Expert surveillance panel on equine influenza vaccine composition

National Institute for Medical Research, Mill Hill, London (United Kingdom) 20 January 2009

Conclusions and Recommendations

Influenza activity in 2008

During 2008, outbreaks of the H3N8 subtype were reported from Brazil, China (People's Rep. of) and Mongolia, Colombia, Czech Republic, Egypt, France, Germany, India, Ireland, Japan, Kuwait, Russia, Sweden, the United Kingdom (UK), and the United States of America (USA). Australia was declared free of influenza in 2008 after an intensive eradication programme.

Source of viruses characterised during 2008

Viruses available for characterisation during 2008 were isolated in the Czech Republic, Germany, Ireland, Japan, Switzerland, the UK, and the USA. Information on field observation, vaccine status and genetic and antigenic characterisation from several laboratories was considered.

Field data

Influenza infection was confirmed in both vaccinated and unvaccinated horses. Most vaccines available contained out of date viruses but insufficient information was available to conclude whether infection occurred in the face of high levels of vaccinal antibody.

Characterisation of viruses isolated during 2008

Sixteen viruses isolated in 2008 were characterised antigenically by haemagglutination inhibition (HI) using ferret and/or horse antisera and/or by sequencing of the haemagglutinin (HA) gene. Sequence data submitted to Genbank were also considered.

Genetic characteristics

All the HA sequences obtained for viruses from different countries were of the American lineage (Florida sublineage) and were similar to those of viruses isolated during 2007, comprising two clades. One (clade 1), which includes sequences of recent viruses from Australia, Japan, North America and the UK, may be composed of two subclades. HA sequences of Japanese isolates from 2008 fell within subclade 1A, represented by A/equine/Ibaraki/2007 and A/equine/Sydney/2007, whereas the sequences of viruses isolated in Egypt and the USA during 2008 fell within subclade 1B, represented by, for example, A/equine/Kentucky/4/2007 or A/equine/Lincolnshire/1/2007. The other (clade 2), represented by, for example, A/equine/Richmond/1/2007, was composed predominantly of sequences of European isolates, but also included that of a virus isolated in Mongolia in late 2007.

No Eurasian lineage viruses were isolated during 2008. The HA sequence of one virus isolated in Switzerland during 2007 was closely related to earlier viruses of the Eurasian lineage, isolated in 1989.

Antigenic characteristics

Analyses, including antigenic cartography (Smith *et al.*, 2004), of HI data available for viruses isolated in 2008 indicated that HAs of the different clades/subclades continued to be antigenically closely related to that of the currently recommended prototype vaccine strain A/equine/South Africa/4/2003.

Conclusions

The panel was of the view that the low number of Eurasian lineage viruses isolated sporadically during the past 5 years does not warrant a recommendation for continued inclusion of a representative of these viruses (A/equine/Newmarket/2/93) in vaccines.

Genetic and antigenic data available to date indicate that the American lineage viruses isolated during 2008 are similar to and exhibit a similar geographical distribution to the viruses circulating during 2007. With the data presently available, there is no evidence to indicate that the genetic differences between viruses isolated in America, Asia or Europe are yet sufficient to affect the efficacy of vaccines containing A/equine/South Africa/4/2003-like viruses.

Level of surveillance

The existence of multiple subclades of American-lineage viruses indicates the continued evolution of these viruses, which eventually will have an impact on vaccine efficacy.

More viruses need to be submitted to determine which clades and subclades of viruses are circulating (or co-circulating) in different parts of the world. The panel wishes to emphasise the importance of continued surveillance and rapid submission of viruses to reference laboratories for characterisation in order that antigenic and genetic drift can be monitored effectively and the information relayed to vaccine manufacturers in a timely manner.

Recommendations

The panel does not recommend inclusion of an H7N7 virus in current vaccines.

The panel no longer supports the need for inclusion of a Eurasian lineage H3N8 virus represented by A/equine/Newmarket/2/93.

Manufacturers should adopt the 2004 recommendations and update the American lineage H3N8 component of their vaccines to an A/equine/ South Africa/4/2003-like virus. (They are advised to consult reference laboratories to ensure that the isolate selected shows broad cross reactivity with viruses from different geographical regions.)

Vaccines

Many vaccines still contain American lineage viruses such as Kentucky/94 and Newmarket/1/93 that were first recommended over 10 years ago. However, because of the practice used by some vaccine manufacturers of updating strains on an *ad hoc* basis, other viruses such as A/eq/Kentucky/97, A/eq/Kentucky/98 A/eq/Kentucky/2002 have also been used. At the time of writing only two vaccines containing an A/eq/ South Africa/4/2003-like virus are available although it is understood that at least one additional vaccine manufacturer is in the process of updating.

Standard reagents

Reference reagents specific for the recommended European lineage vaccine strains are available for standardisation of vaccine content by single radial diffusion (SRD) assay and can be obtained from the National Institute of Biological Standards and Control (NIBSC), email: enquiries@nibsc.co.uk. Preparation of reagents for A/South Africa/4/2003-like viruses is under review.

Four equine influenza horse antisera against A/eq/Newmarket/77(H7N7), A/eq/Newmarket/1/93(H3N8), A/eq/Newmarket/2/93(H3N8) and A/eq/South Africa/4/2003 (H3N8) are available as European Pharmacopoeia Biological Reference Preparations for serological testing of vaccine responses using the single radial haemolysis test. Sera may be sourced from European Directorate for the Quality of Medicines (EDQM) http://www.pheur.org.

SRD reference reagents

NIBSC, Blanche Lane, South Mimms, Potters Bar, Herts EN6 3QG, UK

Fax: (+44-1707) 64.10.50

enquiries@nibsc.ac.uk

EP BRPs for serological testing of equine influenza vaccines

European Directorate for the Quality of Medicines, BP 907,

F-67029 Strasbourg Cedex, France

http://www.pheur.org

OIE primary standards for diagnostic serological testing

Animal Health Trust, Lanwades Park, Kentford, Newmarket,

Suffolk CB8 7UU, UK

Fax: (+44-8700) 50.24.61

info@aht.org.uk

References

Smith *et al.* (2004). Mapping the antigenic and genetic evolution of influenza virus. *Science*, **305** (5682), 371–376.