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Short communication

Epizootic haemorrhagic disease virus in Reunion Island: Evidence for the circulation of a new serotype and associated risk factors

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ABSTRACT

Bluetongue virus (BTV) and epizootic haemorrhagic disease virus (EHDV) are members of the *Orbivirus* genus of the Reoviridae family transmitted between ruminants by the bites of *Culicoides* midges. BTV went undetected in Reunion Island between its first documented emergence in 1979 and two other serious outbreaks with both BTV-3 and EHDV-6 in 2003, and both EHDV-6 and BTV-2 in 2009. In these outbreaks, infected animals developed symptoms including hyperthermia, anorexia, congestion, prostration and nasal discharge.

Samples were collected in 2011 to assess the prevalence of BT and EHD in ruminants native to Reunion Island by serological analysis. A cross-sectional study was undertaken on 67 farms, including a total of 276 cattle, 142 sheep and 71 goats. The prevalence rates of BT and EHD were 58% (95% CI [54.03–62.94]) and 38% (95% CI [33.85–42.63], respectively. Two further suspected outbreaks were confirmed to involve EHDV and BTV/EHDV. A new circulating EHDV serotype 1 of unknown origin was isolated. Our results confirm that the prevalence of both BT and EHD is high and that both are likely currently circulating. A high risk of BTV and EHDV infections was associated with the introduction of ruminants from neighbouring farms without quarantine, the presence of organic and other waste on the farm, and treatment against ectoparasites and insects.

1. Introduction

Epizootic haemorrhagic disease (EHD) is an arthropod-borne disease of wild and domestic ruminants caused by viruses belonging to the species *Epizootic haemorrhagic disease virus* (EHDV) within the genus *Orbivirus* of the Reoviridae family. Bluetongue virus (BTV) is the type species

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of this genus and is both genetically and morphologically related to EHDV (Mertens et al., 2005). EHDV and BTV, both transmitted by biting midges of the genus *Culicoides* (Diptera: Ceratopogonidae), are double-stranded RNA viruses with a 10-segmented genome. The specificity of the interactions of VP2 and VP5 (encoded by genome segments 2 and 6, respectively) with neutralizing antibodies determines the virus serotype (Mecham and Dean, 1988; Mertens et al., 1989). Up to date, twenty-six distinct BTV serotypes have been recognized to cause "bluetongue" (BT) (Maan et al., 2011) and seven serotypes have been identified for EHDV (Anthony et al., 2009). The spread of the vector-borne viral diseases BT and EHD caused several outbreaks of bluetongue disease throughout the Mediterranean basin and in several northern European countries. In North America, EHD has been endemic since 1955 causing seasonal clinical signs including high mortality in white-tailed deer and infrequent BT-like illnesses in cattle and sheep, with for instance, transient viraemia (Thompson et al., 1988). EHD viruses have been isolated from epizootics in Australia, south-east Asia, Africa (Nigeria and South Africa) and more recently in countries surrounding the Mediterranean Basin (Maan et al., 2010).

BTV went undetected in Reunion Island between its first documented emergence in 1979 and two other serious outbreaks with both BTV-3 and EHDV-6 in 2003 (Barré et al., 1985; Bréard et al., 2004, 2005), and both EHDV-6 and BTV-2 in 2009 with infected animals displaying symptoms (Sailleau et al., 2012). To clarify the BTV and EHDV epidemiological situation in Reunion Island, a cross-sectional study of the indigenous domesticated ruminant population was undertaken in 2011 associated with a risk factor analysis in order to identify variables possibly linked to both orbivirus infections. In April 2011, two outbreaks of EHDV were shown to be caused by a new EHDV serotype.

2. Materials and methods

2.1. Study area, design and sampling

A total of 489 ruminant samples (serum and EDTA blood for each sample) were collected from 67 separate farms between February and June 2011. The animals sampled were as follows: 276 cattle, 142 sheep, and 71 goats. The size of the sampling frame was estimated using an α type I error of 5%, an estimated prevalence of 20% and a relative precision of 20% (Toma et al., 2008). Fig. 1 shows the geographical location of the sampling sites used in the study in relation to cattle density. Samples (sera and EDTA blood) were also collected from the two farms where new outbreaks were reported.

2.2. Risk factors analysis

Data concerning farm characteristics, type of production, number of animals, closeness to another farm and sugar cane fields, presence of organic and other waste on the farm, exposure to wind, distance to a permanent water point, type of animal housing, presence of ticks on animals, use of treatment against ectoparasites and insects, animal's contacts with other animals or humans, grazing practice, spreading of manure on pastures, presence of *Tenrec ecaudatus*, rodent control, number of abortions in the herd in the last 12 months, purchasing behaviour,

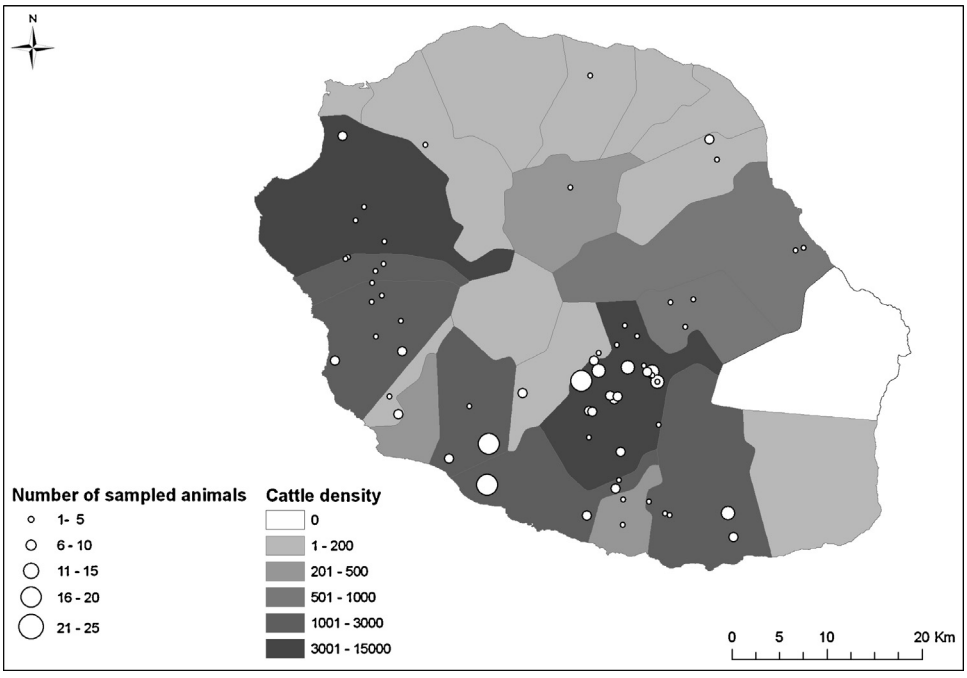

Fig. 1. Location of the sampling sites used in the study in relation to cattle density. Size of the points is proportional to the number of sampled animals.