Distinct groups and antimicrobial resistance of clinical *Stenotrophomonas maltophilia* complex isolates from Korea

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One hundred and twenty-one isolates of *Stenotrophomonas maltophilia* complex were collected from seven Korean hospitals. Species and groups were identified using partial gyrB gene sequences and antimicrobial susceptibility testing was performed using a broth microdilution method. Based on partial gyrB gene sequences, 118 isolates were identified as belonging to *S. maltophilia* complex, including *S. maltophilia*, *S. pavanii*, *Pseudomonas beteli*, *P. geniculata* and *P. hibisciola*. The *S. maltophilia* isolates were further divided into three groups, I to III. *S. maltophilia* groups II and III were clustered into clade A with *S. pavanii* and *P. beteli*; *S. maltophilia* group I was clustered into clade B with *P. geniculata* and *P. hibisciola*. For all *S. maltophilia* complex isolates, the resistance rate to trimethoprim/sulfamethoxazole (TMP/SMX) was very high (30.5%). Antimicrobial resistance rates varied among species or groups of *S. maltophilia* complex. Isolates of clade A showed significantly lower antimicrobial resistance rates than those of clade B; while 25% of clade A isolates were multidrug resistant, 46% of clade B isolates were multidrug resistant (*P*=0.001). The finding of high antimicrobial resistance rates, particularly to TMP/SMX, among *S. maltophilia* complex isolates from Korea, and the existence of distinct groups among the isolates, with differences in antimicrobial resistance rates, suggests consideration of alternative agents to TMP/SMX to treat *S. maltophilia* infections and indicates the importance of accurate identification for appropriate selection of treatment options.

**INTRODUCTION**

*Stenotrophomonas maltophilia* (formerly *Xanthomonas maltophilia*) is a non-fermentative Gram-negative bacillus which is ubiquitous in the environment (Brooke, 2012). It has emerged as one of the important opportunistic pathogens causing nosocomial infections. Although *S. maltophilia* was previously thought to be less pathogenic, infection by this bacterium is now known to be associated with significant morbidity and mortality, especially in immunocompromised patients (Looney et al., 2009). However, it has been difficult to isolate *S. maltophilia* as it is frequently associated with polymicrobial infections or grows slowly in the host. Because several previously proposed species are recognized to be closely related to *S. maltophilia*, it might be referred to as ‘*S. maltophilia* complex’ including *Stenotrophomonas pavanii*, *Stenotrophomonas africana*, *Pseudomonas geniculata*, *Pseudomonas hibisciola* and *Pseudomonas beteli* (Svensson-Stadler et al., 2012). *S. maltophilia* is intrinsically resistant to several antibiotics commonly used to treat nosocomial infections, which can represent a therapeutic challenge and delay in administration of appropriate antibiotics (Brooke, 2012). It is notable that multidrug-resistant (MDR) *S. maltophilia* isolates have been recovered with increasing frequency in recent years in certain parts of the world (Garazi et al., 2012; Nicodemo et al., 2004; Tan et al., 2008). Trimethoprim/sulfamethoxazole (TMP/SMX) is recommended as the first-line therapy against *S. maltophilia* infections. However, resistance to TMP/SMX is increasing (Toleman et al., 2007; Wu et al., 2012).

*Stenotrophomonas maltophilia* isolates from environmental and clinical sources form several genomic groups based on genotypic analyses (Berg et al., 1999; Minkwitz & Berg, 2001). While six 16S rRNA groups have been identified based on the
sequences of a variable region of the 16S rRNA gene (Minkwitz & Berg, 2001), four phylogenetic groups based on the \textit{smeD–smeT} intergenic sequences were also revealed (Gould et al., 2006). In addition, nine genomic groups of the genus \textit{Stenotrophomonas} were proposed based on \textit{gyrB} restriction fragment length polymorphism (RFLP) analysis (Coenye et al., 2004a). The latter study found that the majority of isolates from cystic fibrosis patients grouped into two genomic groups, indicating the existence of particular \textit{S. maltophilia} subgroups of different ecological origin and clinical importance. However, multilocus sequence typing (MLST) analysis did not support the evidence for particularly virulent genogroups, although several genogroups were identified in that study (Kaiser et al., 2009).

The present study reports the genetic diversity and antimicrobial resistance of \textit{S. maltophilia} complex isolates from Korea. We classified the \textit{S. maltophilia} complex isolates into several groups based on partial \textit{gyrB} gene sequences and showed that the antimicrobial resistance rates varied markedly between groups.

**METHODS**

**\textit{S. maltophilia} isolates.** A total of 121 isolates tentatively identified as \textit{S. maltophilia} were included in this study. They were collected from seven tertiary-care hospitals in Korea from 2007 to 2011 and were identified conventionally using VITEK2 systems in the hospitals’ clinical microbiology laboratories. Among them, 85 isolates were from blood, and the others were from sputum (nine isolates), urine (eight isolates), endotracheal aspirate (five isolates), transtracheal aspirate (five isolates), bile (three isolates), pericardial fluid (two isolates), pus (two isolates) and ear discharge (one isolate). The source of one isolate was unknown.

**Species identification and grouping.** To identify the isolates of \textit{Stenotrophomonas} spp., we tried to determine the partial \textit{gyrB} gene sequence of all isolates using primers XgyrBIF (5’-ACGAGTACAA-CCCCAGCACA-3’) and XgyrBIR (5’-CCCATCARGGTGGCTGAAG-AT-3’), which amplified one of the variable regions of the \textit{gyrB} gene, region 2 (Svensson-Stadler et al., 2012). We obtained unambiguous 726 bp sequences from 118 isolates. The \textit{gyrB} sequences of 33 reference strains, which were reported previously (Svensson-Stadler et al., 2012), were retrieved from the GenBank database and were included in the analysis. For species identification and grouping, a phylogenetic tree based on the 151 determined and retrieved \textit{gyrB} gene sequences was constructed using the neighbour-joining method.

**In vitro antimicrobial susceptibility testing.** In vitro susceptibility testing was performed with 118 isolates identified as \textit{S. maltophilia} complex in this study, according to CLSI guidelines (CLSI, 2009). The broth agar dilution method was used for ceftazidime, levofloxacin, piperacillin/tazobactam and tigecycline; the agar dilution method was used for TMP/SMX. For the combination of piperacillin/tazobactam, the criteria for \textit{Enterobacteriaceae} (susceptible \( \leq 2 \) mg l\(^{-1}\); intermediate 4 mg l\(^{-1}\); resistant \( >8 \) mg l\(^{-1}\)). For piperacillin/tazobactam, the criteria of \textit{Acinetobacter} spp. in the CLSI guidelines were used (susceptible \( \leq 16/2 \) mg l\(^{-1}\); intermediate 32/4 to 64/4 mg l\(^{-1}\), resistant \( \geq 128/4 \) mg l\(^{-1}\)). \textit{Escherichia coli} ATCC 25922 and \textit{Pseudomonas aeruginosa} ATCC 27853 were used as control strains. The MICs of control strains were within the acceptable QC ranges. An MDR isolate was defined as one showing resistance to two or more antimicrobial agents.

**Statistical analysis.** Data were analysed using SPSS 11.0 for Windows 2000. Categorical data were tested using \( \chi^2 \) analysis. Differences were considered statistically significant at \( P<0.05 \) for all tests.

**RESULTS**

Based on partial \textit{gyrB} gene sequences (726 bp), 118 isolates were identified as belonging to \textit{S. maltophilia} complex, such as \textit{S. maltophilia}, \textit{S. pavanii}, \textit{P. beteli}, \textit{P. geniculata}, \textit{P. hibisciola} and ‘\textit{S. africana}’ (Fig. 1). We could not obtain unambiguous \textit{gyrB} gene sequences from three isolates, which were excluded from further analyses. Isolates showing \textit{gyrB} gene sequence divergence of \(<4.0\%\) and forming one cluster in the \textit{gyrB} gene tree were identified as belonging to the same species or group of \textit{S. maltophilia} complex (Svensson-Stadler et al., 2012). Remarkably, the \textit{S. maltophilia} isolates, including 10 reference strains, did not cluster into one group. Thus, we classified \textit{S. maltophilia} isolates into three groups. \textit{S. maltophilia} group I included 39 isolates and six \textit{S. maltophilia} reference strains including the type strain, CCUG 5866\(^T\). \textit{S. maltophilia} group I could be further separated into two subgroups, I-1 (32 isolates) and I-2 (seven isolates). \textit{P. geniculata}, which was related to \textit{S. maltophilia} group I, included 10 isolates. One \textit{S. maltophilia} reference strain, CCUG 54442, was classified as \textit{P. geniculata}. Thirty-seven isolates belonged to \textit{S. maltophilia} group II, which included only one reference strain, CCUG 58019. This \textit{S. maltophilia} group II could be further classified into three subgroups, II-1 (28 isolates), II-2 (six isolates) and II-3 (two isolates). Seven isolates and one reference strain (CCUG 35078) were identified as \textit{S. maltophilia} group III. \textit{S. pavanii} clustered with \textit{S. maltophilia} groups II and III and included 18 isolates. Two \textit{P. beteli} and one \textit{P. hibisciola} were also identified. One isolate, SMC1008-158, was closely related to ‘\textit{S. africana}’. \textit{S. maltophilia} group II, \textit{S. pavanii}, \textit{S. maltophilia} group III and \textit{P. beteli} formed one clade (clade A), and \textit{S. maltophilia} group I, \textit{P. geniculata}, \textit{P. hibisciola} and ‘\textit{S. africana}’ formed another clade (clade B) (Fig. 1). Three isolates, K01-43, 08-B-253 and B0811-107, could not be classified to a particular group based on \textit{gyrB} gene sequences, although they were considered to belong to the \textit{S. maltophilia} complex (Fig. 1).

Among 83 isolates from blood, \textit{S. maltophilia} group II was the most frequently identified (30 isolates, 36.1 %), followed by \textit{S. maltophilia} group I (24 isolates, 28.9 %), \textit{S. pavanii} (13 isolates, 15.7 %), \textit{P. geniculata} (seven isolates, 8.4 %) and \textit{S. maltophilia} group III (five isolates, 6.0 %). Thus, 81.1 % of the 37 \textit{S. maltophilia} group II were isolated from blood.

For all \textit{S. maltophilia} complex isolates, the resistance rates to TMP/SMX and levofloxacin were the highest (30.5 %) among the five antimicrobial agents tested (Table 1).
**Fig. 1.** Phylogenetic grouping of 118 clinical isolates and 33 reference strains of *S. maltophilia* complex inferred from partial *gyrB* gene sequences (726 bp). Only reference strains and three unclassified isolates (K01-43, 08-B-253, and B0811-107) are represented in the tree. Species and groups of *S. maltophilia* complex are indicated. This tree was constructed by the neighbour-joining method. *X. campestris* ATCC 33913T was used as an outgroup.
Table 1. Activity of antimicrobial agents against *S. maltophilia* complex isolates

<table>
<thead>
<tr>
<th>Agent</th>
<th>MIC (mg l(^{-1}))</th>
<th>No. of isolates (%)</th>
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<tbody>
<tr>
<td></td>
<td>MIC(_{50})</td>
<td>MIC(_{90})</td>
</tr>
<tr>
<td>Ceftazidime</td>
<td>8</td>
<td>64</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>2</td>
<td>16</td>
</tr>
<tr>
<td>TMP/SMX</td>
<td>2/38</td>
<td>16/304</td>
</tr>
<tr>
<td>P/T</td>
<td>16/4</td>
<td>128/4</td>
</tr>
<tr>
<td>Tigecycline</td>
<td>2</td>
<td>8</td>
</tr>
<tr>
<td>MDR</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

MIC\(_{50}\) and MIC\(_{90}\) of TMP/SMX were 2/38 and 16/304 mg l\(^{-1}\), respectively. The resistance rate to ceftazidime was 28.0%. Of the 118 *S. maltophilia* complex isolates, 11.0% and 11.9% displayed resistance to piperacillin/tazobactam and tigecycline, respectively. We identified 38 MDR isolates (32.2%).

Antimicrobial resistance rates varied among the groups of the *S. maltophilia* complex (Table 2). Overall, isolates of clade A showed significantly lower antimicrobial resistance rates than those of clade B except for levofloxacin. While the TMP/SMX resistance rates of *S. maltophilia* group II, *S. pavanii* and *S. maltophilia* group III of clade A were 16.2%, 33.3% and 42.9%, respectively, 28.2% and 60.0% of *S. maltophilia* group I and *P. geniculata* isolates of clade B were resistant to TMP/SMX, respectively (\(P=0.203\)). In addition to TMP/SMX, ceftazidime resistance rates were also significantly lower in groups of clade A (\(P<0.001\)). Tigecycline-resistant isolates were found in *S. maltophilia* group II (four isolates, 10.8%), *S. maltophilia* group I (four isolates, 10.3%) and *P. geniculata* (three isolates, 30.0%), but no tigecycline-resistant isolates were found in *S. pavanii* and *S. maltophilia* group III (\(P=0.003\)). Although levofloxacin and piperacillin/tazobactam resistance rates did not significantly vary among the groups, they were also high or low in certain groups. Levofloxacin resistance rates were very low in *S. pavanii* and *S. maltophilia* group III isolates (5.6% and 0%, respectively), and *S. maltophilia* group II and *S. maltophilia* group III of clade A and *S. maltophilia* group I of clade B showed very low piperacillin/tazobactam resistance rates (5.4%, 0% and 5.1%, respectively). The MDR rates were also significantly higher in *S. maltophilia* group I and *P. geniculata* of clade A (41.0% and 60.0%, respectively) (\(P=0.001\)).

Although *S. maltophilia* groups I and II isolates could be further divided into two and three subgroups, respectively, antimicrobial resistance rates were not significantly different among the subgroups (data not shown). Among 83 isolates from blood, antimicrobial resistance rates were not significantly different from the others: 30.1% to ceftazidime, 32.5% to levofloxacin, 32.5% to TMP/SMX, 14.5% to tigecycline and 12.0% to piperacillin/tazobactam. One isolate, SMC1102-153, belonging to *P. geniculata*, showed resistance to all five antimicrobial agents tested in this study.

**DISCUSSION**

The most notable finding in this study is the high resistance rate to TMP/SMX. Worldwide surveillance studies showed relatively low resistance rates varying from 4% to 10% (Brooke, 2012; Farrell et al., 2010). A recent report from a Korean hospital also documented a low resistance rate of 6% to TMP/SMX using the agar dilution method (Chung et al., 2012). Thus, the high TMP/SMX resistance rate of 30.5% noted in our study might be unexpected. However, it has been reported that 17.5% of *S. maltophilia* isolates were resistant to TMP/SMX in Taiwan (Wu et al., 2012), and a study from Germany reported that only 34.4% of *S. maltophilia* isolates from sputum of cystic fibrosis patients were susceptible to TMP/SMX (Valenza et al., 2008). The difference in the TMP/SMX resistance rate between different studies in Korea may be due to the different hospitals, isolation period and number of isolates. In addition, most of our isolates were from blood, which might show higher resistance rates. The high TMP/SMX resistance rate found in this study is of concern because the preferred treatment option of *S. maltophilia* infections is TMP/SMX (Brooke, 2012). Thus, continuous surveillance of antimicrobial resistance in *S. maltophilia* is recommended. In contrast to the high resistance to TMP/SMX, piperacillin/tazobactam and tigecycline showed potent activities against *S. maltophilia* complex isolates. This suggests that tigecycline would be an alternative option for treatment of *S. maltophilia* infections in regions of high resistance to TMP/SMX. Tigecycline has been considered as an alternative therapeutic option, mainly as a component of combination therapy (Looney et al., 2009).

To date, the genus *Stenotrophomonas* includes 13 described species (www.bacterio.cict.fr/s/stenotrophomonas.html). However, *‘S. africana’* was revealed to be a later synonym of *S. maltophilia* (Coenye et al., 2004b; Kaiser et al., 2009). *S. pavanii*, which was characterized recently and was proposed as a new species based on DNA–DNA hybridization results (Ramos et al., 2011), showed very high similarities with *S. maltophilia* strains in 16S rRNA and gyrB gene analyses (Svenssson-Stadler et al., 2012). In addition, *Pseudomonas beteli*, *P. geniculata* and *P. hibisciola* were found not to belong to the genus *Pseudomonas* (Anzai et al., 2000). Instead, they were undifferentiated from *S. maltophilia* strains in 16S rRNA gene analysis (>99.2% similarities), and were clustered with *S. maltophilia* strains in gyrB gene analysis (Fig. 1) (Svenssson-Stadler et al., 2012). Thus, it is logical that they are grouped into the *S. maltophilia* complex.

In this study, *S. maltophilia* complex isolates showed genetic diversity based on gyrB gene sequences. High
Table 2. Activity of antimicrobial agents against S. maltophilia complex isolates

TMP/SMX, trimethoprim/sulfamethoxazole; P/T, piperacillin/tazobactam.

<table>
<thead>
<tr>
<th>Agent</th>
<th>Clade A</th>
<th>Clade B</th>
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<tbody>
<tr>
<td></td>
<td>S. maltophilia II (n=37)</td>
<td>S. maltophilia III (n=7)</td>
</tr>
<tr>
<td></td>
<td>S. pavanii (n=18)</td>
<td></td>
</tr>
<tr>
<td>Ceftazidime</td>
<td>1 (2.7)</td>
<td>3 (16.7)</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>13 (35.1)</td>
<td>1 (5.6)</td>
</tr>
<tr>
<td>TMP/SMX</td>
<td>6 (16.2)</td>
<td>6 (33.3)</td>
</tr>
<tr>
<td>P/T</td>
<td>2 (5.4)</td>
<td>3 (16.7)</td>
</tr>
<tr>
<td>Tigecycline</td>
<td>4 (10.8)</td>
<td>0</td>
</tr>
<tr>
<td>MDR</td>
<td>7 (18.9)</td>
<td>3 (16.7)</td>
</tr>
</tbody>
</table>

genetic diversity of S. maltophilia complex has been reported in several studies using pulsed-field gel electrophoresis and enterobacterial repetitive intergenic consensus polymerase chain reaction (ERIC-PCR) (Song et al., 2010; Valdezate et al., 2004). Studies based on MLST demonstrated that S. maltophilia isolates were heterogeneous (Cho et al., 2012; Kaiser et al., 2009). In this study, the partial gyrB gene sequence showed >91.5% identity among S. maltophilia complex isolates. They could be classified into several groups. In previous studies, several S. maltophilia subgroups have been identified based on 16S rRNA gene, L1 and L2 β-lactamase gene sequences, and the sequences of the smeD–smeT intergenic region (Gould et al., 2004, 2006). The 16S rRNA gene sequence variation of S. maltophilia group I isolates in this study was the same as that of K279a, a representative strain of phylogenetic group A (Gould et al., 2004, 2006). S. maltophilia type strain ATCC 13637T (=CCUG 5866T) was designated as phylogenetic group A (Gould et al., 2006). In the gyrB gene tree in this study, strains K279a and CCUG 5866T belonged to S. maltophilia group I. In addition, S. maltophilia group II isolates showed the same 16S rRNA gene sequence variation as N531, a representative strain of phylogenetic group B. The 16S rRNA gene sequences of P. geniculata and P. hibisciola showed the characteristics of phylogenetic group C (Gould et al., 2004). Thus, overall groupings based on 16S rRNA and gyrB genes may be congruent. However, we also found incongruence between groupings based on the 16S rRNA gene and the gyrB gene. For example, isolate B0906-096 belonged to S. maltophilia group II in this study, but showed a close relationship with P. geniculata in 16S rRNA gene analysis (data not shown).

In a previous study, the phylogenetic groups could be identified, but the authors could not find significant differences between phylogenetic groups in terms of their β-lactam resistance and β-lactamase expression (Gould et al., 2006). However, in this study we identified significant differences of resistance rates to some antimicrobial agents. Table 2 shows that high MDR rates in this study are mainly due to S. maltophilia group I and P. geniculata isolates. This means that accurate identification of Stenotrophomonas species is needed to select appropriate antimicrobial agents. Although antimicrobial resistance mechanisms were not investigated in this study, efflux pumps such as SmeABC and SmeDEF are overexpressed in resistant isolates (Brooke, 2012; Liaw et al., 2010). In addition, a class 1 integron was associated with MDR in S. maltophilia (Liaw et al., 2010). Whether high resistance in certain species or groups is intrinsic or acquired is unclear and requires study.

To summarize, in this study we identified distinct groups among S. maltophilia complex isolates. High antimicrobial resistance rates, particularly to TMP/SMX, were also identified. Antimicrobial resistance rates differed among the groups, indicating the need for accurate identification for appropriate selection of treatment options.

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REFERENCES


