

# International Conference on **Influenza**

August 24-26, 2015 London, UK

## Genetic diversity of the pandemic influenza A (H1N1) virus in Saudi Arabia

**Ahmed Mohammed Ashshi**  
Umm Al-Qura University, KSA

**Background & Objectives:** Pandemic influenza A (H1N1) virus emerged and spread globally in the spring of 2009. Saudi Arabia also witnessed a severe H1N1 pandemic virus epidemic with considerable morbidity and mortality in different parts of the kingdom beginning in June 2009. The influenza A (H1N1) pdm09 virus was detected in samples collected between May 2009 and November 2010 from Makkah region. This study provides data on the viral diagnosis and genetic diversity of hemagglutinin (HA) and neuraminidase (NA) genes of influenza A (H1N1) pdm09 virus from Saudi Arabia.

**Methodology:** Nasopharyngeal swabs from 100 clinically infected patients in the peak of the outbreak were collected from Makkah region and processed for viral diagnosis by viral culture and real-time polymerase chain reaction (PCR). HA and NA genes of 10 selected samples were sequenced and analyzed.

**Results:** A total of 100 samples were collected; only 10 samples were found to be positive for influenza A virus infection by real-time PCR. Nucleotide sequence analysis of the HA and NA genes of influenza A (H1N1) from Saudi Arabia showed significant similarities with selected isolates. The phylogenetic tree constructed for both HA and NA genes formed close clusters with selected reference isolates.

**Conclusions:** Nucleotide sequence analysis and phylogenetic relationships of the HA and NA genes of influenza A (H1N1) virus from Saudi Arabia with selected reference isolates indicates that they were genetically close and most probably originated from influenza A(H1N1)pdm09.

[aashshi@yahoo.com](mailto:aashshi@yahoo.com)

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