Human metapneumovirus in bronchoalveolar lavage fluid samples from haematology patients detected by reverse transcriptase polymerase chain reaction

Catharina Linssen1, Petra Wolffs1, Marjolein Drent2, Cathrien Bruggeman1, Bart Span3, Walther van Mook4

Departments of Medical Microbiology1, Respiratory Medicine2, Haematology3 and Intensive Care Medicine4, Maastricht University Medical Center, Maastricht, The Netherlands

Introduction

Human metapneumovirus (hMPV):
- Paramyxovirus
- Respiratory tract infection
- Symptoms comparable to respiratory syncytial virus (RSV)
- Infection described in infants1, the elderly2 and immunocompromised patients2,3
- Bronchoalveolar lavage fluid (BALF) analysis useful in diagnosis pulmonary diseases

Aim

Investigate potential role of hMPV in pulmonary infections in patients with a haematological malignancy by means of reverse transcriptase polymerase chain reaction (RT-PCR) in BALF.

Materials and Methods

Patient inclusion
- April 1999 - June 2006
- University Hospital Maastricht
- Intensive Care Unit and Haematology-oncology ward
- Patients with a haematological malignancy suspected of a pulmonary infection

Exclusion criteria
- < 20 ml recovered volume
- < 60,000 cells/ml
- > 1% Squamous epithelial cells
- > 5% Bronchial epithelial cells
- Excessive amount of debris

BALF work-up
- Total and differential cell count
- Grocott (yeast, fungi, P. jiroveci)
- Ziehl Neelsen (Mycobacteria)
- Quantitative bacterial culture
- Culture yeasts/fungi
- Mycobacterial culture

RT-PCR
- Samples retrieved from -80°C
- Target: Nucleoprotein gene
- RNA isolation: MagNA Pure LC Total Nucleic Acid Isolation Kit
- Primers and probes as described by Dare et al.4

Results

Samples included
- A total of 117 samples from 95 patients included

Cytological data
- Total cell count and differential cell count: no significant difference between groups

Additional data
- In one patient (case 4) 4 BALF samples within one month: the first 3 BALF were hMPV PCR +, the final BALF (collected 1 month after the first) was hMPV PCR -
- 7/117 (6%) of samples were hMPV PCR +

Discussion

- hMPV previously described as cause pneumonia in immunocompromised patients3
- hMPV described as cause of upper respiratory illness in up to 15%5,6
- Co-infection with other viruses up to 15%7
- Infection in ICU-patients (with no haematological malignancy) more common than previously thought?

Conclusion

- 6% of BALF samples from patients in our study population were hMPV RT-PCR +
- hMPV could be considered as a causative agent of pulmonary infections in patients with a haematological malignancy

Table 1. Characteristics of the RT-PCR + patients

<table>
<thead>
<tr>
<th>Variable</th>
<th>Case 1</th>
<th>Case 2</th>
<th>Case 3</th>
<th>Case 4</th>
<th>Case 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, years</td>
<td>58</td>
<td>65</td>
<td>59</td>
<td>51</td>
<td>64</td>
</tr>
<tr>
<td>Gender</td>
<td>M</td>
<td>M</td>
<td>M</td>
<td>M</td>
<td>F</td>
</tr>
<tr>
<td>Underlying disease</td>
<td>Multiple myeloma</td>
<td>Diffuse large B cell NHL</td>
<td>AML</td>
<td>Multiple myeloma</td>
<td>Mantle cell NHL</td>
</tr>
<tr>
<td>Stem-cell</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Ct value</td>
<td>29.03</td>
<td>29.03</td>
<td>26.25</td>
<td>27.01</td>
<td>22.57</td>
</tr>
<tr>
<td>Co-pathogen</td>
<td>S. pneumoniae</td>
<td>HSV-1</td>
<td>none</td>
<td>none</td>
<td>none</td>
</tr>
<tr>
<td>ICU</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Outcome</td>
<td>Survived</td>
<td>Survived</td>
<td>Survived</td>
<td>Survived</td>
<td>Survived</td>
</tr>
</tbody>
</table>

Reference


e-mail: klin@lmib.azm.nl