“Probable contaminants” no more: rapid identification of Gram-positive rods leads to improved clinical care

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Keywords: Actinobaculum schaalii, MALDI-TOF identification

Previously, identification to species level of “non-significant” bacteria (e.g. single specimens with Gram-positive rods or coagulase-negative staphylococci) was generally not performed in our laboratory, including for blood culture isolates. Reasons for this included the low pre-test probability of these bacteria being true pathogens, and the expense of identification methods. Methods used were API strips (bioMérieux, France) and 16s rRNA sequencing, with turnaround times of between 48 hours and two weeks. Consequently, if an isolate was considered significant once the identity was confirmed, attempting to establish the source of bacteremia was difficult, as non-sterile specimens are kept for only 7 days.

Our laboratory recently introduced the Bruker MALDI-TOF identification system utilizing the Biotyper database. Given the ease of species identification this is now performed on all blood culture isolates, regardless of clinical significance, and all other significant isolates (i.e. from a sterile site or a pure/predominant
A 69-year-old man receiving radiotherapy for prostate cancer developed sepsis secondary to a urinary tract infection. Urine was cultured on 5% horse blood agar (HBA) and incubated in 5% CO₂ only at 35°C. Three different organisms were isolated from urine at >10⁸ cfu/L: two colonial types of coagulase-negative staphylococci and a Gram-positive rod, which were deemed non-significant. According to usual laboratory protocols, in the presence of pyuria, positive culture plates are stored for 7 days. Anaerobic and aerobic blood culture bottles from the same day flagged positive on day 2 and 4 respectively with a short Gram-positive rod. Following inoculation of 5% HBA and incubation in 5% CO₂ for 24 hours, a pure organism was isolated. Growth, however, was sufficient only at 48 hours to attempt identification. On day 4 post-collection, the isolate was identified as *Actinobaculum schaalii* by MALDI-TOF with a score of 2.3 (i.e. a reliable score to species level) using the direct colony transfer method. The rod from his urine culture was retrieved and identified as the same organism, using the same method. Interestingly, a urine culture from the same patient a month earlier showed pyuria and Gram-positive rods.

He had been treated empirically with ceftriaxone and improved. Following identification, his antibiotics were changed to amoxicillin for an extended duration, owing to reports of failures of shorter treatment courses for this organism (1) and resistance to commonly prescribed empiric treatments for culture-negative urinary tract infection, like trimethoprim and ciprofloxacin (2).
Antimicrobial susceptibility testing was not pursued on this isolate as the patient had improved and testing would require referral to an external laboratory. On follow-up two months later, the pyuria had resolved with no organisms isolated from the urine.

*A. schaalii* is a slow-growing, often CO₂-requiring organism that has emerged as a significant uropathogen. It is likely to have been under-diagnosed in the past as it may not grow under routine conditions (1). Prior to the introduction of the MALDI-TOF system, identification would have taken on average 8 days using either 16s sequencing or phenotypic methods. Thus this case illustrates the importance of real-time species level identification in making the correct diagnosis and directing appropriate antimicrobial therapy. In addition, it is likely that other isolates previously regarded as contaminants may be pathogens. With the advent of these rapid and inexpensive technologies, we should review what is considered a significant pathogen.

In conclusion, real-time species level identification enables microbiologists to become familiar with novel pathogens and provide timely advice to clinicians. This will allow more rapid directed antimicrobial therapy, which should assist with antimicrobial stewardship, and may lead to improved clinical outcomes.

REFERENCES


