Severe rhinovirus infection in patients requiring Intensive Care Unit admission and in immunocompromised patients: a retrospective study of 42 adults.

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Introduction and objectives

Human Rhinoviruses (HRV) are commonly associated with upper respiratory infection and also play important role in lower respiratory infection. Hospital and community acquired severe HRV infection have been demonstrated previously in immunocompromised as well as immunocompetent patients. Among the three HRV species, HRV-C have been associated with more severe outcome in some studies.

Objectives:

- **To describe the involvement of HRV in lower respiratory infections in patients requiring Intensive Care Unit admission and in immunocompromised patients.**
- **To characterize HRV strains involved by genotyping analysis.**

Methods

A/ Patients: adults (> 18 years)

- **group I: immuno competent patients requiring Intensive Care Unit (ICU) care**
- **group II: immuno compromised patients hospitalized in ICU (group IIa) or in conventional clinical ward (group IIb)**
- **With HRV positive sample**
- **November 2011 to March 2013**

Clinical indication for testing included symptoms of upper respiratory tract infection and lower respiratory tract infection, or surveillance of other infectious or non-infectious conditions.

B/ Data collection: Clinical, laboratory (including bacteriological and parasitological screening) and radiographic data were retrospectively collected.

(i) ***Proven HRV infection*** **if HRV was detected from broncho alveolar lavage fluid (BALF)**

(ii) ***Possible HRV infection*** **if HRV was detected from a nasopharyngeal sample (NP) and no bronchoscopy was performed.**

(iii) **Respiratory infection which occurs after 48h of hospital admission was addressed as hospital-acquired infection.**

C/ Specimen collection: BALF and/or NP aspirate or swab.

D/ Viral detection and HRV genotyping: Prospective molecular screening for :

- HRV, enterovirus, respiratory syncytial virus, metapneumovirus, adenovirus, parainfluenzae virus and bocavirus: all year round.

- influenza A/B virus: from November to May.

HRV prospective detection and genotyping was performed with a one-step RT-PCR targeting the 1A/1B RNA genomic region [1,2]. Other respiratory viruses were screened by real-time (RT)-PCR with the Respiratory MultiWell System (MWS) r-gene® (bioMérieux) kits. BALF specimens have also been tested for genome detection of HSV 1-2 and CMV (Argène ®, bioMérieux), bacterial and fungal stain and culture.

Results

A total of 45 HRV infections were studied (n=42 patients; 3 patients with successive HRV infections). Twelve infections were hospital-acquired (26,7%). Seven patients with proven and two patients with possible HRV pneumonia died during hospital stay (Figure 1).

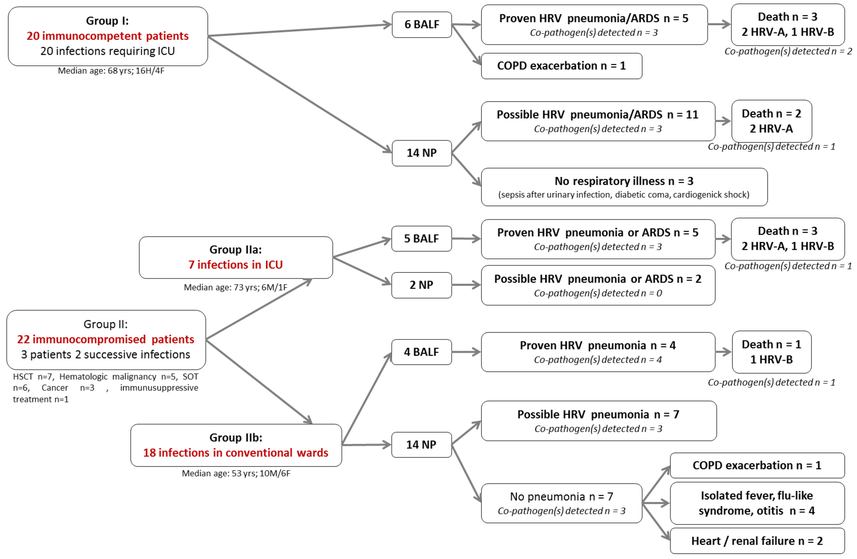


***Figure 1:* Flow diagram of HRV detected in adults, Nov. 2011-March 2013.**

ARDS: acute respiratory distress syndrome, COPD: chronic obstructive pulmonary disease, SOT: solid organ transplant; HSCT: hematopoietic stem cell transplant; BALF: brochoalveolar lavage fluid, NP: nasopharyngeal sample; M/F: male/female.

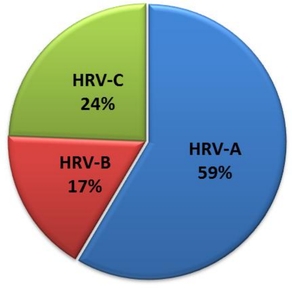


Fig. 2a

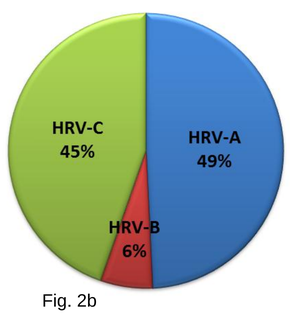
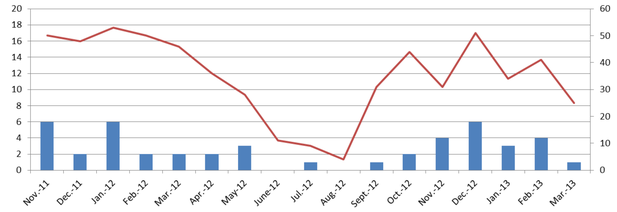


Fig. 2b

***Figures 2a and 2b:* HRV prospective genotyping**

Distribution of the three species of HRV, Nov. 2011–March 2013.
a: studied population (n=41); b: global population (n=524)



Considering all HRV detected in our laboratory, HRV detection in this study had the same monthly distribution trend.

***Figure 3:* Monthly distribution of HRV detection, Nov. 2011-March 2013.**

Bars represent the cases of HRV identification in immuno-compromised patients and immunocompetent requiring ICU care. The line represents all cases of HRV identification in routine practice (secondary right axis).

Phylogenetic analysis of HRV strains detected in studied patients showed that those strains were not grouped in a specific cluster (figure 3).

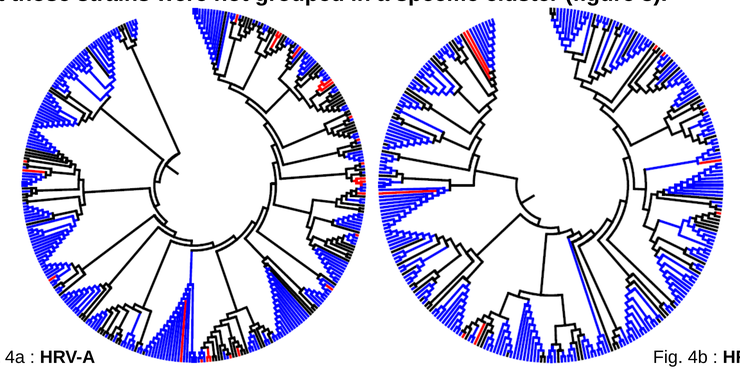


Fig. 4a : **HRV-A**

Fig. 4b : **HRV-C**

***Figures 4a and 4b:* Phylogenetic analysis** *depicting genetic relationships between the HRV strains detected in patients included in the study (red), in patients hospitalized during the study period (blue) and published sequences (black).*
a: HRV-A; b: HRV-C. Phylogenetic tree was reconstructed by the neighbor-joining method, Tamura–Nei's model of evolution, 1000 bootstraps, Mega6.

Conclusions

This study assesses the involvement of HRV in pneumonia, in both immunocompromised and immunocompetent adults. HRV was the only etiologic agent reported in four fatal pneumonia cases.

This observation demonstrates that HRV genome detection should be systematically tested all year round.

In contrast to the literature, HRV-C were not associated with more severe outcome than species A and B. Further investigations are needed to determine the respective role of HRV, underlying condition and frequent in adult pneumonia.

References

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2. Henquell C, Mirand A, Deusebis AL, et al. Prospective genotyping of human rhinoviruses in children and adults during the winter of 2009-2010. J Clin Virol 2012;53:280-4.

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