P1401
Paper Poster Session
Influenza - clinical epidemiology

Detection of mutations in haemagglutinin and neuraminidase genes coding for oseltamivir resistance and enhanced virulence/transmissibility among Indian strains of swine influenza A(H1N1)pdm09 viruses

Nandhini Palani*[1], Sujatha Sistla[1]

[1]*Jipmer, Microbiology, Puducherry, India*

Background: Influenza A virus evolves continuously by acquiring many mutations and multiple molecular determinants to cause increased disease severity. It is crucial to monitor the genetic make-up of this virus specially the surface glycoproteins; hemagglutinin and neuraminidase, to understand their adaptability and evolutionary dynamics in different regions. This can be critical to study the molecular mechanisms involved in the emergence, global spread and resistance mutations in Indian isolates particularly after the controversial commentary regarding under reporting of such mutations from India.

Material/methods: The hemagglutinin (HA) and neuraminidase (NA) genes of a total of 45 representative influenza A(H1N1)pdm09 isolates obtained over a period of 5 years (2011-2015) were sequenced. Phylogenetic analysis was performed with reference to A/California/07/2009 vaccine strain. Molecular characterization of HA and NA segments was carried out to look for amino acid changes recently linked to oseltamivir resistance (NA: H275Y, I223R, N295S, D199N, S247N, Q136K) and enhanced virulence and transmissibility (HA: T200A, D225N, K166Q).

Results: All influenza A(H1N1)pdm09 isolates fell within clade 7 and all possessed H275, indicating the common marker of neuraminidase inhibitor sensitivity. Six strains had N295S mutation (2012-2, 2015-4); three had Q136K (2015-3) which are also considered to be markers of oseltamivir resistance though not as well established as the H275Y mutation. All these strains were from patients who had received oseltamivir as therapy and recovered. Four strains had D225N (2012-3, 2015-1) mutations in HA gene, one of which were isolated from a fatal case (2012). Additional mutations were found in HA in position 100 and 220 in two different strains (2012-1, 2015-1). Of them S100P co-occurred in one of the isolate with N295S mutation (2015).

Conclusions: Although the common mutation associated with oseltamivir resistance was not found in any of our isolates, it is worrying that we encountered some of the less common mutations associated with it. Whether this will translate into clinical, full blown resistance in future needs to be closely monitored. The additional finding of multiple markers of virulence is also a cause for concern.