Equine influenza vaccine composition

Conclusions and recommendations of the OIE Expert Surveillance Panel on Equine Influenza Vaccine Composition Meeting

held at OIE Headquarters
Paris, on 22 March 2017

OIE/Communication Unit

Equine influenza activity in 2016

During 2016, individual animal cases and outbreaks of equine influenza were reported by Ireland, Sweden, the United Kingdom (UK) and the United States of America (USA).

Sources of equine influenza viruses characterised

Equine influenza A (H3N8) viruses were isolated and/or characterised from outbreaks in Ireland, the UK and the USA.

Field data

In Europe there were fewer equine influenza virus infections than in recent years. The clinically affected horses on the seven affected premises in the UK were unvaccinated. A single confirmed case in Sweden had an unknown vaccination history. In Ireland, equine influenza cases were confirmed in both vaccinated and unvaccinated horses but only 10% (approximately) of the horses on the two affected premises had up-to-date vaccination records.

In the USA, outbreaks were detected throughout the year with over 30 confirmed cases from 16 states. No vaccination data were available.

In Asia and South America no equine influenza outbreaks were reported.

Characterisation of viruses identified in 2016

Viruses isolated/identified from outbreaks in Ireland, the UK and the USA were genetically characterised by sequencing the haemagglutinin (HA) and the neuraminidase (NA) genes.

Viruses from the UK and the USA were antigenically characterised by the haemagglutination inhibition (HI) assay, using post-infection ferret antisera and chicken red blood cells.

Genetic characterisation

All HA sequences obtained from viruses were of the American lineage (Florida sublineage). The viruses detected in the USA were characterised as clade 1 viruses and were very similar to those identified in 2015. Viruses detected in Ireland and the UK were characterised as clade 2 viruses. They were similar to viruses from those countries in 2015 in that, compared to the Florida clade 2 reference strain, they had the substitution A144V. This is in contrast to viruses identified in mainland Europe in 2015, which had the substitution I179V.

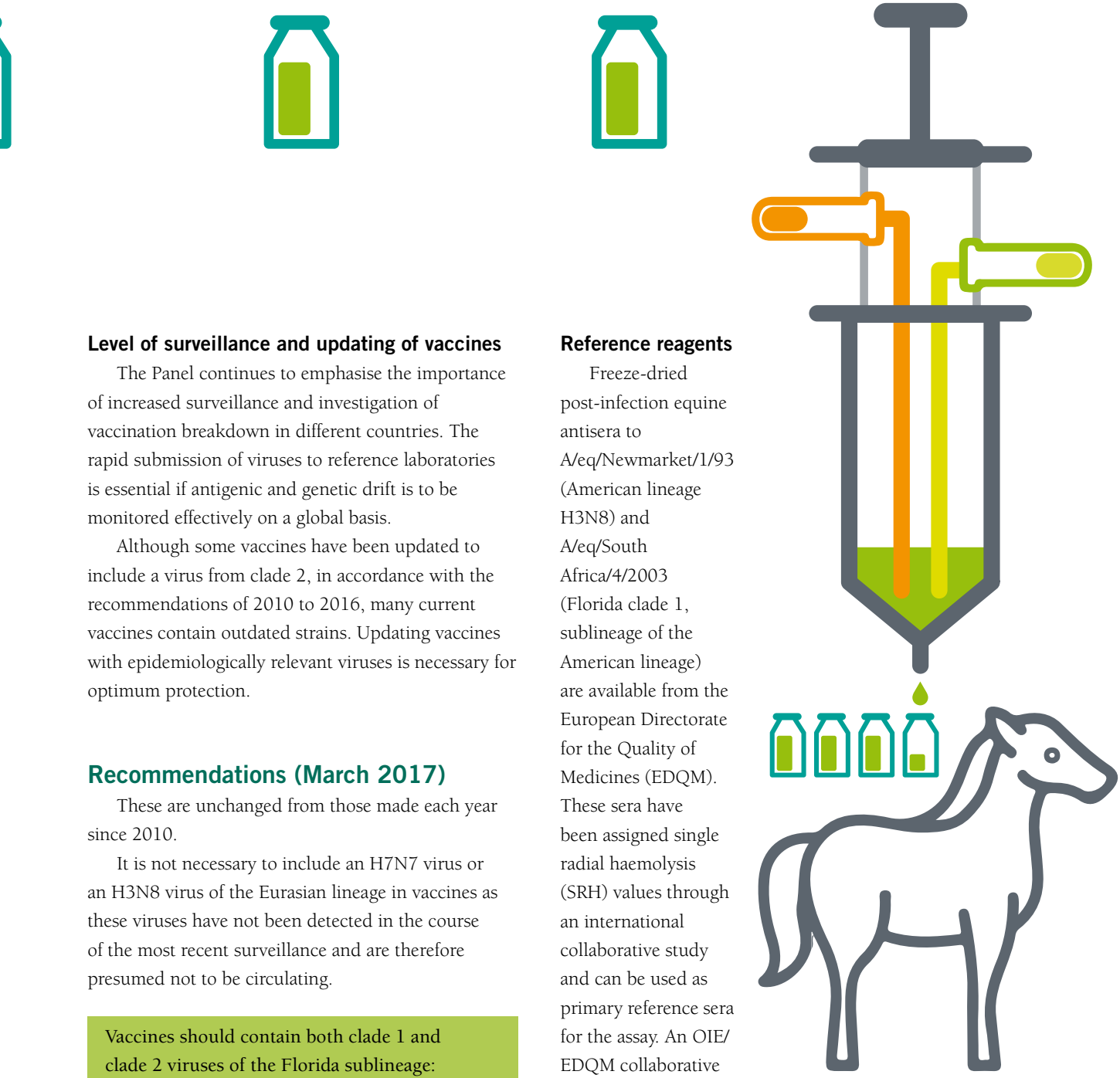
The NA gene sequences of the viruses from clade 1 and clade 2 were also similar to those of the viruses identified in 2015.

Antigenic characterisation

Haemagglutination inhibition data available for viruses isolated in 2016, and antigenic cartography analyses thereof, show that the viruses of the two clades of the Florida sublineage continue to remain closely related antigenically to the recommended vaccine viruses of that lineage.

Conclusion

All viruses isolated and characterised in 2016 were from clades 1 and 2 of the Florida sublineage and were similar to those identified in 2015.



Level of surveillance and updating of vaccines

The Panel continues to emphasise the importance of increased surveillance and investigation of vaccination breakdown in different countries. The rapid submission of viruses to reference laboratories is essential if antigenic and genetic drift is to be monitored effectively on a global basis.

Although some vaccines have been updated to include a virus from clade 2, in accordance with the recommendations of 2010 to 2016, many current vaccines contain outdated strains. Updating vaccines with epidemiologically relevant viruses is necessary for optimum protection.

Recommendations (March 2017)

These are unchanged from those made each year since 2010.

It is not necessary to include an H7N7 virus or an H3N8 virus of the Eurasian lineage in vaccines as these viruses have not been detected in the course of the most recent surveillance and are therefore presumed not to be circulating.

Vaccines should contain both clade 1 and clade 2 viruses of the Florida sublineage:

- clade 1 continues to be represented by A/eq/South Africa/04/2003-like or A/eq/Ohio/2003-like viruses but more recent clade 1 viruses are available from the OIE Reference Laboratories
- clade 2 continues to be represented by A/eq/Richmond/1/2007-like viruses but more recent clade 2 viruses are available from the OIE Reference Laboratories.

Manufacturers producing vaccines for a strictly national market are encouraged to liaise with reference laboratories. The selected viruses should induce responses that are immunogenically relevant to the equine influenza viruses circulating nationally. A sequence determination of both HAs and NAs should be completed before use.

Reference reagents

Freeze-dried post-infection equine antisera to A/eq/Newmarket/1/93 (American lineage H3N8) and A/eq/South Africa/4/2003 (Florida clade 1, sublineage of the American lineage) are available from the European Directorate for the Quality of Medicines (EDQM). These sera have been assigned single radial haemolysis (SRH) values through an international collaborative study and can be used as primary reference sera for the assay. An OIE/EDQM collaborative study is in progress, and a new antiserum against the Florida clade 2 reference strain A/eq/Richmond/1/2007 has been produced and is being standardised internationally.

Recent virus strains, including suitable vaccine candidates for clades 1 and 2, are available from the OIE Reference Laboratories. In the event that an OIE Reference Laboratory cannot supply suitable vaccine candidates for both clades, they will assist the vaccine company to source the viruses from an alternative OIE Reference Laboratory.

Small quantities of ferret antisera for antigenic characterisation are available from the OIE Reference Laboratories in Ireland and the UK.

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OIE Reference Laboratories for equine influenza

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OIE Project brief

Capacity building and surveillance for Ebola Virus Disease EBO-SURSY Project

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Background

The 2014–2016 West African Ebola Virus Disease (EVD) epidemic underscored the risks linked to inadequate disease detection, prevention and response mechanisms, and the importance of strengthening public and animal health systems. The epidemic also raised a series of unanswered questions and defining challenges – at the human-animal-ecosystem interface – that need to be brought into the spotlight so as to reduce the vulnerability of societies to infectious disease threats that spread across national and international borders.

With the objective of contributing to this endeavour, in December 2016, the OIE received a grant from the European Union to implement the project of capacity building and surveillance for Ebola Virus Disease ('EBO-SURSY Project'). In order to implement this project, the OIE has teamed up with the French Agricultural Research Centre for International Development (*Centre de coopération internationale en recherche agronomique pour le développement* – Cirad), French Research Institute for Development (Institut de recherche pour le développement – IRD), the Pasteur Institute and its international network (RIIP).

Project

Through the promotion and adoption of a 'One Health' approach to detect, prevent, control and respond to new and devastating disease threats, this Project will support an enhanced and coordinated response to the (re-) emergence of zoonotic pathogens and address the ongoing efforts to prevent the proliferation and spread of endemic zoonotic pathogens. This Project's purpose is to strengthen laboratory and surveillance