

OIE Expert Surveillance Panel on Equine Influenza Vaccine Composition

24 January 2011, OIE Headquarters

During the meeting of the Biological Standards Commission, at OIE Headquarters, Paris, 8-10 February 2011 (see page 17 of this *Bulletin*), the Commission endorsed the following conclusions and recommendations of the Expert Surveillance Panel on Equine Influenza Vaccine Composition on the composition of equine influenza vaccines for 2011

Conclusions and Recommendations

Influenza activity in 2010

During 2010, outbreaks and/or sporadic cases of equine influenza were reported by Brazil, Finland, France, Germany, Ireland, Sweden, the United Kingdom (UK) and United States of America (USA).

Sources of viruses characterised during 2010

Equine influenza A (H3N8) viruses were isolated and/or characterised from outbreaks in France, Ireland and the UK. At a quarantine station in Japan, equine influenza virus was isolated from a horse imported from Belgium.

Field data

Equine influenza virus infections were confirmed in both vaccinated and unvaccinated horses. Although some vaccines were updated in line with the 2004 recommendations, the current vaccines do not contain the virus strains from the two clades recommended for optimum protection. The detection of virus in a quarantine facility illustrates the continuing risk of the international spread of influenza by infected vaccinated horses.

Characterisation of viruses isolated in 2010

Viruses isolated in 2010 from five outbreaks in France, three in Ireland and seven in the UK were characterised genetically by sequencing of the haemagglutinin (HA) gene. The viruses isolated in the UK were also characterised antigenically by haemagglutination inhibition (HI), using ferret antisera. The virus isolated from the horse in the Japanese quarantine facility was genetically characterised.

Genetic characterisation

All HA1 sequences obtained from viruses were of the American lineage (Florida sub-lineage). All the viruses identified in France and the UK were characterised as A/eq/Richmond/1/07-like, i.e. clade 2 viruses. The virus isolated from the horse exported from Belgium to Japan was also a clade 2 virus. Two of the outbreaks in Ireland were caused by clade 2 viruses and one outbreak was caused by an A/eq/South Africa/03-like, i.e. clade 1 virus.

Antigenic characteristics

The HI data and antigenic cartography analysis of the HI data (Smith *et al.*, 2004) available for viruses isolated in 2010 indicate that they are closely related to A/eq/Richmond/1/07 and clearly different from clade 1 viruses.

Conclusions

No Eurasian viruses were isolated in 2010. The majority of the isolated and characterised viruses were from the American clade 2 lineage (Florida sub-lineage). Only one outbreak investigated in 2010 was associated with a clade 1 virus. There was some evidence of a lack of vaccine efficacy against clade 2 viruses, i.e. that vaccines containing earlier viruses of the American lineage (such as A/eq/Newmarket/1/93) do not provide adequate protection against these viruses.

Level of surveillance

The panel continues to emphasise the importance of increased surveillance in different countries and rapid submission of viruses to Reference Laboratories for

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characterisation. This is essential if antigenic and genetic drift is to be monitored effectively on a global basis and the information relayed to vaccine manufacturers in a timely manner.

Recommendations

It is not necessary to include an H7N7 virus or an H3N8 virus of the Eurasian lineage in the vaccines as these viruses have not been detected in the course of recent surveillance.

Vaccines for the international market should contain both clade 1 and clade 2 viruses of the Florida sub-lineage.

- Clade 1 is represented by South Africa/03-like or Ohio/03-like viruses.

- Clade 2 is represented by Richmond/1/07-like viruses.

Manufacturers producing vaccines for a strictly national market are encouraged to liaise with Reference Laboratories to ensure full use of reference reagents in the selection of cross-reactive and immunogenic local strains.

Reference reagents

Freeze-dried, post-infection equine antisera to A/eq/Newmarket/77 (H7N7), A/eq/Newmarket/1/93 (American lineage H3N8), A/eq/Newmarket/2/93 (Eurasian lineage H3N8), A/eq/South Africa/4/03 (Florida clade 1, sub-lineage of American lineage) and an influenza-negative equine serum are available from the European Directorate for the Quality of Medicines (EDQM). These sera have been assigned single radial haemolysis values through an international collaborative study and can be used as primary reference sera for the assay.

Reference

Smith D.J., Lapedes A.S., de Jong J.C., Bestebroer T.M., Rimmelzwaan G.F., Osterhaus A.D. & Fouchier R.A. (2004). – Mapping the antigenic and genetic evolution of influenza virus. *Science*, **305** (5682), 371-376.