



## **Expert surveillance panel on equine influenza vaccine composition**

6th July 2023 and 27th September 2024  
WOAH Headquarters, Paris

### **Conclusions and Recommendations**

#### **Influenza activity – July 2022 to September 2024**

Since the ESP meeting in July 2022 outbreaks of equine influenza were reported in Africa, Asia, North America, South America and Europe. Equine influenza A(H3N8) viruses were isolated and/or characterised from outbreaks in China, Colombia, France, Ireland, Sweden, the United Kingdom (UK) and the United States of America (USA).

#### **Field Data July 2022- September 2024**

In Europe, sporadic outbreaks were reported in Belgium, France, Germany, Ireland, the Netherlands, Sweden and the UK. Affected equidae included Thoroughbred breeding stock, Sport horses, Showjumpers, Quarter horses, Saddlebreds, Arabians, Standardbreds, ponies and donkeys. The majority of confirmed cases were in unvaccinated horses where clinical signs included pyrexia, nasal discharge, cough, lymphadenopathy, conjunctivitis, inappetence and lethargy. Ataxia was observed on one premises in France. Influenza infection was reported in vaccinated horses in Belgium, France, Ireland, the Netherlands and the UK but in some instances the vaccination schedule had lapsed, or the horses were young, up to three years old, and early in their vaccination career. Predisposing factors related to geographic spread included recent importation of horses, and dispersal after equestrian events such as sales and race meetings.

In North America equine influenza was confirmed in over 30 states in the USA, and in Canada. No vaccination data were available from the USA, but the majority of cases reported in Canada were of unvaccinated horses. In Africa, outbreaks were reported in Libya and in Nigeria. The outbreak in Nigeria was in a donkey market where more than 400 donkeys were gathered. In China, influenza was confirmed in Inner Mongolia, an area with a large population of horses.

In July 2022 reports were also received of outbreaks in Colombia that occurred earlier that year and were possibly linked to participation in both national and international equestrian events. The majority of the affected horses were unvaccinated.

#### **Genetic characterisation of viruses identified 2022-2024**

Viruses isolated/identified in China, Colombia, France, Ireland, Nigeria, Sweden, the UK 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, Nigeria, Sweden, the UK and the USA.

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Only the viruses detected in China were characterised as clade 2, Florida sublineage of the American lineage. Phylogenetic analysis indicated that these viruses were genetically similar to viruses identified in China in the recent past. All other viruses detected were characterised as clade 1, Florida sublineage of the American lineage. Their HA sequences were aligned against the HA of the clade 1-recommended vaccine virus: A/eq/South Africa/2003. All viruses identified and characterised in 2022-2024 were genetically similar to the clade 1 viruses identified in Europe and the USA in 2021 to 2023.

### Antigenic characterisation of viruses identified 2022-2024

Virus neutralisation data showed that the most recent viruses continue to remain antigenically closely related to the recommended clade 1 vaccine viruses. Specific horse antisera against vaccine strains (South Africa/2003 and Ibaraki/2007) cross-neutralised recent clade 1 viruses. Antibody titres against Irish and North American strains isolated in 2022 and 2024 were comparable to those against the homologous vaccine strains.

This close antigenic relationship among the current isolates and vaccine strains was further supported by haemagglutination inhibition titres of viruses with ferret antisera raised against the recommended vaccine strains.

### Conclusions

With the exception of a clade 2 viruses identified in China, all viruses characterised from the outbreaks between July 2022 and September 2024 were of the clade 1 Florida sublineage. They were similar to those identified in Europe and the USA in recent years. Clade 1 viruses are endemic in the USA and since 2019, appear to have supplanted clade 2 viruses in Europe. Recent outbreaks in Africa and South America have also been caused by clade 1 viruses. 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 clade 1 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 scientific 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 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 (September 2024)

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.

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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.