Risk factors for mortality in patients with *Stenotrophomonas maltophilia* bacteremia and clinical impact of quinolone–resistant strains

Eun Jin Kim¹, Yong Chan Kim¹, Jin Young Ahn², Su Jin Jeong²*, Nam Su Ku², Jun Yong Choi², Joon-Sup Yeom² and Young Goo Song²

**Abstract**

**Background:** *Stenotrophomonas maltophilia* is an important nosocomial pathogen. This pathogen has intrinsic or acquired resistance to a number of antibiotics classes. Furthermore, *Stenotrophomonas* infections have been associated with high mortality, mainly in immunocompromised patients. Accordingly, we conducted a retrospective cohort study on the clinical data, microbiological characteristics, and outcomes of patients with *S. maltophilia* (SM) bacteremia.

**Methods:** A retrospective cohort study was conducted at two tertiary care referral hospitals in Seoul, South Korea. Data were collected between January 2006 and December 2015 from electric medical records. Our analysis aimed to identify the risk factors associated with crude mortality, as well as the predictive factors of quinolone-resistant strains in SM bacteremia patients.

**Results:** A total of 126 bacteremia patients were enrolled in the study. The mortality rate was 65.1%. On multivariable analysis, hypoalbuminemia (odds ratio [OR], 5.090; 95% confidence interval [CI], 1.321–19.621; *P* = 0.018), hematologic malignancy (OR, 35.567; 95% CI, 2.517–502.515; *P* = 0.008) and quinolone-resistant strains (OR, 7.785; 95% CI, 1.278–47.432; *P* = 0.026) were independent risk factors for mortality. Alternatively, usage of an empirical regimen with quinolone (OR, 0.172; 95% CI, 0.034–0.875; *P* = 0.034) was an independent protective factor for mortality. The multivariable analysis of predictive factors revealed that high Charlson comorbidity index (OR, 1.190; 95% CI, 1.040–1.361; *P* = 0.011) and indwelling of a central venous catheter (CVC) (OR, 3.303; 95% CI, 1.194–9.139; *P* = 0.021) were independent predisposing factors associated with quinolone-resistant strains in SM bacteremia patients.

**Conclusions:** Our findings suggest that a high Charlson comorbidity score and indwelling of a CVC were significantly independent predictors of quinolone-resistant strains in SM bacteremia patients. Therefore, we need to carefully consider the antibiotic use in SM bacteremia patients with these predictive factors.

**Keywords:** Quinolone-resistant strains, *Stenotrophomonas maltophilia*, Bacteremia
Background

*Stenotrophomonas maltophilia* is a non-fermentative, gram-negative bacillus that is closely related to the *Pseudomonas* species. *Bacterium bookeri*, now known as *S. maltophilia* (SM), was first isolated in 1943 and was subsequently classified as a member of the genus *Pseudomonas* in 1961. Thereafter, it was classified as a member of *Xanthomonas* genus in 1983, and finally it came to rest in the *Stenotrophomonas* genus in 1993 [1]. SM is a bacterium that can occur in almost any aquatic or humid environment [2], and is not considered to be a highly virulent pathogen. Over the last decade, SM has risen to prominence as an important nosocomial pathogen associated with significant case/fatality ratios in certain patient populations, particularly in individuals who are severely debilitated or immunosuppressed [3–5]. Pneumonia and bacteremia are the most common manifestations of SM infection [6]. However, treatment of SM bacteremia is challenging due to the resistance of SM to many broad-spectrum antimicrobial agents. Moreover, SM exhibits high-level intrinsic resistance to a variety of structurally unrelated antibiotics, including: beta-lactams, quinolones, aminoglycosides, tetracycline, disinfectants, and heavy metals [7, 8]. Furthermore, it can acquire resistance through the uptake of resistance genes located on integrons, transposons, and plasmids via horizontal gene transfer and mutations [9, 10]. Thus, choosing the optimal antibiotic for the treatment of SM bacteremia is very difficult. Trimethoprim-sulfamethoxazole (TMP-SMX) should be considered as the empirical choice for clinically suspected SM infections and as the treatment of choice for culture-proven infections by this agent [11, 12]. However, due to concerns regarding adverse events related to TMP-SMX treatment, levofloxacin has also been used as an alternative option [13, 14]. Fluoroquinolone and SMX monotherapies may be equally effective for the treatment of SM infections [15]. But, the overuse of quinolones worldwide has resulted in higher resistance rates in SM [16–18]. Therefore, we investigated the predictive factors of quinolone-resistant strains in SM bacteremia patients.

Methods

Study population and design

A retrospective cohort study was conducted at two tertiary care referral hospitals in Seoul, South Korea. Data were collected between January 2006 and December 2014 from digital medical records. Patients 18 years or older with 1 or more positive blood cultures of SM that met the Centers for Disease Control and Prevention (CDC) criteria for blood stream infection (BSI) [19], were eligible for inclusion. If a patient had multiple episodes of bacteremia, only the data from the first episode were included.
occurrence of SM bacteremia was 57.1 ± 22.5 days. The mean length of stay in the hospital before the onset of bacteremia was 15.07 years and the 68.3% (86/126) of the patients were men. The mean age of the patients was 61.22 ± 15.07 years. 

In vitro antimicrobial susceptibility testing
All bacterial species were identified using conventional methods and/or the ATB 32GN system (bioMerieux, Marcy l’Etoile, France). Antimicrobial susceptibility tests were performed using the disk diffusion method or a VITEK-2 N131 card (bioMerieux, Hazelwood, MO, USA). The results were interpreted based on the Clinical and Laboratory Standards Institute (CLSI) guidelines [22]. SM isolates resistant to TMP-SMX were defined to have a minimal inhibitory concentration (MIC) ≥4/76 mg/mL to TMP-SMX. SM isolates which were resistant to levofloxacin (MIC ≥8 mg/mL) or those with intermediate resistance (MIC = 4 mg/mL) to levofloxacin were defined as quinolone-resistant strains.

Statistical analysis
All statistical analyses were performed using SPSS for Windows (ver. 23.0, SPSS Inc., Chicago, IL, USA). The statistical analyses were performed to assess the factors associated with crude mortality and quinolone susceptibility. Continuous variables were expressed as mean ± standard deviation (SD), and categorical variables were expressed as a number (percentage). The Kolmogorov-Smirnov test was used to analyze the normality of the distribution of parameters. Data that did not show normal distributions were expressed as median and interquartile ranges (IQR). The Student’s t-test was used for continuous variables and the Chi-square test or Fisher’s exact test was used for categorical variables. Variables that did not show normal distributions were compared using the Mann-Whitney test or Kruskal-Wallis test. Univariate and multivariable logistic regression was used to evaluate the risk factors of mortality and the predictive factors of quinolone-resistant strains. Variables with p-values of less than 0.10 in univariate analyses were included in a multivariable logistic regression analysis to identify the risk factors associated with mortality and the predictive factors of quinolone-resistant strains. Results from the multivariate analysis are expressed as an odds ratio (OR) and 95% confidence interval (CI). All statistical tests were two-tailed and a P value of less than 0.05 was considered to be statistically significant.

Results
Baseline characteristics of SM bacteremia patients and comparison of clinical characteristics and outcomes
During the study period, 126 bacteremia patients were enrolled. The mean age of the patients was 61.22 ± 15.07 years and the 68.3% (86/126) of the patients were men. The mean length of stay in the hospital before the occurrence of SM bacteremia was 57.1 ± 22.5 days. The mean Charlson comorbidity index score was 6.5 ± 3.2 and the median APACHE II score was 13.0 (IQR, 9–19).

Multivariable analyses were performed to investigate the risk factors of mortality in SM bacteremia patients. Table 1 shows a comparison of survivors and non-survivors during the entire hospitalization period. Univariate analyses, showed that hematologic malignancy (P = 0.005), indwelling of hemodialysis catheter (P = 0.028), high APACHE II scores (P = 0.001), hypoalbuminemia (P = 0.003), thrombocytopenia (P = 0.004), and low hemoglobin concentration (P = 0.035) were associated with mortality. Also, the length of stay before bacteremia was longer in non-survivors (P = 0.038).

Anatomic origin and microbiologic findings of SM bacteremia are presented in Table 2. Catheter-related infection was the most common primary source of bacteremia (49 cases, 38.9%), followed by intra-abdomen infection (38 case, 30.2%) and respiratory infection (35 cases, 27.8%). The rate of CVC removal was 59.3% (54/91). In our study, 11.9% (15/126) of patients had SM strains resistant to TMP/SMX, and 31.2% (39/126) had strains resistant to quinolone. Only 21 patients (16.7%) were using an empirical regimen with quinolone and there were no cases using an empirical regimen with TMP/SMX. The number of patients under a definitive regimen with quinolone was 32% (40/126), and with TMP/SMX it was 24.8% (31/126).

Mortality risk factors in SM bacteremia patients
On multivariable analysis, hypoalbuminemia (OR, 5.090; 95% CI, 1.321–19.621; P = 0.018), hematologic malignancy (OR, 35.567; 95% CI, 2.517–502.515; P = 0.008) and quinolone-resistant strains (OR, 7.785; 95% CI, 1.278–47.432; P = 0.026) were independent risk factors for mortality. Contrary, usage of an empirical regimen with quinolone (OR, 0.172; 95% CI, 0.034–0.875; P = 0.034) was independent protective factors for mortality (Table 3).

Predicting factors for SM bacteremia with quinolone-resistant strains
Analyses of predictive factors for SM bacteremia with quinolone-resistant strains were performed (Table 4). One patient died immediately on the day of bacteremia and was excluded from this analysis due to death not related to antibiotic adequacy (N = 125 cases). On univariate analysis, high Charlson comorbidity index and long lengths of hospital stay before the onset of bacteremia were significant related factors (P = 0.030 and P = 0.015). Indwelling of CVC, ventilator, and Foley catheter were additional risk factors. Quinolone-resistant SM patients had a significantly higher mortality than the quinolone sensitive group (P = 0.001 and P = 0.013). Based on this multivariable analysis, the Charlson comorbidity index (OR, 1.190; 95%...
Table 1 Baseline characteristics of patients with *S. maltophilia* bacteremia

| Factors                                      | Survivors N = 44 | Non-survivors N = 82 | p value |
|----------------------------------------------|------------------|----------------------|---------|
| **Baseline characteristics**                 |                  |                      |         |
| Age, y, mean ± SD                            | 71.0 (60.5–79)   | 74.5 (61.0–80.25)    | 0.310   |
| Age ≥ 65 years, n(%)                         | 24 (54.5)        | 34 (41.5)            | 0.160   |
| Male, n (%)                                  | 33 (75.0)        | 53 (64.6)            | 0.233   |
| BMI, kg/m², median (IQR)                     | 21.7 (19.4–25.0) | 21.9 (19.0–24.4)     | 0.847   |
| **Comorbidities**                            |                  |                      |         |
| HTN, n (%)                                   | 15 (34.1)        | 32 (39.0)            | 0.585   |
| DM, n (%)                                    | 16 (36.4)        | 23 (28.0)            | 0.336   |
| Cardiovascular disease, n (%)                | 9 (20.5)         | 13 (15.9)            | 0.517   |
| Chronic kidney diseasea, n (%)               | 4 (9.1)          | 4 (4.9)              | 0.449   |
| End stage renal disease, n (%)               | 1 (2.3)          | 7 (8.5)              | 0.259   |
| Chronic liver disease, n (%)                 | 5 (11.4)         | 11 (13.4)            | 0.742   |
| Pulmonary disease, n (%)                     | 4 (9.1)          | 8 (9.8)              | 1.000   |
| Solid tumor, n (%)                           | 18 (40.9)        | 43 (52.4)            | 0.217   |
| Hematologic malignancy, n (%)                | 1 (2.3)          | 17 (20.7)            | 0.005   |
| Solid organ transplantation, n (%)           | 3 (6.8)          | 4 (4.9)              | 0.694   |
| Charlson score, mean ± SD                    | 5.7 ± 3.0        | 6.9 ± 3.2            | 0.049   |
| **Predisposing factors**                     |                  |                      |         |
| Chemotherapy, n (%)                          | 4 (9.1)          | 10 (12.2)            | 0.769   |
| Major surgery a, n (%)                       | 15 (34.9)        | 29 (35.4)            | 0.957   |
| ICU care, n (%)                              | 29 (65.9)        | 54 (65.9)            | 0.995   |
| Length of stay in hospital before bacteremia (days), median (IQR) | 12.0 (3.5–24.5) | 26.0 (14.0–56.0) | 0.038   |
| Central venous catheter, n (%)               | 31 (70.5)        | 59 (72.8)            | 0.777   |
| Hemodialysis catheter, n (%)                 | 2 (4.5)          | 15 (18.8)            | 0.028   |
| Mechanical ventilator, n (%)                 | 19 (43.2)        | 41 (50.6)            | 0.427   |
| Foley catheter, n (%)                        | 28 (63.6)        | 47 (58.0)            | 0.541   |
| **Clinical severity**                        |                  |                      |         |
| Shock, n (%)                                 | 10 (22.7)        | 33 (40.2)            | 0.075   |
| APACHE II score, mean ± SD                   | 11.0 ± 5.8       | 15.4 ± 6.9           | < 0.001 |
| **Laboratory findings**                      |                  |                      |         |
| Neutropenia, n (%)                           | 3 (6.8)          | 15 (18.3)            | 0.079   |
| Hypoalbuminemia, n (%)                       | 18 (6.8)         | 56 (18.3)            | 0.003   |
| Thrombocytopenia, n (%)                      | 9 (20.5)         | 38 (46.3)            | 0.004   |
| Hemoglobin (g/L), mean ± SD                  | 10.1 ± 1.6       | 9.4 ± 1.5            | 0.032   |
| C-reactive protein (mg/L), median (IQR)      | 69.2 (32.2–129.5)| 89.3 (58.5–148.0)    | 0.057   |
| Estimated GFR (ml/min per 1.73m²), median (IQR) | 85.0 (54.2–98.0) | 80.0 (44.0–104.0)    | 0.675   |
| Hospital stay, days                          | 53.0 (20.5–78.0) | 60.0 (35.0–97.0)     | 0.137   |
| Length of stay in ICU, days                  | 30 (11.5–50.0)   | 39 (23.0–67.0)       | 0.640   |

Note. SD Standard deviation, BMI Body mass index, IQR Interquartile range, HTN Hypertension, DM Diabetes mellitus, ICU Intensive care unit, APACHE II Acute Physiologic and Chronic Health Evaluation II score

a Major surgery, any surgical procedure that involves anesthesia or respiratory assistance
CI, 1.040–1.361; \( P = 0.011 \) and indwelling of a CVC (OR, 3.303; 95% CI, 1.194–9.139; \( P = 0.021 \) were identified as independent predisposing factors associated with quinolone-resistant strains in SM bacteremia patients.

### Discussion

Among non-fermenting gram negative bacilli, SM has been reported to be the third most commonly isolated pathogen after *Pseudomonas aeruginosa* and *Acinetobacter baumanii* [23]. Furthermore, SM bacteremia is associated with high mortality rates, the crude mortality estimates range from 21 to 69% [23]. Previous studies have reported that risk factors associated with mortality for SM bacteremia include indwelling of CVC in intensive care units, immunocompromising conditions, exposure to broad-spectrum antibiotic therapy, and long hospital stays [3, 9, 23]. In our study, the mortality rate of 65.1% was similar to the rate reported in previous studies.

#### Table 2

| Infection source          | Survivors \( N = 44 \) | Non-survivors \( N = 82 \) | \( p \) value |
|---------------------------|------------------------|-----------------------------|--------------|
| Pneumonia                 | 12 (27.9)              | 23 (28.0)                   | 0.987        |
| Catheter-related infection| 15 (34.1)              | 34 (42.0)                   | 0.202        |
| Intra-abdominal infection | 16 (36.4)              | 22 (27.2)                   | 0.285        |
| Soft tissue infection     | 0 (0.0)                | 5 (6.2)                     | 0.161        |
| Urinary tract infection   | 1 (2.3)                | 0 (0.0)                     | 0.352        |
| Polymicrobial infection   | 18 (40.9)              | 36 (43.9)                   | 0.746        |

| Antibiotics susceptibility | Survivors \( N = 44 \) | Non-survivors \( N = 82 \) | \( p \) value |
|----------------------------|------------------------|-----------------------------|--------------|
| Quinolone resistance       | 5 (11.6)               | 34 (41.5)                   | 0.001        |
| TMP-SMX resistance         | 3 (6.8)                | 12 (14.6)                   | 0.197        |
| Resistant strain\(^a\)     | 17 (38.6)              | 49 (59.8)                   | 0.024        |

#### Table 3

| Factors                          | OR    | 95% CI            | \( p \) value |
|----------------------------------|-------|-------------------|--------------|
| Hematologic malignancy           | 35.57 | 2.52–502.52       | 0.008        |
| Hypoalbuminemia                  | 5.09  | 1.32–19.62        | 0.018        |
| Quinolone resistance             | 7.79  | 1.28–47.43        | 0.026        |
| Empirical antibiotic - quinolone use | 0.17  | 0.03–0.88         | 0.034        |

Note. BLBLIs Beta-lactam/beta-lactamase inhibitors, TMP-SMX Trimethoprim-sulfamethoxazole

\(^a\)Resistant strain, Quinolone or/and TMP-SMX resistance

\(^b\)Appropriate antimicrobial therapy, the administration of at least one agent to which the index SM isolate was susceptible in vitro
quinolone-resistant SM bacteremia. There have been studies of risk factors related to the acquisition of resistance to levofloxacin in all clinical specimens and to quinolone susceptibility using only respiratory tract specimens with SM [17, 24]. In respiratory tract specimens, a relative factor for resistance to quinolone was the previous use of piperacillin/tazobactam, and risk factors to levofloxacin resistance were exposure to levofloxacin for more than 3 weeks and co-

Table 4 Comparisons of Clinical characteristics between quinolone-susceptible and quinolone-resistant groups

| Factors                     | Susceptible group N = 86 | Resistant group N = 39 | p value |
|-----------------------------|--------------------------|------------------------|---------|
| Age, years                  | 63.0 (51.0–70.0)         | 66.0 (53.5–72.5)       | 0.215   |
| Age ≥ 65 years, n(%)        | 37 (43.0)                | 20 (51.3)              | 0.390   |
| Gender, male                | 57 (66.3)                | 29 (64.6)              | 0.233   |
| Comorbidities               |                          |                        |         |
| HTN                         | 30 (34.9)                | 16 (41.0)              | 0.509   |
| DM                          | 29 (33.7)                | 10 (25.6)              | 0.366   |
| Cardiovascular disease      | 13 (15.1)                | 9 (23.1)               | 0.279   |
| Chronic kidney disease      | 6 (7.0)                  | 2 (5.1)                | 1.000   |
| End stage renal disease     | 4 (4.7)                  | 4 (10.3)               | 0.255   |
| Chronic liver disease       | 12 (14.0)                | 4 (10.3)               | 0.774   |
| Pulmonary disease           | 8 (9.3)                  | 4 (10.3)               | 1.000   |
| Solid tumor                 | 42 (48.8)                | 19 (48.7)              | 0.990   |
| Hematologic malignancy      | 12 (14.0)                | 6 (15.4)               | 0.833   |
| Solid organ transplantation  | 5 (5.8)                  | 2 (5.1)                | 1.000   |
| Charlson score              | 6.1 ± 3.1                | 7.4 ± 3.2              | 0.030   |
| Predisposing factors        |                          |                        |         |
| Chemotherapy                | 11 (12.8)                | 3 (7.7)                | 0.546   |
| Major surgery*              | 28 (32.9)                | 16 (35.4)              | 0.382   |
| ICU care                    | 54 (62.8)                | 29 (74.4)              | 0.205   |
| Hospital stay before bacteremia, days | 17.0 (8.0–34.0) | 30.0 (13.5–57.5)       | 0.015   |
| Central venous catheter     | 57 (66.3)                | 32 (84.2)              | 0.019   |
| Hemodialysis catheter       | 9 (10.5)                 | 8 (21.6)               | 0.100   |
| Mechanical ventilator       | 36 (41.9)                | 24 (63.2)              | 0.029   |
| Foley catheter              | 47 (54.7)                | 28 (73.7)              | 0.046   |
| Clinical findings           |                          |                        |         |
| Shock                       | 23 (26.7)                | 20 (51.3)              | 0.007   |
| APACHE II score             | 13.0 (8.0; 18.0)         | 14.0 (11.0; 21.5)      | 0.115   |
| Laboratory findings         |                          |                        |         |
| Neutropenia                 | 14 (16.3)                | 4 (10.3)               | 0.374   |
| Hypoalbuminemia             | 52 (60.5)                | 21 (53.8)              | 0.487   |
| Thrombocytopenia            | 28 (32.6)                | 19 (48.7)              | 0.084   |
| Hemoglobin, g/L             | 9.8 ± 1.7                | 9.4 ± 1.3              | 0.296   |
| C-reactive protein, mg/L    | 86.8 (41.5–142.5)        | 79.3 (44.5–153.0)      | 0.914   |
| Estimated GFR, ml/min per 1.73m² | 87.0 (51.0–101.0)  | 72.0 (45.4–106.0)      | 0.592   |
| Outcomes                    |                          |                        |         |
| Inappropriate antimicrobial therapy | 23 (26.7) | 16 (42.1)              | 0.089   |
| Hospital stay, days         | 50.0 (26.0–78.0)         | 68.0 (35.0–150.0)      | 0.054   |
| Mortality                   | 48 (55.8)                | 34 (87.2)              | 0.001   |

Note. HTN Hypertension, DM Diabetes mellitus, ICU Intensive care unit, APACHE II Acute Physiologic and Chronic Health Evaluation II score
The data were expressed as mean ± standard deviation, number (%), or median (interquartile range)
* Major surgery, any surgical procedure that involves anesthesia or respiratory assistance
infection/co-colonization with *Klebsiella pneumoniae* resistant to levofloxacin.

In this report, a high Charlson comorbidity index and indwelling of CVC were independent risk factors associated with resistance to quinolone in SM bacteremia. The Charlson comorbidity index is a widely used comorbidity index [21]. A high CCI value means that many coexistent diseases may directly or indirectly affect the choice of antibiotics used and the outcome [25]. Especially, the presence of many coexistent diseases suggests that the previous use of antibiotics, or a prolonged history of hospital admissions, provides opportunities for coexistent diseases to develop. Furthermore, a high CCI value is associated with a greater risk to acquire common antibiotic resistance. This may be due to previous antibiotic uptake or hospital stays, however, this analysis was not part of our study and further studies are needed.

Indwelling of CVC has already been shown to be significantly associated with mortality and bacteremia in previous literature [9]. In particular, removal of CVC has been associated with reduced mortality [26–28]. However, removal of CVC did not influence mortality and quinolone resistance in this report. It is estimated that the rate of patients who adequately removed CVC was only 40%, and therefore did not significantly affect the outcome. SM has the ability to adhere on prosthetic devices such as CVC and form a biofilm. Biofilms can increase antibiotic resistance [11]. Therefore, indwelling of CVC is a risk factor to biofilm formation and, accordingly, to quinolone-resistance. Therefore, it is necessary to actively encourage the removal of CVC.

Previous literature has proven the relationship between inappropriate antimicrobial therapy and mortality in SM infections [23, 27]. Although not relevant to this study, usage of empirical quinolone had a significantly reduced mortality risk. Empirical antibiotic regimens are determined by the severity of patients. Therefore, patients that underwent an empirical quinolone regimen were more likely to have low SM severity and lower mortality. Overall, the periods of empirical antibiotic use were short and there were no patients using TMP / SMX empirically, so whether the empirical use of quinolone actually had a significant impact needs to be analyzed further. Also, SM infections may not be an independent contributor to mortality increase, therefore inappropriate therapy should not have major effects on the outcome of patients [29]. The rate of polymicrobial infections in SM bacteremia was high in the previous literature [23] and in this study as well (42.8%). Thus, high polymicrobial infections may be a confounding factor for appropriate antibiotic use, and this may have affected the mortality risk-factor analysis. Therefore, subgroup analysis was performed in patients with polymicrobial infection. However, there was no significant difference between the two groups regarding mortality (Additional file 1: Table S1).

Significantly, the use of empirical or definitive treatment of carbapenem was higher in the mortality group, although it was not significant in the multivariate analysis. This suggests that the possibility of breakthrough infections by SM in patients being treated with carbapenem is due to intrinsically resistant carbapenem and the selection pressure of SM should be considered [29, 30]. Only 24.8% of patients received TMP/SMX. A high proportion of ICU care and polymicrobial infections may have influenced antibiotic selection. Nevertheless, careful use of carbapenem is necessary, and the possibility for breakthrough infections should be considered.

Our study had several limitations. First, the retrospective design of this study was a major limitation. Second, the history of previous antibiotic use and previous hospital admissions were not investigated. This is especially important, since these are factors related to the acquisition of antibiotic resistance. Third, we could not investigate the susceptibility of other antibiotics except quinolone and TMP/SMX, and our quinolone analysis was limited to levofloxacin only.

**Conclusion**

Quinolone-resistant SM isolates have been emerging and spreading in Korean hospitals, and current therapeutic options are limited for SM bacteremia. Our results suggest that a high Charlson comorbidity index and indwelling of CVC were significant independent predictors of SM bacteremia patients with quinolone-resistant strains. Therefore, we need to carefully consider antibiotics use in patients with SM bacteremia who have these predictive factors.

**Additional file**

Additional file 1: Table S1. Clinical characteristics of polymicrobial infection groups. (DOCX 22 kb)

**Abbreviations**

APACHE II: Acute Physiology and Chronic Health Evaluation II; BSI: Blood stream infection; CDC: Centers for Disease Control and Prevention; CI: Confidence interval; CVC: Central venous catheter; eGFR: Estimated glomerular filtration rate; IQR: Interquartile range; MIC: Minimal inhibitory concentration; OR: Odds ratio; SD: Standard deviation; SM: *S. maltophilia*; TMP-SMX: Trimethoprim-sulfamethoxazole

**Acknowledgements**

This abstract has previously been presented as part of a poster below.

Eun Jin Kim, et al. ‘Predictive Factors Associated With Stenotrophomonas maltophilia Bacteremia Infected by Antibiotic-Resistant Strains.’ Open Forum Infectious Diseases. Vol. 3. No. suppl_1. Oxford University Press, 2016.

**Authors’ contributions**

Conception and design of study: EJK, SJJ Acquisition of data: EJK, YCK, JYA, NSK Data analysis and interpretation: EJK, SJY Drafting of manuscript and critical revision: EJK, SJJ, JYC, JSY, YGS Approval of final version of manuscript: EJK, YCK, JYA, SJJ, NSK, JYC, JSY, YGS.
Funding
This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Availability of data and materials
The datasets used during the current study are available from the corresponding author on reasonable request.

Ethics approval and consent to participate
The study was approved by the institutional review board of the Yonsei University Health System Clinical Trial Center. The informed consent was waived because this study was a retrospective study with review of related data through the electronic medical record. The datasets used and/or analyzed during the current study available from the corresponding author on reasonable request.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

Author details
1 Department of infectious diseases, Ajou University School of Medicine, Suwon, Korea. 2 Department of Internal Medicine and AIDS Research Institute, Yonsei University College of Medicine, 50-1 Yonsei-ro, Seodaemun-gu, Seoul 120-752, Republic of Korea.

Received: 26 March 2019 Accepted: 20 August 2019

Published online: 28 August 2019

References
1. Denton M, Kerr KG. Microbiological and clinical aspects of infection associated with Stenotrophomonas maltophilia. Clin Microbiol Rev. 1998;11(1):57–80.
2. Hoefer D, Monis PT, Grooby WL, Andrews S, Saint CP. Profiling bacterial survival through a water treatment process and subsequent distribution system. J Appl Microbiol. 2005;99(1):75–86.
3. Falagas ME, Kastoris AC, Vouloumanou EK, Rafailidis PI, Kapaskelis AM. Dimopoulos G. Attributable mortality of Stenotrophomonas maltophilia infections: a systematic review of the literature. Future Microbiol. 2009;4(9):1103–9.
4. Micozzi A, Venditti M, Monaco M, Friedrich A, Taglietti F, Santilli S, et al. Bacteremia due to Stenotrophomonas maltophilia in patients with hematologic malignancies. Clin Infect Dis. 2000;31(3):705–11.
5. Labarca JA, Leber AL, Kern VL, Tettico MC, Branikov IE, Bruckner DA, et al. Outbreak of Stenotrophomonas maltophilia bacteremia in allogeneic bone marrow transplant patients: role of severe neutropenia and mucositis. Clin Infect Dis. 2000;30(1):195–7.
6. Gales AC, Jones RN, Forwood KR, Linares J, Sader HS, Verhoef J. Emerging importance of multidrug-resistant Acinetobacter species and Stenotrophomonas maltophilia as pathogens in seriously ill patients: geographic patterns, epidemiological features, and trends in the SENTRY antimicrobial surveillance program (1997-1999). Clin Infect Dis. 2001;32(Suppl 1):S104–13.
7. Zhang L, Li XZ, Poole K. Multiple antibiotic resistance in Stenotrophomonas maltophilia: involvement of a multidrug efflux system. Antimicrob Agents Chemother. 2000;44(2):287–93.
8. Albinos A, Martinez JL. Multiple antibiotic resistance in Stenotrophomonas maltophilia. In: Antimicrob Agents Chemother. 1997;41(5):1140–2.
9. Looney WJ, Nanta M, Muhlemann K. Stenotrophomonas maltophilia: an emerging opportunist human pathogen. Lancet Infect Dis. 2009;9(5):312–23.
10. Sanchez MB. Antibiotic resistance in the opportunistic pathogen Stenotrophomonas maltophilia. Front Microbiol. 2015;6:558.
11. Nicodemo AR, Paez JJ. Antimicrobial therapy for Stenotrophomonas maltophilia infections. Eur J Clin Microbiol Infect Dis. 2007;26(4):229–37.
12. Chung HS, Hong SG, Kim YR, Shin KS, Whang DH, Ahn JY, et al. Antimicrobial susceptibility of stenotrophomonas maltophilia isolates from Korea, and the activity of antimicrobial combinations against the isolates. J Korean Med Sci. 2013;28(1):162–6.
13. Cho SY, Kang CI, Kim J, Ha YE, Chung DR, Lee NY, et al. Can levofloxacin be a useful alternative to trimethoprim-sulfamethoxazole for treating Stenotrophomonas maltophilia bacteremia? Antimicrob Agents Chemother. 2014;58(1):581–3.
14. Bonfiglio G, Cascone C, Azzarelli C, Califso V, Marchetti F, Stefani S. Levofloxacin in vitro activity and time-kill evaluation of Stenotrophomonas maltophilia clinical isolates. J Antimicrob Chemother. 2000;45(1):115–7.
15. Wang YL, Scipione MR, Dubrovskaya Y, Papadopoulos J. Monotherapy with fluoroquinolone or trimethoprim-sulfamethoxazole for treatment of Stenotrophomonas maltophilia infections. Antimicrob Agents Chemother. 2014;58(1):775–82.
16. Chang YT, Lin CY, Lu PL, Lai CC, Chen TC, Chen CY, et al. Stenotrophomonas maltophilia bloodstream infection: comparison between community-onset and hospital-acquired infections. World J Gastroenterol. 2014;20(7):28–35.
17. Pien CJ, Kuo HY, Chang SW, Chen PR, Yeh HW, Liu CC, et al. Risk factors for levofloxacin resistance in Stenotrophomonas maltophilia from respiratory tract in a regional hospital. World J Gastroenterol. 2015;21(57):291–5.
18. Wu H, Wang JT, Shiu YR, Wang HY, Lauderdale TL, Chang SC. A multicenter surveillance of antimicrobial resistance on Stenotrophomonas maltophilia in Taiwan. World J Gastroenterol. 2015;21(5):291–5.
19. Chalson ME, Pompei P, Ales KL, Mackenize CR. A new method of classifying prognostic comorbidity in longitudinal studies: development and validation. J Chronic Dis. 1987;40(5):373–83.
20. Patel JB, Cockerill FR III, Bradford PA, Elipouloos GM, Hindyler JA, Jenkins SG, et al. Clinical and laboratory standards institute. Performance standards for antimicrobial susceptibility testing; 25th informational supplement. Vol. 35 Number 3: CLSI. 2015. [Document M100-S254: CLSI. 2015.
21. Paez JL, Costa SF. Risk factors associated with mortality of infections caused by Stenotrophomonas maltophilia: a systematic review. J Hosp Infect. 2008;70(1):101–8.
22. Baek JH, Kim CO, Jeong SJ, Ku NS, Han SH, Choi JY, et al. Clinical factors associated with acquisition of resistance to levofloxacin in Stenotrophomonas maltophilia. Yonsei Med J. 2014;55(4):987–93.
23. Na HY, Hung IC, Huang YH, Chang YY, Sheng WH, Wang JT, et al. Prognostic factors of health care-associated bloodstream infection in adult patients >140 years of age. Am J Infect Control. 2018;46(2):111–4.
24. Azoka H, Baba M, Yoneyama A. Risk factors for mortality among patients with Stenotrophomonas maltophilia bacteremia in Tokyo, Japan, 1996-2009. Eur J Clin Microbiol Infect Dis. 2010;29(5):605–8.
25. Friedman ND, Korman TM, Fairley CK, Franklin JC, Speelman DW. Bacteremia due to Stenotrophomonas maltophilia: an analysis of 45 episodes. J Infect. 2002;45(1):47–53.
26. Jeon YD, Jeong WY, Kim MH, Jung YI, Ahn MY, Ann HW, et al. Risk factors for mortality in patients with Stenotrophomonas maltophilia bacteremia. Medicine. 2016;95(31):e4375.
27. Ebata H, Hayashi H, Haruki Y, Kondo E, Otsuka F. Clinical characteristics of Stenotrophomonas maltophilia bacteremia: a regional report and a review of a Japanese case series. Intern Med. 2017;56(2):137–42.
28. Sanyal SC, Mokaddas EM. The increase in carbapenem use and emergence of Stenotrophomonas maltophilia as an important nosocomial pathogen. J Chemother. 1999;11(1):28–33.

Publisher’s Note
Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.