Respiratory viruses in bronchoalveolar lavage: a hospital-based cohort study in adults

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ABSTRACT

Background: The epidemiology of respiratory viruses and their potential clinical impact when recovered in lower respiratory specimens has not been established in the hospital setting.

Objective: To investigate the association between positive viral detection and respiratory infection in an at-risk population.

Design: Prospective cohort study.

Setting: Hospital-based.

Patients: 299 adult patients who underwent bronchoalveolar lavage (BAL) procedures.

Measurements: Descriptive epidemiology of 17 different respiratory viruses detected by reverse transcription-polymerase chain reaction (PCR) assays in BAL specimens. Multivariate analysis was conducted to identify the clinical characteristics independently associated with the presence of virus.

Results: Of 522 BAL specimens analysed, 81% were collected in adult transplant recipients or other immunocompromised patients. Overall, PCR assays identified viral nucleic acid in 91 (17.4%) BAL samples. Similar rates of virus-positive BAL were found in the different subpopulations studied (p=0.113). Coronaviruses were the most frequent (32.3%), followed by rhinovirus (22.6%), parainfluenza (19.5%), influenza (9.7%), respiratory syncytial virus, (8.6%), human metapneumovirus (4.2%), and bocavirus (3.1%). Multivariate analysis using mixed models showed that respiratory viral infections were associated with a lack of antibiotic treatment response (OR 2.2, 95% CI 1.2–4.1) and the absence of radiological infiltrate (OR 0.3, 95% CI 0.2–0.8). In lung transplant recipients in whom a respiratory infection was suspected, the respiratory viral detection rate was 24.4% compared to 13.8% overall in other patients (p=0.02).
Conclusions: In this cohort of hospitalised adults, respiratory viruses detected in BAL specimens were associated with respiratory symptoms, absence of radiological infiltrates and a poor response to antibiotic therapy.
Most respiratory tract infections acquired in the community are of viral etiology. In healthy adults, the disease is generally self-limited and restricted to the upper respiratory tract. However, respiratory viruses cause also lower respiratory tract illnesses and even the so-called “common cold” viruses like rhino- and coronavirus can infect the lower respiratory airways \(^1\text{-}^4\). These viral infections are well known to promote complications such as bacterial infections or an exacerbation of a pre-existing, chronic lung disease such as asthma \(^5\).

Lower respiratory tract infections are among the most frequent causes of hospitalisation and although a significant number of cases are presumably linked to an initial viral infection acquired in the community, the viral etiology is rarely evidenced \(^6\text{-}^8\). This is mainly related to the complexity and the costs of nucleic acid detection procedures, as well as the need for appropriate lower respiratory tract specimens \(^9\). In particular, the role of recently discovered viruses such as human metapneumovirus (HMpV), coronavirus NL 63 (HCoV-NL63) and HKU1 (HCoV-HKUI), as well as bocavirus, has not yet been completely assessed in the hospital setting \(^10\text{-}^13\).

In this study, we screened patients who underwent a bronchoalveolar lavage (BAL) procedure by using sensitive nucleic acid detection assays targeting 17 different viruses to assess the potential impact of respiratory virus in hospitalised subjects with lower respiratory tract disease. By definition, this investigation in hospitalized patients will select a population at high risk for complications such as transplant recipients, immunocompromised hosts, or those with co-morbidities and chronic lung diseases. If respiratory viruses do play any significant role, this needs to be assessed first in this at-risk population.
METHODS

Study population and procedures

We conducted a hospital-based prospective cohort study in 299 patients over a 27-month period. All patients who underwent a BAL were eligible, irrespective of the reason/s leading to the procedure. The study was conducted at the University Hospitals of Geneva (Geneva, Switzerland) and included also lung transplant recipients at the University Hospital of Lausanne (Lausanne, Switzerland) which is 60 kilometres from Geneva and an integral part of our transplantation network.

Bronchoscopy was performed by pulmonary physicians based on guidelines which recommend a BAL procedure for immunocompromised hosts with persistent chest X-ray infiltrate and/or respiratory symptoms (cough with or without sputum, dyspnoea exacerbation, chest x-ray infiltrates, unexplained hypoxemia) despite broad-spectrum antibiotic treatment; HIV-positive patients with low CD4 cell count and a suspected pulmonary opportunistic infection; cases of suspected pulmonary tuberculosis and negative sputum analysis; diffuse persistent interstitial infiltrates of unknown origin; exacerbation of respiratory symptoms in patients with chronic interstitial diseases; or nosocomial pneumonia (including intubated patients) without response to broad-spectrum antibiotic therapy. As the indication for the BAL procedure in lung transplant recipients ranged from routine surveillance to respiratory signs and symptoms with or without abnormal radiologic findings, these patients could have several BALs during the study follow-up period. Patients suspected of having primary lung cancer are submitted to bronchial brushing but not to BAL.

BAL was performed following a standardised protocol (technique, sampling and procedure): 30–50 ml of sterile saline solution was instilled two to three times into the distal bronchial tree, either at the site of the radiographic abnormality or in the middle lobe in the absence of radiographic abnormalities.
The study was approved by both institutional ethics committee and signed informed consent was obtained from all patients.

**Data collection**

A baseline case report form was completed shortly before the BAL procedure. Underlying diseases, fever, respiratory symptoms, response to any antimicrobial therapy, reason/s for the BAL procedure, and the presumed diagnosis based on the available evidence and clinical judgment at that time were recorded. Follow-up was conducted at days three and 30 after the BAL procedure.

Since one clinical episode could lead to several BAL procedures within a short period of time, we defined an exclusion strategy to avoid reporting multiple BAL procedures linked to a unique event as independent episodes. Any BAL performed within a four-week period of the previous procedure and yielding the same viral result was excluded from the analysis, but any BAL episode providing a positive result after a negative one was considered, independent of the time elapsed between the two episodes.

**Sample processing**

BAL specimens were pooled and then aliquoted. Appropriate staining was carried out for direct identification of bacteria, mycobacteria, fungi, and parasites. Cultures for bacterial identification were inoculated under standard aerobic conditions on four different media as well as on specific media for *Mycobacterium* detection when indicated. For potentially colonising bacteria, infection was considered as proven only when quantitative culture yielded $>10^3$ cfu/ml of specimen.
Reverse transcription polymerase chain reaction

BAL specimens were inoculated on four different cell lines for viral detection. An aliquot was frozen at -80°C and subsequently used for viral nucleic acid identification. Real-time TaqMan® reverse transcription polymerase chain reaction (RT-PCR) assays for the detection of influenza A, B, and C, respiratory syncytial virus (RSV) A and B, parainfluenza virus (PIV) 1, 2, 3 and 4, human rhinovirus (HRV), enterovirus, HmPV, coronaviruses OC43, 229E, NL63 and HKU1, and bocavirus were performed as previously described. In brief, RNA was extracted in duplicate using 200 µl of the original specimen. The final precipitate extract of each procedure was eluted in 35 µl and pooled to obtain a final 70 µl volume of RNA. Twenty-five µl were used for the retro-transcription step leading to 100 µl of cDNA. Each PCR assay was then conducted with 5 µl of cDNA. All the different steps of the extraction and reverse transcription were conducted in parallel with known positive supernatant of HRV-2-infected cells and appropriate negative controls.

Compared to the previous cited references, the primers and probes targeting HmPV were updated according to De Maertzdorf et al. In addition, we completed the panel by adding RT-PCR assays targeting influenza C (NS gene) and PIV4 (phosphorprotein gene of A and B subtypes). The forward primers, reverse primers, and probes were as follows: forward 5’-GGC TAC CGA TGA AAT CTC TCT CA-3’, reverse 5’-TCT GGT GTT TCA TTT CCC CAA T-3’, probe 5’-JOE-E - TCAAATCAGGAGCCCAGCTCGATCC-TAMRA-3’ for influenza C; forward 5’-TGA CAC TCA ACA AAT YAA AGG TTC A-3’, reverse 5’-ACT CCA GGR TCC ATT ATT TTC ATT G-3’, probe 5’-FAM-TTG CMA CAA TTG AGG GCC TAA TCA C-TAMRA-3’ for PIV4. The analytical sensitivity of the PIV4 was 10 copies/µl. Influenza C analytical sensitivity was assayed using serial dilution of an influenza C/34/WKD virus cell culture supernatant with a detection limit of 10⁻² dilutions.
Statistical analysis

Data are presented for the entire study group and stratified by clinical conditions to assess potential differences in patient characteristics regarding the frequency of respiratory virus among hospitalized patients. Due to varying numbers of repeated measures per patient, we used mixed models to account for the non-independence of samples. Multivariate mixed logistic regression was performed to identify the clinical variables which were independently associated with the presence of virus. Those variables collected immediately before the BAL procedures were included *a priori* based on their clinical relevance. As lung transplant recipients underwent also surveillance BALs, we performed supplementary analyses for this group stratified according to the presence/absence of new symptoms in order to verify how symptoms may predict a virus positivity rate in patients with a low probability of respiratory infection. Analyses were performed using GraphPad Prism 3 (GraphPad Software Inc, San Diego, CA) and STATA (version 10.0; Stata Corp, College Station, TX).

RESULTS

Patients

Of 1242 BALs performed during a 27-month period (November 2003 to March 2006), 522 BAL specimens from 299 patients were analyzed. Exclusion criteria from the analysis included the impossibility to obtain informed consent, multiple BAL procedures for the same clinical episode, and, in most cases, the lack of BAL fluid after routine investigations since no additional bolus of saline solution was instilled only for the purpose of the study. Baseline characteristics of the clinical conditions and symptoms are summarized in Table 1. The mean age was 52 years, and 61% of BAL episodes occurred in male patients.

On average, 1.8 BAL procedure were performed in each case, but this number was significantly higher in lung transplant recipients. Of the 323 (61.9%) episodes in transplant
recipients, 285 (54.6%) were in lung transplants and 38 (7.3%) in solid organ or hematopoietic stem cell recipients. One hundred and ninety-nine episodes (38.1%) occurred in non-transplanted patients; 60 (11.5%) in the presence of a non-HIV immunosuppressive condition; 41 (7.8%) in HIV-infected patients (median CD4 cell count, 77 cells per mm3; range, 2 to 600); and 98 (18.8%) in the absence of immunosuppressive condition. Four hundred twenty-eight episodes (82%) occurred in hospitalized patients; among these, 118 (27.6%) were admitted to the intensive care unit (93% on ventilation support). The presence of radiological infiltrates was evidenced in 46.2% of all episodes. As expected, we observed significant differences between each patient subgroup. Of note, in lung transplant recipients, a suspected respiratory tract infection and/or opportunistic infection or the presence of a radiological infiltrate were significantly less frequent (p < 0.001).

Microbiological analysis

Overall, 91 of 522 episodes (17.4%) were positive for at least one respiratory virus with a positivity rate that ranged between 12.3% and 31.6% according to the group studied (table 1). These differences were not statistically significant. The distribution of the different viral genera and species recovered as well as their relative contribution and seasonality is shown in fig. 1. The viral distribution at the genus level was as follow: human coronavirus, 32.3% (n=30); HRV, 22.6% (n=22); PIV, 19.5% (n=19); influenza, 9.7% (n=9); RSV, 8.6% (n=8); HMpV, 4.2% (n=4); and bocavirus, 3.1% (n=3) (fig. 1A). In five episodes, two different viruses were detected concomitantly.

The proportion of documented bacterial infection was 23.7% in virus-negative cases compared to 13.2% of those virus-positive (table 2). The median total cell count (interquartile range [IQR]) in the BAL fluid was similar between the virus-negative and -positive groups: 20 (24) and 23 (34) cells 10⁶/100 mL, respectively.
Four hundred fifty-six BAL specimens (87%) were sent for viral culture. Eleven (2.4%) were inconclusive because of bacterial contamination, 363 (79.6%) remained negative, and 82 (18%) were positive (cytomegalovirus (CMV), 52 cases (63.4%); HSV, 11 (13.4%); PIV, 10 (12.1%); RSV, 5 (6.1%); HRV, 3 (3.6%); and influenza A, 1 (1.2%)). Of the 19 episodes with a positive respiratory virus culture, four had a negative PCR result. In contrast, among all episodes that were PCR-positive for a respiratory virus, only 18 (19.8%) had a concomitant positive culture. CMV was found in 12.1% of virus-negative cases and in 9.9% of virus-positive cases and herpes simplex virus (HSV) in 1.1% and 2.2%, respectively.

**Clinical features according to virological results**

At the time of the BAL procedure, the physician in charge who was blinded to the virological and microbiological results suspected a respiratory tract infection in 71 of 91 (78.0%) episodes that revealed to be respiratory virus-positive compared to 219 of 431 (50.8%) of those that remained negative (OR, 2.3, 95% CI, 1.4 to 3.8). A respiratory opportunistic infection was suspected in 32 of 91 (35.1%) respiratory virus-positive episodes compared to 97 of 431 (22.5%) negative episodes (OR, 2.0, 95% CI, 1.2 to 3.2). Fifty-one (56%) of subsequently virus-positive episodes had been treated with antibiotics before the BAL procedure compared to 124 (28.8%) of those that remained negative (OR, 1.7, 95% CI 1.1 to 2.9). In multivariate analysis, controlling for baseline condition, signs or symptoms available immediately before the BAL procedure without knowledge of the microbiological results, the recent introduction of an antibiotic treatment (OR, 2.2, CI 95% 1.2 to 4.1), as well as the absence of a new radiological infiltrate (OR, 0.3, CI 95% 0.2 to 0.8) were significantly associated with the presence of respiratory viruses (table 3). Patients under mechanical ventilation were as likely as others in the intensive care unit to be virus-positive (OR, 0.3, 95% CI 0.1 to 1.5). Forty of 299 patients died within one month following the BAL procedure.
(13.4%). Of these, eight had a virus-positive BAL compared to 32 with a virus-negative BAL (OR, 1.3, 95% CI, 0.5 to 3.6).

Separately, we also analysed lung transplant recipients who represented the larger subgroup of patients enrolled. This analysis showed that the overall incidence of any respiratory symptoms (defined by the presence of at least one of the following: cough; sputum; dyspnoea; fever; or radiological infiltrate) among patients with a respiratory infection suspected before the BAL procedure was 73.7% compared to 38.6% of those without any previous suspicion (p<0.001). Importantly, in the group with a suspicion of respiratory infection, the respiratory viral detection rate was 24.4% compared to 13.8% in other cases (p=0.02). These two observations confirmed an association between the presence of symptoms and a positive viral detection.

DISCUSSION

This study shows that by using sensitive molecular assays, respiratory viruses are recovered in up to 17.4% of BAL specimens performed in a tertiary care hospital. Among all viruses screened, coronaviruses and rhinoviruses are the most frequent. A series of analyses of associated clinical conditions indubitably and consistently supported that these viral infections were associated with respiratory symptoms and complications. In particular, in the subgroup of lung transplant recipients, we were able to demonstrate that the detection of viral nucleic acid was significantly associated with respiratory symptoms and this corroborates its role in symptom production. The completeness of the molecular assays, the use of highly standardised lower respiratory specimens, and the fact that cases were not selected on pre-defined clinical conditions strengthen the accuracy of our findings.

Subjects enrolled were those that underwent a bronchoscopic procedure as a part of their clinical work-up to identify the cause of a potential respiratory infection. Although this
approach limited the spectrum of respiratory diseases studied, this had the advantage to provide high quality lower respiratory tract specimens and to focus on hospitalized patients, those most at risk of complications. The viral detection rate was relatively similar across all subgroups studied. The temporal association between symptoms and the presence of a respiratory viral infection defined by a positive PCR assay was carefully assessed. Univariate analysis using the associated clinical, radiological or microbiological findings revealed a significant association between the presence of an acute respiratory disease and a positive PCR. In multivariate analysis, the non-response to antibiotherapy targeting a respiratory tract infection and the absence of radiological infiltrates were significantly associated with the presence of a positive viral detection. Analysis of the subgroup of lung transplant recipients in whom the BAL procedure is often performed as part of routine follow-up further confirmed the association between symptoms and viral infections. In a consistent manner, the viral infections concentrated clearly in lung transplant recipients in whom respiratory symptoms were exacerbated and a respiratory infection suspected. This is also consistent with previous studies 6,18.

By targeting 17 different viruses using similar sensitive nucleic detection assays applied on the most standardized lower respiratory tract specimens, and by avoiding the selection of cases for specific symptoms, our study is likely to provide a representative epidemiological pattern of lower respiratory tract viral infection in hospitalised adults. In this regard, the so-called “common cold” viruses, rhino- and coronavirus, are the most frequently encountered and represented 23% and 32% of our positive cases, respectively. This mirrors the epidemiology of the adult population living in the community. The ability of these viruses to cause lower respiratory tract diseases has been reported previously 6,9,13,19,20 and HRV is known to cause complications in asthma and chronic obstructive pulmonary disease patients as well as in lung transplant recipients. Coronavirus infections are also associated with lower
respiratory diseases and pneumonia. Taken together, this highlights the significant impact of rhino- and coronaviruses compared to other more classical viruses such as influenza RSV and PIV, the latter three being the only target of many routine diagnostic procedures. Some viruses such as HMpV, influenza C, enterovirus and PIV4 were very infrequent or absent in this adult population, perhaps reflecting a previous protective immunity or other seasonal aspects. Similarly, relatively few cases of bocavirus infections (3%) were diagnosed. Most bocavirus studies have focused on children and only few reports have studied adults in whom the incidence seems significantly lower. The use of new molecular tools targeting all respiratory viruses represents an opportunity to revisit the respective role of each of these agents. Nevertheless any conclusion drawn from this type of study needs to take into account the seasonality and the potential inability to detect new viral subtypes. Of note, our detection assays target viral RNA or DNA which does not prove per se the presence of fully competent and replicating virus. Although this could be considered as a limitation, it must be kept in mind that most of these viruses are not cultivable and that viral RNA is not equipped to survive in respiratory secretions without facing degradation or clearance by daily mucus production. Thus, a positive RT-PCR assay is most likely proof of an ongoing or a recent viral infection. Viral shedding has been shown to persist for days and even weeks in very young children and other immunocompromised patients.

It is noteworthy that viruses such as influenza, or to a lesser extent RSV, for which an antiviral treatment might be available, accounted for only one-fifth of all positive cases in this adult population. This emphasizes the potential for therapy targeting other respiratory viruses which are still orphan of specific antiviral treatment.

Our study shows that respiratory viruses are detected in approximately one of five hospitalised adults presenting lower respiratory tract complications leading to a BAL procedure. When sensitive nucleic acid detection assays are used in this population, rhino-
and coronaviruses are the leading agent detected. Our analysis supports a relationship between a positive viral detection and the presence of lower respiratory symptoms, as well as a poor response to antibiotherapy.
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COMPETING INTEREST

None

ETHICS APPROVAL

Ethical approval for this study was obtained from the ethics committees of the University Hospitals of Geneva and the University Hospital of Lausanne.

JG participated in the development of the study design, implemented the study, and was in charge of data management and analysis, and the writing and revision of the manuscript.
PMS assisted in the study design, supervised the study in Geneva, collected data, and participated in the analysis, and the writing of the manuscript.
JDA assisted in the study design, supervised the study in Lausanne, collected data, participated in the analysis of the data, and the writing of the manuscript.
TR participated in the study design, helped to oversee the implementation, supported the recruitment of the patients and assisted with manuscript preparation.
PM helped to process the samples and to implement the study in Lausanne and assisted with manuscript preparation.
YT was in charge of the development of the molecular assays used, supervised the laboratory analysis, and assisted with manuscript preparation.

CT was in charge of the development of the molecular assays used, supervised the laboratory analysis, and assisted with manuscript preparation.

POB was in charge of the data management, analysis and the statistical methods, and participated actively in the writing and revision of the manuscript.

LK (guarantor) had the initial idea for the study, designed the protocol, supervised the laboratory analysis and was the recipient of the funding. He participated in the data analysis, wrote the manuscript, and revised article drafts for publication. LK takes responsibility for the integrity of the data and the accuracy of the data analysis. All authors have seen and approved the final version.

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<table>
<thead>
<tr>
<th>No immunosuppressive conditions (n=98)</th>
<th>HIV-infected (n=41)</th>
<th>Other immunosuppressive conditions (n=60)</th>
<th>Lung transplant recipients (n=285)</th>
<th>Other transplant recipients (n=38)</th>
<th>All (n=522)</th>
</tr>
</thead>
<tbody>
<tr>
<td>No of BAL* included in the study</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
<td>1.1 (0.2)</td>
<td>1.1 (0.3)</td>
<td>1.2 (0.3)</td>
<td>3.6 (1.1)</td>
<td>1.8 (1.9)</td>
</tr>
<tr>
<td>[median, maximum]</td>
<td>[1, 3]</td>
<td>[1, 2]</td>
<td>[1, 9]</td>
<td>[3, 14]</td>
<td>[1, 14]</td>
</tr>
<tr>
<td>Respiratory tract infection suspected</td>
<td>71.5 %</td>
<td>95.1 %</td>
<td>86.7 %</td>
<td>27.7 %</td>
<td>92.1 %</td>
</tr>
<tr>
<td>Respiratory opportunistic infection</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>52.7 %</td>
</tr>
<tr>
<td>suspected</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tuberculosis suspected</td>
<td>20.4 %</td>
<td>73.2 %</td>
<td>51.7 %</td>
<td>8.8 %</td>
<td>60.5 %</td>
</tr>
<tr>
<td>Fever</td>
<td>19.4 %</td>
<td>73.2 %</td>
<td>16.7 %</td>
<td>0 %</td>
<td>10.5 %</td>
</tr>
<tr>
<td>Influenza-like illness</td>
<td>51.0 %</td>
<td>70.7 %</td>
<td>48.3 %</td>
<td>10.9 %</td>
<td>94.7 %</td>
</tr>
<tr>
<td>Respiratory symptoms</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>33.5 %</td>
</tr>
<tr>
<td>Cough</td>
<td>49.0 %</td>
<td>70.7 %</td>
<td>55.0 %</td>
<td>31.6 %</td>
<td>57.9 %</td>
</tr>
<tr>
<td>Dyspnoea</td>
<td>55.1 %</td>
<td>56.1 %</td>
<td>68.3 %</td>
<td>29.5 %</td>
<td>63.2 %</td>
</tr>
<tr>
<td>Sputum, Rhinopharyngitis</td>
<td>48.0 %</td>
<td>41.5 %</td>
<td>43.3 %</td>
<td>21.1 %</td>
<td>31.6 %</td>
</tr>
<tr>
<td>Any respiratory symptoms</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>31.0 %</td>
</tr>
<tr>
<td>New radiological infiltrates</td>
<td>75.5 %</td>
<td>85.4 %</td>
<td>81.7 %</td>
<td>47.0 %</td>
<td>79.0 %</td>
</tr>
<tr>
<td>Antibiotic treatment targeting a respiratory tract infection</td>
<td>84.7 %</td>
<td>82.9 %</td>
<td>85.0 %</td>
<td>14.7 %</td>
<td>81.6 %</td>
</tr>
<tr>
<td>Respiratory virus-positive n (%)</td>
<td>39.8 %</td>
<td>34.2 %</td>
<td>43.3%</td>
<td>26.0 %</td>
<td>43.4%</td>
</tr>
<tr>
<td></td>
<td>12 (12.3)</td>
<td>7 (17.1)</td>
<td>12 (20.0)</td>
<td>48 (16.8)</td>
<td>12 (31.6)</td>
</tr>
</tbody>
</table>

*BAL = bronchoalveolar lavage
TABLE 2: Microbiological findings associated with the presence of respiratory virus

<table>
<thead>
<tr>
<th></th>
<th>Virus-negative (n=431)</th>
<th>Virus-positive (n=91)</th>
</tr>
</thead>
<tbody>
<tr>
<td>No microorganisms or colonisation, n (%)</td>
<td>237 (55.0)</td>
<td>76 (83.5)</td>
</tr>
<tr>
<td>Bacterial infection, n (%)</td>
<td>124 (23.7)</td>
<td>12 (13.2)</td>
</tr>
<tr>
<td><em>Mycobacterium</em> tuberculosis or atypical mycobacteria, n (%)*</td>
<td>7* (1.6)</td>
<td>2 (2.2)</td>
</tr>
<tr>
<td><em>Pneumocystis jiroveci</em>, n (%)</td>
<td>14 (3.2)</td>
<td>1 (1.1)</td>
</tr>
</tbody>
</table>

*Atypical *Mycobacterium* was identified in two cases (one lung transplant recipient and one HIV-infected subject).
**TABLE 3: Clinical predictors of respiratory virus at the time of the bronchoalveolar lavage procedure***

<table>
<thead>
<tr>
<th>Predictors</th>
<th>OR (95% CI)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Baseline Conditions</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No immunosuppressive conditions</td>
<td>Reference group</td>
<td></td>
</tr>
<tr>
<td>HIV</td>
<td>1.0 (0.3 – 3.2)</td>
<td>0.98</td>
</tr>
<tr>
<td>Other immunosuppressive condition</td>
<td>1.6 (0.6 – 4.2)</td>
<td>0.39</td>
</tr>
<tr>
<td>Lung transplantation</td>
<td>1.6 (0.6 – 4.0)</td>
<td>0.32</td>
</tr>
<tr>
<td>Other transplantation</td>
<td>2.4 (0.8 – 7.0)</td>
<td>0.10</td>
</tr>
<tr>
<td><strong>Signs or symptoms</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>New radiological infiltrate</td>
<td>0.3 (0.2 – 0.8)</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>Treated with antibiotics**</td>
<td>2.2 (1.2 – 4.1)</td>
<td>0.01</td>
</tr>
<tr>
<td>Sputum</td>
<td>1.9 (1.0 – 3.7)</td>
<td>0.07</td>
</tr>
<tr>
<td>Opportunistic infection suspected</td>
<td>1.8 (0.9 – 3.6)</td>
<td>0.10</td>
</tr>
<tr>
<td>Cough</td>
<td>1.5 (0.8 – 3.0)</td>
<td>0.25</td>
</tr>
<tr>
<td>Respiratory infection suspected</td>
<td>1.5 (0.7 – 3.2)</td>
<td>0.26</td>
</tr>
<tr>
<td>Dyspnœa</td>
<td>0.7 (0.4 – 1.3)</td>
<td>0.29</td>
</tr>
<tr>
<td>Fever</td>
<td>1.5 (0.7 – 3.3)</td>
<td>0.26</td>
</tr>
<tr>
<td>Flu-like illness</td>
<td>1.2 (0.6 – 2.7)</td>
<td>0.57</td>
</tr>
<tr>
<td>Rhinopharyngitis</td>
<td>0.9 (0.5 – 2.0)</td>
<td>0.89</td>
</tr>
</tbody>
</table>

(*mixed logistic regression model, clustered on patient)

**antibiotic treatment targeting a respiratory tract infection**
FIGURE 1: Distribution and seasonality of respiratory viruses among 91 virus positive bronchoalveolar lavage specimens collected over a period of 27 months in a tertiary care hospital.

Figure 1A: Distribution of the different viral genera and species

Corona, coronavirus; Metapneumo, metapneumovirus; Para, parainfluenza virus; RSV, respiratory syncytial virus

RSV: in one case RSV was not typable
Figure 1B: Relative contribution of each viral genus according to the season

- **Winter**: 2.6% Bocavirus, 34.2% Corona, 18.4% Influenza, 7.9% Meta pneumonia, 13.2% Parainfluenza, 15.8% RSV
- **Autumn**: 4.0% Bocavirus, 20.0% Corona, 4.0% Influenza, 20.0% Meta pneumonia, 52.0% Parainfluenza, 18.2% RSV
- **Summer**: 9.1% Bocavirus, 18.2% Corona, 36.4% Influenza, 36.4% Meta pneumonia, 5.0% Parainfluenza, 5.0% RSV
- **Spring**: 50.0% Bocavirus, 5.0% Corona, 5.0% Influenza, 35.0% Meta pneumonia, 5.0% Parainfluenza, 5.0% RSV

**RSV**, respiratory syncytial virus
Figure 1C: Monthly rate of respiratory virus positivity
Respiratory viruses in bronchoalveolar lavage: a hospital-based cohort study in adults

Jorge Garbino, Paola M Soccal, John-David Aubert, Thierry Rochat, Pascal Meylan, Yves Thomas, Caroline Tapparel, Pierre-Olivier Bridevaux and Laurent Kaiser

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