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Molecular Epidemiology of *Serratia marcescens* in a Hospital

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Serratia marcescens is an important nosocomial pathogen, particularly regarding catheter-related bacteremia, urinary tract infections, and respiratory infections. Pulsed-field gel electrophoresis (PFGE) is useful in determining the molecular epidemiology of various pathogens including *S.*

marcescens (1).

In May 2003, two inpatients (P1 and P2) successively developed sepsis in a surgical ward of a hospital with 925 beds. Blood cultures of the two patients revealed the presence of *S. marcescens*. Both patients P1 and P2 had been inserted with vascular catheters for 12 days and 4 days, respectively, before developing sepsis. The two isolates from the respective patients had identical PFGE patterns. Epidemiological investigation conducted by the infection control team in the hospital, however, was unable to identify the source of the infection. PFGE-based surveillance of *S. marcescens* was then conducted to assess the possible risk of an outbreak of *S. marcescens* infections.

A total of 23 clinical isolates of *S. marcescens*, including the above two isolates and 21 isolates obtained from 21 inpatients during August and September 2003, were analyzed for chromosomal DNA typing by using a counter-clamped homogeneous electric field system (CHEF Mapper™: Bio-Rad Laboratories, Hercules, Calif., USA), and for antibiotic resistance (WalkAway™: Dade Behring, Deerfield, Ill., USA).

Twenty different PFGE patterns of the *SpeI* DNA digests of the isolates were detected (Figs. 1A and 1B). PFGE patterns A, J, and K (Fig. 1A) were shared respectively by

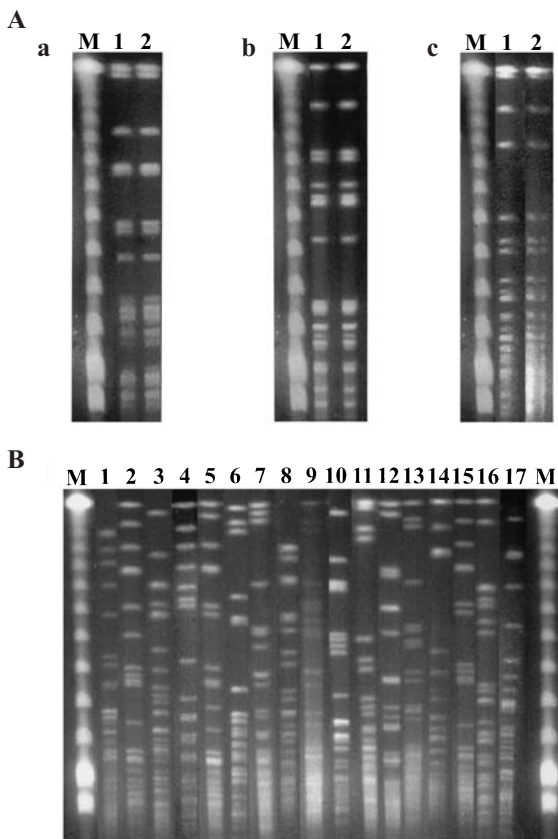


Fig.1. Pulsed-field gel electrophoresis of *SpeI*-digested genomic DNA from *S. marcescens* isolates.

A: a) PFGE pattern K (isolates No. S6 and S7), b) PFGE pattern J (isolates No. S15 and S18), c) PFGE pattern A (isolates No. S21 and S38), M: low range PFG Marker.

B: lane 1: isolate No. S14, lane 2: No. S16, lane 3: No. S19, lane 4: No. S23, lane 5: No. S24, lane 6: No. S25, lane 7: No. S27, lane 8: No. S28, lane 9: No. S29, lane 10: No. S31, lane 11: No. S32, lane 12: No. S33, lane 13: No. S34, lane 14: No. S36, lane 15: No. S37, lane 16: No. S39, lane 17: No. S40.

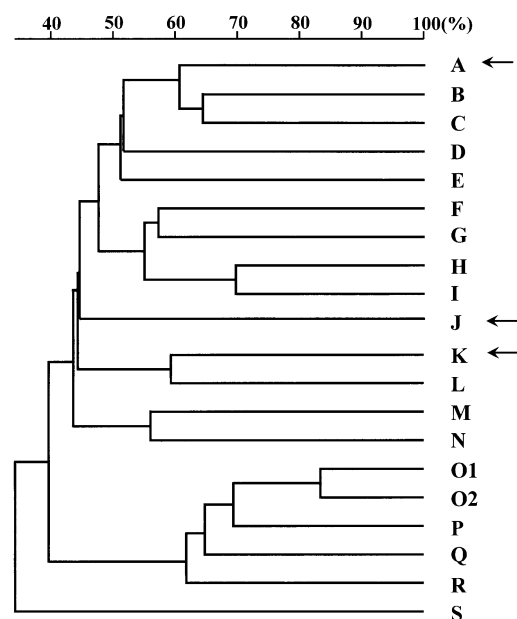


Fig. 2. Band-based cluster analysis of PFGE patterns of *S. marcescens* isolates.

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Table 1. Antibiotic pattern classified by antibiotic pattern of 18 antibiotics against *S. marcescens*

| Antibiotic pattern | Antibiotics | | | | | | | | | | |
|--------------------|-------------|------|-----|-----|-----|-----|------|-----|-----|-----|------|
| | ABPC | PIPC | CTM | CMZ | CTX | CAZ | FMOX | AZT | S/C | AMK | MINO |
| a | R | R | R | R | R | S | R | S | R | R | S |
| b | R | S | R | S | R | S | R | S | S | S | S |
| c | R | I | R | R | S | S | R | S | S | S | S |
| d | R | I | R | R | R | I | I | I | S | S | S |
| e | R | R | R | S | S | R | S | R | S | S | S |
| f | R | R | R | S | S | S | S | S | S | I | S |
| g | R | I | R | S | S | S | S | S | S | S | S |
| h | R | S | R | S | S | S | S | S | S | S | S |
| i | R | S | R | S | I | S | I | S | S | S | S |
| j | I | S | R | S | S | S | S | S | S | S | S |
| k | I | S | R | S | S | S | I | S | S | S | S |
| l | R | S | I | S | S | S | S | S | S | S | S |
| m | S | S | R | S | I | S | S | S | S | S | R |
| n | S | S | S | S | S | S | S | S | S | S | S |

All isolates were resistant to CCL and CEZ, but sensitive to CPR, GM, IPM, LVFX, and ST.
 ABPC: ampicillin, PIPC: piperacillin, CTM: cefotiam, CMZ: cefmetazole, CTX: cefotaxime, CAZ: ceftazidime,
 CCL: cefaclor, CEZ: cefazolin, CPR: ceftiofloxacin, FMOX: flomoxef, AZT: aztreonam, S/C: sulbactam/cefoperazone,
 AMK: amikacin, MINO: minocycline, GM: gentamicin, IPM: imipenem/cilastatin, LVFX: levofloxacin,
 ST: sulfamethazole/trimethoprim, R: resistant, S: sensitive, I: intermediate.

Table 2. Phenotypic and genotypic characterization of *S. marcescens* isolates

| Patient no. | Isolates no. | Specimen | Date | Ward | PFGE pattern | Antibiotic pattern |
|-------------|--------------|----------------------|--------|------|--------------|--------------------|
| P1 | S6 | Venous blood | 12-May | 8N | K | k |
| P2 | S7 | Venous blood | 19-May | 8N | K | i |
| P3 | S14 | Venous blood | 12-Aug | 16 | H | c |
| P4 | S15 | Venous blood | 15-Aug | 12S | J | d |
| P5 | S16 | Sputum | 20-Aug | 8N | O1 | h |
| P6 | S18 | Urine | 22-Aug | 12S | J | j |
| P7 | S19 | Sputum | 25-Aug | 12N | F | o |
| P8 | S21 | Urine | 27-Aug | 7N | A | i |
| P9 | S23 | Sputum | 28-Aug | 7N | L | h |
| P10 | S24 | Sputum | 29-Aug | 11N | P | h |
| P11 | S25 | Sputum | 1-Sep | ICU | I | k |
| P12 | S27 | Urine | 8-Sep | 6N | B | a |
| P13 | S28 | Sputum | 8-Sep | 7N | G | i |
| P14 | S29 | Sputum | 8-Sep | 9S | R | e |
| P15 | S31 | Urine | 10-Sep | 7N | S | l |
| P16 | S32 | Sputum | 9-Sep | 5S | C | i |
| P17 | S33 | Sputum | 16-Sep | 10N | Q | i |
| P18 | S34 | Urine | 16-Sep | 9S | D | f |
| P19 | S36 | Urine | 18-Sep | 7S | M | i |
| P20 | S37 | Venous blood | 22-Sep | 7N | O2 | m |
| P21 | S38 | Urine | 22-Sep | 7N | A | b |
| P22 | S39 | Pleural cavity drain | 24-Sep | 12N | N | k |
| P23 | S40 | Urine | 26-Sep | 9S | E | n |

isolates from different pairs of the patients (see below). The other 17 PFGE patterns were unique to each isolate (Fig. 1B). Band-based cluster analysis of these patterns (Molecular Analysis™: Bio-Rad) revealed a low level of similarity among the isolates except for patterns O1 and O2 that formed a cluster (a cluster was defined as a group of patterns sharing more than 70% similarity) (Fig. 2).

The majority of the *S. marcescens* isolates were resistant to ABPC, CCL, and CEZ, but sensitive to CAZ, IMP, and LVFX. They were resistant to 2-10 of 18 tested drugs (Table 1). Fifteen different drug resistance patterns were observed. No correlation was found between the antibiotic patterns and

PFGE patterns (data not shown).

Three pairs of isolates having identical PFGE patterns were obtained from different patients in the same ward on similar dates. The strains with pattern K (isolate Nos. S6 and S7) were isolated from patients P1 and P2 in ward 8N in May. Those with pattern J (Nos. S15 and S18) were from patients P4 and P6 in ward 12S in August. Those with pattern A (Nos. S21 and S38) were from patients P8 and P21 in ward 7N in August and September. It was noteworthy that all these pairs of patients had undergone catheterization concurrently. The patients may have been infected with the pathogen from the same source related to catheters.

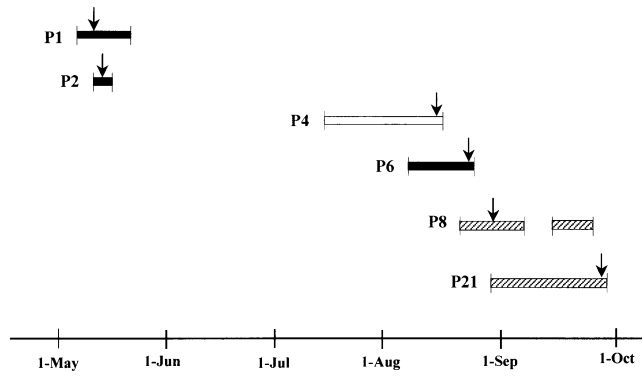


Fig. 3. Duration of catheterization. Intravenous, central venous, and urinary tract catheterization are represented by filled, open, and hatched boxes, respectively. Vertical arrows indicate the date of isolation of *S. marcescens*.

Catheterization was thus found to have a high risk of *S. marcescens* infection. In the hospital, its application including its duration was revised and a single use of heparin solution for the heparin lock technique was implemented. None of the patients involved in the above outbreak suffered serious consequences.

REFERENCE

1. Miranda, G., Kelly, C., Solorzano, F., Leanos, B., Coria, R. and Patterson, J. E. (1996): Use of pulsed-field gel electrophoresis typing to study an outbreak of infection due to *Serratia marcescens* in a neonatal intensive care unit. *J. Clin. Microbiol.*, 34, 3138-3141.