	0	0	0	0
Melibiose	0	0	0	0	0
α-Methyl-D-glucoside	0	100	80	86	14
Raffinose	1	0	9	0	0
L-Rhamnose	1	0	0	0	17
Salicin	**0**	**0**	**0**	**100**	**3**
D-Sorbitol	0	0	0	0	0
Sucrose	**15**	**100**	**100**	**100**	**100**
Trehalose	98	100	62	0	14
D-Xylose	**98**	**0**	**100**	**100**	**100**
Mucate, acid production	0	0	0	0	0
Tartrate, Jordan's	87	100	89	14	94
Esculin hydrolysis	**0**	**0**	**0**	**100**	**3**
Acetate utilization	20	0	12	14	11
Lipase (corn oil)	92	100	35	14	91
DNase (25°C)	50	0	12	100	81
$No_3^- \rightarrow NO_2^-$	95	100	80	57	97
ONPG[f]	0	0	10	0	0
Tyrosine clearing	91	0	100	100	100

[a] Data from O'Hara et al. (71).
[b] Key reactions for differentiation of the five species are shown in bold.
[c] Only one strain of *P. myxofaciens* studied.
[d] *P. vulgaris* biogroup 3 has been characterized by DNA-DNA hybridization into four genomospecies. Genomospecies 3 is being named *Proteus hauseri*; genomospecies 4 to 6 will remain unnamed because they are difficult to separate phenotypically (71).
[e] TSI, triple sugar iron.
[f] δ-Nitrophenyl-D-galactopyranoside.

Antimicrobial Susceptibility

The indole-negative *P. mirabilis* strains are generally more susceptible to antimicrobials than are *P. vulgaris*, *P. penneri*, and *P. hauseri*. *P. mirabilis* has intrinsic resistance to nitrofurantoin and tetracycline but is generally susceptible to the amino- and ureido-penicillins (ampicillin, amoxicillin, and piperacillin), cephalosporins (cefazolin, cefoxitin, cefuroxime, cefotaxime, ceftazidime, ceftriaxone, ceftizoxime, and cefepime), aminoglycosides (amikacin, gentamicin, and tobramycin), imipenem, ciprofloxacin, and trimethoprim-sulfamethoxazole (34, 82, 101, 112). However, high levels of ciprofloxacin resistance have been reported for *P. mirabilis* and *Providencia* spp. in hospitals where use of this agent is unrestricted (100). The intrinsic resistance to tetracycline can be used as an identification marker for this organism.

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TABLE 7. Database entries of *Proteus*, *Providencia*, and *Morganella* for human isolates[a]

Species	API 20E v. 10.1	BBL Crystal v. 3.0	RapID onE v. 1.93	Vitek		MicroScan		Biolog v. 3.5	Midi v. 3.9
				GNI v. R 6.01	GNI+ v. R 6.01	Conv. v. 22.26	Rapid v. 22.26		
Morganella morganii	×[b]	×	×	×	×	×	×	×	×
Proteus mirabilis	×	×	×	×	×	×	×	×	×
Proteus penneri	×	×	×	×/vulgaris[c]	×/vulgaris	×	×	×/vulgaris	×
Proteus vulgaris	×	×	× (2 grp)	×/penneri[c]	×/penneri	×	×	×/penneri	×
Providencia alcalifaciens	×	×	×	×	×	×	×	×	×
Providencia rettgeri	×	×	×	×	×	×	×	×	×
Providencia rustigianii		×	×			×	×	×	×
Providencia stuartii	×	×	×	×	×	×[d]	×	×	×

[a] Updated from reference 65. v. refers to the software version.
[b] ×, in the database.
[c] ×/vulgaris and ×/penneri indicate that an additional off-line test is necessary to separate these two species.
[d] Will also detect *P. stuartii* urea positive.

In 1979, Chow et al. reported an outbreak of *P. mirabilis* that was resistant to ampicillin, cephalothin, tetracycline, chloramphenicol, carbenicillin, colistin, trimethoprim-sulfamethoxazole, streptomycin, and the aminoglycosides (16). An outbreak of *P. mirabilis* that was resistant to both gentamicin and the antiseptic chlorhexidine, as well as seven other antimicrobial agents, was reported as the cause of urinary tract infections in 90 patients in England in 1987 (21). The source of the outbreak was linked to the introduction of a catheter care policy involving chlorhexidine.

In an unusual outbreak in a hospital nursery, the strain of *P. mirabilis* that was responsible for bacteremias and meningitis in newborns was tetracycline susceptible. This very unusual antimicrobial pattern was used as a marker to trace the epidemiology (12).

P. penneri is generally more resistant to penicillin than is *P. vulgaris*, and its susceptibility pattern more closely reflects that of *M. morganii* than that of *P. vulgaris*. These *Proteeae* are generally susceptible to cefoxitin, broad-spectrum cephalosporins (cefotaxime, ceftriaxone, ceftizoxime, and ceftazidime), cefepime, aztreonam, aminoglycosides, ciprofloxacin, tazobactam, and imipenem (34, 112) and may be resistant to cefazolin, cefprozil, cefuroxime, cefamandol, cefdinir, cefoperazone, loracarbef, ampicillin, and the ureidopenicillins (5).

In a 1996 study, Fuchs et al. reported that the discrepancy between disk diffusion testing and broth microdilution testing for *P. vulgaris* was noteworthy (34). In that study, 100% of 25 *P. vulgaris* isolates were susceptible to four broad-spectrum cephalosporins by disk diffusion but only 64 and 40% were susceptible to cefotaxime and ceftriaxone, respectively, by broth microdilution. Laboratorians should be aware of this possible discrepancy in testing and should evaluate the results conservatively.

THE GENUS *PROVIDENCIA*

Current Classification

The genus *Providencia* consists of five species: *P. alcalifaciens*, *P. heimbachae*, *P. rettgeri*, *P. rustigianii*, and *P. stuartii*.

In 1904, Rettger isolated a previously undescribed organism from chickens during an epidemic resembling fowl cholera, but he did not submit the isolate to detailed study until 14 years later, when it was further characterized and named *Bacterium rettgerei* by Hadley et al. (Table 2) (41).

In 1920, Ornstein described an organism that he named *Bacillus inconstans* (75). This strain was isolated from the human intestine and would later be determined to be the first description of a strain of the genus *Providencia*. Over the years, many literature references, including Shaw and Clarke (88), have cited Ornstein's work as having been published in 1921. However, the original publication, as well as the 1921 edition of *Index Medicus* (36), has revealed that this work was actually published in 1920.

In 1941, Rustigian and Stuart studied a strain designated 33111 and learned that it attacked urea readily (83). The next year, Cope and Kilander published a study on a group of 83 "atypical" organisms that were biochemically similar to "*Shigella paradysenteriae*" Flexner but were antigenically distinct from the well-recognized types of *Shigella* (17). In 1943, Stuart et al., in a collaboration with Cope, realized that both of their laboratories were studying the same organism, whose strains then numbered 48, and that those organisms were clearly members of the genus *Proteus* (98). These strains were positive for both urea and indole, as were the strains of *Shigella rettgeri* studied by St. John-Brooks 20 years earlier (97). Neter in 1942 had already suggested that "*S. rettgeri*" be eliminated from the genus *Shigella* (70), a suggestion that now had sufficient justification. Rustigian and Stuart recommended that these strains be redescribed as *Proteus rettgeri*, even though, unlike other *Proteeae*, they were positive for D-mannitol fermentation (84).

Changes were also taking place in the classification of a similar group of organisms being referred to as "anaerogenic paracolon 29911" (98). In 1943, Stuart had initially studied 23 of these strains, which were not *Proteeae* because there were no homologous reactions with *Proteus* antisera. The following year, Gomes described "*Eberthella alcalifaciens*" (38), which would later become the type species of *Providencia*. In 1951, Kauffmann designated the anaerogenic paracolon 29911 strains of Stuart (1943) as the Providence group because Stuart worked at Brown University in Providence, R.I. (53). Kauffmann showed that the only reliable difference between these Providence strains and those in the genus *Proteus* was the inability of the Providence strains to decompose urea. An additional 35 strains of the Providence group isolated from urine specimens were described by Brooke in 1951 (11). By 1952, Kauffmann and Edwards had assigned the genus *Providencia* to this group, with the species being *providenciae* (56).

The years 1952 to 1962 saw a lot of taxonomic instability involving this genus. In another proposal in 1953, Kauffmann created a separate genus for *Proteus rettgeri* that was called "*Rettgerella*" (54). He reversed this opinion in 1954 (55).

In 1954, Singer and Bar-Chay suggested (92) and Buttiaux et al. proposed (13) that the Providence group of Stuart be placed into the genus *Proteus* as *Proteus stuartii*, because their physi-

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ological characteristic of smell as well as their biochemical characteristics were so similar to those of *Proteus rettgeri*. Singer also established that transformation of phenylalanine into phenylpyruvic acid was a valuable differential test for the separation of the *Proteus*-Providence group, which are positive in this test, from other members of the *Enterobacteriaceae*, all of which were thought at this time to be negative in this test.

Ewing et al., also in 1954, further subdivided the Providence group into two biochemical groups designated 1 and 2 based on the production of gas from glucose as well as the fermentation patterns in adonitol and inositol (28). They also reported that the Providence strains appeared to be an intermediate group between *Proteus morganii* and *Proteus rettgeri* but differed from the *Proteus* species based on their failure to utilize urea.

During 1955, Shaw and Clarke, utilizing additional biochemical tests, were able to reinforce the relationship of the Providence group of cultures to those within the genus *Proteus*. They wrote that the first reported description of a Providence culture appeared to be that of "*Bacillus inconstans*" Ornstein 1920, so that the type species of the Providence isolates should actually be *Proteus inconstans* (88). In the same journal that month, Proom made a valid argument against including both the Providence group and strains of *P. rettgeri* in the genus *Proteus* since several of their biochemical characteristics were dissimilar from those of other members of the genus. His alternative was to establish a new genus to include the Providence group and *Proteus rettgeri* isolates (79).

In what might be considered landmark papers in 1958 and 1962, Ewing reviewed the taxonomy of the *Proteeae* (25, 26). He agreed that the Providence group could not be incorporated into the genus *Proteus* and stated that the correct generic term for the Providence group should be *Providencia* and the proper species name would be *Providencia inconstans*. However, he further contended that there was insufficient evidence to either exclude *Proteus rettgeri* from the genus *Proteus* or create this new genus to contain only the Providence group and *Proteus rettgeri*. He also proposed that the existing genus *Morganella*, first proposed in 1943 (35), might include the species *morganii*, *rettgeri*, and *inconstans*. Apparently this proposal was never acted upon by the Judicial Commission.

In the 1962 report, Ewing regarded the specific epithet "*providenciae*" as invalid, since the species was neither defined nor characterized (26). However, an original culture of *Eberthella alcalifaciens* de Salles Gomes 1944 was available that had been defined, characterized, and validly published (38). Phenotypically, *E. alcalifaciens* had been shown to closely resemble the description of the *Providencia* strains. Ewing was satisfied that the phenotypic characteristics were similar enough to recommend that the type species for *Providencia* should be *Providencia alcalifaciens*. As a result of continued work, *Providencia* subgroups A and B of Ewing could now be even more clearly divided. Subgroup A became *P. alcalifaciens*, and subgroup B became *P. stuartii* (26). Ten years later, in 1972, Ewing et al. delineated four biogroups of *P. alcalifaciens* and two biogroups of *P. stuartii* based on the production of gas from glucose and the production of acid from adonitol and inositol (27).

The ability of *Proteus rettgeri* to produce acid from salicin, L-rhamnose, D-mannitol, adonitol, D-arabitol, and erythritol formed the basis used by Penner et al. in 1975 to divide these strains into five biogroups (77). Two years later, Farmer et al. (30) proposed that *P. rettgeri* biogroup 5 be reclassified as *Providencia stuartii* urea positive.

In a 1978 study, Brenner et al. reclassified several organisms based on DNA-DNA hybridization (9). *Proteus rettgeri* became *Providencia rettgeri*, and the assignment of *Proteus rettgeri* biogroup 5 to the genus *Providencia* as *P. stuartii* was confirmed.

DNA hybridization in 1983 resulted in *P. alcalifaciens* biogroup 3 being named *Providencia rustigianii* to honor Robert Rustigian, who did early studies on the *Proteus* group (48). This report also confirmed that *P. alcalifaciens* biogroup 4 was the same as *P. stuartii*. The four species of *Providencia* could now be separated by their ability to hydrolyze urea and produce acid from *i*-inositol, adonitol, D-arabitol, trehalose, and D-galactose. Later that same year, Müller, working independently in Germany, published a report describing *Providencia friedericiana*, which was isolated from fecal specimens of five varieties of penguins (67). Three years later, DNA hybridization studies would prove that *P. friedericiana* and *P. rustigianii* were identical, and the name *P. rustigianii* would be given priority over *P. friedericiana* because it was published and validated first (47). Coincidentally, in 1986, Müller et al. described another new species, *Providencia heimbachae*, also isolated from the feces of penguins (69). This specific name was selected to honor Friederike Heimbach, who isolated 12 of the original strains.

In 1987, Owen et al. confirmed the G+C content of the type strains of *Providencia* and reported that the genus had a narrow and homogenous range of 39 to 43 mol% (76). Table 5 lists the respective type strains for the *Providencia* genera.

16S rRNA Classification

To date, no sequencing of the 16S rRNA genes of *Providencia* has been reported or deposited.

Phenotypic Identification of the Species

Conventional methods. As with the genus *Proteus*, members of the genus *Providencia* are positive in tests for phenylalanine deaminase. They are negative in tests for lysine and ornithine decarboxylase and arginine dihydrolase, and they produce acid from D-mannose (Table 4). With the identification of *P. heimbachae* as a fifth species in the genus, additional phenotypic tests were necessary to separate the five species (Table 8).

Fischer et al. successfully employed L-glutamic acid decarboxylase to differentiate between *P. rettgeri* and *P. stuartii* (33), but the method is very cumbersome, making it unappealing to clinical laboratories. The production of acid from trehalose or D-arabitol will generally separate the two species. Also, 75% of *P. rettgeri* species will produce acid from erythritol. *P. rettgeri* is the only species of the *Proteeae* that will produce this positive reaction.

Commercial methods. The commercial identification products currently available do not include *P. heimbachae* in their databases (Table 7). Until recently, with the discovery of an isolate from feces, this organism had not been reported as having been isolated from a human specimen (72). Accuracy rates for commercial products range from 79% (100% to genus level) for the API 20E system (107) to 100% for the Vitek GNI and GNI+ cards (73, 74). Bourbeau and Heiter also reported 100% accuracy with both the GNI and the GNI+ card (8). Studies involving the Crystal ID-E/NF panel report accuracies of 83% (74) and 100% (107) using 35 and 14 strains, respectively. The MicroScan Rapid Neg ID3 panel can be expected to accurately identify 100% of the test strains (2).

Clinical Significance

Human isolates of *Providencia* species have been recovered from urine, throat, perineum, axilla, stool, blood, and wound specimens. *P. heimbachae* and *P. rustigianii* have also been isolated from penguins (48, 69).

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TABLE 8. Differentiation of *Providencia* species[a]

Test	% Positive at 48 h[b] for:				
	P. alcalifaciens	*P. heimbachae*	*P. rettgeri*	*P. rustigianii*	*P. stuartii*
Indole production	**99**	**0**	**99**	**98**	**98**
Methyl red	99	85	93	65	100
Voges-Proskauer	0	0	0	0	0
Citrate, Simmons'	**98**	**0**	**95**	**15**	**93**
Hydrogen sulfide (on TSI[d] agar)	0	0	0	0	0
Urea, Christensen	**0**	**0**	**98**	**0**	**30**
Phenylalanine deaminase	98	100	98	100	95
Lysine decarboxylase	0	0	0	0	0
Arginine dihydrolase	0	0	0	0	0
Ornithine decarboxylase	1	0	0	0	0
Motility (36°C)	96	46	94	30	85
Gelatin hydrolysis (22°C)	0	0	0	0	0
Growth in KCN	**100**	**8**	**97**	**100**	**100**
Malonate utilization	0	0	0	0	0
D-Glucose					
Acid production	100	100	100	100	100
Gas production	85[c]	0	10	35	0
Acid production from:					
D-Adonitol	**98**	**92**	**100**	**0**	**5**
L-Arabinose	1	0	0	0	1
D-Arabitol	**0**	**92**	**100**	**0**	**0**
Cellobiose	0	0	3	0	5
Dulcitol	0	0	0	0	0
Erythritol	**0**	**0**	**75**	**0**	**0**
Glycerol	15	0	60	5	50
i(*myo*)-Inositol	**1**	**46**	**90**	**0**	**95**
Lactose	0	0	5	0	2
Maltose	1	54	2	0	1
D-Mannitol	**2**	**0**	**100**	**0**	**10**
D-Mannose	100	100	100	100	100
Melibiose	0	0	5	0	0
α-Methyl-D-glucoside	0	0	2	0	0
Raffinose	1	0	5	0	7
L-Rhamnose	**0**	**100**	**70**	**0**	**0**
Salicin	1	0	50	0	2
D-Sorbitol	1	0	1	0	1
Sucrose	15	0	15	35	50
Trehalose	**2**	**0**	**0**	**0**	**98**
D-Xylose	1	8	10	0	7
Mucate, acid production	0	0	0	0	0
Tartrate, Jordan's	90	69	95	50	90
Esculin hydrolysis	0	0	35	0	0
Acetate utilization	40	0	60	25	75
Lipase (corn oil)	0	0	0	0	0
DNase (25°C)	0	0	0	0	10
$NO_3^- \rightarrow NO_2^-$	100	100	100	100	100
ONPG[e]	1	0	5	0	10
Tyrosine clearing	100	100	95	100	98

[a] Data from reference 28a.
[b] Key reactions for differentiation of the five species are shown in bold.
[c] *P. alcalifaciens* biogroup 1 produces gas from glucose fermentation; biogroup 2 does not.
[d] TSI, triple sugar iron.
[e] δ-Nitrophenyl-D-galactopyranoside.

When Gomes first described *Eberthella* (now *Providencia*) *alcalifaciens* in 1944, the strain with which he worked was isolated from an 11-month-old child with dysentery (38). Haynes and Hawkey found a higher incidence of *P. alcalifaciens* in patients with diarrhea than in healthy patients and suggested that this organism may be a cause of diarrhea, particularly in children (44). Albert et al. have shown that *P. alcalifaciens* is capable of invading HEp-2 monolayers in rabbits, but the relevance to human disease is not clear (1).

P. stuartii has long been recognized as a pathogen for nursing home patients with chronic indwelling urinary catheters. A total of 21 to 61% of urinary tract specimens in this population contain either *P. mirabilis* or *P. stuartii*, and the organisms may even result in a fatal bacteremia (105).

There have been rare incidents of *P. rettgeri* causing nosocomial infections. Traub et al. reported an outbreak of urinary tract infections caused by a highly resistant lactose-fermenting strain of *P. rettgeri* (102). While the organism was easily traceable because of this unusual biochemical characteristic, no common source of the outbreak was discovered. In a similar report, 10 patients had urinary tract infections caused by a highly resistant strain of *P. rettgeri*, and one death was believed to have been caused by these infections (22). The spread of infection was probably by contact with hospital personnel; the

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outbreak ended after the use of disposable gloves and contact isolation procedures were implemented. Other similar problems have been reported in the literature (61).

Antimicrobial Susceptibility

P. rettgeri and *P. stuartii* are generally resistant to gentamicin and tobramycin but susceptible to amikacin. Urine isolates are susceptible to the expanded-spectrum oral cephalosporins, including cefaclor, cefuroxime, cefetamet, cefpodoxime, ciprofloxacin, and amoxicillin-clavulanic acid (18). *Providencia* spp. are also susceptible to thienamycin, ceftazidime, cefotaxime, ceftizoxime, and moxalactam. Alternative choices for antimicrobial therapy would include ceftriaxone, mezlocillin, imipenem, and trimethoprim-sulfamethoxazole (94).

In a continuous monitoring study of imipenem and ciprofloxacin use with nonfastidious clinical isolates, Fass et al. reported that the susceptibility of *P. stuartii* to ciprofloxacin decreased from 100 to 46% over a 6-year period in their institution, illustrating the potential for emerging resistance in this group and the need for routine susceptibility tests (31). Virtually all *Morganella* spp., *Proteus vulgaris*, *Proteus penneri*, and *Providencia* strains are capable of producing inducible β-lactamases that will hydrolyze primary and extended-spectrum penicillins and cephalosporins (99). For these reasons, the susceptibility of *Providencia* isolates needs to be monitored and specialized testing may be required.

A hospital-acquired outbreak of multiply resistant *P. rettgeri* occurred in 1976 and involved 127 patients over a 22-month period in Tennessee (52). These strains were resistant by disk diffusion to 15 antimicrobials and by broth microdilution to 3 antimicrobials. Exposure to multiple antimicrobials coupled with simultaneous gentamicin administration, polymyxin-neomycin bladder irrigation, or indwelling urinary tract devices predisposed the patients to infections with resistant strains.

THE GENUS *MORGANELLA*

Current Classification

The genus *Morganella* currently consists of one species, *Morganella morganii*, with two subspecies, *morganii* and *sibonii*.

During 1905, Castellani described a bacterium that he isolated from a human case of "fever" similar to typhoid fever. In 1914, he studied this isolate plus two additional identical strains. He called these "*Bacterium columbense*" after Colombo, the city in Ceylon where he worked, and noted that they were probably neither the paracolon nor paratyphosus D bacteria reported by other workers (Table 3) (14). Many years later, these strains would be classified by Fulton into the genus *Morganella* (35).

In 1906, while studying the etiology of summer infantile diarrhea, Morgan described a non-lactose-fermenting organism that was completely different from the Flexner type of "*Bacillus dysenteriae*" that was implicated as the cause of the pediatric disease then occurring in the Phillipines, Germany, and the United States (66). This organism was to become known as Morgan's bacillus and in 1919 would be named "*Bacillus morganii*" by Winslow et al. (111). It was positive in tests for indole production and the fermentation of carbohydrates but negative for the liquefaction of gelatin.

Seventeen years after Winslow had named Morgan's bacillus "*Bacillus morganii*," Rauss performed more extensive experiments on this group of bacteria (80). His work showed that these strains exhibited a spreading phenomenon, which he called emanation, and although it was less marked than that exhibited by *Proteus*, it made these strains, in his mind, definitely part of the *Proteus* group. Indeed, in the fifth edition of *Bergey's Manual of Determinative Bacteriology*, published in 1939, this organism was called *Proteus morganii* (4).

A major development that occurred in 1943 was the work by Fulton, which showed that "*Bacterium columbense*"Castellani 1914 was actually the same organism as *Proteus morganii* Winslow 1919. He proposed the genus name *Morganella* for these strains, which were negative for the fermentation of lactose or sucrose but produced indole (35). The type species would be *M. morganii* Morgan 1906, with an additional species, "*M. columbensis*."

In a review article in 1962, Ewing reported that the isolate of "*Bacterium columbense*" Castellani had been reidentified as *Escherichia coli* (26), thus negating this organism from the genus *Morganella* in which it had been placed by Fulton in 1943. This deletion would have resulted in *M. morganii* being the only species remaining in the valid genus *Morganella*. Therefore, the species *morganii* was relegated to the genus *Proteus* for another 16 years.

Since 1976, it has been known that trehalose fermentation could divide the genus into more than one biogroup (89). Studies by Hickman et al. in 1980 suggested that positive lysine and ornithine decarboxylase reactions correlated with additional divisions with the genus (45). In their 1978 study, Brenner et al. confirmed the assignment of *P. morganii* to the genus *Morganella* based on DNA-DNA hybridization (9). In 1985, Farmer et al. proposed that the nonmotile members of Hickman's lysine-positive group be designated *M. morganii* biogroup 1 (29).

In an extensive study of these groups in 1992, also based on DNA hybridization, Jensen et al. defined two subspecies containing four and three biogroups, as shown in Table 8 (50). *M. morganii* subsp. *morganii* contains four biogroups. Biogroup A contains the type strain of the species (ATCC 25830). Biogroup B is the previous biogroup 1 of Farmer.

The type strains for the two subspecies of *Morganella* are listed in Table 5.

16S rRNA Classification

To date, no sequencing of the 16S rRNA genes of the genus *Morganella* has been performed.

Phenotypic Identification of the Species

Conventional methods. *M. morganii* subsp. *morganii* is separated from *M. morganii* subsp. *sibonii* based almost entirely on its negative reaction for the fermentation of trehalose (Table 9). Within biogroups A, B, C, and D, separation is based on reactions with lysine and ornithine decarboxylases.

M. morganii subsp. *sibonii* contains three biogroups. Separation within biogroups E, F, and G is based on reactions with lysine and ornithine decarboxylases, production of indole, and growth in the presence of KCN.

Additional studies by Janda et al. using 73 strains from 14 clinical laboratories and 1 reference laboratory confirmed the relationship between rapid glycerol fermentation and nonmotility and showed that biogroup A was the predominant strain isolated in clinical laboratories (49a). The study also showed the inability of *Morganella* strains to invade either HEp-2 or Vero cell lines.

Commercial methods. *M. morganii* subsp. *morganii* is contained in the databases of the major identification systems, both manual and automated (Table 7). At present, *M. morganii* subsp. *sibonii* is not contained in any identification database.

The accuracy of identification in these systems is usually

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TABLE 9. Differentiation of *Morganella morganii* subspecies and biogroups[a]

Test	% of hybridized strains positive at 48 h for[b]:						
	M. morganii subsp. *morganii* biogroup				*M. morganii* subsp. *sibonii* biogroup		
	A[c]	B[d]	C	D	E	F	G
Indole production	**100**	**100**	**100**	**100**	**100**	**75**	**56**
Methyl red	100	95	100	100	100	75	89
Voges-Proskauer	0	0	0	0	0	0	0
Citrate, Simmons'	0	0	0	0	0	0	0
Hydrogen sulfide (on TSI[e] agar)	0	15	25	0	0	0	22
Urea, Christensen	100	96	100	100	100	100	100
Phenylalanine deaminase	100	96	100	100	100	100	100
Lysine decarboxylase	**0**	**100**	**0**	**100**	**100**	**75**	**0**
Arginine dihydrolase	0	0	0	0	0	0	0
Ornithine decarboxylase	**100**	**80**	**0**	**0**	**100**	**0**	**89**
Motility (36°C)	0	0	50	0	100	75	89
Gelatin hydrolysis (22°C)	0	0	0	0	0	0	0
Growth in KCN	**100**	**80**	**100**	**100**	**100**	**100**	**67**
Malonate utilization	0	5	0	0	0	0	0
D-Glucose							
Acid production	100	100	100	100	100	100	89
Gas production	100	88	100	100	100	75	78
Acid production from:							
D-Adonitol	0	0	0	0	0	0	0
L-Arabinose	0	0	0	0	0	0	0
D-Arabitol	0	0	0	0	0	0	0
Cellobiose	0	0	0	0	0	0	0
Dulcitol	0	0	0	0	0	0	0
Erythritol	0	0	0	0	0	0	0
Glycerol	50	100	50	100	0	0	0
i(*myo*)-Inositol	0	0	0	0	0	0	0
Lactose	0	0	0	0	0	0	0
Maltose	0	0	0	0	0	0	0
D-Mannitol	0	0	0	0	0	0	0
D-Mannose	100	92	100	100	100	100	89
Melibiose	0	0	0	0	0	0	0
α-Methyl-D-glucoside	0	0	0	0	0	0	0
Raffinose	0	0	0	0	0	0	0
L-Rhamnose	0	0	0	0	0	0	0
Salicin	0	0	0	0	0	0	0
D-Sorbitol	0	0	0	0	0	0	0
Sucrose	0	0	0	0	0	0	11
Rehalose	**0**	**0**	**0**	**0**	**100**	**100**	**100**
D-Xylose	0	0	0	0	0	0	0
Mucate, acid production	0	0	0	0	0	0	0
Tartrate, Jordan's	50	96	100	100	100	100	100
Esculin hydrolysis	0	0	0	0	0	0	0
Acetate utilization	0	0	0	0	0	0	0
Lipase (corn oil)	0	0	0	0	0	0	0
DNase (25°C)	0	0	0	0	0	0	0
$NO_3^- \rightarrow NO_2^-$	100	84	100	33	100	100	100
ONPG[f]	50	15	75	33	0	0	0
Tyrosine clearing	100	89	100	100	100	100	88

[a] Modified from reference 50.
[b] Key reactions for the differentiation of subspecies and biogroups are shown in bold.
[c] Includes type strain ATCC 25380.
[d] Formerly biogroup 1.
[e] TSI, triple sugar iron.
[f] δ-Nitrophenyl-D-galactopyranoside.

100% (8, 73, 74, 81, 107, 113). The only product that contains trehalose is the ID32E (bioMérieux, Inc., Marcy l'Etoile, France), but *M. morganii* subsp. *sibonii* is not in its database.

Clinical Significance

M. morganii is an opportunistic secondary invader that was originally thought to be the cause of summer diarrhea (66). In 1986, Müller isolated *M. morganii* significantly more often from patients with gastrointestinal disease than from healthy controls (68). Case reports implicating this organism as a cause of disease, although rare, are scattered throughout the literature. For example, *M. morganii* has caused neonatal sepsis in an 11-day-old boy (85), a brain abscess in a neonate (104a), and a tubo-ovarian abscess (originally mistaken for vasculitis attributed to Henoch-Schonlein purpura) in a 15-year-old girl (78). Reports involving *M. morganii* infections in immunocompromised individuals include chorioamnionitis and neonatal sei-

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zures in a pregnant woman (51), a postoperative foot infection in a diabetic (37), and pyomyositis (1a) and meningitis (63a) in AIDS patients. Schonwetter and Orson also described a case of atypical pyoarthritis due to *M. morganii* in an elderly patient (86). This case was atypical in that it had a very benign clinical presentation with minimal inflammatory response over a prolonged period. Sica et al. reported a patient with acute lymphoblastic leukemia who underwent a resolvent splenectomy for immune pancytopenia following an allogeneic bone marrow transplant (90). The patient developed pericarditis, from which *M. morganii* was isolated. The authors conclude that splenectomy could have been a predisposing factor for the development of this unusual complication.

One report of nosocomial infections with *M. morganii* involved three cases of septicemia in a cardiac surgery unit, for which no common source was discovered. Two of the three cases patients a polymicrobic infection including *P. mirabilis*. Two of the three cases were fatal (109). Another report described 13 *M. morganii* infections scattered over four services and five floors of a hospital; this outbreak was eventually resolved when strict aseptic techniques, i.e., hand washing, were reinforced (104).

Additional human sources from which the organism has been isolated include urine, gallbladder, stool, sputum and other respiratory samples, and assorted wound sites.

Antimicrobial Susceptibility

M. morganii is susceptible to many of the currently used antimicrobial agents, including ceftazidime, cefepime, aztreonam, imipenem, tazobactam, ciprofloxacin, tobramycin, and gentamicin. Strains are often resistant to the newer cephalosporins, including cefprozil, cefuroxime, loracarbef, cefdinir, and cefetamet (7). They can also be resistant to cefazolin, cefixime, cefpodoxime, and ampicillin.

As with strains of *Providencia* spp., *Morganella* spp. are capable of producing β-lactamases. When automated susceptibility testing is performed on these organisms, a 3- to 6-h time frame may not be adequate for expression of all of the bacterial resistance mechanisms and could result in a report of false susceptibility (32). False resistance also may occur in testing with aztreonam because elongation of cells just before lysis can be interpreted by the instrument as growth (6). York et al. reported on the inability of the MicroScan Walk/Away rapid susceptibility panels to detect resistance to expanded- and broad-spectrum cephalosporins with some *Morganella* and indole-positive *Proteus* isolates (113). Laboratorians must monitor susceptibility results involving these antimicrobials when using commercial systems.

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