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Seroprevalence and spatial distribution of maedi-visna virus and pestiviruses in Catalonia (Spain)

A. Alba [a,*], A. Allepuz [a,b], E. Serrano [a], J. Casal [a,b]

[a] *Centre de Recerca en Sanitat Animal (CReSA), UAB-IRTA, Campus de la Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain*
[b] *Departament de Sanitat i Anatomia Animals, Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain*

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Abstract

During the period 2004–2005 a serological survey was conducted in sheep flocks in Catalonia (North-Eastern Spain) in order to determine the seroprevalence of maedi-visna virus (MVV) and pestiviruses, such as Border Disease Virus (BDV), to investigate their spatial distribution and to obtain information about associations between them for planning and prioritizing the control measures in this region. A random sample of 241 sheep flocks stratified by counties was analyzed. A total of 5120 and 3611 animals were tested using different indirect ELISA methods for MVV and pestiviruses, respectively. The results showed that MVV and pestiviruses were very widespread in Catalonia. Ninety percent of sheep flocks were positive for MVV and sixty four percent were positive for *Pestivirus* genus. The spatial distributions of both viral pathogens were not homogenous: MVV seroprevalence within flock was higher in North-Western and Western Catalonia, whereas the antibody proportion of pestiviruses at the flock-level and within flock was higher in North-Western Catalonia. Large flocks had higher seroprevalences within flock than smaller ones. Mixed flocks showed higher risk of MVV infection than purely sheep flocks and there was a statistical association between MVV and pestivirus seroprevalence.

Keywords: Maedi-visna; Pestiviruses; Sheep flocks; Antibody prevalence; Spatial distribution; North-Eastern Spain

1. Introduction

Maedi-visna virus and pestiviruses, such as Border Disease Virus (BDV), are important viral pathogens which infect small ruminant species worldwide causing substantial economic losses. These pathogens are similar in that there is no efficient therapy available to treat them, they need to be controlled at flock-level and they cause a persistent infection. The circulation of these viral agents can be detected in most infected sheep flocks by serological assays.

Maedi-visna virus (MVV) belongs to the Small Ruminants Lentiviruses (SRLVs) of the *Retroviridae* family. This virus causes persistent infections and chronic disease after a prolonged incubation period in their hosts, culminating in multiorgan pathology with an invariably fatal outcome (Clements and Zink, 1996; Pépin et al., 1998). The maedi syndrome is described as a fatal, progressive pneumonia in mature sheep; and visna is a

* Corresponding author. Tel.: +34 93 581 45 57; fax: +34 93 581 44 90.
E-mail address: ana.alba@cresa.uab.es (A. Alba).

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clinical syndrome which causes a meningoencephalitis (Pritchard and Dawson, 2000). The most important routes of transmission are: from an infected ewe to its offspring via colostrum and milk (Pritchard and Dawson, 2000) and horizontal transmission by respiratory secretions in some flocks with a high density of animals (Berriatua et al., 2003).

The disease is widespread in many countries of the world, particularly in European countries. Data on the prevalence of SRLVs cannot be directly compared at present, due to the differences in sensitivity and specificity of diagnostic tests and the variety of sampling methods used. However, available data showed that no European country, except Iceland, could be considered to be free of SRLVs infection as defined by the Office International des Epizooties (no positive animal detected after a survey with a sample large enough to detect 1% of flocks infected with a probability of 99%) (Peterhans et al., 2004). Published studies in Spain showed that in some regions, such as the Basque Country, over 95% of flocks were infected (Berriatua et al., 2003).

The genus *Pestivirus* includes four species: Border Disease Virus (BDV), bovine viral diarrhoea virus type 1 (BVDV-1), BVDV type 2 (BVDV-2) and classical swine fever virus (CSFV) (Fauquet et al., 2005). BDV and BVDV are not strictly host specific and can cross infect cattle, sheep, goats, pigs and non-domesticated species (Krametter-Frötscher et al., 2007b; Nettleton and Entrican, 1995), whereas CSFV has been isolated only in pigs (Krametter-Frötscher et al., 2007b; Harkness, 1985). BDV causes a congenital disease of sheep characterised by still-birth, abortion and the birth of weak lambs with nervous symptoms and sometimes an abnormally hairy birthcoat. Transmission of these kinds of viruses occurs by oral and/or intranasal routes. Persistently infected sheep act as a primary reservoir by shedding viruses through their excretions and secretions. Lambs of infected ewes are at risk of becoming persistently infected with BDV and thereby perpetuating the disease cycle. The seroprevalence of BDV at flock-level was estimated in previous studies in other Spanish regions as Basque Country, Madrid, Castilla-León and Asturias and the detected levels were 68%, 50%, 48% and 10%, respectively (Valdazo-González et al., 2006; Berriatua et al., 2006; Mainar-Jaime and Vázquez-Boland, 1999). In other published studies in several different European countries, the seroprevalence at flock-level also turned out to be very high, being detected in 67.6% of flocks in Austria in communal alpine pasturing (Krametter-Froetscher et al., 2007a), between 60% and 80% of flocks in Switzerland (Stalder et al., 2005), and 30.4% (ranging between 0 and 70% depending on the region) in Northern Ireland (Graham et al., 2001).

The aims of this study were to determine the antibody seroprevalence of MVV and pestiviruses (as BDV) among ovine flocks in Catalonia and to examine their spatial distribution.

2. Material and methods

2.1. Population

A cross-sectional serological survey in sheep flocks was conducted in Catalonia. This region is located in North-Eastern Spain and has an area of 31,930 km^2 which is divided in 41 counties. The target sheep population is around 638,429 adult animals distributed in 3482 flocks. Approximately 22% of these animals are from autochthonous pure breeds and most sheep flocks are raised for meat production (Anonymous, 2004).

2.2. Study design

A stratified random sample was selected taking into account a proportional allocation by counties to determine the seroprevalence at flock-level affected by MVV and pestiviruses. The sample size was calculated considering an expected flock seroprevalence of 80% with a precision of 5% for a 95% confidence level and 5% of possible losses. The sample size studied in this survey was 241 sheep flocks. In each flock, 24 samples were randomly obtained from animals older than 18 months. At the beginning, from these samples, 14 were tested to determine the presence or absence of antibodies against MVV and/or pestiviruses; this sample allowed us to detect at least one serological positive animal if seroprevalence within flock was higher than 20%. In those flocks which resulted positive for MVV and/or pestiviruses antibodies, the remaining 10 samples were tested to estimate the prevalence of seropositive animals within flock with a precision of 20% for a confidence level of 95%. The sample sizes were calculated with WinEpiscope 2.0 software (Thrusfield et al., 2001). A total of 5476 serums from 241 sheep flocks were obtained during the period 2004–2005 through the Official Campaign for Brucellosis Eradication. In each flock sampled, data on census, flock type (purely sheep or mixed with goats) and geographical coordinates were collected.

2.3. Serological tests

The detection of antibodies against MVV was performed using a commercially available ELISA test (ELITEST-MVV; HYPHEN Biomed) which contains a synthetic peptide corresponding to an immunodominant region of the transmembrane protein gp46 and a recombinant p25 (capsid protein).

The test used for the detection of pestiviruses, such as BDV, was a commercially available ELISA kit (BD p80