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Abstract *Corynebacterium striatum* is often dismissed as a contaminant when cultivated from blood samples; indeed, it is a skin saprophyte that may therefore be introduced into the clinical specimen accidentally. Nevertheless, the organism can be responsible for true bacteraemias, and multidrug resistance spread among nosocomial strains is of increasing concern. Specific criteria for testing have not been defined yet, but we however suggest to report clear resistances (i.e. absence of any inhibition zones with the disc test), in order to try to understand this species behaviour under antibiotic exposure. In this context, features of a blood isolate (strain DSM 45711) are here depicted.

Keywords *Corynebacterium striatum* · Multidrug resistance · Bacteraemia

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Brief report

Corynebacterium striatum is emerging as a cause of bloodstream infections, even associated with endocarditis; also, it shows the potential to cause pneumonia, meningitis and arthritis, although it has been frequently dismissed as a blood and airway sample contaminant in the past (Boltin et al. 2009; Renom et al. 2007; Bowstead and Santiago 1980; Brandenburg et al. 1996; Scholle 2007). Multidrug resistance (MDR) is getting increasingly observed among strains of the species, with few therapeutic options being available; particularly, glycopeptides, linezolid, daptomycin, quinupristin/dalfopristin and tigecycline may be the only drugs effective, in vitro, against these organisms. Indeed, *C. striatum* MDR has been known to potentially affect all of these compounds, except for vancomycin that is therefore the drug of choice in the absence of laboratory data or pending antibiotic susceptibility testing results (Renom et al. 2007; Bowstead and Santiago 1980; Brandenburg et al. 1996; Scholle 2007).

An MDR *C. striatum* strain was collected (Fig. 1) in our clinical microbiology laboratory (*Spirito Santo* Hospital, Pescara, Italy) from the blood sample of a 60-year-old myelodysplastic syndrome bacteraemic host; exactly, four bioMérieux (Marcy L'Etoile, France) BacT/Alert bottles for aerobe bacteria/fungi were suddenly collected after patient's fever onset (temperature value was 38.0 °C), and detected as positive after 24 h incubation. Observation under a microscope showed non-motile, Gram positive (after staining) coryneforms that were identified as *C. striatum* through both the Vitek2 ANC card and 16S rRNA sequencing (performed at the Department of Biomedical Sciences, Campus Biomedico University, Rome, Italy). The strain was then deposited

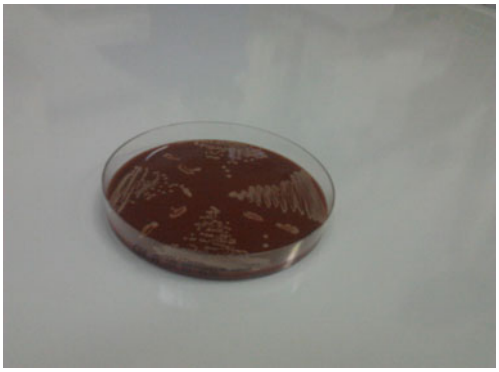

Fig. 1 Strain DSM 45711 yellow-pigmented colonies on Chocolate agar (growth medium by Liofilchem®, Roseto degli Abruzzi, Italy)

into the DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen, GmbH-Braunschweig, Germany) as strain DSM 45711. Susceptibility testing showed MDR (Table 1), including tigecycline resistance; particularly, an agar diffusion test along with MIC determination (Table 1, Fig. 2) was performed and interpreted according to EUCAST version 2.0. Given the absence of corynebacteria-specific breakpoints, inhibition zone diameters and MICs have been evaluated based on those for coagulase-negative staphylococci (CNS); concomitantly, empirical vancomycin had been successfully administered, while waiting for testing results, leading to the septic episode clinical resolution. Also, follow-up blood cultures performed after 48 h from starting treatment were negative. The patient did not suffer from endocarditis and had no catheter, so the source of the infection remained unexplained.

DSM 45711 represents a further MDR strain (Table 1) within the species, exerting tigecycline resistance too (if MIC values are interpreted according to EUCAST criteria for CNS). A few further considerations should be done in this ambit.

Corynebacteria *tetA*/*tetB* gene-encoded pumps extrude oxacillin, while the mechanism for resistance to beta-lactams other than oxacillin is unclear (Campanile et al. 2009); hence, nowadays it is unknown whether oxacillin-resistant corynebacteria should be considered as almost pan-beta-lactam resistant, like *mecA* gene-positive (methicillin/oxacillin/cefoxitin resistant) staphylococci (that only respond to ceftobiprole and ceftaroline) (Savini et al. 2012). A polymerase chain reaction was carried out (at the Tor Vergata University of Rome, Italy) to search this genetic element, but DSM 45711 was not found to harbour it, as expected. Betalactams have to be tested individually, then, independently of oxacillin (methicillin/cefoxitin) activity; also, in our opinion, clear resistances at least (i.e. molecules showing absence of any inhibition zones) should be reported to clinicians, with the purpose to target the therapy and more deeply understand the behaviour of coryneforms under antibiotic exposure. Moreover, specific criteria to test and interpret

Table 1 Susceptibility profile of *C. striatum* DSM 45711

	IZD (in mm)[a]/ MICs (mg/L)[b]	Interpretation according to CNS criteria
Penicillin G	6	R
Ampicillin	6	R
Ampicillin-sulb.	6	R
Oxacillin	6	R
Cefoxitin	6	R
Ceftriaxone	6	R
Ceftazidime	6	R
Imipenem	6	R
Meropenem	6	R
Ciprofloxacin	6	R
Levofloxacin	6	R
Moxifloxacin	6	R
Erythromycin	6	R
Clindamycin	6	R
Gentamicin	6	R
Amikacin	22	R
Tetracycline	12	R
Cotrimoxazole	6	R
Rifampin	6	R
Chloramphenicol	6	R
Fosfomycin	6	R
Vancomycin	MIC 0.38	S
Teicoplanin	MIC 0.19	S
Daptomycin	MIC 0.125	S
Linezolid	30	S
Tigecycline	MIC 0.75	R

CNS coagulase-negative staphylococci

[a] Inhibition zone diameter, obtained by agar disc test (antibiotic discs by Liofilchem®, Roseto degli Abruzzi, Italy) according to EUCAST version 2.0, valid from January 1, 2012

[b] MICs (minimum inhibitory concentrations) obtained by MIC Test Strips (Liofilchem®, Roseto degli Abruzzi, Italy)

antibiotic susceptibility testing with coryneforms are strongly needed, in order to avoid under- and overestimation of in vitro drug activities, provide patients with adequate treatments and improve the clinical outcome.

Again, a reliable aetiologic diagnosis of bacteraemic episodes must rely on a correct sampling; particularly, culture of more than one blood specimen is crucial to define the pathogenic role of *C. striatum* isolates; the species belongs in fact to the commensal skin flora and may therefore contaminate blood bottles.

Finally, once corynebacteria are isolated, 16S rRNA sequencing must confirm the phenotype-based identification. Although Vitek2 successfully characterized DSM 45711, in fact, it is known that commercial systems may fail (Rennie et al. 2008); the risk is that strains may not be correctly

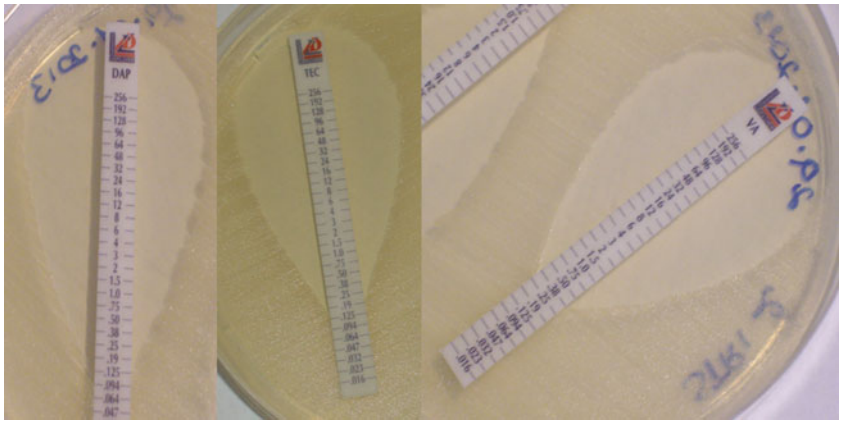

Fig. 2 Strain DSM 45711 MICs (see Table 1) for daptomycin (*left*), teicoplanin (*middle*), and vancomycin (*right*) (MIC Test Strips and Mueller-Hinton II agar by Liofilchem®, Roseto degli Abruzzi, Italy)

identified, with knowledge of individual species epidemiology and pathogenicity consequently remaining fragmentary and confused.

To conclude, along with single reports of disease, *C. striatum* outbreaks have been reported too (Campanile et al. 2009); key measures such as a proper preparation of the phlebotomy site along with caretakers' hand cleansing and use of sterile gloves (to be changed after each patient's handling) should be recommended therefore to prevent, respectively, blood sample contamination by skin commensal organisms (and subsequent falsely positive blood cultures), as well as patient-to-patient dissemination of strains and/or resistance determinants within the hospital wards.

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