Monitoring bluetongue disease (BTV-1) epidemic in southern Spain during 2007

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ABSTRACT

On the 25th of July 2007, bluetongue virus (BTV) serotype 1 was detected in Andalusia, southern Spain for the first time. A total of 4436 farms infected with BTV-1 were confirmed during that year: 3162 in sheep flocks, 113 in goat flocks, 7 in cattle herds and 1154 in mixed farms (sheep, goat and/or cattle in the same farm). The most common clinical signs were: fever, depression, lethargy, facial edema, and salivation (observed in more than 70% of the infected farms). Lesions in oral mucosa, lameness and dyspnea were also frequently observed.

Median morbidity rate in sheep and goat flocks were 6.3% and 2.7% respectively. Median mortality rate was 2.2% in sheep flocks and 1.2% in goat flocks. Median case fatality rate was 29.8% in sheep flocks and 45% in goat flocks. Morbidity and mortality rates were not significantly higher in sheep flocks than in goat flocks ($p > 0.05$), whereas case fatality rate was significant higher in goat flocks compared to sheep flocks ($p < 0.05$). Neither clinical signs nor mortality were observed in cattle herds.

The spatial distribution of the risk of BTV infection over Andalusia by municipality was evaluated by means of a hierarchical Bayesian model. The results evidenced that the risk was not homogeneous over the territory, being higher in the western part of the region. The likelihood of BTV infection was increased between 1.01 and 1.16 times by an increase of 10,000 domestic ruminants, and between 1.01 and 1.69 times by the presence of red deer (*Cervus elaphus*) in the municipality.

1. Introduction

Bluetongue (BT) is an arthropod-borne, viral, non-contagious disease caused by a virus which belongs to the genus *Orbivirus* within the *Reoviridae* family. Bluetongue virus (BTV) is transmitted by biting midges of the genus *Culicoides*, and can infect different species of ruminants. To date, 24 distinct BTV serotypes have been identified. BT is a reportable disease of considerable socioeconomic impact and is of major importance in the international trade of animals and animal products.

Before 1998, BT was considered an exotic disease in Europe, with the exception of Cyprus, where since 1924 the disease was detected several times (Polydorou, 1978). In the western Mediterranean basin, BT disease, caused by

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serotype 10, was first reported in Morocco in 1956, from where it seemed to spread to the south of Spain and Portugal by wind (Sellers et al., 1978). Between 1956 and 1960 it caused the death of approximately 179,000 sheep in the Iberian Peninsula (Manso-Ribeiro et al., 1957; Lopez and Botija, 1958).

In the last years, almost all countries of the Mediterranean basin and Western Europe have been affected by different serotypes (Mellor et al., 2008). In 1998 the disease appeared in Greece and in the next year it spread to Turkey and Bulgaria. No more cases were detected until January 2000 when a case was declared in Tunisia, which was attributed to serotype 2. In the second semester of 2000, BTV-2 was also detected in Algeria, Morocco, Italy (Sardinia, Sicily, and the southern mainland), Corsica (France) and Majorca and Minorca Islands (Spain). New cases were detected in Corsica in July 2001 and in several regions of Italy during the next years. In April 2002 three new serotypes (BTV-4, BTV-8 and BTV-16) appeared in Italy, probably originating from eastern Mediterranean countries (Calistri et al., 2004; Giovannini et al., 2004). In October 2003 BTV-4 affected also Corsica and Minorca (Spain). In August 2004 BTV-4 affected Morocco, and by October the first cases appeared in Andalusia and Extremadura (Spain). By November, the same serotype was detected in Portugal near the Spanish border. A total of 322 cases were declared in Spain: 268 in Andalusia, 50 in Extremadura and 4 in Ceuta (northern Africa). The infection reappeared in the Iberian Peninsula in 2005, and although the number of cases was low (n = 88), the disease affected several Spanish regions: Castile-La Mancha, Castile and Leon and Madrid (RASVE, 2009).

In October 2006, a new serotype (BTV-1) appeared in the eastern Maghreb, and few weeks later cases were declared in Sardinia (Italy). In addition, during 2006, BTV-8 emerged in Central Europe, where no previously known vectors were present, and spread rapidly between different countries (Saegerman et al., 2008). BTV-1 continued to spread in 2007 and was detected in Portugal by September and southwest France by November (Wilson and Mellor, 2009). The serotype is still active and new outbreaks have been detected in northern and eastern France (International Society for Infectious Diseases, 2009), which may pose a great risk for the neighbouring countries as their ruminant populations are not vaccinated against BTV-1.

Information relative to BTV-1 is still very limited, and data on the impact of this serotype in the affected European countries has not been reported to date. The objectives of the present study were (i) to describe the evolution and main findings of the epidemic that affected Andalusia in 2007, and (ii) analyse the spatial distribution of the BTV relative risk of infection at the end of the epidemic.

2. Materials and methods

2.1. Data collection

Andalusia is a region located in the south of Spain and has an extension of 87,597 km². The ruminant population is about 2.6 million sheep, 1.2 million goats and 0.6 million

cattle. The total number of sheep, goat, cattle and mixed farms is of 13346, 10789, 8745 and 4339, respectively (data provided by the Autonomous Government of Andalusia). Epidemiological data were collected during clinical inspections by the veterinary authorities, as part of the official visits to the farms, using a standardized questionnaire. Data relative to date of visit; type of farm (sheep, goat, cattle and mixed); number of animals in the farm; reason for the visit (suspicion, surveillance, sampling in the affected radius); number of animals with clinical signs compatible with BT; number of deaths associated to BT and date when clinical signs were first observed, were collected. Furthermore, information on the clinical signs observed and the mortality in the affected farms were also collected. Data on clinical signs and mortality were available from 88.3% (n = 3919) of the farms affected in Andalusia during 2007.

A case was defined as a farm where at least one animal (sheep, goat or cattle) was confirmed by the national reference laboratory as positive by means of RT-PCR analysis according to the OIE guidelines. Morbidity rate was expressed as the number of animals with signs indicative of BT in a farm divided by the average number of animals at risk in that farm. Mortality rate was expressed as the number of deaths associated to BT in a farm divided by the average number of animals at risk in that farm. Case fatality rate at farm level was expressed as the proportion of the animals clinically affected by BT that died in the affected farms.

In order to statistically assess between-species differences in morbidity, mortality and case fatality rates we used a generalized linear mixed model with the glimmix procedure implemented in the statistical software package SAS 9.1 version. It was assumed that morbidity, mortality and case fatality rates followed a binomial distribution and an R-Side residual effect was included in the model in order to control for possible overdispersion with respect to the variance of the binomial distribution. Differences were considered statistically significant when *p*-value <0.05.

2.2. Spatial analysis

As most of the cases were detected by clinical suspicion and clinical disease was observed mainly in sheep, to avoid biasing the analysis, only the cases that affected sheep farms were included in the model. The aggregation level used was the municipality (i = 1, . . ., 770). For each municipality we estimated the relative risk ($r[i]$) of BTV infection as the ratio:

$$r[i] = \frac{\text{CI}[i]}{\text{CIT}}$$

where CI[i] represented the estimated cumulative incidence in each municipality and CIT was the overall observed cumulative incidence in the affected region defined by the 770 municipalities with recorded BT cases. In spatial data sets, observations that are close in space tend to be more similar than observations that are far apart. This can arise because transmission requires close proximity or because environmental determinants of disease themselves are spatially heterogeneous (Clements