ELSEVIER

Contents lists available at ScienceDirect

Journal of Clinical Virology

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



Short communication

Acute respiratory infections among returning Hajj pilgrims—Jordan, 2014



Mohammad Mousa Al-Abdallat ^{a,1}, Brian Rha ^{b,*,1}, Sultan Alqasrawi ^a, Daniel C. Payne ^b, Ibrahim Iblan ^c, Alison M. Binder ^{b,d}, Aktham Haddadin ^e, Mohannad Al Nsour ^f, Tarek Alsanouri ^e, Jawad Mofleh ^f, Brett Whitaker ^b, Stephen L. Lindstrom ^g, Suxiang Tong ^b, Sami Sheikh Ali ^a, Rebecca Moritz Dahl ^h, LaShondra Berman ^g, Jing Zhang ^b, Dean D. Erdman ^b, Susan I. Gerber ^b

- ^a Communicable Diseases Directorate, Jordan Ministry of Health, Amman, Jordan
- b Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA
- ^c Jordan Field Epidemiology Training Program, Amman, Jordan
- ^d Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA
- ^e Directorate of Laboratories, Jordan Ministry of Health, Amman, Jordan
- ^f Eastern Mediterranean Public Health Network, Amman, Jordan
- g Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA
- h Maximus Federal, Atlanta, GA, USA

ARTICLE INFO

Article history: Received 7 November 2016 Received in revised form 9 January 2017 Accepted 30 January 2017

Keywords: Hajj Respiratory tract infections Jordan MERS-CoV Viruses

ABSTRACT

Background: The emergence of Middle East Respiratory Syndrome coronavirus (MERS-CoV) has prompted enhanced surveillance for respiratory infections among pilgrims returning from the Hajj, one of the largest annual mass gatherings in the world.

Objectives: To describe the epidemiology and etiologies of respiratory illnesses among pilgrims returning to Jordan after the 2014 Hajj.

Study design: Surveillance for respiratory illness among pilgrims returning to Jordan after the 2014 Hajj was conducted at sentinel health care facilities using epidemiologic surveys and molecular diagnostic testing of upper respiratory specimens for multiple respiratory pathogens, including MERS-CoV.

Results: Among the 125 subjects, 58% tested positive for at least one virus; 47% tested positive for rhino/enterovirus. No cases of MERS-CoV were detected.

Conclusions: The majority of pilgrims returning to Jordan from the 2014 Hajj with respiratory illness were determined to have a viral etiology, but none were due to MERS-CoV. A greater understanding of the epidemiology of acute respiratory infections among returning travelers to other countries after Hajj should help optimize surveillance systems and inform public health response practices.

Published by Elsevier B.V.

1. Background

Each year, 2–3 million pilgrims from over 180 countries travel to the Hajj in the Kingdom of Saudi Arabia (KSA), where crowded conditions pose potential risks for transmission of respiratory tract infections, the most common infections acquired by Hajj pilgrims [1–3]. The emergence of Middle East Respiratory Syndrome

coronavirus (MERS-CoV) prompted additional travel guidance and enhanced surveillance following Hajj, including in Jordan, which has reported cases of MERS-CoV and shares its eastern and southern borders with KSA [1,4]. Based upon the number of Hajj visas issued, approximately 5600 pilgrims from Jordan traveled to KSA for the 2014 Hajj. In October 2014, Jordan established targeted surveillance of acute respiratory illnesses in Hajj pilgrims returning to Jordan.

In this report, we present the results of a surveillance initiative to describe cases of acute respiratory illnesses in Hajj pilgrims returning to Jordan and detect etiologies of disease, which included

^{2.} Objectives

 $^{^{\}ast}$ Corresponding author at: Centers for Disease Control and Prevention, 1600 Clifton Road, NE, Mailstop A-34, Atlanta, GA 30333, USA.

E-mail address: wif8@cdc.gov (B. Rha).

¹ These authors contributed equally to this work.

Table 1Characteristics of Hajj Pilgrims, Jordan, 2014.

Characteristic	All patients (n = 125)	
	n/total	%
Demographics		
Age groups (years)		
18-64	88/118	75
65+	30/118	25
Sex		
Male	76/123	62
Female	47/123	38
Clinical characteristics		
Symptoms		
Fever	51/125	41
Cough	95/125	76
Sore throat	62/125	50
Nasal discharge	46/125	37
Difficulty breathing	20/125	16
Comorbid conditions		
Diabetes	17/125	14
Hypertension	28/125	22
Heart disease	10/125	8
Kidney disease	1/125	1
Cancer	1/125	1
Bronchial asthma	2/125	2
Current smoker	24/107	22
Currently pregnant	3/42	7
Travel history		
Exposures		
Contact with sick person during Hajj	31/119	26
Contact with animal during Hajj	3/115	3
Visited market	20/22	91
Visited slaughterhouse	2/22	9
Visited health care facility prior to enrollment	36/99	36
Visited Hospital	5/24	21
Visited Center	19/24	79
Healthcare facility in KSA	13/31	42
Healthcare facility in Jordan	18/31	58
Mode of transportation	•	
Bus	93/125	74
Car	15/125	12
Plane	17/125	14

testing for MERS-CoV and other pathogens known to cause acute respiratory illnesses.

3. Study design

During October 8–23, 2014, a two-week period immediately following the conclusion of Hajj, 12 hospitals and outpatient clinical sentinel surveillance sites in the south, north, and central regions of Jordan conducted surveillance for respiratory illness among returning pilgrims. Pilgrims returning to Jordan with symptoms of respiratory infection were instructed to present to sentinel health facilities via health information cards at points of reentry, and through posted notices and healthcare workers at the sentinel health facilities. Persons were considered for enrollment in surveillance if they (1) traveled to the 2014 Hajj, and (2) presented with respiratory illness. Institutional Review Board approval was obtained in Jordan for this public health response, and verbal consent was obtained prior to enrollment. Targeted demographic and clinical information were collected (listed in Table 1) by in-person interview using a brief, standardized questionnaire.

Nasopharyngeal and oropharyngeal (NP/OP) swabs were sought from all enrolled subjects using flocked swabs. Swab specimens were combined in 2–3 mL of viral transport media, stored at 4 °C, and transported to the Central Public Health Laboratory in Amman, Jordan, within 48 h of collection and divided into aliquots. Total nucleic acid extraction was performed on 140 μL of sample from one aliquot per subject using a QIAamp Viral RNA Mini Kit (QIAGEN), and then tested using Centers for Disease Control and

Table 2Respiratory pathogens detected among Hajj Pilgrims, Jordan, 2014.

Respiratory pathogen	All patients ($n = 125$)	
	n/total	%
Virus		
MERS coronavirus	0/125	0
Human coronavirus 229E	8/125	6
Human coronavirus NL63	4/125	3
Human coronavirus OC43	4/125	3
Human coronavirus HKU1	0/125	0
Influenza A ^a	4/125	3
Influenza B	2/125	2
Influenza C	0/125	0
Respiratory syncytial virus	1/125	1
Parainfluenza virus 1 ^b	1/125	1
Parainfluenza virus 2	0/125	0
Parainfluenza virus 3	2/125	2
Parainfluenza virus 4	0/125	0
Human metapneumovirus	0/125	0
Rhino/enterovirus	59/125	47
Parechovirus	0/125	0
Adenovirus	1/125	1
≥2 viruses ^c	13/125	10
Bacteria		
Bordetella pertussis	0/125	0
Chlamydophila pneumoniae	0/125	0
Mycoplasma pneumoniae	0/125	0
Legionella pneumophila	0/125	0

- ^a All influenza A-positive specimens were subtype H3N2.
- ^b One specimen tested positive for parainfluenza virus 1 by panviral PCR.

Prevention (CDC) real-time reverse transcription PCR (rRT-PCR) assays for influenza A, B (procedures available upon request at https://www.cdc.gov/flu/clsis/), and MERS-CoV [5].

Frozen specimen aliquots were sent to CDC in Atlanta, Georgia, USA, for additional testing of non-MERS-CoV respiratory pathogens (listed in Table 2). Total nucleic acids were extracted from 300 μ L of each specimen aliquot using the NucliSENS easyMAG system (bioMerieux) and tested on a multi-pathogen TaqMan Array card (ThermoFischer Scientific) using CDC-developed singleplex rRT-PCR assays [6–8].

Influenza-positive samples were further confirmed and influenza A-positive samples were sub-typed as human seasonal A(H3) or A(H1)pdm09 using CDC influenza rRT-PCR assays (procedures available upon request at https://www.cdc.gov/flu/clsis/), while influenza-negative samples were additionally tested with broadly reactive panviral family/genus PCRs that were designed to amplify genomic sequences from both known and potentially novel members of the viral families/genera, including those known to be associated with respiratory diseases: Adenoviridae [9], Coronavirinae [10], Orthomyxoviridae [11], Paramyxovirinae [12], Parvovirinae (unpublished in-house PCR), Polyomaviridae [13], and Reoviridae (orthoreovirus) [14].

Differences among subjects were assessed for significance (α = 0.05) using χ^2 , Fisher's exact, and Wilcoxon rank sum tests, where appropriate. All data were analyzed using SAS version 9.3 (SAS Institute, Cary, NC).

4. Results

Epidemiologic data and respiratory specimens were collected from 125 subjects (Table 1) with a median age of 51.5 years (range 25–86). Common underlying medical conditions reported included hypertension (22%), diabetes (14%), and heart disease (8%); 22% of those responding reported current smoking. Onset of symptoms

^c Specimens testing positive for two viruses included those with co-detection of rhino/enterovirus with human coronavirus 229E(n=3), NL63(n=2), or OC43(n=2), influenza A(n=2), parainfluenza virus B(n=2), or adenovirus B(n=1). In addition, one specimen tested positive for three viruses: rhino/enterovirus, human coronavirus B(n=1).

Download English Version:

https://daneshyari.com/en/article/5667996

Download Persian Version:

https://daneshyari.com/article/5667996

<u>Daneshyari.com</u>