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Prevalence of serotypes of *Xanthomonas maltophilia* from world-wide sources

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SUMMARY

Since its development in 1988, a serologic typing scheme for *Xanthomonas maltophilia*, based on 31 O antigens, has been successfully used to serotype isolates involved in nosocomial outbreaks in the United States. To determine if this serotyping scheme would be useful in typing *X. maltophilia* isolates from world-wide sources, we obtained additional isolates from 10 countries; of 900 isolates tested, 795 (88·3%) were typable. In order of predominance, the three most common serotypes were 10, 3 and 19. These three serotypes were most frequently associated with respiratory and blood isolates. This serotyping system is useful as an epidemiologic screening method for universal typing of outbreaks of *X. maltophilia* infections.

INTRODUCTION

Xanthomonas maltophilia has emerged as an important nosocomial pathogen in recent years [1–3]. Isolation of *X. maltophilia* is increasing in frequency [4–6], and strains are often resistant to many commonly used antibiotics [1, 7–12]. *X. maltophilia*, generally considered to be an opportunistic nosocomial pathogen, is most commonly isolated from immunocompromised patients who have had prior antimicrobic therapy, or undergone surgical procedures, respiratory tract intubation, or urinary tract catherization.

Since its development in 1988, a serologic classification scheme, based on 31 O antigens [13], has been used to type *X. maltophilia* isolates, involved in nosocomial infections, submitted to the Centers for Disease Control from sources in the United States. This report describes the results of serologic reactions of 900 clinical and environmental isolates of *X. maltophilia* received from world-wide sources to determine if these antisera would be useful in typing *X. maltophilia* isolates from locations throughout the world.

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MATERIALS AND METHODS

Cultures

Three hundred and eight strains of *X. maltophilia* were obtained from 10 countries: France, Canada, England, Belgium, Spain, Germany, the Netherlands, New Zealand, Japan, and Finland, and 592 isolates submitted to the Centers for Disease Control from US sources were serotyped. Of these 900 strains, 772 were from human and 60 were from environmental sources; the sources of 70 strains were unavailable. These strains included epidemic and endemic infections. The identification of all isolates was confirmed by using conventional biochemical methods.

Serotyping

Serotyping of *X. maltophilia* isolates was performed as previously described [13]. Briefly, isolates were harvested by centrifugation (1126 g) after 18–24 h incubation with shaking at 32 °C in veal infusion broth (Difco Laboratories, Detroit, Michigan). The cell sediment was resuspended in 2 ml of 0·01 M phosphate-buffered saline (pH 7·2) and then vortexed; next, the suspension was placed in flowing steam (100 °C) for 2 h, cooled, and then remixed. Slide agglutination was performed with the cell suspension adjusted to approximately a No. 8 McFarland standard. One drop of antigen suspension was added to single drops of each of the 31 antisera. The slide was rocked back and forth for 1 min and then examined for evidence of agglutination.

Statistical methods

The χ^2 and P value were calculated using Epi Info Version 5 [14].

RESULTS

Overall, 795 of the 900 (88·3%) of all isolates could be assigned to a specific O group (Table 1). Seventy-six (8·4%) strains did not agglutinate in the 31 antisera. Eleven (1·2%) could not be typed because they autoagglutinated. Eighteen (2·0%) agglutinated in two or more antisera (polyagglutination). Distribution of *X. maltophilia* isolates by site was as follows (%): respiratory, 37·0; blood, 15·1; wound, 11·4; urine, 9·3; environmental, 6·7; body fluid, 2·1; stool, 1·1; ear, 1·1; eye, 0·3; unknown, 7·8; and miscellaneous, 8·0. The most prevalent serotype was 10 (23·6%), followed by serotypes 3 (11·6%) and 19 (10·9%). Serotypes 10, 3, 19, 8 and 13 were the five predominant serogroups and represented 55·5% of the isolates tested. For serogroups 10 and 19, respiratory isolates comprised a majority of the specimens. Serogroup 3 isolates were about evenly divided among respiratory and blood isolates. No isolates agglutinated in antiserum from serogroup 11. More data are needed to determine if differences in specimen source distribution account for some of the differences in serotype distribution.

A serologic trend, associated with serogroup 10, has been recognized in hospital outbreaks in the United States (117/151 *v.* 61/263, χ^2 [Yates uncorrected] =

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Table 1. *Results of O agglutination of 900* X. maltophilia *isolates from human and environmental sources*

Sero-type	Immunizing strain*	No. of isolates from human and environmental sources*											Total	Percent of total
		RE	BL	WO	UR	EN	ST	EY	ER	BF	UK	Misc.		
1	873-3	0	1	0	0	0	0	0	0	0	0	0	1	0·1
2	447	0	0	2	0	0	0	0	0	1	0	0	3	0·3
3	PM-56	31	36	5	8	15	2	0	1	1	4	1	104	11·6
4	363-4	9	2	3	3	0	0	1	0	0	0	1	19	2·1
5	229	2	0	1	1	0	1	0	0	0	1	0	6	0·7
6	557	1	4	1	4	3	0	0	1	0	2	0	16	1·8
7	PM-97	1	0	0	0	2	0	0	0	0	1	0	4	0·4
8	810-2	12	3	6	11	0	0	0	0	0	3	7	42	4·7
9	556	10	6	2	6	3	1	0	0	0	7	1	36	4·0
10	558	122	24	19	7	12	1	1	2	3	9	12	212	23·6
11	294	0	0	0	0	0	0	0	0	0	0	0	0	0
12	555	12	2	1	1	0	0	0	0	0	3	1	20	2·2
13	109-4	13	4	4	3	6	0	0	0	1	3	8	42	4·7
14	653-4	2	2	2	0	0	0	0	1	0	0	2	9	1·0
15	611	7	3	3	2	0	0	0	0	1	5	1	22	2·4
16	560	15	1	4	2	3	2	0	0	1	4	5	37	4·1
17	PM-61	0	2	0	2	0	0	0	0	1	1	0	6	0·7
18	788-3	5	1	3	3	0	0	0	0	0	3	3	18	2·0
19	609	23	17	13	10	3	1	0	2	5	11	13	98	10·9
20	PM-143	5	2	1	3	0	0	0	0	1	0	1	13	1·4
21	PM-41	3	4	3	0	0	0	0	0	0	1	1	12	1·3
22	PM-62	5	3	5	0	0	0	0	2	0	2	4	21	2·3
23	PM-94	3	0	0	0	1	0	1	1	0	1	0	7	0·8
24	PM-283	0	0	1	1	0	0	0	0	0	0	1	3	0·3
25	PM-219	3	1	0	2	0	0	0	0	0	0	0	6	0·7
26	PM-225	3	3	0	1	0	0	0	1	1	0	0	9	1·0
27	PM-289	1	1	0	1	0	0	0	0	0	0	0	3	0·3
28	PM-314	1	0	0	3	2	0	0	0	0	0	0	6	0·7
29	PM-525	5	1	3	2	0	0	0	0	0	0	0	11	1·2
30	PM-528	3	0	1	1	0	0	0	0	0	0	0	5	0·6
31	PM-540	2	0	0	0	0	0	0	0	0	2	0	4	0·4
Autoagglutination		3	0	2	1	4	0	0	0	0	0	1	11	1·2
Polyagglutination		9	3	2	1	0	0	0	0	2	1	0	18	2·0
Non-typable		22	10	16	5	6	2	0	0	0	6	9	76	8·4
Total		333	136	103	84	60	10	3	11	18	70	72	900	

* RE, respiratory; BL, blood; WO, wound; UR, urine; EN, environmental; ST, stool; EY, eye; ER, ear; BF, body fluid; UK, unknown; Misc., miscellaneous.

41·832, P value $< 0·0001$); 56·3% of these strains were isolated from respiratory tract specimens. No other serologic trends with respect to country were noted.

DISCUSSION

Xanthomonas maltophilia is frequently isolated from clinical specimens [15, 16] and has an emerging role in nosocomial infections [1–6, 12]. Recently, a rapid and simple screening method to assist in epidemiologic characterization of *X. maltophilia* was developed [13]. This serotyping scheme has been successfully used to help evaluate strains implicated in nosocomial outbreaks in the United States (unpublished observations) [17]. All of the serologic studies, however, have been done on isolates submitted to CDC from sources within the United States. It was unclear whether or not this typing system would be effective on isolates from international sources.

Of all *X. maltophilia* isolates tested, 88·3% were typable, indicating that *X. maltophilia* throughout the world share similar antigens. Relatively low rates of autoagglutination and polyagglutination were noted. However, the rate in the 'non-typable' category is significant and may indicate that other antigen types of *X. maltophilia* exist and that appropriate antisera should be developed to enable a more world-wide approach to serologic characterization.

Results from our study indicate that serotypes 10, 3, and 19 are the most common world-wide serogroups and are most often found in respiratory and blood specimens.

In our experience, serotyping of *X. maltophilia* is an effective epidemiologic screening method. Additionally, we have shown that groups of strains of the same serotype can be further characterized into distinct subgroups by multilocus enzyme electrophoresis (MEE) [17]. The availability of more than one epidemiologic typing method will make it easier to identify the source of at least some outbreaks caused by *X. maltophilia*. Until MEE or molecular epidemiologic techniques become more routinely available, serology is the method of choice for the initial screening of suspected nosocomial isolates of *X. maltophilia*.

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REFERENCES

1. Gilardi GL. *Pseudomonas maltophilia* infections in man. Am J Clin Pathol 1969 **51**: 58–61.
2. Sutter VL. Identification of *Pseudomonas* species isolated from hospital environment and human sources. Appl Environ Microbiol 1968; **16**: 1532–8.
3. Gardner P, Griffin WB, Swartz MN, Kunz LJ. Nonfermentative gram-negative bacilli of nosocomial interest. Am J Med 1970; **48**: 735–49.
4. Morrison AJ, Hoffman KK, Wenzel RP. Associated mortality and clinical characteristics of nosocomial *Pseudomonas maltophilia* in a university hospital. J Clin Microbiol 1986; **24**: 52–5.
5. Muder RR, Yu VL, Dummer JS, Vinson C, Lumish RM. Infections caused by *Pseudomonas maltophilia*. Expanding clinical spectrum. Arch Intern Med 1987; **147**: 1672–4.
6. Khardori N, Eltig L, Wong E, Schable B, Bodey G. Nosocomial infections due to *Xanthomonas maltophilia* (*Pseudomonas maltophilia*) in patients with cancer. Rev Infect Dis 1990; **12**: 997–1003.
7. Felegie TP, Yu VL, Rumans LW, Yee RB. Susceptibility of *Pseudomonas maltophilia* to antimicrobial agents, singly and in combination. Antimicrob Agents Chemother 1979; **16**: 833–7.
8. Moody MR, Young VM, Kenton DM. In vitro antibiotic susceptibility of pseudomonads other than *Pseudomonas aeruginosa* recovered from cancer patients. Antimicrob Agents Chemother 1972; **2**: 344–9.
9. Gilardi GL. Infrequently encountered *Pseudomonas* species causing infections in humans. Ann Intern Med 1972; **77**: 211–5.
10. Nord CE, Wadstrom T, Wretlind B. Synergistic effect of combinations of sulfamethoxazole, trimethoprim, and colistin against *Pseudomonas maltophilia* and *Pseudomonas cepacia*. Antimicrob Agents Chemother 1974; **6**: 521–3.
11. Yu VL, Felegie TP, Yee RB, Pasculle AW, Taylor FH. Synergistic interaction in vitro with use of three antibiotics simultaneously against *Pseudomonas maltophilia*. J Infect Dis 1980; **142**: 602–7.
12. Zuravleff JJ, Yu VL. Infections caused by *Pseudomonas maltophilia* with emphasis on bacteremia: case reports and a review of the literature. Rev Infect Dis 1982; **4**: 1236–46.
13. Schable B, Rhoden DL, Hugh R, et al. Serological classification of *Xanthomonas maltophilia* (*Pseudomonas maltophilia*) based on heat-stable O antigens. J Clin Microbiol 1989; **27**: 1011–4.
14. Dean AG, Dean JA, Burton AH, Dicker RC. Epi Info, Version 5: a word processing, database, and statistics program for epidemiology on microcomputers. Centers for Disease Control, Atlanta, Georgia, USA, 1990.
15. Pedersen MM, Marso E, Pickett M. Nonfermentative bacilli associated with man: III. Pathogenicity and antibiotic susceptibility. Am J Clin Pathol 1970; **54**: 178–92.
16. Holmes B, Lapage SP, Easterling BG. Distribution in clinical material and identification of *Pseudomonas maltophilia*. J Clin Pathol 1979; **32**: 66–72.
17. Schable B, Villarino ME, Favero MS, Miller JM. Application of multilocus enzyme electrophoresis to epidemiologic investigations of *Xanthomonas maltophilia*. Infect Control Hosp Epidemiol 1991; **12**: 163–7.