

Pandemic influenza A(H1N1)2009: molecular characterisation and duration of viral shedding in intensive care patients in Bordeaux, south-west France, May 2009 to January 2010

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From May 2009 to January 2010, the Virology Laboratory at the University Hospital of Bordeaux received more than 4,000 nasopharyngeal samples from the Aquitaine region (south-west France) for the diagnosis of pandemic influenza A(H1N1)2009. Eighty-three infected patients deteriorated and were admitted to intensive care units. Our study focused on 24 of these patients. Positivity for influenza A(H1N1)2009 was monitored by realtime PCR and duration of viral shedding was determined. The first available sample of each patient was analysed for bacterial, fungal and viral co-infection. We observed six bacterial (or bacterial/fungal) co-infections and one viral co-infection with respiratory syncytial virus. The samples were analysed for the presence of the neuraminidase H275Y (N1 numbering) mutation, which confers resistance to oseltamivir, by realtime PCR of the neuraminidase gene. No H275Y mutation was observed in any of the viral strains screened in this study. In parallel, a fragment of the haemagglutinin gene encoding amino acid residues 173 to 362 was sequenced to detect mutations that had been reported to increase the severity of the disease. Two patients were infected by strains bearing the D222G (H3 numbering) mutation. The viral shedding of A(H1N1)2009 in this study ranged from four to 28 days with a median of 11 days.

Introduction

During the influenza A(H1N1)2009 pandemic, the virology laboratory at the University Hospital of Bordeaux received from May 2009 to January 2010 more than 4,000 samples collected from the Aquitaine region (south-west France), an area with three million inhabitants. Some 1002 (24.9%) samples were confirmed as positive for pandemic influenza A(H1N1)2009 by realtime PCR. During this period, the three intensive care units (ICUs) of the University Hospital of Bordeaux received 83 patients with severe clinical conditions including acute respiratory distress syndrome (ARDS).

Six of them required extracorporeal membrane oxygenation (ECMO) support. We could study those six and an additional 18 influenza-positive ICU patients in detail to address the following points: to establish the presence of microbial co-infection on admission, to obtain molecular data on the oseltamivir resistance-associated H275Y mutation [1] in the neuraminidase gene, to screen for already identified mutations in the haemagglutinin (HA) gene that may have an influence on the virulence of the virus [2-5], and to evaluate the duration of viral shedding.

Methods

Patients with confirmed influenza A(H1N1)2009 were selected retrospectively for this study after their admission to the ICU for influenza complications, for example respiratory failure or exacerbation of an underlying chronic condition requiring surveillance or assistance. The patients in this study were admitted to the ICU between May 2009 and January 2010.

The detection of influenza A(H1N1)2009 viral RNA was carried out in nasal swabs, bronchoalveolar lavage fluids or respiratory secretions. Pandemic influenza A(H1N1)2009 was diagnosed using the Roche detection kit for influenza A (RealTime ready Influenza A(H1N1) detection set) and operated on a Roche LightCycler 480.

We screened each patient at admission for viral, bacterial and fungal co-infections. Viral respiratory co-infections were investigated using a multiplex PCR assay (Seegene Seeplex RV5-ACE screening) which allows the detection of influenza A, influenza B, respiratory syncytial virus (RSV) A/B, adenovirus A/B/C/D/E, parainfluenzavirus 1/2/3, bocavirus 1, metapneumovirus, human rhinovirus and coronavirus OC43/229E/NL63/HKU1. Bacterial and fungal co-infections were diagnosed after culture and/or serology.

The H275Y (N1 numbering) mutation conferring resistance to oseltamivir was investigated on admission on the first specimen by a fluorescence resonance energy transfer (FRET)-based assay designed in the virology laboratory in Bordeaux as previously described [6].

For sequencing of the HA gene, influenza A RNA was reverse-transcribed using the Titan One Tube RT-PCR kit (Roche) with primers HA1S (ATGAAGGCAATACTAGTAGTTATGCTATATAC) and HA1AS (TTAAATACATATTCTACTGTAGAGACCC). cDNA was then subjected to a nested PCR to amplify a fragment encoding for amino acid residues 173-362 with primers HA3S (CCAAAGCTCAGCAAATCCTAC) and HA3AS (ATCTCGTCAATGGCATTCTGT). The sequences were aligned to the reference strain A/California/06/2009 using Clustalw and Jalview softwares.

Duration of viral shedding was determined as the period between the onset of symptoms and the last positive PCR for influenza A(H1N1)2009 with exception of some cases for whom onset of symptoms could not be determined (the first positive PCR being used as Do of viral shedding). As there was no standard protocol for the follow-up of influenza patients, sampling could have stopped while the patients were still positive for influenza A(H1N1)2009. Using such a method we may have underestimated the duration of the shedding but were not dependent on a negative PCR to evaluate the shedding.

Results

We studied 24 patients admitted to the ICU for severe influenza A(H1N1)2009 between May 2009 and January 2010. All the data collected are summarised in Table 1. The patients had a median age of 51.5 years ranging from 2 to 85 years and the female:male sex ratio was 0.45. Eight patients were immunocompromised (one with lung carcinoma with metastasis, one with co-infection with human immunodeficiency virus (HIV) and hepatitis C virus (HCV), two with leukaemia, two with lymphoma and two patients under follow-up for transplantation), seven had chronic cardiovascular and/or pulmonary diseases, four were obese (BMI>30), and nine had no comorbidity. During the study four patients died.

We were able to collect data concerning antiviral treatment for 20 of the 24 patients. The 20 patients had received the neuraminidase inhibitor oseltamivir. The median time of oseltamivir treatment initiation in the 17 patients for whom this information was available, was five days after the onset of symptoms (range: 1-12 days).

Screening on admission for microbial co-infections revealed only one viral co-infection with respiratory syncytial virus (RSV) and six bacterial or fungal co-infections: *Staphylococcus aureus*, *Haemophilus influenzae*, *Streptococcus agalactiae*, *Branhamella catarrhalis*,

Enterobacter cloacae, *Mycoplasma pneumoniae* and *Candida albicans* (Table 1)

We were able to follow up positivity for influenza A(H1N1)2009 viral RNA in 18 patients for whom we had several specimens. The median duration of viral shedding was 11 days (4-28 days, Table 2). Immunodepression was associated with prolonged viral shedding, with six of the eight immunocompromised patients PCR-positive 14 or more days after onset of symptoms (Table 1); the two other patients who also shed virus for longer than 14 days were obese. Immunocompetent and immunocompromised patients shed virus for a median duration 10 days and 16 days, respectively.

The H275Y mutation was not detected in any of our patients, nor was any other mutation at position 275 of the neuraminidase gene.

We amplified 26 HA sequences from 21 patients (two patients were investigated with several successive samples). The different substitutions of our isolates compared to the reference strain are shown in the Figure. Three samples from two different patients exhibited the D222G substitution. The first (Patient 1 in Table 1) was a patient with morbid obesity (body mass index>40) presenting a severe ARDS requiring ECMO support for nine days and mechanical ventilation for a further 20 days. The HA sequence of virus isolated from their bronchoalveolar lavage fluid showed a mixed population at codon 222: D222EG. As shown in Table 1, she exhibited prolonged viral shedding of 28 days (already published [7]) but recovered and was discharged after one month. The second case (Patient 8 in Table 1) had a lymphoma and chronic obstructive pulmonary disease. Viral shedding lasted for a minimum of 14 days (from the first to the last positive sample), and the patient died after 19 days of hospitalisation. Four influenza A-positive samples from this patient were subjected to HA sequencing. The first sample, a nasal swab, did not contain the D222G substitution, nor did the second one which was a respiratory secretion. Interestingly, the D222G was identified in the third and fourth specimens obtained from secretions 12 and 14 days after the first sample. A mixed population (D222DG) was noted in the fourth specimen. In addition to the D222G mutation, isolates from all four samples contained a V321F substitution in HA that did not match any HA sequences published as of May 2010.

Other substitutions are listed in Table 3 and include S203T (13/26 sequences), and less frequently D222E (4/26), Y230H (1/26), M257I (1/26), Q293H (1/26), I295V (2/26), K305R (1/26), V321I (2/26) and V321F (5/26).

Discussion

In Aquitaine, 13–25% of the population were infected with influenza A(H1N1)2009 during the pandemic [8]. Between May 2009 and January 2010, 83 patients suffered from a complicated influenza and were admitted

TABLE 1

Clinical and microbiological features of influenza A(H1N1)2009 patients requiring intensive care, Bordeaux, May 2009 - January 2010 (n=24)

Patient	Age group (years)	Sex	ECMO	Outcome	Immunodepression	Respiratory symptom	Cardiac symptom	Obesity ^a	Viral co-infection	Bacterial or fungal co-infection	Median time of NAI treatment initiation (days)	Viral shedding (days)	D222G in HA
1	15-44	F	Yes					Yes			5	28	Yes
2	45-64	M	Yes		Hairy cell leukaemia			Yes			7	27	
3	45-64	F	Yes	Deceased	Cardiac transplantation						1	19	
4	45-64	M	Yes		Chronic lymphocytic leukaemia						ND	17	
5	15-44	M			HIV/HCV					<i>Haemophilus influenzae</i> / <i>Candida albicans</i>	8	16	
6	45-64	F	Yes					Yes			6	14	
7	45-64	M		Deceased	Lung cancer	Asthma					9	14	
8	45-64	M		Deceased	Lymphoma	COPD					5	14	Yes
9	45-64	M									12	12	
10	15-44	M								<i>Streptococcus agalactiae</i>	4	10	
11	45-64	M				Respiratory failure					ND	10	
12	45-64	M		Deceased						<i>Staphylococcus aureus</i>	8	10	
13	45-64	F	Yes			Asthma		Yes			8	9	
14	45-64	F				COPD					9	7	
15	45-64	M			Lymphoma						ND	7	
16	0-15	F								<i>Enterobacter cloacae</i> / <i>Mycoplasma pneumoniae</i>	3	4	
17	45-64	F					Cardiopathy				ND	4	
18	15-44	M									4	4	
19	45-64	F							RSV	<i>Candida albicans</i>	2	ND	
20	15-44	F									ND	ND	
21	65+	F									ND	ND	
22	65+	F				Chronic bronchitis					ND	ND	
23	0-15	M								<i>Branhamella catarrhalis</i>	1	ND	
24	15-44	M			Lung transplantation						1	ND	

COPD: Chronic obstructive pulmonary disease; ECMO: extracorporeal membrane oxygenation; F: female; HA: haemagglutinin; HCV: hepatitis C virus; HIV: human immunodeficiency virus; M: male; NAI: neuraminidase inhibitor; ND: not determined; RSV: respiratory syncytial virus.

^a Obesity was defined as a body mass index >30.

median delay before initiation of treatment was five days, which exceeds the recommended time for the administration of oseltamivir at the latest 48 hours after the onset of symptoms [22]. Late treatment due to delayed admission to the ICU and comorbidities could account for prolonged viral shedding because of a slower viral clearance [23]; it has been shown that treatment initiated one to three days after infection significantly shortens viral shedding duration [24]. However, Patient 3 was shedding virus particles for 19 days despite rapid administration of oseltamivir.

As among the currently licensed drugs only neuraminidase inhibitors remain useful to treat influenza A(H1N1)2009, it is of particular importance to monitor the resistance/sensitivity of viral isolates to oseltamivir. Unfortunately worrying levels of oseltamivir-resistant isolates of the seasonal influenza A(H1N1) have emerged in Europe [25,26]. In these viruses, the most frequent mutation conferring resistance to oseltamivir is the H275Y substitution [27] in the neuraminidase gene, which does not cause cross-resistance to zanamivir.

Among the 26 isolates analysed, we have not observed any H275Y substitution. These data are in accordance with the literature showing that the prevalence of resistant A(H1N1)2009 viruses is at present very low. As of August 2010, 304 cases of oseltamivir resistance in this strain have been reported worldwide [28], all of which were due to the H275Y mutation in NA.

The HA protein is one of the determinants of virulence and host specificity through its interaction with the sialic acid receptor on the cell surface. While avian influenza viruses preferentially bind to alpha2,3-linked sialic acid, human viruses prefer the alpha2,6 linkage [29]. It has been shown that two positions in HA are involved in determining sialic acid binding preference, namely amino acid residues 187 and 222 (190 and 225 in H3 numbering) [30]. A D222G mutation causes

a shift to preferential binding to alpha2,3 receptors. This mutation has recently been described in influenza A(H1N1)2009 isolates from patients with severe disease or fatal outcome in several countries [2,4,5,31,32], but has also been detected in association with a mild disease [33].

Two D222G substitutions were observed in our study. Both patients experienced a severe clinical course of disease. One required ECMO and the estimated viral shedding lasted 28 days [7], while the other died after 19 days and was at the time probably still positive for influenza A(H1N1)2009, although no autopsy was performed. In the deceased patient, this mutation was not present on admission but appeared 12 days after the first positive sample, therefore suggesting a selection event. We propose that the long duration of viral shedding allowed the virus to evolve and acquire this substitution. Whether or not this mutation accounted for the severity of the disease in this patient remains to be investigated.

Interestingly, the 1918 Spanish influenza isolate NY18 carried the combination D190/G225 and had double specificity for both alpha2,3- and alpha2,6-linked sialic acid [30]. It has been shown in ferrets that this viral isolate fails to transmit efficiently but remains virulent [30,34]. Alpha2,3 sialic acid receptors are found in the lower respiratory tract in humans [35]. Like the avian influenza A(H5N1) virus, strains with mutations that affect receptor binding might be less efficiently transmitted but could have an increased pathogenicity [4].

In addition to the D222G substitution, we observed four D222E substitutions in this study (Table 3, Figure). Although these patients had prolonged viral shedding, we could not clearly establish a link with the severity of the disease as they all, except Patient 9, presented comorbidities. Studies have shown that the proportion of D222E is similar in mild and severe cases [32].

In parallel, we found Q293H and I295V mutations whose pejorative role has been mooted but remains to be confirmed [3].

Conclusion

In 24 patients hospitalised in the ICU for pandemic influenza A(H1N1)2009 infection, the requirement for ECMO was mainly associated with comorbidities (immunodepression/pulmonary disease/obesity) and long viral shedding despite oseltamivir treatment.

All strains were found susceptible to oseltamivir. The D222G substitution was observed in only two patients and we hypothesise that this mutation is selected for in the lower respiratory tract but is not transmitted. Microbial co-infections were detected, but with one exception it was not clear whether they contributed to the severity of the disease. We think that the influenza virus alone was responsible for the severe disease and the evolution toward ARDS.

TABLE 3

Frequency of haemagglutinin substitutions identified in influenza A(H1N1)2009 isolates from intensive care patients, Bordeaux, May 2009- January 2010 (n=21 patients)

Mutations in HA	Frequency (among the 26 sequences)	Number of patients exhibiting this mutation
S203T	50%	12
D222G	8%	2
D222E	15%	4
Y230H	4%	1
M257I	4%	1
Q293H	4%	1
I295V	8%	2
K305R	4%	1
V321I	8%	2
V321F	19%	1

HA: haemagglutinin.

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