

Preliminary Outbreak Assessment

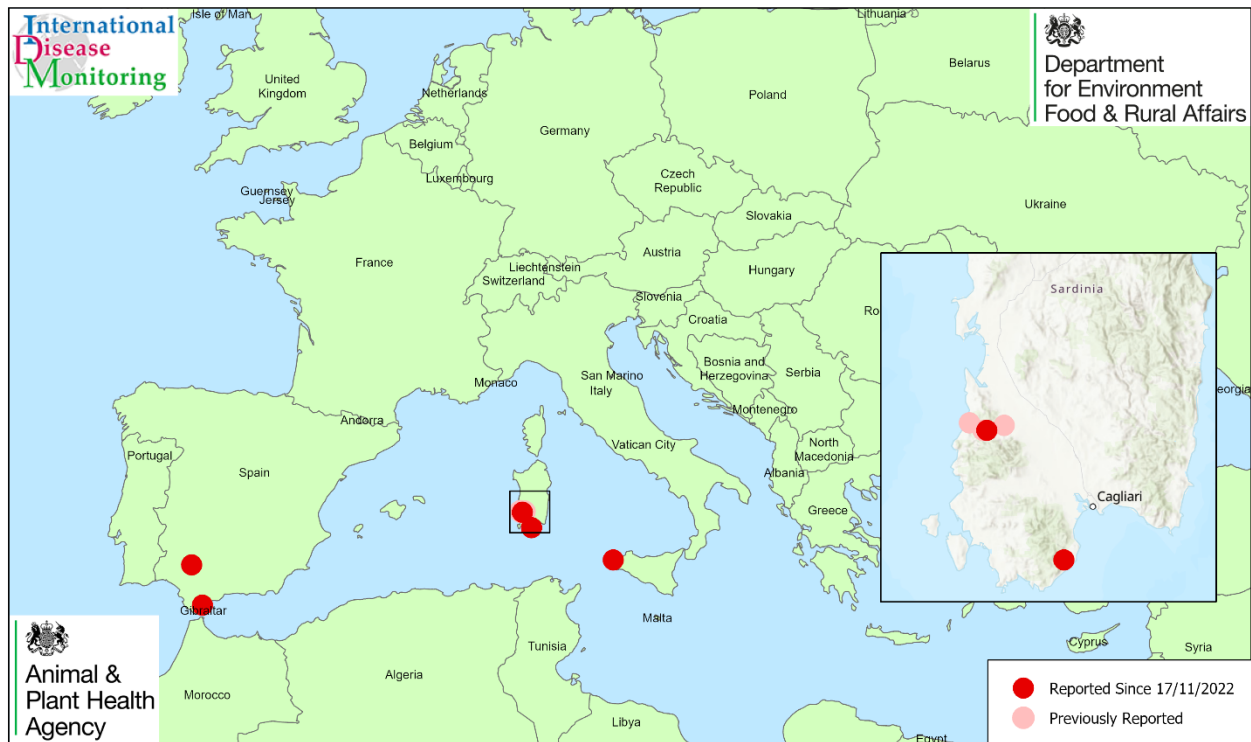
Epizootic Haemorrhagic Disease in Europe

24 November 2022

Disease report

Following the initial report of the emergence of Epizootic Haemorrhagic Disease (EHD) in Europe with outbreaks in cattle in Sardinia and Sicily, 2 outbreaks have now been confirmed for the first time on cattle farms in southern Spain. One farm had 1,098 cattle and is located in Seville and the second farm had 139 cattle and is located in Cádiz. In total 12 cattle were confirmed positive with EHD in Spain according to WOA (World Organisation for Animal Health). Disease in Spain was confirmed by the Central Veterinary Laboratory of Algete on 17 November 2022 and reported by the WOA on 23 November. According to a media report, suspicion of EHD was raised when clinical signs and lesions were reported to the official veterinary services within the Junta of Andalucía. Samples were then taken and tested positive for the EHD virus by polymerase chain reaction (PCR) (Agronomist ABC, 2022). Although EHD has been confirmed in 2 farms to date, clinical signs consistent with EHD have been reported in 25 cattle farms in Cádiz and 8 in Seville (Agronomist ABC, 2022). Movement of live animals from the provinces of Cádiz, Huelva, Málaga, Córdoba, Sevilla and Badajoz to other Member States is restricted and within Spain, movement of live animals from affected regions (Campo de Gibraltar (Algeciras) and La Janda (Medina Sidonia) in Cádiz, and Sierra Norte (Cazalla de la Sierra) and Vega de Sevilla (Cantillana) in Seville) has been restricted (Agronomist ABC, 2022).

In addition, since our first report there has been a further outbreak of EHD in cattle confirmed in Sardinia and a case in wild red deer as reported by the WOA. The cattle farm was in Arbus and had 11 cattle, one of which was confirmed with EHD. The red deer was located in a natural park in Pula, near the southern coast of Sardinia.



Map Prepared by IDM

Date: 24/11/2022

Absolute Scale: 1:21,000,000

Epizootic Haemorrhagic Disease in Southern Europe November 2022

0 390 780 1,170 Km

Situation assessment

The EHD virus (EHDV) has been notifiable to the WOAHP since 2008 and EHD is notifiable in the EU Animal Health Law, Commission Implementing Regulation 2018/1882/EU. The virus infects many ruminant species and may manifest as haemorrhagic disease, although sub-clinical infection may also occur (WOAHP, 2019). Due to the clinical presentation, bluetongue is a key differential diagnosis, along with foot-and-mouth disease (FMD) in deer and cattle. Additional differential diagnoses in cattle are bovine viral diarrhoea (BVD), infectious bovine rhinotracheitis, vesicular stomatitis, malignant catarrhal fever, and bovine ephemeral fever (WOAHP, 2019). The EHDV is transmitted by arthropod vectors, predominantly *Culicoides* biting midge species, with some European species highlighted as potential competent vectors (EFSA, 2009). Increasing temperatures through climate change may promote transmission of EHDV in *Culicoides* midges as has been well documented for bluetongue viruses (Jones et al., 2019). This could include both expansion in the range of competent vectors and increased transmission efficiency by the midge due to the shorter extrinsic incubation period (EIP) at higher temperatures. After initial infection in the midge midgut, the virus has to move to the salivary glands to be transmitted by biting, before the midge dies. The time for this (the EIP) shortens with increasing temperature such that the survival time of the midge is greater than the EIP allowing transmission through taking subsequent blood meals.

To date, there are 8 recognised serotypes of EHDV, though it is likely that more exist (Pirbright, 2022). The serotype of EHDV responsible for the ongoing outbreaks in Europe

is not available at the time of writing. Prior to the recent outbreaks of EHD in Europe, the disease has been confirmed in a number of neighbouring countries across the Middle East and North Africa such as Turkey, Morocco, Algeria (all EHDV-6), Tunisia (EHDV-6 and EHDV-8) and Israel (EHDV-7), dating as far back as 1950 for Israel. In North America, EHD occurs from mid-summer through to late autumn, in line with vector seasonality. Serotypes 1, 2 and 6 have been confirmed in North America to date. Australia has shown the greatest heterogeneity with serotypes 1, 2, 5, 6, 7 and 8 all reported across the country (Australian Government, 2014).

EHDV is present in neighbouring countries to Europe, across the Middle East and North Africa. In late September 2021, over 200 confirmed outbreaks of EHD occurred in central/western Tunisia and these were caused by an EHDV-8 serotype (Sghaier et al., 2022). Four outbreaks of EHDV in Tunisia were reported by WOAHA during this time period. There have been further reports of EHD in Tunisia since August 2022, though no further information on the serotype is currently available (ProMed, 2022). Media reports from Italy suggested that vectors carrying EHDV may have blown into Sardinia via desert winds (Italy 24, 2022). Genetic analysis has confirmed the virus found in Sardinia has a direct North African origin, with more than 99.9% homology to EHDV-8 strains detected in Tunisia in 2021 and 2022 ([Biorxiv 2022](#)), further genetic analysis for the Sicilian samples is ongoing. Although no information was available on the possible route of entry of EHD into Spain at the time of writing, the proximity of southern Spain to the north coast of Morocco would be consistent with vector blow-over, similar to that proposed for Sardinia.

Conclusion

Further outbreaks of EHD have been confirmed in southern Europe both in Sardinia and in Spain for the first time. The case in the wild red deer in Sardinia is significant as the first case confirmed in wildlife, which could potentially behave as a reservoir of infection over time. However, given that Sardinia is an island and restrictions are in place, this would not pose a risk to neighbouring territories unless infected vectors blow over into Corsica for example. The situation in Spain will be closely monitored as infection of roaming wildlife with EHD within mainland Europe holds significantly greater potential for spread. Several candidate *Culicoides* biting midge species have been identified as potential vector species in Europe. Fully disseminated infections have been identified in *Culicoides obsoletus* and *Culicoides scoticus* following experimental infection with EHDV (Maurer et al., 2021), and EHDV has also been detected in a single field-caught *Culicoides punctatus* specimen in Japan (Yanase et al., 2005). These 3 species are widespread across northern Europe and the UK and have huge local abundance on livestock farms during the vector active season. Different strains of EHDV from North America have been shown to be transmitted with different efficiencies in *Culicoides sonorensis* (McGregor et al. 2019). However, at this time of year as we head into the winter months, any potential vectors that are present in the UK would be at low population numbers. Transmission rates at the lower temperatures would be low too. The minimum temperature required for EHDV replication within the midge is 15.2 degrees Celsius (Wittmann et al., 2002). This is higher than that for BTV and also for African horse sickness virus (AHSV), another midge borne virus, thus further

lowering the likelihood of transmission, particularly during the colder months, relative to BTV. The main route of entry of EHDV into the UK would be via movement of live viraemic animals and/or infected vectors into the UK from an affected area. There have been no recent trade consignments of live cattle received in the UK from Sardinia, Sicily or Spain since 01 September 2022. At present, we consider the risk of introduction of EHDV into the UK via movement of live animals and/or vectors to be **negligible**. We will continue to monitor the situation.

Authors

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