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Allison R. McMullen
Washington University School of Medicine in St. Louis

Neil Anderson
Washington University School of Medicine in St. Louis

Meghan A. Wallace
Washington University School of Medicine in St. Louis

Angela Shupe
Washington University School of Medicine in St. Louis

Carey-Ann D. Burnham
Washington University School of Medicine in St. Louis

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When Good Bugs Go Bad: Epidemiology and Antimicrobial Resistance Profiles of *Corynebacterium striatum*, an Emerging Multidrug-Resistant, Opportunistic Pathogen

Allison R. McMullen,* Neil Anderson, Meghan A. Wallace, Angela Shupe, Carey-Ann D. Burnham

Department of Pathology & Immunology, Washington University in St. Louis School of Medicine, St. Louis, Missouri, USA

ABSTRACT Infections with *Corynebacterium striatum* have been described in the literature over the last 2 decades, with the majority being bacteremia, central line infections, and occasionally, endocarditis. In recent years, the frequency of *C. striatum* infections appears to be increasing; a factor likely contributing to this is the increased ease and accuracy of the identification of *Corynebacterium* spp., including *C. striatum*, from clinical cultures. The objective of this study was to retrospectively characterize *C. striatum* isolates recovered from specimens submitted as part of routine patient care at a 1,250-bed, tertiary-care academic medical center. Multiple strain types were recovered, as demonstrated by repetitive-sequence-based PCR. Most of the strains of *C. striatum* characterized were resistant to antimicrobials commonly used to treat Gram-positive organisms, such as penicillin, ceftriaxone, meropenem, clindamycin, and tetracycline. The MIC_{50} for ceftaroline was >32 μg/ml. Although there are no interpretive criteria for susceptibility with telavancin, it appeared to have potent *in vitro* efficacy against this species, with MIC_{50} and MIC_{90} values of 0.064 and 0.125 μg/ml, respectively. Finally, as previously reported in case studies, we demonstrated rapid *in vitro* development of daptomycin resistance in 100% of the isolates tested ($n = 50$), indicating that caution should be exhibited when using daptomycin for the treatment of *C. striatum* infections. *C. striatum* is an emerging, multidrug-resistant pathogen that can be associated with a variety of infection types.

KEYWORDS *Corynebacterium*, *Corynebacterium striatum*, antimicrobial agents, opportunistic infections, susceptibility testing, telavancin

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Address correspondence to Carey-Ann D. Burnham, cburnham@path.wustl.edu.

* Present address: Allison R. McMullen, Augusta University, Augusta, Georgia, USA.

A.R.M. and N.A. contributed equally to this work.

Recent advances in organism detection and identification have facilitated an improved understanding of the clinical significance of some bacterial species previously thought to be largely commensal organisms, such as the "coryneform" bacteria. While the pathogenicity of certain *Corynebacterium* spp., such as *Corynebacterium diphtheriae*, has been well established and described in the literature, non-*diphtheriae Corynebacterium* spp. are increasingly being associated with disease in immunocompetent and immunocompromised patients. A 2012 case series linked *Corynebacterium* spp. to significant respiratory disease in 27 patients, whereas a similar 2013 case series linked *Corynebacterium* spp. to respiratory disease in 10 patients (1, 2). Interestingly, while the majority of respiratory infections in each study were caused by the established respiratory pathogen *Corynebacterium pseudodiphtheriticum*, both studies found

Corynebacterium striatum to be a cause for a large proportion of infections (26% and 20%, respectively).

Several microbiome surveys have established *Corynebacterium striatum* as a common component of the skin microbiota (3–6). In addition, infections with *Corynebacterium striatum* have been described in the literature over the last 2 decades. Similar to other skin flora, the majority of the described infections have been limited to isolated bacteremia, central line infections, and occasionally, endocarditis (7–16). Over recent years, the scope of these infections has broadened to include respiratory, wound, medical hardware/devices, and even urinary tract infections (16–23). While the reasons for this increased association with multiple pathological processes may not be entirely apparent, a likely contributing factor is the increased ease and accuracy of the identification of *Corynebacterium* spp., including *C. striatum*, from clinical cultures (24, 25).

Compared to other Gram-positive skin flora, *C. striatum* is relatively resistant to antimicrobial therapy. Effective treatment usually requires aggressive source control (i.e., heart valve or central line removal) or prolonged therapy with intravenous antibiotics with broad Gram-positive activity (10, 11, 13, 14). A recent survey of over 100 *C. striatum* isolates derived from various patient specimens in a U.S. hospital over a 10-year period found resistance to many commonly used antimicrobials (23). Vancomycin was found to be the only universally active antibiotic. Isolated case reports have suggested that infections can be successfully treated with linezolid or daptomycin (10–13). However, prolonged therapy with linezolid is cost prohibitive and often complicated by neutropenia and/or drug-drug interactions. While therapy with daptomycin may have a more favorable side effect profile, the failure of prolonged daptomycin therapy has been documented in multiple case reports (16, 22). This failure of therapy has been attributed to the rapid emergence of isolates with a resistant phenotype under selective antibiotic pressure (16).

The objective of this study was to retrospectively characterize *Corynebacterium striatum* isolates from specimens submitted as part of routine patient care, including trends in antibiotic resistance. In addition, we sought to characterize the *in vitro* activity of telavancin against multidrug-resistant *C. striatum*.

RESULTS

Epidemiology. *C. striatum* isolates were reported most commonly in wound and respiratory specimens from patients ranging from 50 to 69 years of age (Table 1). The characteristics of patients with *C. striatum* recovered in clinical specimens did not differ significantly by gender from those recovered in patients with coagulase-negative staphylococci (CNS) ($P = 0.95$) or *Staphylococcus aureus* isolates ($P = 0.95$). There was a significantly higher percentage of patients in the 60- to 69-year age range with *C. striatum* than with *S. aureus* ($P = 0.02$). Compared to CNS and *S. aureus*, *C. striatum* isolates were more often isolated from wound specimens, tissue specimens, and bone specimens ($P < 0.01$). Approximately 46.1% (119/256) of the *C. striatum* isolates were from monomicrobial cultures (Table 2). The most common monomicrobial specimen sources were blood (18%), tracheal aspirates (13%), and tissue (13%). In polymicrobial cultures, *C. striatum* was accompanied by normal flora in 55% of the cultures, one other organism in 27% of the cultures, two other organisms in 10% of the cultures, and three other organisms in 3% of the cultures. Organisms commonly coisolated with *C. striatum* included *S. aureus* (36/137 [26.3%]), CNS (15/137 [10.9%]), and *Pseudomonas aeruginosa* (15/137 [10.9%]). Of the *C. striatum* isolates recovered from respiratory specimens, 75% (46/61) were from tracheal aspirates (26% monomicrobial, 49% polymicrobial) (Table 3). Of the blood isolates, 91% (21/23) were from peripheral draws.

Identification. In a comparison of the Bruker Biotyper and the Vitek MS, there was 100% agreement (85/85 isolates) for all isolates tested. Both instruments also had 100% agreement in identification for four isolates previously misclassified as *C. striatum* (*Corynebacterium tuberculostearicum*, $n = 1$ and *Corynebacterium simulans*, $n = 3$); all were previously misclassified by RapID CB Plus, except for an isolate of *C. simulans* misclassified by Bruker matrix-assisted laser desorption ionization–time of flight mass

TABLE 1 Patient characteristics for laboratory-reported *C. striatum* compared to *Staphylococcus* spp. in clinical specimens[a]

Characteristic[b]	*Corynebacterium striatum* (*n* = 256)		Coagulase-negative *Staphylococcus* (*n* = 1,537)		*Staphylococcus aureus* (*n* = 2,655)	
	No.	%	No.	%	No.	%
Sex						
Male	141	55.1	852	55.43	1,469	55.33
Female	115	44.9	685	44.57	1,186	44.67
Age (yr)						
<20	3	1.2	18	1.17	39	1.47
20–29	15	5.9	123	8.00	345	12.99
30–39	19	7.4	148	9.63	272	10.24
40–49	26	10.2	188	12.23	355	13.37
50–59	65	25.4	326	21.21	533	20.08
60–69	72	28.1	379	24.66	578	21.77
70–79	36	14.1	237	15.42	353	13.30
80–89	16	6.3	97	6.31	160	6.03
>90	4	1.6	21	1.37	20	0.75
Source						
Wound	67	26.2	180	11.71	449	16.91
Respiratory	61	23.8	3	0.20	455	17.14
Tissue (lymph node)	36	14.1	78	5.07	180	6.78
Bone	30	11.7	22	1.43	37	1.39
Blood	23	9.0	669	43.53	381	14.35
LVAD	7	2.7	5	0.33	7	0.26
Urine	3	1.2	296	19.26	141	5.31
Other, sterile[c]	14	5.5	211	13.73	348	13.11
Other, nonsterile[d]	15	5.9	73	4.75	657	24.75

[a]All isolates were isolated from clinical samples from 1 January 2013 to 31 December 2015.
[b]LVAD, left ventricular assist device.
[c]Includes aspirate, biopsy, catheter tip, cerebrospinal fluid, hardware, joint fluid, pleural fluid, peritoneal fluid, shunt, stones, synovial fluid, and valve specimens.
[d]Includes cervical, cyst, cornea, drainage, genital, lesion, ocular swab, placenta, sinus, stool, ulcer, urethra, vaginal, vesicle, and wound specimens.

spectrometry (MALDI-TOF MS) analysis at the time of initial culture. In a comparison of the MALDI-TOF MS results to RapID CB Plus results when available historically ($n = 43$), it was found that the RapID CB Plus misclassified three isolates as *C. striatum*. Of these isolates, two were *C. simulans* isolates which had colony morphologies similar to those of *C. striatum*, although they had susceptibility profiles differing from the typical *C. striatum* profile (i.e., the isolate was susceptible to all drugs tested). The other was a *C. tuberculostearicum* isolate which had a susceptibility profile similar to the typical *C. striatum* profile but had a different colony morphology. In a comparison of these three organisms morphologically, both *C. striatum* and *C. simulans* have large white colonies, whereas *C. tuberculostearicum* has small pinpoint colonies (Fig. 1).

Antimicrobial susceptibility testing. Antibiotic susceptibility breakpoints used were derived from CLSI document M45, 3rd edition (26). For most of the isolates, susceptibility testing revealed resistance to most of the drugs tested (Table 4). It was demonstrated that for cefotaxime, ceftriaxone, meropenem, ciprofloxacin, tetracycline, penicillin, and clindamycin, the MIC_{50} would be classified as resistant. Interpretive criteria are not available for ceftaroline, but the MIC_{50} and MIC_{90} were both >32 μg/ml. For vancomycin, linezolid, and daptomycin, the MIC_{50} would be classified as susceptible. The 87 isolates tested for telavancin susceptibility exhibited an MIC_{50} of 0.064 μg/ml and an MIC_{90} of 0.125 μg/ml.

Development of daptomycin resistance. Upon overnight incubation of 50 isolates with daptomycin, 100% of the isolates became nonsusceptible to the drug (Table 5). Interestingly, overnight incubation with daptomycin also had an effect on vancomycin

TABLE 2 Monomicrobial cultures with *C. striatum* by site

Specimen type[a]	No. (% total cultures)
Blood	22 (18)
Tracheal aspirate	16 (13)
Tissue	15 (13)
Wound	14 (12)
Bone	11 (9)
LVAD	7 (6)
Bronchoalveolar lavage fluid	7 (6)
Synovial fluid	6 (5)
Nonsterile site[b]	5 (4)
Peritoneal fluid	3 (3)
Pleural fluid	2 (2)
Abscess	2 (2)
Bronchial washing	1 (1)
Aspirate	1 (1)
Lung tissue (autopsy)	1 (1)
Graft	1 (1)
Urine	1 (1)
Unknown	4 (3)
Total	119

[a]LVAD, left ventricular assist device.
[b]Includes cervical, cyst, cornea, drainage, genital, lesion, ocular swab, placenta, sinus, stool, ulcer, urethra, vaginal, vesicle, and wound specimens.

and telavancin MICs. The vancomycin MIC_{50} and MIC_{90} increased from 0.38 μg/ml to 0.50 μg/ml and from 0.50 μg/ml to 0.75 μg/ml, respectively. Following incubation with daptomycin, the telavancin MIC_{50} and MIC_{90} (48-h read) dropped from 0.016 μg/ml to 0.012 μg/ml and 0.023 μg/ml to 0.016 μg/ml, respectively.

Molecular typing. For the 85 isolates available for molecular typing, there were 12 strain types detected; each strain type was given an alpha designation. The most common strain type detected was F, accounting for approximately half of the isolates (44/85 [52%]). The next most common strain type was D (10/85), and the remaining isolates were classified into 10 different strain types (Table 6). All types appeared to be equally distributed among different specimen sources. There did not appear to be any major differences between the susceptibility testing results for the different types.

DISCUSSION

Although coryneforms are commonly considered commensals of the skin and mucosal surfaces, some species are associated with specific disease manifestations. Herein, we describe the epidemiology and antimicrobial resistance profiles of the emerging multidrug-resistant pathogen *C. striatum*.

The commonality of *C. striatum* in respiratory specimens, particularly monomicrobial tracheal aspirates, supports previous studies suggesting that *C. striatum* is an emerging respiratory pathogen (1, 20, 27). The specific association with tracheal aspirates may be

TABLE 3 Comparison of monomicrobial and polymicrobial cultures with *C. striatum*

Culture source	No. of monomicrobial cultures (% of specimen type)	No. of polymicrobial cultures (% of specimen type)	Total (%)
Tracheal aspirate	16 (26)	30 (49)	46 (75)
Bronchoalveolar lavage fluid	7 (11)	4 (7)	11 (18)
Bronchial washing	1 (2)	2 (3)	3 (5)
Sputum	0 (0)	1 (2)	1 (2)
Total from respiratory cultures	24 (39)	37 (61)	61
Peripheral blood draw	20 (87)	1 (4)	21 (91)
Central line blood draw	2 (9)	0 (0)	2 (9)
Total from blood cultures	22 (96)	1 (4)	23

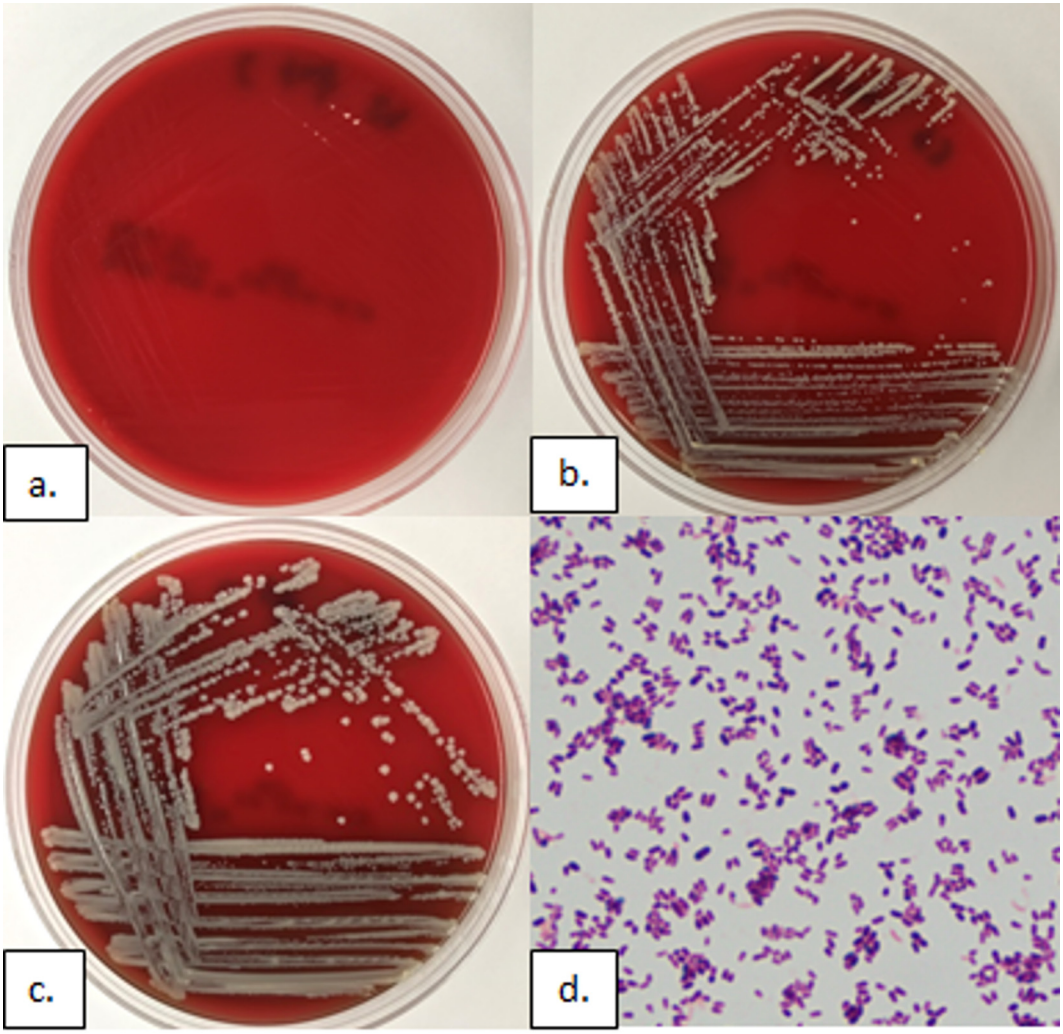

FIG 1 Morphological characteristics of *C. tuberculostearicum*, *C. simulans*, and *C. striatum*. (a) Colony morphology of *C. tuberculostearicum*. At 24 h of growth on sheep blood agar, colonies are pinpoint and barely visible. (b) Colony morphology of *C. simulans*. At 24 h of growth on sheep blood agar, colonies are large and white. (c) Colony morphology of *C. striatum*. At 24 h of growth on sheep blood agar, colonies are large and white. (d) Gram stain of *C. striatum* showing typical coryneform morphology of palisading Gram-positive bacilli.

explained by increased biofilm production allowing the organism to adhere to instruments used for endotracheal intubation, a mechanism explored by Souza et al. (20). Similar to previous studies, *C. striatum* was commonly isolated from a variety of other specimen types, including tissue, wounds, left ventricular assist devices, and blood cultures. Notably, the majority of positive blood specimens were collected from peripheral sites rather than central lines, suggesting that while *C. striatum* can cause infection of endovascular devices, this is not necessarily the only factor contributing to bacteremia. In addition, our findings demonstrate that *C. striatum* is isolated from different types of clinical specimens from those of other skin commensals, such as coagulase-negative *Staphylococcus* spp., raising the possibility that *C. striatum* may have a different predilection for wound, tissue, and bone infections from some other bacteria that are considered to be a component of normal skin flora.

In a comparison of the identification results for *C. striatum* isolates from two commercially available MALDI-TOF MS identification systems (Bruker MS and Vitek MS), we observed that the two systems perform similarly for *C. striatum* identification. In contrast, some misidentifications were observed using the RapID CB Plus phenotypic identification system. Misidentification of *C. simulans* as *C. striatum* by the RapID CB Plus

TABLE 4 Antimicrobial susceptibility profiles of *C. striatum* isolates

Antimicrobial tested	No. of isolates tested	% susceptible[a]	MIC data (μg/ml)		
			MIC_{50}	MIC_{90}	Range
Penicillin	43	16	8	32	0.25 to >256
Cefotaxime	16	0	>256	>256	>256
Ceftriaxone	124	1	>256	>256	0.25 to >256
Ceftaroline	87	NA	>32	>32	0.25 to >32
Meropenem	87	4	>32	>32	0.125 to >32
Vancomycin	207	100	1	2	0.5 to 2.0
Daptomycin	91	98	0.125	0.25	0.032 to >256
Telavancin	87	NA	0.064	0.125	0.008 to 0.125
Tetracycline	206	38	64	>256	0.064 to >256
Ciprofloxacin	203	7	>32	>32	0.032 to >32
Clindamycin	140	1	>256	>256	0.064 to >256
Linezolid	120	100	0.50	0.50	0.125 to 2.0

[a]Based on CLSI M45, 3rd edition (26). NA, no interpretative data available.

was observed in our investigation, and this has also been described previously (28). This is perhaps not surprising, since these two organisms share 98% 16S rRNA gene sequence homology and biochemically are very similar. In fact, the species name "*simulans*" is derived from the fact that this organism is "similar" to *C. striatum*. However, based on the two *C. simulans* isolates included in our study, these similarities do not extend to antibiotic resistance profiles. In sharp contrast to the broad antibiotic resistance seen in *C. striatum*, both *C. simulans* isolates included in this study were susceptible to all antibiotics tested. Although the antibiotic susceptibility pattern of *C. simulans* has not been well characterized in the literature, Cazanave et al. previously described a *C. simulans* prosthetic joint isolate that was susceptible to penicillin and vancomycin (29). Our findings suggest that laboratories relying on phenotypic identification methods should consider possible misidentification when a *C. striatum* isolate is found to be broadly susceptible to antimicrobial agents and seek an alternative identification method. Although the misidentification of *C. tuberculostearicum* as *C. striatum* by the RapID CB Plus has not been specifically described, a high rate of misidentification of *C. tuberculostearicum*, as with other *Corynebacterium* spp., has been shown by other investigators (30). Misidentifications of *C. striatum* as *C. tuberculostearicum* can be avoided by careful attention to the colony morphology, which should be large for *C. striatum* (nonlipophilic) and small for *C. tuberculostearicum* (lipophilic) (30).

Our findings describing the resistance of *C. striatum* to many of the commonly used antibiotics with Gram-positive activity are consistent with other recent surveys of *C. striatum* resistance (23, 31). Several recent studies have explored the efficacy of ceftaroline for uncommonly isolated Gram-positive organisms, including *C. striatum* (32, 33). Sader et al. examined the efficacy of ceftaroline in 19 *Corynebacterium* sp. isolated clinical specimens obtained from 2008 to 2011, of which eight were identified as *C. striatum* (32). The study found varied efficacy of ceftaroline (MIC_{50}, 0.5 μg/ml; MIC_{90}, >32 μg/ml) among the *Corynebacterium* spp., although the investigators did not

TABLE 5 Effects of 24-h daptomycin exposure on isolate susceptibility

Drug tested	Incubation with daptomycin	MIC_{50}/MIC_{90} (μg/ml)[a]				No. susceptible/ total no. (%)[b]	No. nonsusceptible/ total no. (%)[b]
		MIC_{50} at 24 h	MIC_{90} at 24 h	MIC_{50} at 48 h	MIC_{90} at 48 h		
Daptomycin	Preincubation	0.094	0.125	NP	NP	48/50 (96)	2/50 (4)
	Postincubation	>256	>256	NP	NP	0/50 (0)	50/50 (100)
Vancomycin	Preincubation	0.25	0.38	0.38	0.50	50/50 (100)	0/50 (0)
	Postincubation	0.38	0.50	0.50	0.75	50/50 (100)	0/50 (0)
Telavancin	Preincubation	0.012	0.016	0.016	0.023	NA	NA
	Postincubation	0.012	0.016	0.012	0.016	NA	NA

[a]NP, not performed.
[b]Based on CLSI M45, 3rd edition (26). NA, no interpretative data available.

TABLE 6 Distribution of repetitive-sequence PCR types of *C. striatum* isolates

REP-PCR type (*n*)[a]	No. (%) of monomicrobial isolates	Blood	Bone	Pleural fluid	Graft	Joint	LVAD[b]	Tissue	Wound	Unknown
F (44)	31 (70)	15	12	1	0	4	3	5	4	0
D (10)	5 (50)	1	2	0	0	1	1	4	1	0
I (6)	1 (17)	0	1	0	0	1	0	4	0	0
A (5)	3 (60)	1	2	0	0	0	0	1	0	1
H (4)	2 (50)	1	3	0	0	0	0	0	0	0
J (4)	3 (75)	1	1	1	0	0	0	1	0	0
C (5)	4 (80)	0	1	0	1	3	0	0	0	0
K (3)	2 (66)	0	1	0	0	0	1	0	1	0
B (1)	1 (100)	1	0	0	0	0	0	0	0	0
E (1)	0 (0)	0	0	0	0	0	0	0	1	0
G (1)	0 (0)	0	0	0	1	0	0	0	0	0
L (1)	1 (100)	1	0	0	0	0	0	0	0	0

[a]REP-PCR, repetitive-sequence PCR.
[b]LVAD, left ventricular assist device.

specifically report the susceptibility results for *C. striatum*. Another study published in 2013 by Goldstein et al. had similar results (33). Goldstein et al. examined ceftaroline efficacy in organisms isolated from diabetic foot wounds from the previous 11 years. Similar to Sader et al., these authors tested 36 *Corynebacterium* spp., of which 10 were identified as *C. striatum* and demonstrated varied activity against ceftaroline among *Corynebacterium* spp. (MIC_{50}, 0.125 μg/ml; MIC_{90}, 2 μg/ml), although they did not specifically report the activity in *C. striatum* isolates. Our findings of nearly universal resistance to ceftaroline by *C. striatum* specifically may account for the varied resistance observed when mixed populations of *Corynebacterium* spp. are tested for resistance. Our findings suggest that for *C. striatum* infection, ceftaroline is unlikely to be a viable therapeutic option. We hypothesize that this resistance is due to the modification of penicillin-binding proteins.

Our study is the first to measure *in vitro* telavancin activity against a large collection of *C. striatum* strains. While interpretive criteria do not exist for telavancin and *C. striatum*, an MIC_{90} of 0.125 μg/ml would be interpreted as susceptible for *Staphylococcus* species (34). Although additional studies are needed to substantiate the relationship between *in vitro* susceptibly data and clinical response, telavancin may represent a viable therapeutic option for infection with *C. striatum*.

The rapid emergence of daptomycin resistance is an established phenomenon for some strains of *C. striatum*; a previous publication demonstrated this phenomenon in approximately 58% (7/12) of susceptible *C. striatum* isolates (16). In our study, we found that 100% (48/48) of susceptible *C. striatum* isolates exhibited this phenotype, demonstrating that the development of daptomycin resistance is common. Furthermore, previous studies have shown that this is a stable phenotype and that these isolates can remain resistant to daptomycin following at least 10 serial passages (16). Overall, these data suggest that caution should be taken when using this drug for the treatment of *C. striatum* infections, even for those isolates that initially exhibit *in vitro* susceptibility.

Although subtle, and possibly within the margin of error for MIC testing, the phenotype of elevation in vancomycin MICs following incubation with daptomycin is intriguing and has not been previously described for *C. striatum*. However, a similar phenomenon has been described when *Staphylococcus aureus* isolates are exposed to vancomycin, resulting in a phenotype with cell wall thickening and in an elevated MIC for both vancomycin and daptomycin (35). Interestingly, we observed an opposite effect for telavancin.

Several published studies have suggested that the presence of multidrug-resistant *C. striatum* in the environment is the result of clonal spread of a specific strain. A 2009 case series from Italy examined 36 strains isolated from three hospitals over a 3-year period (9). Using pulsed-field gel electrophoresis, this group demonstrated that all isolates were from a single clone containing several genes conferring antibiotic resistance. A second 2013 study performed in Brazil examined 15 separate *C. striatum*

isolates isolated from tracheal aspirates for clonality (27). Using pulsed-field gel electrophoresis, this group showed that most multidrug-resistant isolates were related to a single clone, which may have spread due to an enhanced ability to create biofilms (20). The findings differ from those of our current study, which describe the epidemiology of *C. striatum* infection in a nonoutbreak setting. Although a dominant strain type was detected, nearly half (41/85 [48%]) of the isolates were distributed among 12 other strain types. The resistance phenotype was not unique to the dominant clone, as the majority of *C. striatum* isolates included in the analysis were multidrug resistant. Furthermore, clonality did not appear to account for any trends in type of infection or resistance profile to any specific antimicrobial agent.

Strengths of our study are its size and temporal span, facilitating the interrogation of epidemiology and antimicrobial resistance profiles. Additional strengths are the availability of comprehensive susceptibility testing data and the assessment of the potential for the development of daptomycin resistance among a large sampling of isolates. Finally, our strain typing data illustrated that these findings are not driven by an expansion of a single clone and thus may represent the characteristics of *C. striatum* in general. Our study is limited by the fact that it is a retrospective, single-center study; thus, the results may not be generalizable to other settings. Furthermore, while the included *C. striatum* isolates were reported based on site and organism predominance, their presence does not necessarily confirm pathogenicity. Finally, MIC determination was performed using only one method. Confirmation of results, especially shifts in vancomycin MICs after daptomycin exposure with a second method, would strengthen this study.

In summary, our data support the characterization of *C. striatum* as an emerging multidrug-resistant pathogen. Vancomycin, linezolid, and telavancin demonstrate good *in vitro* activity against the organism, while resistance to penicillin, cephalosporins, ciprofloxacin, meropenem, tetracycline, and clindamycin is common.

MATERIALS AND METHODS

Study overview. Following institutional review board (IRB) approval, we performed a retrospective review of 256 *C. striatum* isolates recovered from a variety of clinical specimens submitted to the microbiology laboratory of Barnes-Jewish Hospital, a 1,250-bed, tertiary-care hospital, from 2012 to 2015. All isolates were identified and reported as a part of routine patient care based on specimen source and abundance. Specifically, *C. striatum* was only reported in polymicrobial cultures when there was evidence that it was a potential pathogen (predominant organism grown, coryneforms observed in the direct specimen Gram stain, present with polymorphonuclear leukocytes, positive in multiple blood culture sets, etc.). The following information was obtained for each isolate: specimen type, presence of other microorganisms, identification methodology, and results of any susceptibility testing performed. A chart review of each corresponding patient was performed in order to obtain gender and age. For comparison, the same review was performed for CNS and *Staphylococcus aureus* isolates obtained during the same time period.

Identification. *C. striatum* isolates were originally identified either by RapID CB Plus (Remel, Lenexa, KS) or MALDI-TOF MS (Bruker Biotyper, Bruker Daltonics, Inc., Billerica, MA), as per the standard operating procedures at the time of isolation. These identifications were retrospectively retrieved by chart review at the time of the study. A subset of these isolates that had been stored at −70°C was further characterized for the purposes of the study. The identification of these frozen isolates was confirmed using both the Vitek MS IVD version 2.3.3 (bioMérieux, Durham, NC) and the Bruker Biotyper version 5. The percent agreement between the methods used was obtained.

Antimicrobial susceptibility testing. For the all isolates included in the study, susceptibility testing was initially performed when deemed clinically appropriate as a part of routine patient care using gradient diffusion Etest (bioMérieux, Durham, NC). The subset of frozen isolates that were further characterized received additional susceptibility testing evaluating meropenem, ceftaroline, linezolid, telavancin, and daptomycin using gradient diffusion (Etest) on Mueller-Hinton agar with sheep blood. The results were read at 24 and 48 h and interpreted using CLSI interpretative breakpoints (CLSI document M45, 2nd and 3rd editions) (26, 36).

Development of daptomycin resistance. To further characterize the ability of *C. striatum* to develop resistance to daptomycin, 50 daptomycin-susceptible isolates were incubated overnight with daptomycin Etests, as per a previously published protocol (16). In brief, each isolate was inoculated into two 5-ml tubes of tryptic soy broth at an optical density of a 0.5 McFarland standard. A daptomycin Etest was cut in half, and both halves of the Etest were submerged into one tube, whereas the other tube served as the growth control. Tubes were incubated at 35°C room air under constant agitation overnight. Isolates that were turbid after incubation were tested for MICs to daptomycin, vancomycin, and telavancin using

gradient diffusion (Etest) assays. The MIC_{50} and MIC_{90} for each drug were obtained and compared pre- and postincubation.

Molecular typing. Strain typing was performed on the 85 previously frozen isolates confirmed to be *C. striatum*. Isolates with different typing results were compared by isolate source and susceptibility pattern. Organism DNA was extracted using the Mo Bio BiOstic bacteremia DNA isolation kit (Mo Bio, Carlsbad, CA) and stored at −20°C prior to use. Strain typing was performed by repetitive-sequence PCR using the primer RW3A. Analysis of PCR products was performed using the DiversiLab bacterial barcodes system (bioMérieux, Durham, NC) (16, 37). Each unique strain type was given an alpha designation.

Statistical analysis. All data were assessed for statistical significance using Fisher's exact test analysis; a *P* value less than 0.05 was used to establish significance.

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