



Expert surveillance panel on equine influenza vaccine composition

8th July 2021 and 7th July 2022 by Videoconference

Conclusions and Recommendations

Influenza activity – April 2020 to July 2022

Since the previous meeting in April 2020, outbreaks of equine influenza were reported in Africa, Asia, North and South America, the Middle East and Europe. Equine influenza A(H3N8) viruses were isolated and/or characterised from outbreaks in China, France, Ireland, Israel, Sweden, the United Kingdom (UK), Canada, and the United States of America (USA).

Field Data 2020-2022

In Europe, sporadic outbreaks were reported in Belgium, Estonia, Finland, France, Germany, Ireland, Italy, the Netherlands, Sweden and the UK. The majority of confirmed cases were in unvaccinated horses where clinical signs included pyrexia, nasal discharge, cough, lymphadenopathy, conjunctivitis and lethargy. Influenza infection was reported in vaccinated horses in Estonia, France, Germany, Ireland, the Netherlands and the UK but in some instances the vaccination schedule had lapsed.

Most equine influenza outbreaks on premises during the reporting period were associated with introduction of unvaccinated horses or horses of unknown vaccination status. In Israel an outbreak was reported in horses recently imported from Europe but the outbreak was confined to the quarantine facility. In the USA, influenza was confirmed in over 30 states during the two-year period (2020-2022). Fatalities were reported among donkeys in Missouri and wild-caught horses in Colorado, in 2022. In Colorado, pneumonia and mortality were reported primarily in horses that had been gathered as a result of a severe wildfire in the summer of 2021. More typical self-limiting respiratory disease signs were reported in other horses at the facility at the same time. In Africa, outbreaks were detected in Tunisia. In China, influenza virus was isolated from a subclinical case in Zhejiang province.

Genetic characterisation of viruses identified 2020-2022

Viruses isolated/identified in China, France, Ireland, Sweden, the UK, Canada, and the USA were characterised genetically by sequencing of haemagglutinin (HA) genes.

Additionally, the neuraminidase (NA) genes were sequenced for viruses isolated/identified from outbreaks in France, Ireland, the UK and the USA.

The HA sequences were aligned against the respective HAs of the clade-recommended vaccine viruses: A/eq/South Africa/2003 (for clade 1 viruses) and A/eq/Richmond/1/2007 (for clade 2 viruses).

The virus detected in China was characterised as clade 2, Florida sublineage of the American lineage.

All other viruses detected were characterised as clade 1, Florida sublineage of the American lineage and were genetically similar to the clade 1 viruses identified in Europe and the USA in 2019.

Antigenic characterisation of viruses identified 2020-2022

Horse antiserum raised against a 2019 virus isolated in Ireland cross-neutralised the recent isolates indicating a close antigenic relationship. Two viruses generated by reverse genetics, one with the HA from a virus isolated in the USA in 2020 and one with the HA from a virus isolated in Ireland in 2021, were antigenically characterised with mono-specific horse antisera raised against recommended vaccine strains. Virus neutralisation data showed that the viruses continue to remain antigenically closely related to the recommended clade 1 vaccine viruses.

The close antigenic relationship among the current isolates and vaccine strains characterised by neutralisation data were further supported by haemagglutination inhibition titres of 2020 and 2021 isolates with ferret antisera raised against recommended vaccine strains and a 2019 virus isolated in the UK.

Conclusions

With the exception of a clade 2 virus identified in China, all viruses isolated and characterised from the outbreaks detected between April 2020 and July 2022 were of the clade 1 Florida sublineage. They were similar to those identified in Europe and the USA in 2019. Clade 1 viruses are endemic in the USA and since 2019, appear to have supplanted clade 2 viruses in Europe. Although the clade 1 viruses have gradually diverged genetically from the WOAHA recommended vaccine strains, the neutralisation data with mono-specific post-vaccination horse antisera indicated that they continue to remain antigenically similar to the viruses recommended for inclusion in vaccines. These data are corroborated by haemagglutination inhibition assays with mono-specific ferret antisera. The panel agreed that there is no current evidence-based justification for revising the recommendations on vaccine composition.

Level of Surveillance and Updating of Vaccines

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

Recommendations (July 2022)

These are currently 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 over the course of many years of surveillance and are therefore presumed not to be circulating.

Vaccines should contain both clade 1 and clade 2 viruses of the Florida sublineages.

The recommendation for the coming year is:

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 WOAHP 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 WOAHP reference laboratories.

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

Reference reagents

Freeze-dried post-infection equine antisera to A/eq/South Africa/4/2003 (Florida clade 1) and to A/eq/Richmond/1/2007 (Florida clade 2) are available from the EDQM. These antisera have been assigned Single Radial Haemolysis values through international collaborative studies and can be used as primary reference antisera for the assay.

Recent virus strains, including suitable vaccine candidates for clades 1 and 2, are available from the WOAHP reference laboratories in Japan, Ireland and the USA. In the event of a WOAHP reference laboratory being unable to supply suitable vaccine candidates for either or both clades, they will assist the vaccine company to source the viruses from an alternative WOAHP reference laboratory.

Ferret or horse antisera for antigenic characterisation are available from the WOAHP reference laboratory in Ireland and Japan, respectively.

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