JOURNAL OF CLINICAL MICROBIOLOGY, Dec. 2010, p. 4623–4626 Vol. 48, No. 12
0095-1137/10/$12.00 doi:10.1128/JCM.01216-10

Clinical Features of Infections and Colonization by *Acinetobacter* Genospecies 3[▽]

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Received 16 June 2010/Returned for modification 13 August 2010/Accepted 1 October 2010

Two hundred twenty-one isolates of *Acinetobacter baumannii* and 15 of *Acinetobacter* genospecies 3 (AG3) were consecutively collected in a 30-day period during the nationwide project GEIH-Ab2000. Nosocomial acquisition ($P = 0.01$), intensive care unit admission ($P = 0.02$), and antibiotic pressure ($P = 0.03$) were observed to be lower in the AG3 group. AG3 isolates were more frequently implied in wound infections ($P = 0.05$), while *A. baumannii* tended to be recovered from respiratory samples ($P = 0.08$). To our knowledge, this is the first report analyzing the clinical differences among *Acinetobacter* genospecies, with our findings suggesting that clinical features of AG3 may not be equivalent to those traditionally described for *A. baumannii*.

Among the species in the *Acinetobacter* genus, *Acinetobacter baumannii* is the most frequently isolated in clinical samples and the one of greatest clinical interest. However, since molecular tools are not usually available for routine clinical practice, other *Acinetobacter* species with similar phenotypes are usually misidentified as *A. baumannii*. When the prevalence of these genospecies is assessed with genetic tools, many authors identify *Acinetobacter* genospecies 3 as the most commonly isolated species after *A. baumannii* or even the most frequently isolated (2, 13). Nonetheless, despite its remarkable prevalence, clinical data regarding infections produced by *Acinetobacter* genospecies 3 are scarce (8, 9).

The present study aimed to describe the clinical features of colonization and infections by *Acinetobacter* genospecies 3 and their differences from those of *A. baumannii*.

Twenty-eight Spanish hospitals participated in the GEIH-Ab2000 project in November 2000. During a 30-day period, all new isolates of *A. baumannii* were included and sent to a reference laboratory. Bacterial identification at the genus level was performed following conventional phenotypic methods (5), whereas identification of the genospecies was determined

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▽ Published ahead of print on 13 October 2010.

by amplified rRNA gene restriction analysis and by DNA sequencing of the 16S rRNA gene (1). For each case, only the first isolate was studied.

For each case, the following variables were recorded: hospital ward, gender, age, type of sample, underlying diseases, invasive procedures, and antimicrobial agents received during the previous month. *A. baumannii* was considered to have been nosocomially acquired if the sample had been obtained more than 2 days after the patient's admission. The clinical significance (colonization or infection) of the *A. baumannii* isolation and type of infection in each case was assessed according to Centers for Disease Control and Prevention criteria (6, 7). Sepsis, severe sepsis, septic shock, and multiorgan failure were defined according to standard criteria. Patients were observed until discharge or death or until 30 days after the sample had been obtained if the patient was still hospitalized.

Paired categorical and continuous variables were compared using χ^2 or Fisher's exact test and the Mann-Whitney U test, respectively. Significance was set at a P value of <0.05. Statistical analyses were performed with SPSS v.15.0.

Separate data obtained from this project have been published elsewhere (1, 4, 5, 10–12).

During the study period, 240 isolates presumptively identified as *A. baumannii* by local laboratories were sent to the reference laboratory: 221 were identified as *A. baumannii*, 15 as *Acinetobacter* genospecies 3, and 3 as other *Acinetobacter* species, and 1 case was not an *Acinetobacter* species (12). In the *A. baumannii* and *Acinetobacter* genospecies 3 groups, 9 and 2 cases, respectively, were excluded due to lack of data essential to the study. Therefore, 212 cases of *A. baumannii* (AB group) and 13 cases of *Acinetobacter* genospecies 3 (AG3 group) were included. No case aggregation was observed for *Acinetobacter* genospecies 3 isolates, which came from 10 different hospitals.

The main clinical data are summarized in Table 1.

Most samples in the AG3 group were recovered from patients admitted in non-intensive care unit (ICU) wards ($n = 11$; 69.2%), and 23.1% of samples corresponded to outpatients ($n = 3$, including 1 urine culture, 1 wound exudate swab, and the ascitic fluid from a patient receiving peritoneal dialysis). Most isolates were recovered from wound swab or abscess culture ($n = 6$; 46.1%), and infections were usually located on skin and soft tissues (57.1% of cases with infection; $n = 4$). No cases in this group developed severe sepsis or septic shock, and only one patient, who was colonized only by *Acinetobacter* genospecies 3, died.

These features differ from those observed for patients with *A. baumannii* isolates. ICU admission (15.4% versus 50%) and nosocomial acquisition (76.9% versus 97.2%) were both significantly higher in the AB group, and the median number of antimicrobial agents previously administered was also superior ($P = 0.03$). *A. baumannii* preferably colonized or infected the respiratory tract, but this trend did not reach statistical significance. No significant differences were observed regarding mortality or severity of episodes of infection, although they both were higher in the AB group.

To our knowledge, this is the first study specifically describing the clinical features of infection and colonization by *Acinetobacter* genospecies 3 and their differences from those of *A. baumannii*. Only two studies have reported limited clinical data about *Acinetobacter* genospecies 3. Idzenga et al. (9) described an outbreak of this genospecies in four patients from a Dutch ICU. Clinical information is scarce, since authors focus on demonstrating the cross-transmission of the pathogen and its microbiologic features. Horrevorts et al. (8) prospectively included 56 isolates of *Acinetobacter* spp. from a neonatal ICU. DNA-DNA hybridization tests were performed on 38 of them, with 76.3% being identified as *Acinetobacter* genospecies 3. The clinical information provided refers to the whole sample, not specifically to genospecies 3 cases. Moreover, this information might be limited to a specific population (critically ill neonates) and to the epidemiologic circumstances of the health center itself. Clinical differences among genospecies were not assessed in any of these reports.

In our study, the clinical profile of patients colonized or infected by *Acinetobacter* genospecies 3 was noticeably different from that observed for patients with *A. baumannii* infections. Nosocomial acquisition was not so frequent and, when it was described, usually occurred in conventional wards, not in ICUs. Therefore, antibiotic pressure on the AG3 group was markedly inferior. *Acinetobacter* genospecies 3 was more frequently implied in skin and soft tissue infections, including surgical wound infection, while colonization and infection of the respiratory tract seemed to be less frequent than that observed for *A. baumannii*. We also found a nonsignificant trend suggesting a better prognosis for infections by *Acinetobacter* genospecies 3, though this fact was probably conditioned by the type of infections observed in this group and the higher rate of inappropriate empirical treatment in the AB group. Nevertheless, some authors have suggested that there might be relevant pathogenic differences among the genospecies of *Acinetobacter* (3).

The prevalence of *Acinetobacter* genospecies 3 in our study (15/240; 6.25%) is considerably lower than that observed by other authors (2, 13), who have described prevalences of up to 39%. The differences probably lie in the specific epidemiologic situation of each center.

This new clinical information seems to provide a proper context for microbiologic data published so far. We and other authors previously reported better antimicrobial susceptibility for *Acinetobacter* genospecies 3 than for *A. baumannii* (10, 13). These differences might arise from a different ecology and pathogenesis, as suggested by our results.

The study has some limitations. The size of the AG3 group is relatively small and might be underpowered for evaluating certain differences. Moreover, the results observed in our sample might conflict with the clinical situation in other geographic areas or even in different epidemiologic circumstances. However, the multicentric, nationwide design of the study aims to provide the results with a broader perspective. We cannot define if the three cases of *Acinetobacter* cenospecies 3 isolated in outpatients were true community-acquired infections or were related to health care assistance, since this concept was not defined at the time the study was performed. Finally, the study was carried out 10 years ago, and there may be some differences from the current epidemiologic situation. However, the value of

TABLE 1. Main clinical features of infections and colonization by *Acinetobacter* genospecies 3 and *Acinetobacter baumannii*

Characteristic of patients[a]	No. of cases with patient characteristic/total cases (%) or median value ± SD[b]		*P* value[c]
	Acinetobacter genospecies 3	*Acinetobacter baumannii*	
Demographic features			
Age	56 ± 20.7	60 ± 20.3	0.8
Female gender	4/13 (30.8)	60/212 (28.3)	1.0
Any comorbidity	9/13 (69.2)	152/212 (71.7)	1.0
Diabetes mellitus	5/13 (38.5)	32/212 (15.1)	**0.04**
Neoplastic disease	2/13 (15.4)	35/212 (16.5)	1.0
Obesity	0/13 (0)	20/212 (9.4)	0.6
Hepatopathy	0/13 (0)	8/212 (3.8)	1.0
Renal insufficiency	1/13 (7.7)	10/212 (4.7)	0.5
COPD	2/13 (15.4)	28/212 (13.2)	0.7
Heart failure	2/13 (15.4)	26/212 (12.3)	0.7
Transplantation	0/13 (0)	4/212 (1.9)	1.0
Immunosuppression	1/13 (7.7)	14/212 (6.6)	0.6
Predisposing external factors			
Central venous catheter	5/13 (38.5)	139/211 (65.6)	0.07
Urinary catheterization	7/13 (53.8)	164/211 (77.4)	0.08
Recent surgery	3/13 (23.1)	101/211 (47.6)	0.09
Parenteral nutrition	0/13 (0)	53/211 (25)	**0.04**
Previous ICU admission	4/13 (30.8)	145/212 (68.4)	**0.01**
Mechanical ventilation	3/13 (23.1)	115/211 (54.2)	**0.04**
Previous antibiotic therapy	7/13 (53.8)	166/210 (79)	0.07
No. of previous antimicrobial agents	0.5 ± 1.2	2 ± 6.9	**0.03**
Clinical features			
Nosocomial acquisition	10/13 (76.9)	206/212 (97.2)	**0.01**
Days of stay prior to the isolation	4 ± 11.4	15 ± 27.9	**0.02**
Cases from ICU	2/13 (15.4)	106/212 (50)	**0.02**
Type of sample			
Respiratory sample	2/13 (15.4)	85/209 (40.7)	0.08
Blood/catheter culture	1/13 (7.7)	17/209 (8.1)	1.0
Urine culture	3/13 (23.1)	50/209 (23.9)	1.0
Wound swab or abscess culture	6/13 (46.1)	48/209 (22.9)	0.08
Infection/colonization			
Colonization	5/12 (41.6)	98/212 (46.2)	0.7
Infection	7/12 (58.3)	114/212 (53.8)	0.7
Site of infection*			
Respiratory tract*	1/7 (14.3)	55/112 (49.1)	0.1
Urinary tract*	1/7 (14.3)	17/112 (15.2)	1.0
Skin/soft tissue*	4/7 (57.1)	24/112 (11.3)	**0.05**
Bloodstream*	1/7 (14.2)	8/112 (7.1)	0.4
Incorrect empirical treatment*	1/7 (14.3)	38/110 (34.5)	0.4
Severe sepsis or septic shock*	0/7 (0)	29/111 (26.1)	0.2
Days of stay after isolation	16 ± 11.2	20 ± 11.1	0.4
Crude mortality			
All cases	1/11 (9.1)	39/209 (18.7)	0.7
Infection cases*	0/7 (0)	29/112 (26.1)	0.2

[a] COPD, chronic obstructive pulmonary disease. Only infection cases were included for the analysis of variables marked with "*" (colonization cases excluded).
[b] Continuous variables are expressed as median values ± standard deviations. When the total for a variable is expressed as a value inferior to the total number of cases, this corresponds to unavailable data. For *Acinetobacter* genospecies 3, $n = 13$ cases; for *Acinetobacter baumannii*, $n = 212$ cases.
[c] Statistically significant values are in boldface.

this study lies in the novel report of qualitatively different clinical features of the infections produced by other genospecies of *Acinetobacter*, which may not be equivalent to those traditionally described for *A. baumannii*. This constitutes an interesting starting point for future, larger studies, which would be necessary to confirm these findings.

This study was partially supported by a research grant from Merck Sharp & Dohme, Spain, and by the Red Española de Investigación en Patología Infecciosa (Instituto de Salud Carlos III; C03/14).

Special thanks go to Michael McConell for his valuable advice on English elaboration.

We have no conflict of interest to report.

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