

The Equine Flu in South America

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In the pre-virological era equine flu outbreaks were described based on clinical signs and on disease spreading pattern. Human flu cases were also described concomitant with those animal outbreaks. By that time there was none/or little knowledge about the agent that was causing those clinical signs in humans and animals. The equine influenza (EI) would cause serious impact in cities where horses were the major type of transportation^[1].

With science evolution, the agent that was causing flu was first identified from pigs^[2], from humans in 1933^[3] and from equines in 1956 (H7N7 subtype) and in 1963 (H3N8 subtype)^[4]. The H7N7 EIV subtype is considered to be extinct since 1980^[5] and H3N8 subtype continues to cause outbreaks worldwide.

The techniques HA - hemagglutination assay, HI - inhibition of hemagglutination assay and virus isolation in embryonated chicken eggs, are deeply used to study EIV outbreaks^[6]. With the advance of molecular techniques, globalization and the high visibility of journals/articles/communications, the

epidemiology of EIV started to be more deeply studied.

Initially, the EIVs H3N8 subtypes were defined in a single phylogenetic group^[7] that evolved into two lineages, American and Eurasian, according to the geographic region^[8]. The American lineage diverged into South America, Kentucky and Florida sub-lineages^[9]. The strains from the Florida sub-lineage suffered two mutations in the hemagglutinin and diverged into Florida Clade 1 (FC1) and Clade 2 (FC2)^[9,10] represented by the strains A/equine/South Africa/4/03 and A/equine/Newmarket/5/03, respectively^[11]. The FC1 and FC2 strains are responsible for the EIV outbreaks that occurred worldwide in the last years and are the predominant EIVs^[12-21].

In South America, EIV outbreaks caused by the H3N8 subtype were described in Brazil in 1963, 1969, 1985, 1988, 2001, 2012 and 2015^[16,21-28], in Chile in 1963, 1985, 1992, 2006 and 2012^[29-31], in Argentina in 2001 and 2012^[30,32] and Uruguay in 2012^[30]. The H3N8 EIVs that were sequenced were more identical to the North American strains than to the European EIVs^[16,21,28,30,33].

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In 2012, outbreaks occurred in the United States, Argentina, Brazil, Uruguay and Dubai. The strains had high nucleotide identity and belonged to FC1^[16,19,21,30]. According to Perglione *et al* (2016), the outbreak might have initiated in South America and went to Dubai. Brazil has reported 129 confirmed EIV outbreaks to the OIE in 2012 [World Animal Health Information Database (WAHID) Interface - http://www.oie.int/wahis_2/public/wahid.php/Countryinformation/Reporting].

An outbreak occurred in Brazil in 2015 in a veterinary hospital in the city of São Paulo (State of São Paulo) and different variants were found suggesting the evolution the virus suffered during the same outbreak^[28].

Before 2012, only a few studies about the circulating EIVs in South America were described. The surveillance studies of EIV in South America provide information about which strains are causing the outbreaks and control/prevention actions that might be applied such as the use of epidemiologically relevant strains in EIV vaccination^[11].

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