

Bacteraemia Caused by *Kytococcus schroeteri* in a Pneumonia Patient

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Abstract

The genus *Kytococcus* are pigmented, non-encapsulated, non-motile, aerobic, catalase-positive, Gram-positive cocci in pairs or tetrads. We report a case of *Kytococcus schroeteri* isolated from a blood specimen of a patient with pneumonia. The isolate was Gram-variable and difficult to identify using conventional biochemical tests.

Keywords: *Kytococcus schroeteri*; Gram-variable; 16S rDNA sequencing; Bacteraemia

Introduction

Kytococci are a part of the normal skin microbiota of humans and can cause infections, particularly in patients with prosthetic devices or immunodeficiency. Due to insufficient identification methods and an intrinsic resistance to several β -lactams, infections due to *Kytococci* are a challenge to clinical microbiologists and clinicians [1]. Here, we report the first Korean case of bacteraemia due to *Kytococcus schroeteri* in a patient with pneumonia.

Case Report

A 55-year-old man was admitted to a tertiary-care hospital in Seoul, Korea, for evaluation of fever and dyspnea. The patient had no history of hypertension or diabetes mellitus. The patient had been living in a sanatorium because of quadriplegia resulting from a cerebral infarction diagnosed at age 20 years. Laboratory tests showed a leukocyte count of $12.89 \times 10^9/L$ (neutrophil 83.6%) and a C-reactive protein level of 156.0 mg/L (normal range, 0.1-6.0 mg/L). A chest X-ray showed a large amount of pleural effusion and marked peribronchovascular markings in the left lung. Percutaneous catheter drainage of the pleural effusion was performed, but the pleural fluid culture did not yield any bacterial growth. The predominant organism of sputum cultures was α -*Streptococcus* species, which is thought to be part of the normal flora. A blood culture performed the day the patient was admitted showed Gram-positive cocci growth (isolate GNKS01) in an anaerobic blood culture vial, one of six total (three aerobic and three anaerobic).

Subculture of the blood culture fluid yielded small, slightly yellow-pigmented, convex, catalase-positive, and non-haemolytic colonies on 5% sheep blood agar after 24 h of incubation in 6% CO₂ at 35°C. Routine Gram staining of the smeared preparation showed Gram-variable cocci in pairs or tetrads (Figure 1). However, the isolate appeared to be Gram-positive after shortening the destaining time from 3–4 sec to 1–2 sec. Morphologic evaluation using scanning electron microscopy (FE SEM S-800, Hitachi, Tokyo, Japan) showed spherical cells (1.0–1.5 μ m in diameter) in pairs or tetrads (Figure 2).

Biochemical features were tested using the GP identification card with Vitek 2 system (bioMérieux, "Marcy-l'Étoile", France). However, the commercial card failed to identify the organism. Analysis using matrix-assisted laser desorption/ionization mass spectrometry (MALDI Biotyper, Bruker Daltonics, Bremen, Germany) also failed to identify the organism. 16S rDNA gene sequencing was performed with a universal bacteria primer set, 27F (5'-AGA GTT TGA TCC TGG CTC AG-3') and 1541R (5'-AAG GAG GTG ATC CAG CCG CA-3'), using an automatic sequencer (ABI 3730xl, AB, Weiterstadt, Germany), and the partial 16s rDNA sequences of the isolate GNKS01 were

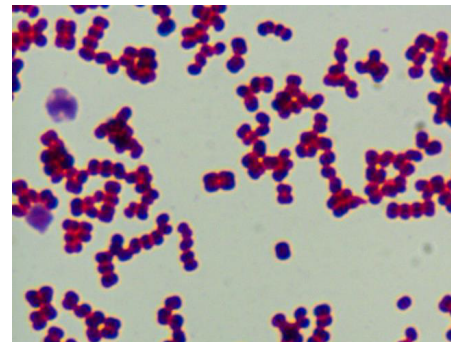


Figure 1: Routine Gram staining of the isolate GNKS01 showed Gram-variable cocci in pairs or tetrads.

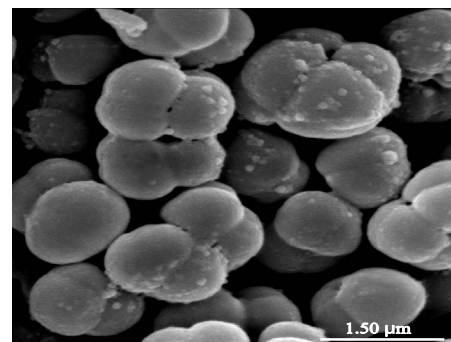


Figure 2: Electron micrograph of *K. schroeteri* isolated from blood specimen. Magnification, 20,000X.

100% identical to those of DSM 13884^T, the type strain of *K. schroeteri* (GenBank Accession No. AJ297722.1), according to a BLAST search (<http://blast.ncbi.nlm.nih.gov/>).

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Antimicrobial susceptibility testing was performed with the disk diffusion method. Minimal inhibitory concentrations (MICs) of antimicrobials were determined with Etest strips (bioMérieux) on Mueller-Hinton agar (Asan Pharmaceutical, Seoul, Korea) following the guidelines of the Clinical and Laboratory Standards Institute [2]. The isolate GNKS01 exhibited similar antimicrobial susceptibility patterns to the type strain DSM 13884^T (Table 1). However, the isolate GNKS01 was susceptible to erythromycin, while the type strain DSM 13884^T was resistant.

The patient was treated with tazobactam and ciprofloxacin. He showed good clinical response, and symptoms and elevated inflammatory markers resolved after 10 days.

Discussion

The genus *Kytococcus* belongs to the family *Dermacoccaceae*, which is a part of the suborder *Micrococccineae* and the order *Actinomycetales*. The genus *Kytococcus* was separated from the genus *Micrococcus* based on phylogenetic (16S rRNA gene sequencing) and chemotaxonomic (menaquinone composition, peptidoglycan types, and cellular fatty acid composition) analysis in 1995 [3]. *Kytococci* are pigmented, non-encapsulated, non-motile, aerobic, catalase-positive, and Gram-positive cocci that appear in pairs or tetrads. The genus consists of three species: *Kytococcus sedentarius*, *Kytococcus aerolatus*, and *Kytococcus schroeteri*. *K. sedentarius* is a normal saprophyte of the human skin but seldom causes human infections [4]. *K. aerolatus* was first identified from an indoor air sample and has never been reported to cause human infections [5]. *K. schroeteri* was first described in 2002, isolated from blood cultures of a patient with prosthetic valve endocarditis and distinguished from *K. sedentarius* based on physiological tests and chemotaxonomic investigations [6]. Though *K. schroeteri* is a part of the normal human skin flora, it causes systemic human infections associated with prosthetic devices and immunodeficiency. To date, *K. schroeteri* has been identified as a human pathogen in 17 cases; prosthetic valve endocarditis was the most common clinical presentation (n=8) [6-13], followed by pneumonia in immunocompromised patients (n=5) [14-17], ventriculoperitoneal shunt infection (n=2) [1,18], postoperative spondylodiscitis (n=1) [19], and implant-related septic arthritis (n=1) [20].

Antimicrobial agent	DSM 13884 ^T		GNKS01	
	DDT	MIC (µg/ml)	DDT	MIC (µg/ml)
Ampicillin	R	ND	R	ND
Penicillin G	R	ND	R	ND
Erythromycin	R	ND	S	ND
Tetracycline	S	0.5	S	0.75
Teicoplanin	S	ND	S	ND
Vancomycin	S	0.125	S	0.094
Linezolid	S	ND	S	ND
Tigecycline	S	0.094	S	0.094
Quinupristin/Dalfopristin	S	ND	S	ND
Tobramycin	I	ND	R	ND
Amikacin	S	1.5	S	1
Trimethoprim/sulfamethoxazole	S	0.125	S	0.125
Ciprofloxacin	S	1	I	1
Gentamicin	S	0.38	S	0.5

Abbreviation : DDT, disk diffusion test; MICs, minimal inhibitory concentrations; S, susceptible; I, intermediate; R, resistant; ND, not done

Table 1: Antimicrobial susceptibilities of the type strain DSM 13884^T and the *K. schroeteri* clinical isolate from blood culture as determined by the disk diffusion and the Etest.

K. schroeteri is a Gram-positive coccus; however, the isolate GNKS01 showed Gram-variable results in routine Gram staining. A former case report described a similar phenomenon in which identification was hampered because the microorganism was misidentified as Gram-negative cocci [1]. The authors attributed the cause of the abnormal Gram stain reaction to treatment with β-lactams or the inflamed tissue from which the *K. schroeteri* was isolated [1]. However, when we performed routine Gram staining for the type strain DSM 13884^T, we also observed Gram-variable results. Thus, we assume that *K. schroeteri* may have a property that allows it to be easily destained, which could result in its misinterpretation as Gram-negative cocci.

In this case report, *K. schroeteri* GNKS01 was isolated from a blood specimen of a patient with pneumonia. However, the patient's pleural fluid did not yield any bacterial growth, and the sputum culture did not show any growth other than α-*Streptococcus* species. Given that the patient did not have any focal infections other than pneumonia, we consider the possibility that his bacteraemia originated from respiratory infection.

In summary, we report a case of *K. schroeteri* bacteraemia successfully treated with tazobactam and ciprofloxacin in a patient with pneumonia. We found that Gram-staining results of *K. schroeteri* can be easily misinterpreted as Gram-negative cocci. Additionally, identification of the *Kytococcus* spp. isolates using commercially available identification cards and MALDI-TOF MS systems was difficult, indicating the necessity of 16S rDNA gene sequencing.

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