Clinical and Microbiological Characteristics of Community-Acquired 
*Staphylococcus lugdunensis* Infections in Southern Taiwan

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Most *Staphylococcus lugdunensis* strains (49/59, 83%) were related to clinical infections, were susceptible to most antimicrobial agents with an overall oxacillin-resistant rate of 5% (3/58), and carried relatively great genetic diversity. Community-acquired infections (41/49, 84%) were dominant, often developed in patients with comorbidities, and had rather benign clinical courses without mortality.

*Staphylococcus lugdunensis*, a member of coagulase-negative staphylococci (CoNS) first described in 1988 by Freney et al. (5a), often causes skin and soft tissue infections; severe infections attributed to this organism are not rare (1, 8). Its clinical course and microbiological characteristics may resemble those of the coagulase-positive *Staphylococcus aureus* (4, 6) and has been associated with more invasive infections (2, 4, 8, 11, 13). The purpose of this study was to investigate the clinical and microbiological characteristics of *S. lugdunensis* isolates at a tertiary hospital in southern Taiwan.

A total of 59 *S. lugdunensis* isolates from 57 patients were collected at National Cheng Kung University Hospital between August 2005 and September 2009. CoNS was identified by conventional methods and the GP card Vitek 2 (bioMérieux, Marcy l’Etoile, France). The further confirmation was carried out using 16S rRNA sequencing. *S. lugdunensis* isolates that were the only or predominant pathogen from wound or pus culture or derived from sterile body fluid or bloodstream were included for analysis.

Oxacillin and cefoxitin susceptibilities were tested by the MIC dilution method. Cefoxitin and other antimicrobial susceptibilities were evaluated by the disk diffusion method (3). *S. aureus* ATCC 25923 and ATCC 29213 were used as quality control strains. Pulsed-field gel electrophoresis (PFGE) of SmaI-digested genomic DNA samples of *S. lugdunensis* isolates was carried out with a CHEF Mapper XA apparatus (Bio-Rad Laboratories, Hercules, CA), according to the instruction manual. PFGE patterns were interpreted in accordance with the criteria of Tenover et al. (14). *S. lugdunensis* strains were analyzed for staphylococcal cassette chromosome mec element (SCCmec) typing and amplification of the mecA and 16S rRNA genes by multiplex PCR and traditional PCR, respectively (10, 15). The purified PCR products were directly sequenced using the automated ABI Prism 3730 DNA sequencer (Applied Biosystems, Foster, CA).

A total of 49 of 59 *S. lugdunensis* strains (83%) derived from 48 patients were related to clinically significant infections. Diabetes mellitus (11/48, 23%), malignancy (6/48, 13%), and end-stage renal disease (5/48, 10%) were the most common comorbidities. The majority of *S. lugdunensis* infections (41/49, 84%) were community acquired. Skin and soft tissue infection (44/49, 90%) was the major type of clinical presentation. All three bacteremia episodes were catheter related and developed in the intensive care unit. None of the three patients had clinical features of infective endocarditis. Transthoracic echocardiography was not performed in any case. Two patients

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>Community acquired (n = 46) No. (%) of sensitive isolates</th>
<th>Nosocomial (n = 12) No. (%) of sensitive isolates</th>
<th>Total (n = 58) No. (%) of sensitive isolates</th>
<th>P valuea</th>
</tr>
</thead>
<tbody>
<tr>
<td>Penicillin</td>
<td>24 (52) 3 (25) 27 (47) 0.1148</td>
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<tr>
<td>Oxacillin</td>
<td>46 (100) 11 (92) 57 (98) 0.2069</td>
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<tr>
<td>Cefoxitin</td>
<td>46 (100) 10 (83) 56 (97) 0.0399</td>
<td></td>
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<tr>
<td>Clindamycin</td>
<td>35 (76) 8 (67) 43 (77) 0.4865</td>
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<tr>
<td>Gentamicin</td>
<td>46 (100) 8 (67) 54 (93) 0.0012</td>
<td></td>
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<tr>
<td>Co-trimoxazole</td>
<td>45 (98) 11 (92) 56 (97) 0.3739</td>
<td></td>
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<tr>
<td>Erythromycin</td>
<td>32 (70) 7 (58) 39 (67) 0.5023</td>
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<tr>
<td>Levofloxacin</td>
<td>46 (100) 12 (100) 58 (100)</td>
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<tr>
<td>Moxifloxacin</td>
<td>45 (98) 12 (100) 57 (98)</td>
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<tr>
<td>Vancomycin</td>
<td>46 (100) 12 (100) 58 (100)</td>
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<tr>
<td>Teicoplanin</td>
<td>46 (100) 12 (100) 58 (100)</td>
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</table>

a Community-acquired group versus nosocomial group, examined by Fisher’s exact test (two tailed).
FIG. 1. Genetic relationships and Smal pulsed-field gel electrophoresis (PFGE) patterns of 49 S. lugdunensis isolates from 48 patients. PFGE groups are designated A to P; B, E, F, I, J, K, M, O, and P denote unclustered isolates. R denotes oxacillin resistance, S denotes isolates from skin and soft tissue infection, T denotes isolates from catheter-related infection, U denotes isolates from urinary tract infection, and X denotes isolates from bacteremia.
showed improvement soon after catheter removal and antimi-
crobial therapy, and one patient died 9 days after catheter-
related bacteremia even treated with vancomycin. S. lugdu-
nensis was cultured as the only pathogen in 32 specimens (65%). S. lugdunen-
sis was the predominant pathogen in 17 specimens (16
patients) with polymicrobial infections or colonization. The
most common coisolate identified was another CoNS isolate (8
patients), and the others included oxacillin-resistant Staphylo-
coccus aureus, group B streptococci, group D streptococci,
Peptostreptococcus species, Bacteroides fragilis, Enterococcus
species, Gram-positive bacilli, micrococci, and Stenotrophomo-
nas maltophilia. These coisolates did not influence the treat-
ment or clinical course. All the community-acquired S. lug-
dunensis infections had rather benign clinical courses without
mortality. The results of the antimicrobial susceptibility test
are shown in Table 1. The oxacillin MICs for 57 of 58 strains
(98%) of S. lugdunensis were ≤2 μg/ml, and cefoxitin MICs for
56 of 58 strains (97%) were ≤4 μg/ml. The overall oxacillin-
resistant rate was 5% (3 in 8), according to the recommenda-
tions of the CLSI in 2010 (3). All three oxacillin-resistant S. lug-
dunensis isolates had the mecA gene and were derived from
nosocomial infections. The genetic relationships and SmaI PFGE
patterns of 49 S. lugdunensis infection isolates are shown in Fig. 1.
Sixteen pulsotypes were identified from 49 isolates. The following
two major PFGE pulsotypes accounted for 25 (51%) of the 49
isolates: pulsotype C (18 isolates) and pulsotype L (7 isolates).
Nine did not cluster with any other isolates.

Community-acquired S. lugdunensis bacteremia is associ-
ated with endocarditis in up to 50% of patients and could be
fatal (2, 4). Bücher et al. (1) reported that S. lugdunensis is
isolated from 13% of 159 abscesses from general practice
during a 6-month period. Recurrent and invasive S. lug-
dunensis infections were seen in 7 (1.4%) and 14 (2.9%) of
491 patients in 4 years (1). Our study revealed that the major
isolates of S. lugdunensis infections were derived from com-

munity-acquired infections with common comorbidity of di-
abetes mellitus, malignancy, and end-stage renal disease.
These results are different from the results reported by
Kleiner et al. showing that the major comorbidity of S. lug-
dunensis infections was related to surgery or recent trauma (47%)
(7). Skin and soft tissue infection was the most common type of infection. Only one death occurred, the patient with nosocomial catheter-related bacteremia.

Sixteen pulsotypes identified from our 49 S. lugdunen-
sis isolates indicated relatively great genetic diversity among
our clinical strains related mainly to community-acquired
infections. However, pulsotype C containing 18 isolates and
pulsotype L containing 7 isolates suggest the possibility of
transmission of S. lugdunensis from human to human.

S. lugdunensis is classified as a CoNS species in the routine
microbiological laboratory. If a positive culture result for S. lug-
dunensis is reported, the clinical significance other than
contamination should be considered seriously. In addition to
the clinical presentation and course resembling those of S. aureus, S. lugdunensis shares the same CLSI antimicrobial sus-
cceptibility and resistance breakpoints with S. aureus. There are
higher oxacillin MIC values in susceptibility and resistance for
treatment of S. lugdunensis than those for treatment of other
CoNS (MIC of ≤2 and MIC of ≤4 μg/ml versus MIC of ≤0.25
μg/ml and MIC of ≤0.5 μg/ml, respectively) (3). In our clinical
infection isolates, oxacillin-susceptible strains decreased to 4 of
49 (8.2%) if S. lugdunensis is not identified from the CoNS
species. Delayed or incorrect diagnosis of S. lugdunensis infections
may result in misidentified antimicrobial resistance and overuse
of more powerful second-line antibiotics for treatment.

S. lugdunensis, unlike other CoNS species, has high suscep-
tibility to most antibiotics (5). The overall oxacillin-resistant
rate was 5% (3/58), which was similar to that in previous
reports (12). All three oxacillin-resistant S. lugdunensis isolates
had the mecA gene in this study, in contrast to other reports
that most oxacillin-resistant S. lugdunensis strains lacked the
mecA gene (9, 13). For the three mecA gene-positive isolates in
this study, one had an oxacillin MIC of ≥4 μg/ml, and two had
MICs of 2 μg/ml; two had cefoxitin MICs of ≥8 μg/ml, and one
had a MIC of 4 μg/ml. Current MIC breakpoints for oxacillin
or cefoxitin recommended by the CLSI could not predict the
presence of the mecA gene. Our data revealed a zone diameter
for cefoxitin of ≤22 mm, which correlated with the presence of
the mecA gene.

In summary, S. lugdunensis has emerged as an important
organism in both community-acquired and nosocomial in-
fecions. The majority of S. lugdunensis strains in our study
were clinically significant, derived mainly from community-

acquired infections in patients with comorbidity of diabetes
mellitus, malignancy, and end-stage renal disease. They
were susceptible to most antimicrobial agents and carried
relatively great genetic diversity. Community-acquired S.
lugdunensis infections had rather benign clinical courses
without mortality.

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