Burden of Influenza in Hospitalized Mexican Patients During the 2018-2019 Season


1 Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Mexico City; 2Instituto Nacional de Pediatría, Mexico City; 3Instituto Nacional de Enfermedades Respiratorias, México City; 4Hospital General Dr. Aurelio Valdivieso, Oaxaca; 5Hospital General de Durango and Hospital General 450, Durango, Mexico; 6Hospital General Dr. Manuel Gea González, Mexico City; 7Hospital Infantil de México Federico Gómez, Mexico City; 8Hospital General de Tapachula, Chiapas, México; 9Hospital Regional de Alta Especialidad Oaxaca, México; 10Hospital Regional de Alta Especialidad Ciudad Salud, Tapachula, Chiapas, México.

Results form the 2018-2019 influenza season

A total of 2227 hospitalized patients with community acquired respiratory illness were assessed for eligibility during the 2018-2019 season. Of them, 866 (39%) met selection criteria and consented participation: 441 (51%) patients were ≥5 years old and 425 (49%) patients were <5 years old. In the ≥5 years old group 244 (55%) were male; in the <5 years old group 220 (52%) were male.

Of 866 enrolled patients, 226 (26%) tested positive for influenza. Influenza subtype A(H1N1)pdm09 predominated during the season [163 (70%) cases], followed by influenza A(H3N2) [17 (7%) cases] and non-typeable influenza A [7 (3%) cases]. Influenza B tested positive in 45 (19.5%) patients; of them 20 (9%) were subtype B-Yamagata, 15 (7%) B-Victoria and 10 (4%) non-typeable influenza B.

Among influenza positive patients there were 49 (22%) admissions to the ICU, 70 (31%) required invasive mechanical ventilation and 39 (17%) died; 85% of the patients were not vaccinated.

The table and the graphs below show the cumulative frequency and seasonal distributions of respiratory viruses in hospitalized patients participating in the study.

Consecutive influenza seasons: 2015-2019

The phylogenetic tree (shown below) is based on the hemagglutinin (HA) genes of influenza A(H1N1) collected during consecutive seasons; genetic differences are compared to the A/California/04/2009 consensus sequence. Amino acid substitutions delineating major branches are shown. Date of collection follows names of viruses. Clade 6B.1 predominated during the 2018-2019 season. Amino acid substitutions are shown in the table below the phylogenetic tree.

Key aspects & challenges

The GIHSN-Mexico has successfully implemented a hospital surveillance system for severe influenza and other respiratory viruses. Data obtained provides an indication of changes in the epidemiology of severe influenza, and potentially contributes to the refinement of clinical care guidelines and policy.

Challenges include: the sustainability of the surveillance system and timely dissemination of the results to the scientific community and public health agencies.

Site presentation

To establish the Mexico branch of the GIHSN, 11 hospitals have been included since September 2015, 5 in the Mexico City area and 6 in the following Mexican States: Durango, Oaxaca and Chiapas. Potential study patients are assessed throughout the whole calendar year. Influenza season is defined as the first two weeks in which influenza is being identified and there is a continuous increase thereafter. The end of the season occurs with the decline of influenza positive cases followed by two-influenza-weeks. Hospitalized patients ≥1 month of age (no upper age limit) are eligible for the study.

Methods

Hospitalized, non-institutionalized patients residing in a pre-defined hospital catchment area, reporting symptoms of a predefined set of conditions described as possibly associated with a recent influenza infection within 7 days prior to admission and not having been discharged from a hospital in the previous 30 days are included in the study. Trained doctors and nurses collect relevant information by a combination of face-to-face interview of patients and attending physicians, and by reviewing clinical records. Nasopharyngeal swabs are collected from all patients entering the inclusion criteria and tested by reverse transcription-polymerase chain reaction (RT-qPCR) for influenza and a multiplex PCR (RespiFinder®) for other viruses and bacteria. Influenza-positive samples are sub-typed. Patients are considered vaccinated if they had received the current season’s influenza vaccine by at least 14 days before symptom onset. The study was approved by a Central Research Ethics Committee. Informed written consent/assent when appropriate is required for enrollment.

The phylogenetic tree (shown below) is based on the hemagglutinin (HA) genes of influenza A(H1N1) collected during consecutive seasons; genetic differences are compared to the A/California/04/2009 consensus sequence. Amino acid substitutions delineating major branches are shown. Date of collection follows names of viruses. Clade 6B.1 predominated during the 2018-2019 season. Amino acid substitutions are shown in the table below the phylogenetic tree.

The GIHSN-Mexico has successfully implemented a hospital surveillance system for severe influenza and other respiratory viruses. Data obtained provides an indication of changes in the epidemiology of severe influenza, and potentially contributes to the refinement of clinical care guidelines and policy.

Challenges include: the sustainability of the surveillance system and timely dissemination of the results to the scientific community and public health agencies.

Site presentation

To establish the Mexico branch of the GIHSN, 11 hospitals have been included since September 2015, 5 in the Mexico City area and 6 in the following Mexican States: Durango, Oaxaca and Chiapas. Potential study patients are assessed throughout the whole calendar year. Influenza season is defined as the first two weeks in which influenza is being identified and there is a continuous increase thereafter. The end of the season occurs with the decline of influenza positive cases followed by two-influenza-weeks. Hospitalized patients ≥1 month of age (no upper age limit) are eligible for the study.

Methods

Hospitalized, non-institutionalized patients residing in a pre-defined hospital catchment area, reporting symptoms of a predefined set of conditions described as possibly associated with a recent influenza infection within 7 days prior to admission and not having been discharged from a hospital in the previous 30 days are included in the study. Trained doctors and nurses collect relevant information by a combination of face-to-face interview of patients and attending physicians, and by reviewing clinical records. Nasopharyngeal swabs are collected from all patients entering the inclusion criteria and tested by reverse transcription-polymerase chain reaction (RT-qPCR) for influenza and a multiplex PCR (RespiFinder®) for other viruses and bacteria. Influenza-positive samples are sub-typed. Patients are considered vaccinated if they had received the current season’s influenza vaccine by at least 14 days before symptom onset. The study was approved by a Central Research Ethics Committee. Informed written consent/assent when appropriate is required for enrollment.

Consecutive influenza seasons: 2015-2019

The phylogenetic tree (shown below) is based on the hemagglutinin (HA) genes of influenza A(H1N1) collected during consecutive seasons; genetic differences are compared to the A/California/04/2009 consensus sequence. Amino acid substitutions delineating major branches are shown. Date of collection follows names of viruses. Clade 6B.1 predominated during the 2018-2019 season. Amino acid substitutions are shown in the table below the phylogenetic tree.

Key aspects & challenges

The GIHSN-Mexico has successfully implemented a hospital surveillance system for severe influenza and other respiratory viruses. Data obtained provides an indication of changes in the epidemiology of severe influenza, and potentially contributes to the refinement of clinical care guidelines and policy.

Challenges include: the sustainability of the surveillance system and timely dissemination of the results to the scientific community and public health agencies.

Site presentation

To establish the Mexico branch of the GIHSN, 11 hospitals have been included since September 2015, 5 in the Mexico City area and 6 in the following Mexican States: Durango, Oaxaca and Chiapas. Potential study patients are assessed throughout the whole calendar year. Influenza season is defined as the first two weeks in which influenza is being identified and there is a continuous increase thereafter. The end of the season occurs with the decline of influenza positive cases followed by two-influenza-weeks. Hospitalized patients ≥1 month of age (no upper age limit) are eligible for the study.

Methods

Hospitalized, non-institutionalized patients residing in a pre-defined hospital catchment area, reporting symptoms of a predefined set of conditions described as possibly associated with a recent influenza infection within 7 days prior to admission and not having been discharged from a hospital in the previous 30 days are included in the study. Trained doctors and nurses collect relevant information by a combination of face-to-face interview of patients and attending physicians, and by reviewing clinical records. Nasopharyngeal swabs are collected from all patients entering the inclusion criteria and tested by reverse transcription-polymerase chain reaction (RT-qPCR) for influenza and a multiplex PCR (RespiFinder®) for other viruses and bacteria. Influenza-positive samples are sub-typed. Patients are considered vaccinated if they had received the current season’s influenza vaccine by at least 14 days before symptom onset. The study was approved by a Central Research Ethics Committee. Informed written consent/assent when appropriate is required for enrollment.

The phylogenetic tree (shown below) is based on the hemagglutinin (HA) genes of influenza A(H1N1) collected during consecutive seasons; genetic differences are compared to the A/California/04/2009 consensus sequence. Amino acid substitutions delineating major branches are shown. Date of collection follows names of viruses. Clade 6B.1 predominated during the 2018-2019 season. Amino acid substitutions are shown in the table below the phylogenetic tree.

Key aspects & challenges

The GIHSN-Mexico has successfully implemented a hospital surveillance system for severe influenza and other respiratory viruses. Data obtained provides an indication of changes in the epidemiology of severe influenza, and potentially contributes to the refinement of clinical care guidelines and policy.

Challenges include: the sustainability of the surveillance system and timely dissemination of the results to the scientific community and public health agencies.