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Short Communication

A fatal case of urosepsis due to *Corynebacterium riegelii*

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Abstract

Corynebacterium species other than *Corynebacterium diphtheriae* rarely cause infections in human but rather reside in flora, however they have been reported to cause opportunistic infections in both immunocompromised and immunecompetent patients. Here we report for the first time a case of an elderly female patient presenting with a fatal urosepsis caused by a recently defined pathogen, *Corynebacterium riegelii*, identified on second day after patient hospitalization leading to a progressive worsening and death of the patient on 6th day.

Key words: *Corynebacterium riegelii*, urosepsis, PCR amplification.

Corynebacterium riegelii, a recently defined *Corynebacterium* species, was first isolated and identified by Funke *et al.* (1997, 1998) from females with urinary tract infections, however fatal infections have never been reported (Winn *et al.*, 2006).

A 79 years-old female was admitted to the psychiatry ward with difficulty in cooperation, loss of orientation and delirium and was put on antipsychotic and antihypertensive drugs. Physical exam was not remarkable. Laboratory findings showed white blood cell (WBC) count: 15.100/mm^3 (80% neutrophils, 20% lymphocytes), hemoglobin: 12.7 g/dL, Blood Urea Nitrogen: 126 mg/dL, creatinine: 1.4 mg/dL, C-Reactive protein: 25 mg/dL (normal < 5 mg/dL) and a normal platelet count of 166.000 platelets/mm^3. Urinalysis showed pyuria with a WBC of 40-45 cells per high-power field (HPF). As she developed fever and signs of urinary tract infection on the second day of hospitalization, she was diagnosed with pyelonephritis and urosepsis. Following 2 sets of blood and urine cultures, she was started ciprofloxacin (200 mg iv every 12 hours) empirically. She developed tachypnea, respiratory distress, progressive increase in blood urea nitrogen and serum creatinine and died on 6th day of hospitalization. Blood cultures remained negative, however, urine cultures obtained on second and third days of admission revealed > 10^5 cfu/mL diphtheroid bacilli in pure culture. Colonies were green colored, 2-3 mm in diameter and opaque on Cystein-Lactose-Electrolyte-Deficient (CLED) agar (Becton Dickinson, USA) and non-hemolytic on sheep blood agar, non-motile, non-sporulated Gram positive bacilli. The methods used for determination of the biochemical profiles have been described previously (Funke *et al.*, 1998). API Coryne strips revealed a profile number of 2001224 at 48 hours, and API 50CH reactions were performed with the 50 CHE medium (bioMérieux, Marcy l'Etoile, France). The isolate was catalase (+), esculin (-), urease (+), CAMP (-) and was preliminarily identified as *C. riegelii*.

The MICs were determined by E-test (AB Biodisk Sonla, Sweden) on Mueller Hinton agar at 35 °C in ambient air for 20 h (Martinez-Martinez *et al.*, 1995). The results were as follows: vancomycin: 0.25 mg/L, co-trimoxazole 2 mg/L, penicillin-G: 0.125 mg/L, ciprofloxacin: 0.064 mg/L, nalidixic acid: 16 mg/L, amikacin: 0.25 mg/L.

The identification of the isolate was also confirmed by 16S rRNA gene sequencing. For this purpose, bacterial DNA was obtained from overnight culture using a commercial DNA purification kit (High Pure PCR Template Preparation kit, Roche Diagnostics, Mannheim, Germany).

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Primers described previously were used during the PCR amplification and sequencing (Jonasson *et al.*, 2002; Weisburg *et al.*, 1991). The sequence obtained was compared with the sequences deposited at the GenBank using BLASTN 2.2.18+ program (Zhang *et al.*, 2000). The sequenced segment of 1457 bp had 100% homology with the reference strain deposited in GenBank under the accession number EU848548.

Strong urease activity(*i.e.*, positive within 5min in Christensen's urea broth) is one of the typical features of *Corynebacterium riegelii*. It forms white, non-lipophylic, non-hemolytic colonies on blood agar. Slow acid production from maltose but not from sucrose and glucose is a distinctive feature. API Coryne has been successfully used for *C. riegelii* identification. Bernard *et al.* (2002) reported four *C. riegelii* isolates: two from blood culture which were reported for the first time, one from urine culture and one from cord blood. He reported that none of the isolates produced propionic acid but the two strains tested for O-129 were found to be sensitive. Funke *et al.* (1998) determined MICs of various antimicrobial substances and found that *C. riegelii* strains were susceptible to cephalothin, chloramphenicol, ciprofloxacin, fusidic acid, gentamicin, penicillin, rifampin, tetracycline, and vancomycin but were resistant to cefetamet, ceftibuten, and fosfomycin.

Various identification systems have been used recently with great success including API Coryne. Amplification of 16S rRNA genes and sequencing is another tool used for identification (Tang *et al.*, 2000). More recently, Van den Velde *et al.* (2007) have suggested that species of corynebacteria would be more correctly identified based on their cellular fatty acid profiles (ie, for the C14 to C20 fatty acids).

As there was no other comorbidity to cause progressive clinical worsening and no other pathogen isolated, the patient's death was attributed to urosepsis due to *C. riegelii*. The microorganism was possibly acquired prior to admittance and only manifested afterwards. There were no documented prior infections with *C. riegelii* in any other patient in the hospital.

Although ciprofloxacin was started empirically and continued based on susceptibility results, there is no clinical data in the literature regarding clinical efficacy of ciprofloxacin to infections with *C. riegelii.*

Coryneform bacteria from urine samples, even when growing in pure cultures, are usually considered contaminants by many clinical laboratories. It should be kept in mind that *C. riegelii* may cause fatal urinary tract infections. We therefore emphasize the importance of identifying coryneform bacteria to the species level whenever they are recovered in pure culture from clinical specimens. More data is required regarding clinical features and treatment strategies on infections with recently defined Corynebacterium species.

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