

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.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

LETTER TO THE EDITOR VIROLOGY

Enterovirus D68 nosocomial outbreak in elderly people, France, 2014

A. Bal^{1,2}, I. Schuffenecker^{1,2}, I.-S. Casalegno^{1,2}, L. Josset^{1,2}, M. Valette^{1,2}, N. Armand³, P. B. Dhondt⁴, V. Escuret^{1,2} and B. Lina^{1,2}

1) Hospices Civils de Lyon, Groupement Hospitalier Est, Laboratoire de Virologie, Centre National de Référence des Enterovirus et Parechovirus, Centre National de Référence des virus Influenzae, Bron, 2) Université de Lyon, Université Claude Bernard Lyon I, Faculté de Médecine Lyon Est, Lyon, 3) Equipe Mobile d'Hygiène, Centre hospitalier de Valence, Valence and 4) EHPAD Résidence Les Collines, St Donat sur l'Herbasse, France

Original Submission: 8 April 2015; Revised Submission: 28

April 2015; Accepted: 5 May 2015

Editor: T. Avšic-Zupanc

Article published online: 15 May 2015

Corresponding author: B. Lina, Laboratoire de Virologie - Bât A3, 59 Boulevard Pinel, F-69677 Bron Cedex, France E-mail: bruno.lina@chu-lyon.fr

Sir.

In the context of the re-emergence of enterovirus D68 (EV-D68) infection, the main concern is to understand its full epidemiology spectrum [1]. In this letter, we report for the first time an outbreak of nosocomial respiratory infections in elderly people due to EV-D68. These new data are of prime importance to further detect and manage such nosocomial infections.

On 21 October 2014, an ongoing respiratory outbreak in the Alzheimer disease unit of a nursing home was reported to the National Reference Centre for influenza viruses (Bron, France). Thirteen patients were present in the Alzheimer disease unit at the time of the epidemic and all had an individual bedroom. The mean age was 89 years (range 79-101 years); eight of the 13 patients had an underlying disease: one had chronic obstructive pulmonary disease and seven had cardiovascular disease. Of the 13 patients, seven required help to move and six were bedridden. Interactions between patients occurred only in the living room, where each patient had a predefined seat. Bedridden patients spent the shortest time in the living room because it was strictly limited to lunch time. The other patients could carry out other activities in the living room besides eating lunch. Hence there was prolonged contact in the living room mainly for these patients.

On 20 October (Day I (DI)), four patients developed signs of upper respiratory tract infection (cough and rhinorrhoea without fever). The next day (D2), three new patients developed similar clinical signs. On 23 October (D4), nasal swabs were collected from these three most recently symptomatic patients, as recommended by the French guidelines for epidemic management in nursing homes [2] and sent to our laboratory. During the evening, medical staff noticed that an additional patient was starting to cough. All the patients developed only mild respiratory symptoms, no complications were described. There were no further reported cases among other patients of the nursing home or among the medical staff.

Virus RNA extraction from nasal samples was performed using the NucliSens Easy Mag instrument (BioMérieux, Lyon, France). Real-time PCR was then used for the detection of influenza A and B viruses, respiratory syncytial virus, human metapneumovirus, adenoviruses A to F, coronavirus E223 and OC43, bocavirus, parainfluenzaviruses I to 4 and rhinovirus/ enterovirus. Samples from two of the patients tested positive with a commercial real-time PCR (MWS r-gene™ respiratory panel; BioMérieux) that detects both rhinovirus and enterovirus and negative with other PCRs. The sample from the third patient was negative for all PCRs. The two positive samples were next transferred to the National Reference Centre for Enteroviruses for further characterization. EV-D68 infection was confirmed for the two patients by a recently implemented specific real-time RT-PCR [3]. Sequencing of the complete VPI of the two EV-68-positive specimens was performed. The two sequences were 100% identical, belonged to clade B, and were similar to those viruses currently circulating in the USA and France [4] (Fig. 1).

Three days after the first cases occurred in the Alzheimer disease unit, the medical staff implemented droplet precautions. These consisted of wearing facemasks for the staff, restricting access to visitors in the unit and reinforcing hand hygiene using hydro-alcoholic solution. The symptomatic patients were isolated in their bedrooms, and the living room was closed. These infection control measures were stopped 8 days after the last patients developed their clinical signs.

In this report, we describe an EV-D68 outbreak in elderly people. We identified two confirmed cases (i.e. symptomatic patients with a biologically confirmed EV-D68 infection), five probable cases (i.e. patients symptomatic within 48 hours of direct and prolonged contact with a confirmed case) and one excluded case (symptomatic but with EV-D68 PCR negative and no prolonged and direct contact with a confirmed case). Patients developed mild respiratory symptoms with a median duration of 6 days (range: 3-10 days). The outbreak lasted 11

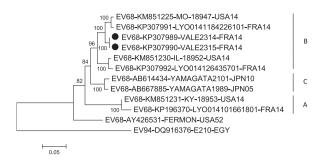


FIG. 1. Phylogenetic analysis based on complete VPI coding sequences of enterovirus D68 (EV-D68) strains. The analysis included the two sequences determined from the respiratory specimens collected from the patients of this study (shown by a dot), eight selected sequences from clinical strains and belonging to genogroups A, B and C (as defined by Tokarz et al. in 2012 [4]), and the prototype EV-D68 strain. The prototype coxsackievirus EV-D94 strain was used as an outgroup virus. Genetic distances were calculated with the Tamura–Nei model of evolution. The tree was constructed by the neighbour-joining method using MEGA5 and validated using 1000 bootstrap pseudo-replicates. Designation of strains is as follows: serotype of the strain–GenBank accession number–laboratory number of the isolate–three-letter country ISO code–year of detection. The ID^{VPI} sequences determined in this study were deposited in GenBank database (KP307989–KP307992).

days and stopped 9 days after the implementation of droplet infection control measures.

A few publications describe nosocomial transmission of EV-D68 [3,5], but no outbreak has been previously reported in an elderly healthcare centre.

The source of the outbreak is unknown. It can be speculated that the four primary cases were exposed to contagious healthcare workers or visitors. Afterwards, no healthcare workers recalled having respiratory symptoms the week before the outbreak but we cannot exclude this hypothesis as EV-D68 asymptomatic cases have been reported in adults. However, despite the fact that healthcare workers work in three different units, the outbreak was limited to only one unit, which suggests that they were unlikely to have been involved in transmission to the secondary cases. This transmission was more likely a patient-to-patient transmission in the living room. Indeed, the seven confirmed or probable cases had prolonged contact in this room, no cases were reported after its closure and the incubation period is considered to be short (median: 1.9 days; 95% CI 1.4–2.4 days) [1].

Influenza viruses, parainfluenza viruses, adenoviruses and respiratory syncytial viruses are the most frequent aetiologies of healthcare-acquired viral respiratory diseases.

This report highlighted the following points: (i) EV-D68 should be considered as an agent of nosocomial outbreaks, (ii) EV-D68 should be specifically searched for when molecular detection of rhinovirus/enterovirus is positive in such a context, and (iii) the rapid implementation of hygiene measures (reinforced hand disinfection, facial masks, segregation of the cases) is the main factor to efficiently block the chain of transmission.

Transparency declaration

B. L. has served as consultant to and received support for travel from BioMérieux. No financial support was provided to BL for the consultant activities.

Acknowledgements

The authors thank Dr Jacques Sartre and the staff of the nursing home for assistance in sample collection and patient management; and Delphine Falcon, Chantal Gousse and Clio Socratous for technical assistance in samples analyses.

References

- [1] European Centre for Disease Prevention and Control (ECDC). Rapid Risk Assessment—Enterovirus D68 detections in the USA, Canada and Europe, 17 September 2014. Stockholm: ECDC; 2014. Available online from:http://www.ecdc.europa.eu/en/publications/Publications/enterovirus-68-USA-Canada-rapid-risk-assessment.pdf.
- [2] Haut Conseil de la Santé publique (HCSP). Conduite à tenir devant une ou plusieurs infections respiratoires aiguës dans les collectivités de personnes âgées (September 2014). Available online from: http://www. hcsp.fr/Explore.cgi/avisrapportsdomaine?clefr=288.
- [3] Poelman R, Schölvinck EH, Borger R, Niesters HG, van Leer-Buter C. The emergence of enterovirus D68 in a Dutch University Medical Center and the necessity for routinely screening for respiratory viruses. J Clin Virol 2015;62:1–5.
- [4] Tokarz R, Firth C, Madhi SA, Howie SR, Wu W, Sall AA, et al. Worldwide emergence of multiple clades of enterovirus 68. J Gen Virol 2012;93:1952–8.
- [5] Rahamat-Langendoen J, Riezebos-Brilman A, Borger R, Van der Heide R, Brandenburg A, Schölvinck E, et al. Upsurge of human enterovirus 68 infections in patients with severe respiratory tract infections. J Clin Virol 2011;52:103–6.