A canine urinary tract infection representing the first clinical veterinary isolation of *Acinetobacter ursingii*

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Abstract

Acinetobacter species can be important opportunistic pathogens in humans, especially in healthcare settings. We report here the first isolation of *Acinetobacter ursingii* from an animal species; it was isolated from a canine urinary tract infection, and phenotypic identification proved unreliable.

Keywords: *Acinetobacter ursingii*, canine, molecular diagnostics, urinary tract infection, veterinary microbiology
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Acinetobacter species cause a wide range of infections, in humans with those most frequently isolated belonging to the *Acinetobacter calcoaceticus–Acinetobacter baumannii* complex [1]. While other species are pathogenic, much less is known about their epidemiology, and their laboratory identification can be unreliable [2,3]. A Gram-negative bacilli, isolate 76496, was cultured from free-catch urine received from an 8.5-year-old male Border Terrier submitted for diagnosis to Easter Bush Pathology, University of Edinburgh.

The dog had a history of acute kidney injury of unknown origin, resulting in permanent reduction of renal function (chronic kidney disease). The animal was presented for a routine checkup. The urine culture was pure, with a viable count of $>10^6$ CFU/mL. While this does not confirm the isolate as the definite cause of chronic kidney disease, and a free catch can be susceptible to contamination, the heavy growth and purity indicates clinical significance. Phenotypic identification using Vitek2 and Analytical Profile Index (API) failed to give a reliable identification. In the case of VITEK 2, a low-discrimination result with bionumber 0040001101501000 was returned using the Gram-negative identification card. Three possible organisms were listed: *Pseudomonas fluorescens, Acinetobacter lwoffii* and *Bordetella bronchiseptica.* A repeat analysis gave the result as 'unidentified' with a similar bionumber: 0040000101501000. The API 20 NE strip (for nonfastidious, nonenteric Gram-negative rods) gave an 'acceptable identification to the genus' result for *Acinetobacter* with the numerical code 0000071 and *Acinetobacter junii/johnsonii* (63.1%) and *Acinetobacter baumannii/calcoaceticus* (26.1%) given as the significant taxa. 16S rDNA sequencing was therefore used to identify the isolate. A 16S rDNA was amplified by PCR with primers fD1 and rP2 [4] and sequenced on both strands with primers fD1 and rP2, and 519r, 536f, 357f and 1385r [5]. Using EzBioCloud [6] this 1402 bp partial 16S sequence yielded a 100% match to that of the *Acinetobacter ursingii* type strain DSM 16037 (accession no. AIEA01000080 at positions 29–1430). Susceptibility testing by disc diffusion found the isolate susceptible to all antimicrobials tested: ampicillin, amoxicillin/clavulanate, cephalexin, clindamycin, enrofloxacin, erythromycin, and trimethoprim/sulfonamide. This antibiogram may indicate a possible community or environmental source rather than being nosocomially acquired.

The dog received a 1-week course of amoxicillin/clavulanate, resulting in a negative culture from a follow-up urine sample 10 days after cessation of treatment.

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First identified in 2001, *A. ursingii* has been isolated from various human infections including urinary tract infection [2,7,8]. Dortet et al. [2] describe similar problems with the phenotypic identification of *A. ursingii* to those encountered here, and they suggest that therefore the true prevalence of *A. ursingii* infection may be underestimated. Notably, $^{9}/_{10}$ of their studied *A. ursingii isolates* gave an API 20 NE numerical code of 0000071, identical to our isolate, leading them to propose that such a result represents a 'reasonably reliable' approach to identify *A. ursingii* [2]. The poor reliably of VITEK 2 for the identification of *A. ursingii* has also been reported [3].

To our knowledge, this report is the first veterinary isolation of *A. ursingii,* and this organism must be considered as a possible aetiologic agent in veterinary diagnostic laboratories. This is particularly the case where phenotypic tests are inconclusive but indicative of an *Acinetobacter* species, with identification by molecular approaches advisable. Given the potential for *Acinetobacter* species to carry multidrug resistance (although that was not the case here) and to cause nosocomial infections, it is important for veterinary microbiology to accurately identify these and track their epidemiology.

Conflict of interest

None declared.

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