Short Communication

Prevalence, Identification, and Antimicrobial Susceptibility of Staphylococcus lugdunensis from Various Clinical Specimens in Korea

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SUMMARY: Staphylococcus lugdunensis is an unusually virulent coagulase-negative staphylococcus (CoNS) that can cause many types of infection. All culture specimens were collected from patients at Inje University Busan Paik Hospital between October 2005 and March 2006. S. lugdunensis was identified using the phenotypic biochemical tests and 16S rDNA sequencing. Among 358 CoNS, three strains were identified as S. lugdunensis. All three isolates showed positive results in the clumping factor test, but the L-pyrrolidonyl-beta-naphthylamide hydrolysis test was positive in only one and the ornithine decarboxylase test in two. Two of the three isolates were correctly identified by API Staph, but none of them was identified correctly by the Vitek I system. All three strains were penicillin resistant secondary to beta-lactamase production. S. lugdunensis was an unrecognized but infrequent cause of infection.

Staphylococcus lugdunensis is a member of the coagulase-negative staphylococcus (CoNS) first described by Frény et al. (1) in 1988. It has been considered part of the resident flora of the surface of the human skin in the inguinal and breast areas (2), but it is an unusually virulent CoNS and can cause many types of infection with a clinical course much like that of infections caused by Staphylococcus aureus, as the two species seem to share virulence determinants (3). Only a few studies have determined the frequency of S. lugdunensis in clinical specimens, which show the organism to account for about 5% of all CoNS (4, 5). However, there are no data on the prevalence of S. lugdunensis from clinical specimens in Korea. The aims of this study were to determine the prevalence of the organism in various clinical specimens and to evaluate the biochemical characteristics and antimicrobial susceptibilities of S. lugdunensis isolates.

All CoNS isolates were collected from patients at a tertiary-care university hospital between October 2005 and March 2006. We performed colony morphology examination, gram staining, and catalase and tube coagulase tests to confirm that the colonies were CoNS; these are the usual methods employed in our clinical microbiology laboratory. If the colonies were correctly identified by API Staph, but none of them was identified correctly by the Vitek I system. All three strains were penicillin resistant secondary to beta-lactamase production. S. lugdunensis was an unrecognized but infrequent cause of infection.

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mercial biochemical test results.

The important key reactions that identify *S. lugdunensis* are the clumping factor, ODC, and PYR test. All three isolates showed positive results for clumping factor, but the PYR test was positive in only one strain, and the ODC test was positive in two strains. Two of the three *S. lugdunensis* isolates were correctly identified at the species level by API Staph Kit, but Vitek I GPI showed incorrect results in all three strains because the biochemical profile for this species is not yet included in the manufacturer’s database. Even though this limitation has been overcome to some degree by the launching of the Vitek II system, we must keep the limitation in mind because the Vitek I is commonly used in Korea at present.

Among the 358 isolates of CoNS, 55 strains showed positive results in only one of the three major biochemical reactions of clumping factor, ODC, and PYR. For 45 of these 55 strains, we performed the partial 16S rDNA sequencing and verified that none of them was *S. lugdunensis*. The strains showing PYR only and ODC only positive results were, for the most part, *Staphylococcus haemolyticus* and *Staphylococcus epidermidis*, respectively. We determined the antibiotic resistance patterns of the three isolates by the disk diffusion method and the MICs of the Vitek GPS card and interpreted the results according to CLSI guidelines (6). In our study, all three strains were penicillin resistant secondary to beta-lactamase production. One isolate was resistant to penicillin only, another to penicillin and tetracycline, the other to penicillin and gentamicin. None of the three isolates in this study was oxacillin resistant (tested against cefoxitin). All three *S. lugdunensis* isolates were susceptible to erythromycin, ciprofloxacin, cotrimoxazole, clindamycin, and vancomycin.

There are a few reports concerning the prevalence of *S. lugdunensis* in clinical specimens. Herchline and Ayers (4) identified *S. lugdunensis* in 10% of 2,260 staphylococcal isolates and reported that the number of *S. lugdunensis* isolates identified increased over the study period. Haile et al. (5) reported that *S. lugdunensis* accounted for 6% of 500 CoNS recovered from urine. The results of our study suggest that *S. lugdunensis* may be an unrecognized and not rare clinical isolate, but the frequency of *S. lugdunensis* from clinical specimens is very low in Korea when compared with reports from other countries. Although respiratory specimens are one of the most common sources of CoNS in clinical specimens, we found no *S. lugdunensis* in respiratory specimens in this study, so we verified that this organism is not a frequent resident of the respiratory tract, as noted previously (4). All isolates in reports from the USA and Spain were clumping-factor positive (7,8), and our study showed concordance with these results. However, others reported different results, as 35.3% of *S. lugdunensis* were clumping-factor negative (9), so the clumping factor test by itself is insufficient as a basis for suspicion.

Commercial systems designed to identify all CoNS are not very specific, lack sufficient information in their database, or show variable results when compared with other systems (9,10). Thus careful interpretation is required for accurate identification of *S. lugdunensis* using the characteristic biochemical testing or commercial systems. It has been suggested that penicillin resistance is rare in *S. lugdunensis* because of the lack of beta-lactamase and the *mecA* gene, but it seems that this is not correct all the time. Beta-lactamase activity is present in some *S. lugdunensis* isolates (approximately 40% [5] and 24% [11]). In our study, all three strains were penicillin resistant as a result of beta-lactamase production. These data preclude the generalization of universal penicillin and cephalosporin susceptibility in *S. lugdunensis* (2,4,12).

In this study, we evaluated the prevalence of *S. lugdunensis* from various clinical specimens in Korea. We ascertained that *S. lugdunensis* might be an unrecognized and not rare clinical isolate, but the frequency of *S. lugdunensis* in clinical specimens was very low.

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**REFERENCES**