Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Journal of Clinical Virology 56 (2013) 82–83

Contents lists available at SciVerse ScienceDirect

Journal of Clinical Virology

journal homepage: www.elsevier.com/locate/jcv

Letter to the Editor

Rhinovirus genetic diversity among immunosuppressed and immunocompetent patients presenting with a severe respiratory infection

Keywords:
Human rhinovirus
Genotyping
Severe infection

To the Editor,

Three species of HRV are currently known: A, B and C. HRV C has been detected primarily in children and immunosuppressed patients in association with severe disease.[1–7] HRV species and their associated clinical outcomes in different patient groups are not well defined.[8–10]

We evaluated the occurrence and clinical outcomes of HRV species infections in two distinct populations, immunocompetent and immunosuppressed patients.

A total of 400 swab/nasal wash samples were collected from two populations of hospitalized patients at Hospital São Paulo. Adults patients in a Hematopoietic Stem Cell Transplantation program (HSCT, $n = 202$) and patients (children and adults) hospitalized due to severe acute respiratory syndrome who were suspected of having an influenza A (H1N1)pdm09 infection (SII – suspect of influenza virus infection, $n = 198$).

The inclusion criteria for HSCT was the presence of acute respiratory illness of probable viral etiology. For the SII population was suspicion of severe influenza A (H1N1)pdm09 virus infection with a negative test for this virus.

Criteria for a severe clinical outcome were admission to the intensive care unit (ICU), length of hospitalization and mortality.

Viral RNA was extracted using the QIAamp Viral RNA Extraction Kit (Qiagen, Germany). RT-PCR was accomplished as described previously.[11] DNA sequencing was performed with the BigDye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, USA). The phylogenetic relationships were assessed by maximum likelihood (Topali software v2.5.). All data were analyzed with SPSS version 11.0 (SPSS Inc., USA).

HRV was detected in 11% (22/202) of HSCT patients and in 31.3% (62/198) of SII patients ($p < 0.001$). The hospitalization length was longer for the HRV positive cases from the HSCT group than for those of the SII group ($p < 0.001$) but no significant differences were identified for ICU admission or mortality.

A phylogenetic analysis was performed for 92% (77/84) of the samples and 54.6% (42/77) were HRV A, 11.7% (9/77) were HRV B, and 33.8% (26/77) were HRV C. HRV C was predominant among children but for adult patients' species distribution was similar. Indeed the clinical outcomes were similar ($p > 0.05$) for both patient groups regardless of the species (Table 1) and when each species was compared between the two groups.

Table 1
HRV species distribution, ICU admission, hospitalization time and mortality among the HSCT and SII patients.

	HSCT				
	HRV A (%)	HRV B (%)	HRV C (%)	*p*	Total (%)
ICU admission					
Yes	2 (50.0)	0 (0.0)	2 (50.0)	0.49	4 (23.5)
No	8 (61.5)	2 (15.4)	3 (23.1)		13 (76.5)
Total	10 (58.8)	2 (11.8)	5 (29.4)		17 (100.0)
Time of hospitalization					
Mean	11.1	21.5	30.2		
Median	0.5	21.5	24.0		
Range	0–45	12–31	1–51	0.23	
n	8	2	5		
SD	17.2	13.4	21.2		
Death					
Yes	3 (100.0)	0 (0.0)	0 (0.0)	0.32	3 (16.7)
No	8 (53.3)	2 (13.3)	5 (33.3)		15 (83.3)
Total	11 (61.1)	2 (11.1)	5 (27.8)		18 (100.0)
	SII				
	HRV A	HRV B	HRV C	*p*	Total
ICU admission					
Yes	9 (47.4)	3 (15.8)	7 (36.8)	0.74	19 (37.3)
No	18 (56.3)	3 (9.4)	11 (34.4)		32 (62.7)
Total	27 (53.9)	6 (11.8)	18 (35.3)		51 (100.0)
Time of hospitalization					
Mean	10.2	9	11.3		
Median	7	9	6		
Range	1–68	5–12	1–73	0.94	
n	25	6	17		
SD	13.3	2.8	17.7		
Death					
Yes	2 (66.7)	0 (0.0)	1 (33.3)	0.78	3 (5.9)
No	25 (52.1)	6 (12.5)	17 (35.4)		48 (94.1)
Total	27 (52.9)	6 (11.8)	18 (35.3)		51 (100.0)

SD, standard deviation; HSCT, patients in the Hematopoietic Stem Cell Transplantation program; SII, patients suspected of having an influenza virus infection.

Some authors[12,13] did not observe any difference in the infection outcomes of HRV and influenza A (H1N1)pdm09 infections, as defined by intensive care unit admission and mortality, but species were not considered in their study. In the present study we attempted to identify differences in clinical outcomes in more detail using an HRV genotyping analysis.

The severe outcomes previously linked to HRV C infection[1,8,9] and not the other two species should be reevaluated. Parameters such as age, immune status, and enrollment of community or hospitalized patients, may have differed between the studies. In this context, we reported elsewhere that younger ages may have a greater association with HRV C occurrence in both community and hospital settings.[10]

1386-6532/$ – see front matter
http://dx.doi.org/10.1016/j.jcv.2012.09.001

In conclusion, HRV can play a role in severe respiratory infections, but the outcomes are not dependent on the viral agent or host factors, such as species diversity or immune status.

Contributions

Ellen Ricci Monteiro da Silva and Aripuana Watanabe authors contributed in study design, laboratory tests, data analysis, manuscript writing and revision. Emerson Carraro, Celso Granato and Nancy Bellei authors involved in study design, data analysis, manuscript writing and revision.

Funding

Financial support of Fundação de Amparo a Pesquisa do Estado de São Paulo (FAPESP Project number: 2010/09978-5) and Coordenação de aperfeiçoamento de pessoal de nível superior (CAPES).

Competing interests

None of the authors has declared competing interests.

Ethical approval

The present study was approved by the Ethics Committee of Sao Paulo Hospital and the Federal University of Sao Paulo (number: 0710/10).

References

1. Lau SKP, Yip CC, Lin AW, Lee RA, So LY, Lau YL, et al. Clinical and molecular epidemiology of human rhinovirus C in children and adults in Hong Kong reveals a possible distinct human rhinovirus C subgroup. *J Infect Dis* 2009;**200**(7):1096–103.
2. Greenberg SB. Respiratory viral infections in adults. *Curr Opin Pulm Med* 2002;**8**(3):201–8 [Review].
3. Garbino J, Crespo S, Aubert J-D, Rochat T, Ninet B, Deffernez C, et al. A prospective hospital-based study of the clinical impact of non-severe acute respiratory syndrome (non-SARS)-related human coronavirus infection. *Clin Infect Dis* 2006;**43**:1009–15.
4. Tapparel C, Cordey S, Junier T, Farinelli L, Van Belle S, Soccal PM, et al. Rhinovirus genome variation during chronic upper and lower respiratory tract infections. *PLoS One* 2011;**6**(6):e21163.
5. Nicholson KG, Kent J, Ireland DC. Respiratory viruses and exacerbations of asthma in adults. *Br Med J* 1993;**307**:982–6.
6. Seemungal T, Harper-Owen R, Bhowmik A, Moric I, Sanderson G, Message S, et al. Respiratory viruses, symptoms and inflammatory markers in acute exacerbations and stable chronic pulmonary disease. *Am J Respir Crit Care Med* 2001;**164**:1618–23.
7. Ison MG, Hayden FG, Kaiser L, Corey L, Boeckh M. Rhinovirus infections in hematopoietic stem cell transplant recipients with pneumonia. *Clin Infect Dis* 2003;**36**:1139–43.
8. Miller EK, Edwards KM, Weinberg GA, et al. A novel group of rhinoviruses is associated with asthma hospitalizations. *J Allergy Clin Immunol* 2009;**123**(1): 98–104.
9. Miller EK, Khuri-Bulos N, Williams JV, Shehabi AA, Faouri S, Al Jundi I, et al. Human rhinovirus C associated with wheezing in hospitalised children in the Middle East. *J Clin Virol* 2009;**46**(1):85–9.
10. Moreira LP, Kamikawa J, Watanabe AS, Carraro E, Leal E, Arruda E, et al. Frequency of human rhinovirus species in outpatient children with acute respiratory infections at primary care level in Brazil. *Pediatr Infect Dis J* 2011;**30**(7):612–4.
11. Savolainen C, Mulders MN, Hovi T. Phylogenetic analysis of rhinovirus isolates collected during successive epidemic seasons. *Virus Res* 2002;**85**:41–6.
12. Chan PA, Mermel LA, Andrea SB, McCulloh R, Mills JP, Echenique I, et al. Distinguishing characteristics between pandemic 2009–2010 influenza A (H1N1) and other virusesin patients hospitalized with respiratory illness. *PLoS One* 2011;**6**(9):e24734 [Epub 2011 September 16].
13. Kraft CS, Jacob JT, Sears MH, Burd EM, Caliendo AM, Lyon GM. Severity of human rhinovirus infection in immunocompromised adults is similar to that of 2009 H1N1 influenza. *J Clin Microbiol* 2012;**50**(3):1061–3 [Epub 2012 January 11].

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31 August 2012