Clinical Features of Infections and Colonization by Acinetobacter Genospecies 3

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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 isolated 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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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 χ² 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. Horrevoets 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 genospecies 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
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.

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

| Characteristic of patients | Acinetobacter genospecies 3 | Acinetobacter baumannii | P value
|---------------------------|-----------------------------|-------------------------|---------
| 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 (0.7) | 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
| 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) | 145/211 (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 ± 1.4 | 15 ± 2.9 | 0.02
| Cases from ICU | 2/13 (15.4) | 100/212 (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 (21.3) | 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) | 32/209 (18.7) | 0.7
| Infection cases* | 0/7 (0) | 29/112 (26.1) | 0.2

* COPD, chronic obstructive pulmonary disease. Only infection cases were included for the analysis of variables marked with *+* (colonization cases excluded).

** 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.

† Statistically significant values are in boldface.

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We have no conflict of interest to report.

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