CONCISE COMMUNICATION

Air Contamination around Patients Colonized with Multidrug-Resistant Organisms

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Care-related infections are a major public health concern. Their transmission can be associated with environmental factors. This study looks at air contamination around 45 patients colonized with multidrug-resistant organisms (MDROs). We found that 30 hospital rooms (67%) were contaminated with MDRO species and 10 rooms (22%) were contaminated with at least 1 MDRO.

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The dissemination of multidrug-resistant organisms (MDROs) is a major issue for hospital patients and staff alike.[1] The environment plays a major part in the occurrence of nosocomial infections because these MDROs can survive on various surfaces.[2] The aim of our study was to describe airborne bacterial contamination in hospitalization rooms of clinically contaminated MDRO patients.

METHODS

We prospectively included 45 patients with MDRO colonization. Often, patients are rehabilitation patients who regularly suffer from MDRO colonization or infection. All patients except 2 were in individual rooms. The rooms were all naturally ventilated (no mechanical ventilation or air conditioning system). Room windows and doors were kept closed during air samplings. Sampling was performed at 2 separate times: before nursing care (T1) and, whenever possible, during nursing care (T2).

Sampling of airborne bacteria was performed using 2 bioimpactors (Sampl'Air, AES) placed 1 m away from the patient, at a height of 1 m 20 cm, which collected 1 m^3 of air (100 L/minute during 10 minutes). The aspirated air impacted directly on the plate agar, which was then removed from the device and incubated at 37°C for 24–48 hours to allow viable organisms to grow. Colony-forming units (CFUs) were counted, and the corresponding values for bacteria/m^3 were analyzed. The susceptibility to antibiotics (phenotyping identification) was studied by agar disk diffusion according to the French Society of Microbiology Antibiogram Committee recommendations.

MDROs included methicillin-resistant *Staphylococcus aureus* (MRSA), extended-spectrum β-lactamase (ESBL)-producing enterobacteria, vancomycin-resistant *Enterococcus faecium*, *Pseudomonas aeruginosa*, and other gram-negative bacilli resistant to at least 3 of the 5 following groups of antibiotics: piperacillin-tazobactam or ticarcillin-clavulanate, ceftazidime or cefepime, carbapenems (imipenem, meropenem), aminoglycosides (gentamicin, tobramycin, amikacin), and fluoroquinolones (ciprofloxacin). Multidrug-resistant coagulase-negative *Staphylococcus* (MR-CNS) were resistant to methicillin, rifampin, aminoglycosides, and fluoroquinolones.

Epidemiologic typing of sample isolates (strains common to both clinical and air samples) was performed by PFGE (Pulsaphor system, Pharmacia LKB Biotechnology) according to established protocols.[3] An air sample was considered positive if at least 1 of the 2 air samples was positive for at least 1 MDRO. We defined the sample combinations as follows: (C+) as positive clinical sample with MDROs; (C−) as negative clinical sample (control group); (A+) as positive air sample (for MDRO); (C+/A+)* as positive paired clinical/air sample; (C+/A+) as positive paired clinical/air sample with at least 1 MDRO common to both samples; $(C+/A+)^{id}$ as identical phenotyping and genotyping strain of paired clinical/air MDRO sample; T1 as time of air sampling occurring outside nursing care; and T2 as time of air sampling during nursing care (standard technical and personal care).

RESULTS

Our study included a total of 45 MDRO-carrier patients (C+) occupying 44 different rooms in 4 different care units over a 5-month period. There were 22 (C+) patients in the infectious diseases (ID) unit, 12 in the neurologic rehabilitation (NR) unit, 7 in the adult surgery (AS) unit, and 4 in the pediatric oncology (PO) unit. Two patients shared a double occupancy room in the NR unit.

The following 62 clinical MDRO strains were identified: ESBL-producing enterobacteria ($n = 34$; 55%), MRSA ($n = 15$; 24%), *Acinetobacter baumanii/calcoaceticus* complex: 5 (8%), *Acinetobacter* species ($n = 2$; 4%), *Pseudomonas* species ($n = 5$; 8%), vancomycin-resistant *E. faecium* ($n = 1$; 2%).

Among the 45 (C+) patients, 30 (66%) had a positive air sample (C+/A+) and 15 (33%) had a negative air sample (C+/A−) (Table 1). A control group was designed with the 11 consecutive patients (all hospitalized in the ID unit) with a negative clinical MDRO detection. For each of these (C−) patients, a paired clinical/air sample was taken. No patient in the control group tested positive for air contamination.

We identified 38 airborne MDRO strains: ESBL-producing enterobacteria ($n = 8$; 21%), *Acinetobacter* species ($n = 13$; 34%), MRSA ($n = 5$; 13%), *Pseudomonas* species ($n = 4$; 11%), and MR-CNS ($n = 8$; 21%). There is a large variability

TABLE 1. Number of Patients in (C+) and (C−) Groups, regarding Their Air Sample Status

Group of patients	Air sample		Total no. of patients
	A+ sample	A− sample	
(C+) patients study group	(C+/A+) patients, $n = 30$ (66%)	(C+/A−) patients, $n = 15$ (33%)	45
(C−) patients control group	(C−/A+) patients, $n = 0$ (0%)	(C−/A−) patients, $n = 11$ (100%)	11

NOTE. A+, air positive sample with multidrug-resistant organisms (MDROs); A−, air negative sample for MDROs; C+, clinically positive with a MDROs; C−, clinically negative; C+/A+, paired clinically positive and air positive sample.

in the number of collected MDROs: 7.86 ± 5.76 UFC/m^3 MRSA, 2.25 ± 2.22 UFC/m^3 enterobacteria, 19.44 ± 56.44 UFC/m^3 *Acinetobacter* species, and 4.5 ± 6.06 UFC/m^3 *Pseudomonas* species.

Among the 45 (C+) patients, 10 (22%) had at least 1 identical MDRO strain in their paired clinical/air sample (C+/A+)*: a total of 15 identical MDROs were found (1 patient's paired sample showed up to 3 identical MDROs). Phenotyping and genotyping analysis confirmed the strain similarity in all the paired samples (C+/A+)^{id}. No unit specificity seemed to arise.

E. faecium was clinically present only once in the AS unit but not in the air. *S. epidermidis* was found quite often in the air of different care units ($n = 8$).

Fourteen air samples were taken in the hallway of the ID, AS, and NR units; 64% of them were found contaminated with *A. calcoaeciticus* or MRSA (1–5 CFU/mL). The ID unit was found to be the most contaminated area (number of positive air samples and bacterial burden).

For one of the first tested patients, air samplers were placed in different areas of the room—near the floor, in the bathroom, and around the bed—both before and during nursing care. Some strains were found in several paired samples (E-BLSE, MRSA), suggesting that the same strain could circulate in different rooms and across units.

The 2 tetraplegic patient colonized with MDROs (one with MRSA and *K. pneumoniae* BLSE and the other with *K. pneumoniae* BLSE, *P. aeruginosa*, and *S. marcescens*) were hospitalized in the same room. The identical (C+/A+)^{id} *P. aeruginosa*, *S. marcescens*, and MRSA were found in air samples. Of the 30 paired positive (C+/A+) patients, air sampling was conducted at T1 and T2 for 20 of them and showed that in 58% of cases, the sample taken at T2 revealed a greater amount of CFU/m^3 than at T1 (Figure 1).

DISCUSSION

Our study showed that in 67% of cases, when a patient was clinically colonized with MDROs, the air in his room was also contaminated with MDROs. For 22% of patients, at least one of the airborne strains was identical to the clinical ones, which was confirmed by antibiogram and PFGE profile. Air can become more concentrated with MDROs during human activity, as demonstrated by Shiomori et al[4] for MRSA.

Many studies have shown air contamination in healthcare facilities with different microorganisms such as MRSA,[5,6] more recently with *Pneumocystis jirovecii*[7] and *Clostridium difficile*[8] but also with *Pseudomonas aeruginosa*.[9] The case of both tetraplegic patients hospitalized in the same room suggests that the air may be cross-contaminated for certain types of strain but not for others.

No MR-CNS was found in MDRO carriers; it was never found in non-MDRO carriers. We know that CNS is a transmission medium for genes of antibiotic resistance.[9] We still need to determine whether MR-CNS could be a marker for air contamination.

Many questions remain unanswered, mainly regarding the various types of aerial contaminants, their survival in the environment, and their degree of transmission. The lack of existing standards in study methodology makes it difficult to compare results across multiple studies, which in turn affects the relevance and efficacy of the work conducted in this field.

MDROs in the air surrounding the patient may lead to potential contamination of healthcare workers or patients. We need to generate survey data and explore the relationship

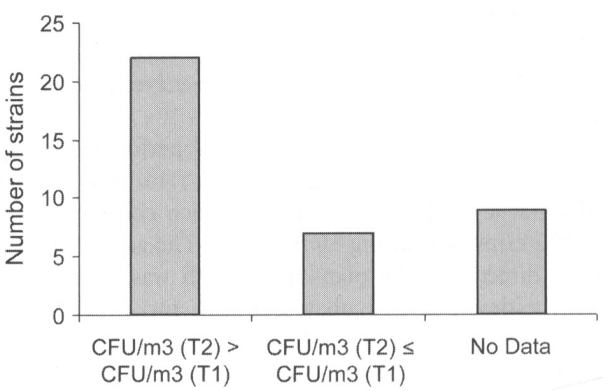

FIGURE 1. Comparison of the level of air contamination (CFU/m^3) regarding the nurse activity. T1, time of air sampling occurring outside nursing care; T2, time of air sampling during nursing care; CFU, colony-forming unit; ND, no data.

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between carrier patients, air transmission, and nosocomial infections.

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