The Prevalence of Microorganisms in H1N1 Patients Compared to Seasonal Influenza in a Sample of Iraqi Patients[#]

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Abstract

This study provides valuable information on secondary microbial infections in H1N1 patients compared to Seasonal Influenza in Iraqi Patients. Nasopharynx swabs were collected from (12) patients infected with Seasonal influenza (11 from Baghdad and 1 Patient from south of Iraq) ,and (22) samples from patients with 2009 H1N1 (20 from Baghdad and 2 from south of Iraq). The results show that the patients infected with 2009 H1N1 Virus were younger than healthy subjects and those infected with seasonal influenza. And the difference reached to the level of significance ($p< 0.01$) compared with healthy subjects.Two cases infected with 2009 H1N1 virus (9.1%) were from south of the Iraq and remaining 20 cases were from Baghdad . Polymicrobial isolates from nasopharynx swab were observed in patients infected with 2009 H1N1 virus. Polybacterial infections (2-7 microorganisms) and fungal infection were reported in 21 out of 22 patients (95.5%) and 5 out of 22 (22.7 %) respectively.The predominant isolated microorganisms were *Streptococcus pyogenes* , *Staphylococcus aureus* and *Streptococcus pneumoniae* were found in 95.2 % , 95.2 % and 90.5 % respectively .The results also show that seven microorganisms were isolated from 10 (47.6 %) patients infected with 2009 H1N1 , no microorganism was isolated from patients infected with seasonal influenza or healthy persons.

Key words: Seasonal Influenza , 2009 H1N1, Nasopharynx swabs

الخلاصة

هدفت الدراسة الحالية الى معرفة المسببات المايكروبية الثانوية عند المصابين بفايرس أنفلونزا الخنازير (فايرس H1N1) ومقارنتها بتلك المعزولة من المصابين بالأنفلونزا الموسمية (Seasonal Influenza) عند المرضى العراقيين ، أذ تم جمع نماذج من الأنف والحنجرة من ١٢ مصاب بالأنفلونزا الموسمية (١١ من بغداد و مصاب واحد من جنوب العراق) ، و ٢٢ مصاب بفايرس H1N1 (٢٠ من بغداد و ٢ من جنوب العراق). أظهرت النتائج ان المصابين بفايرس H1N1 هم من الفئات العمرية الأقل مقارنة بالمصابين بالأنفلونزا الموسمية والأصحاء ، وان هناك أصابات مايكروبية متعددة عند المصابين بفايرس H1N1 تصل الى أكثر من نوع مايكروبي واحد (بكتيري وفطري) ، وان الأنواع البكتيرية السائدة هي *Streptococcus pyogenes* و *Staphylococcus aureus* بنسبة عزل ٩٥,٢٪ و *Streptococcus pneumoniae* بنسبة عزل ٩٠,٥٪. كذلك أظهرت النتائج عزل ٧ أنواع بكتيرية من عشر مرضى مصابين بفايرس H1N1 بينما لم تعزل من المصابين بالأنفلونزا الموسمية والأصحاء.

Introduction

In late March and early April 2009, an outbreak of H1N1 influenza A virus infection was detected in Mexico, with subsequent cases observed in many other countries including the United States (1) . On June , 2009, the World Health Organization raised its pandemic alert level to the highest level, phase 6, indicating widespread community transmission on at least two continents (2,3).Between 1958 and 2005, 37 cases of swine influenza among civilians were reported . Six cases (17 percent) resulted in death. Forty-four percent of infected individuals had known exposure to pigs. Cases were reported in the United States, former Czechoslovakia, the Netherlands, Russia, Switzerland, and Hong Kong (4).Influenza virus is present in respiratory secretions of infected persons. As a result, influenza virus can be transmitted through sneezing and coughing via large-particle droplets . Transmission via contact with surfaces that have been contaminated with respiratory droplets or by aerosolized small-particle droplets may also occur. In addition to respiratory secretions, certain other bodily fluids (eg, diarrheal stool) should also be considered potentially infectious (5).

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Influenza predisposes individuals to developing bacterial community-acquired pneumonia .During each of the influenza pandemic of the 20th century , secondary bacterial pneumonia was a frequent cause of illness and death and *Streptococcus pneumoniae* was reported as the most common etiology .these findings also apply to seasonal influenza (6).The aim of this work was to study the prevalence of microorganisms in H1N1 Compared to Seasonal Influenza in Nasopharyngeal swabs of Iraqi Patients.

Materials and Methods

1. Sampling: Nasopharyngeal swabs were collected from (11) patients infected with Seasonal influenza from Baghdad and (1) Patient from south of Iraq ,and (20) samples from patients with 2009 H1N1 from Baghdad and (2) from south of Iraq during the period 1/1/2009 to 15/2/2010 .
2. Bacterial isolates : Samples were streaked onto Blood , Chocolate and MRS agar , under aerobic and anaerobic conditions , the plates were incubated at 37C for 24-72 h.

The isolates were subjected to the microscopic and biochemical tests for the diagnosis as mentioned in (7,8).

Results

Table 1. Shows that the patients infected with 2009 H1N1 Virus were younger than healthy subjects and those infected with seasonal influenza. And the difference reached to the level of significance ($p < 0.01$) compared with healthy subjects .Two cases infected with 2009 H1N1 virus (9.1%) were from south of Iraq and the remaining 20 cases were from Baghdad . Polymicrobial isolates from nasopharyngeal swabs were observed in patients infected with 2009 H1N1 virus.Polybacterial infections (2-7 microorganisms) and fungal infection were reported in 21 out of 22 patients (95.5%) and 5 out of 22 (22.7 %) respectively (Table 2).The predominant isolated microorganisms were *Streptococcus pyogenes* , *Staphylococcus aureus* and *Streptococcus pneumoniae* wich was found in 95.2 % , 95.2 % and 90.5 % respectively, while Actinomycetes are isolated from 47.6% (10 out 21) (Table 2).Table 3 shows that seven microorganisms were isolated from 10 (47.6 %) patients infected with 2009 H1N1 ,no microorganism was isolated from patients infected with seasonal influenza or healthy subjects.

Table 1: The charactereristics of the study .

	Healthy subjects (n=11)	Patients with Seasonal influenza	Patients with 2009 H1N1
Gender : (male:Femal)	7:4	6:6	11:11
Age(year):			
Median	38	32.5	30
Mean ± SD	40.9 ± 13.7	36.3±15.4	27.4±12.6 *
Residency:			
Baghdad	11	11	20
South of Iraq		1	2

* $p < 0.01$ compared with healthy subjects.

Table 2 : The frequency (%) of microorganisms isolated from nasopharynx swabs.

Microorganisms	Frequency
Streptococcus pyogenes	20(95.2)
Staphylococcus aureus	20(95.2)
Streptococcus pneumoniae	19(90.5)
Streptococcus mitis	12(57.1)
Haemophillus influenzae	15(71.4)
Actinomycetes	10(47.6)
Candida albicans	5(23.8)

Table 3: Distribution of 2009 H1N1 cases according to the number of microorganisms.

No. of Microorganisms	Frequency (%) of patients
0	1(4.5)
1	0(0)
2	1(4.5)
3	0(0)
4	6(27.3)
5	1(4.5)
6	3(13.6)
7	10(45.5)

Discussion

In April 2009, a novel influenza virus (2009 influenza A [H1N1] virus) was first reported in humans . This was followed by case series of patients with severe 2009 influenza A (H1N1) viral infection (3). This report provides valuable information on secondary bacterial infections in H1N1 patients compared to Seasonal Influenza in Iraqi Patients. The rate of infection in the United States has been highest among individuals ≤24 years of age (9).Tsigrelis *etal* (10) describe two patients with early onset secondary bacterial pneumonia due to *S. aureus* that occurred as a complication of 2009 H1N1 viral infection. The emergence of pneumonia caused by community-associated methicillin-resistant *S. aureus* (CA-MRSA) during the 2003–2004 and subsequent influenza seasons has further altered the microbiological spectrum of secondary bacterial pneumonia in the setting of influenza (11,12). During the 1968–1969 influenza pandemic, there was a large increase in the number of patients presenting to a hospital in Atlanta, Georgia, US, in January 1969 with acute respiratory infections which led to the admission of all patients with clinical or radiographic evidence of pneumonia. Pneumococcus was the most common aetiology but cases of pneumonia related to *S. aureus* increased, in relative terms, more that due to any other organism, from 6% of cases during the previous influenza season to 19 % during the pandemic. In contrast, 61% of community-acquired pneumonia (CAP) cases were caused by pneumococcus during the previous influenza season compared to 48 % during the pandemic [10] . Although secondary bacterial pneumonia due to *Staphylococcus aureus* was a major cause of death in patients with influenza during prior pandemics but it has not been well characterized during the study of Morens *et al* . (13). In a review of 37 cases of human infections with swine influenza virus reported between 1958 and 2005, six cases (17 percent) resulted in death, all of which were due to pneumonia. Influenza virus was the only pathogen identified from the lungs in four patients; in one individual, *Streptococcus viridans*, *Neisseria spp*, and *Klebsiella spp* were also identified in addition to influenza virus (14 , 15).

Conclusions

the patients infected with 2009 H1N1 Virus were younger than healthy subjects and those infected with seasonal influenza. And the difference reached to the level of significance ($p< 0.01$) compared with healthy subjects .

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