

Abstract no: 127**Presentation at ESCV 2016: Poster 66****Microbiological evaluation of respiratory tract infections in pilgrims returning from countries affected by Middle East respiratory syndrome coronavirus (MERS-CoV)**

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Since September 2012, the World Health Organization (WHO) has been notified of 1728 laboratory-confirmed cases of infection with Middle East respiratory syndrome coronavirus (MERS-CoV), including at least 624 related deaths (disease outbreak news of April 26, 2016). Although MERS-CoV appears to be transmitted through respiratory droplets between humans with close contact, dromedary camels are likely to be a zoonotic source of MERS-CoV infection in humans. Early detection of MERS-CoV infection among international travelers exposed to camels or healthcare facilities in the Middle East remains essential. All travelers returning from MERS-CoV-affected areas to Paris (France) are given particular attention and those with fever and/or respiratory symptoms are referred to a dedicated infectious disease unit as the Infectious Disease Department of La Pitié-Salpêtrière University Hospital in Paris. The aim of this study was to investigate the microbiological etiologies of respiratory tract infections (RTI) among these specific travellers from the beginning of the 2015 Hajj and Umrah pilgrimage period (September 2015) to April 2016.

Upon admission, patients were isolated and nasopharyngeal swabs, sputum samples and, for persons on ventilators, bronchoalveolar lavage specimens were collected by trained nurses. We examined which etiological respiratory pathogens were identified during screening for MERS-CoV in symptomatic travellers returning to Paris during September 2015 to April 2016 period, from MERS-CoV endemic regions (published WHO bulletins). Firstly, samples were screened with a specific MERS-CoV real-time reverse transcription PCR targeting region upstream of the E gene (upE), as recommended by WHO. The second step of the etiologic diagnosis entailed an investigation for other respiratory viruses (influenza A/B viruses, respiratory syncytial virus, metapneumovirus, rhinovirus-enterovirus, parainfluenza viruses, other human coronaviruses) using Respiratory MWS r-gene[®] kits (bioMérieux) and for bacteria using standardized culture procedures.

A total of 31 symptomatic travellers mainly returning from Saudi Arabia (mean age 63.1 years, range 21–92 years; 58% male) were included during the study period and overall 48 respiratory clinical specimens were collected. None of the tested specimens were positive for MERS-CoV. Since a negative result should not absolutely rule out the possibility of MERS-CoV infection, notably if specimen is collected late or very early in the illness, some patients were screened twice. The vast majority of viral RTI, sometimes

associated with bacteria superinfection, in these pilgrims returning home, were due to seasonal influenza A viruses (29%), rhinoviruses (23%), and other coronaviruses (7%) distinct from the MERS-CoV. Four patients were presenting acute lobar pneumonia, none were formally diagnosed. However, all were cured with antibiotics, as the presentation suggested pneumococcal infection. One case of Q fever, another known zoonosis transmitted by dromedary camels, and one case of *Legionella pneumophila*-associated disease were diagnosed among tested pilgrims.

Continuous surveillance should be implemented to ensure the timely detection of possible imported cases of MERS-CoV and their immediate isolation in order to avoid secondary cases. However, clinicians should be aware that influenza viruses and rhinoviruses are the most commonly identified pathogens in returning pilgrims with acute RTI.

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Abstract no: 136**Presentation at ESCV 2016: Poster 67****Determination of genotype distribution and the various polymorphisms in cytomegalovirus (CMV) strains**

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Human cytomegalovirus has different genotypes, by determining these genotypes in different disease groups, the association of one and more than one infections can be found. In genotyping, frequently seen genetic polymorphisms gB (UL55) and gH (UL75) performed in envelope's glycoprotein. In our study phylogenetic analysis of 50 CMV (+) patient's gB and gH gene regions were done. In this study DNA sequence analysis performed and the result was evaluated by MEGA 6.0 program. According to phylogenetic analysis the results were; 48–50 patient gene region were amplified, 23 (%48) of these patients were gB1, 8 (%16) were gB2, 11 (32%) were gB3 genotype and one patient was gB4. According to UL 75 (gH) gene region the patients genotype was observed as; 6 (%12) were gH1 and 44 (%88) were gH, while in five of patients gB2/3 mix genotype was found (Table 1). According to gene regions, gB1 and gH2 were reported in more ratios.

According to sequence analysis results more polymorphism was observed. In the polymorphisms, the peptide change which belong to gB region frequently seen in gp166 while gH region is observed in general. We found S51Stop, K56E and T57H polymorphisms in all of the our patient's gH region, which is not found in the previous studies. The reason behind not finding S51Stop, K56E and T57H polymorphisms in previous studying is these polymorphisms are

Table 1

Gene region	Patients' numbers (n)	Genotype (n/%)				
		1	2	3	4	2/3
UL55 (gB)	50	23 (%46)	8 (%16)	11 (%22)	1 (%2)	5 (%10)
UL75 (gH)	50	6 (%12)	44 (%88)	–	–	–