Multilocus Sequence Typing for Clonality Analysis of Antimicrobial-Resistant *Stenotrophomonas maltophilia* Strains

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Stenotrophomonas maltophilia is an opportunistic nosocomial pathogen and is being isolated worldwide with increasing frequency. *S. maltophilia* isolates are often highly resistant to most of the currently used antimicrobial agents, including carbapenems, aminoglycosides, and fluoroquinolones. A variety of antimicrobial resistance mechanisms, including efflux pumps and integrons, have been reported in *S. maltophilia*. In Korea, the isolation rate of *S. maltophilia* is increasing, but few studies have reported the resistance mechanisms of this pathogen. Cho et al. [1] reported the first study on efflux pumps in clinical isolates of *S. maltophilia* in Korea.

Efflux pumps have been shown to play a role in multidrug resistance in *Pseudomonas aeruginosa*, *Burkholderia cepacia*, and *S. maltophilia*. The findings of the study by Cho et al. have indicated that overexpression of SmeABC efflux pumps is important for the fluoroquinolone (ciprofloxacin and levofloxacin) resistance of *S. maltophilia*. The conclusions of this study are interesting from an epidemiological perspective.

Multilocus sequence typing (MLST) has recently been used to type many pathogenic bacteria and fungi. MLST has many advantages over other molecular typing methods; it is easy to perform and produces unambiguous results, and the sequence data can be shared and compared among different hospitals [2]. However, to date, MLST has seldom been applied for typing

clinical *S. maltophilia* isolates. The report by Kaiser et al. [3] described the development of an MLST scheme for *S. maltophilia*. They applied MLST to *S. maltophilia* based on partial sequences (444 to 558 bp) of 7 housekeeping genes. The online database (<http://pubmlst.org/smaltophilia/>) includes 40 to 55 alleles for each of the 7 target gene sequences and 56 multilocus allelic profiles or sequence types (ST), which is considerably lower than the numbers deposited in databases for other bacteria.

Cho et al. [1] used MLST to study the molecular epidemiology of *S. maltophilia* at a university hospital in Korea. The 33 clinical isolates recovered over a 1-yr period exhibited 26 different STs. Of these, 28 isolates exhibited new STs (23 distinct STs), whereas only 5 isolates exhibited previously described STs (3 STs). Their study proved that the MLST scheme for *S. maltophilia* represents a discriminatory typing method with stable markers and that it is appropriate for studying population structures.

The genetic diversity of the *S. maltophilia* isolates in the study by Cho et al. indicates that most of these resistant bacteria may be of a polyclonal nature. However, the authors have emphasized on the clonal nature of the emergence of antimicrobial-resistant *S. maltophilia*, as shown in a phylogenetic analysis of MLST types. Three or 4 isolates showing a high level of resistance to ciprofloxacin and overexpression of the SmeABC efflux system were observed in groups A and A' of the MLST cluster, respectively. Ad-

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ditionally, the group B isolates (4 isolates) were highly resistant to ceftazidime and cefepime. This finding suggests that MLST data can provide evidence of the emergence and spread of antimicrobial-resistant clones of *S. maltophilia*.

Molecular epidemiological studies provide important tools to prevent the further spread of antimicrobial-resistant nosocomial pathogens. MLST can be used as an alternative to pulsed-field gel electrophoresis (PFGE) in clinical microbiology. Many studies have suggested that these techniques have similar powers of discrimination for several pathogens, but this discriminatory power differs among species. MLST generally provides information on the evolutionary history, population structure, and long-term global epidemiology of pathogens, whereas PFGE is better for investigation of outbreaks and potential transmission events over a short period of time [2]. Therefore, after further validation and comparison with PFGE by using a larger collection of isolates, MLST may play a role in clinical microbiology by facilitating the investigation of molecular epidemiology of *S. maltophilia* strains.

The present MLST analysis provides valuable data regarding the current epidemic status of antimicrobial-resistant *S. maltophilia* isolates and their antimicrobial efflux mechanisms under hospital settings. The increase in the prevalence of nosocomial *S. maltophilia* infections is principally because of the changing

characteristics of hospitalized patients and use of antibiotics. In this regard, the work of Cho et al. is important because it highlights the fact that MLST is a useful method to elucidate the trends of resistance in *S. maltophilia* isolates associated with nosocomial infections. Moreover, this technique will facilitate identification of the clonality and evolutionary relatedness of antimicrobial-resistant *S. maltophilia* isolates.

Authors' Disclosures of Potential Conflicts of Interest

No potential conflict of interest relevant to this article was reported.

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