

Emerging Diseases, Outbreaks & Case Studies &

16th Annual Meeting on **Influenza** March 28-29, 2018 | Orlando, USA

Molecular epidemiology of a novel re-assorted epidemic strain of equine influenza virus in Pakistan in 2015-16

Amjad khan, Muhammad Hassan Mushtaq, Mansur Ud Din Ahmad, Jawad Nazir, Asghar Khan and Shahid Hussain Farooqi
University of Veterinary and Animal Sciences, Pakistan

A widespread epidemic of equine influenza (EI) occurred in nonvaccinated equine population across multiple districts in Khyber Pakhtunkhwa Province of Pakistan during 2015-2016. An epidemiological surveillance study was conducted from Oct 2015 to April 2016 to investigate the outbreak. EI virus strains were isolated in embryonated eggs from suspected equines swab samples and were subjected to genome sequencing using M13 tagged segment specific primers. Phylogenetic analyses of the nucleotide sequences were concluded using Geneious. Haemagglutinin (HA), Neuraminidase (NA), Matrix (M) and nucleoprotein (NP) genes nucleotide and amino acid sequences of the isolated viruses were aligned with those of OIE recommended, FC-1, FC-2, and contemporary isolates of influenza A viruses from other species. HA and NA genes amino acid sequences were very similar to Tennessee/14 and Malaysia/15 of FC-1 and clustered with the contemporary isolates recently reported in the USA. Phylogenetic analysis showed that these viruses were mostly identical (with 99.6% and 97.4% nucleotide homology) to, and were reassortants containing chicken/

Pakistan/14 (H7N3) and Canine/Beijing/10 (H3N2) like M and NP genes. Genetic analysis indicated that A/equine/Pakistan/16 viruses were most probably the result of several re-assortments between the co-circulating avian and equine viruses, and were genetically unlike the other equine viruses due to the presence of H7N3 or H3N2 like M and NP genes. Epidemiological data analysis indicated the potential chance of mixed, and management such as mixed farming system by keeping equine, canine and backyard poultry together in confined premises as the greater risk factors responsible for the re-assortments. Other factors might have contributed to the spread of the epidemic, including low awareness level, poor control of equine movements, and absence of border control disease strategies.

Speaker Biography

Amjad Khan has completed his PhD from the University of Veterinary and Animal Sciences, Lahore. He currently a Research Associate working in a project on surveillance of influenza viruses in Pakistan. He has published more than 20 research articles in peer reviewed journals.

e: dramjadkhan77@gmail.com