LABÉO
Pôle d'analyses et de recherche
de Normandie

LABÉO notice

(March 11, 2021)

The CES Valencia Spring Tour 2021 is a competition which lasts for 4 weeks with a total of 850 horses. The accomodation of the horses is a big tet with 450 boxes. A French horse showed fever on the 14th of February and another one on the 16th of February with development of neurological signs the day after. These horses are the first identified with fever but it is more than sure that some horses had fever before but were not known. On the 20th of February 10 horses showed fever and 48H later 52 showed fever. Since the begining of the crisis in Valencia many horses have shown neurological signs. A total of 11 horses have died (data on the 9th of March). These informations were reported by Pr Anne Courouce (Oniris, RESPE) wich was mandated by the French Equestrian Federation in Valencia.

EHV-1 was rapidly identified by PCR as the virus responsible of these epizootie. However, because of the number of positive and sick horses, there is a question about the virulence of the strain.

We isolated the EHV-1_Valencia virus at LABÉO (France) and obtained preliminary information about the genotype (ORF30 2254 nt position) (Nugent et al 2006) and clade using Multilocus Sequence Testing (MLST) for EHV1 (Garvey et al 2018).

Genotype A/G/C2254 data:

This genotype was first described by Nugent et al (2006). Strains carrying a guanine (G2254; D752) were strongly associated with neuropathogenicity while whose carrying an adenine (A2254; N752) were strongly associated with non-neurological outbreaks.

Several studies based on field isolates since suggested that abortion is largely associated with A2254 ;N752 EHV-1 strains while in the case of EHM the genotype/pathotype association is less obvious. This has been recently reported by Gabrielle Sutton who identified in 2020

(Viruses. 2020 Oct 13;12(10)) a new variant with genotype C2254/H752. To-date this genotype C2254 was reported in only one stud.

The EHV1_Valencia strain is a A2254 genotype.

This was observed on 30 different samples (NPS) obtained from horses from different countries sampled by Pr Anne Couroucé.

Information about the clade:

A MLST approach (Garvey et al; 2018; Sutton et al. 2019) can distinguish the majority of EHV1 U_L clades described by Bryant et al. (2018). This MLST approach is based on identification of several SNP in different ORFs (Nugent et al 2006 ; Garvey et al., 2018).

Preliminary results from LABÉO suggest that EHV1 Valencia belongs to Clade 11 but further analysis is needed to confirm the Clade and remove a doubt about Clade 10. This analysis is being carried out in collaboration with the OIE Reference laboratory at the Irish Equine Centre. Clade 11 and clade 10 today only reported strains from UK, IRL and F.

In 2018, at LABÉO we identified strains belonging to Clades 7, 8, 10, 11 and 13 showing that different strains were in circulation in France and responsible for outbreaks of EHV1 associated disease.

Whole genome sequencing will be necessary to determine if EHV1_Valencia is a previously unidentified strain and to try to identify virulence markers of this virus.

Notice written by Dr Stéphane Pronost (LABÉO), Pr Anne Couroucé (ONIRIS, RESPE), Dr Christel Marcillaud-Pitel (RESPE) with the kind participation of Pr Ann Cullinane (Irish Equine Centre).