## EPIDEMIOLOGICAL SITUATION OF BOVINE VIRAL DIARRHEA VIRUS (BVDV) INFECTION IN A DAIRY CATTLE POPULATION FROM THE ASTURIAS REGION OF SPAIN

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Bovine viral diarrhea virus (BVDV) is a pestivirus infection affecting cattle and other ruminants. The major source of infection among cows is the presence of persistently infected (PI) animals in the herd.<sup>1</sup> Other less likely mechanisms of virus transmission would be the presence of transiently infected animals, the use of contaminated semen, by workers' clothing or instruments and by biting flies.<sup>4</sup> In general, in absence of PI animals, self-clearance will occur within the herd.<sup>5</sup>

Screening herds for BVDV-antibody carriers has been shown to be of interest both to discriminate PI animals (usually seronegative) and to determine the herd's infection status and its susceptibility to infection.<sup>1</sup> The purpose of the present study is to learn on the distribution of BVDV infection on a non-vaccinated population of dairy cattle from the Asturias region (North Spain) and on the factors associated with it. In addition, the possible role of BVDV infection on the development of *Neospora caninum* (NC) abortion is also studied.

## **Material and Methods**

From a previous survey to estimate NC prevalence on 48 dairy herds, <sup>6</sup> 28 herds (60%) that had never been vaccinated against BVDV infection were selected. Only cows >1 year old were included in the study. A commercial ELISA<sup>i,7</sup> was used to test for antibodies against BVDV. Herd and cow information was obtained through personal interview with the farmer at time of bleeding.

Individual and herd seroprevalences were estimated and antibody-age profiles plotted. Data obtained were used to assess whether cow seropositivity was related to herd size, location, abortion, age, cow origin, number of seropositive cows in the herd and distance to the closest dairy farm, by means of a multivariable random-effects logistic regression model.<sup>ii</sup> To test whether the risk for abortion for cows being seropositive to both NC and BVDV infections increased as compared with that for cows being seropositive only to NC, an unconditional logistic regression model was developed. In this case, abortion was the outcome variable and NC infection status, BVDV infection status and the interaction between both the independent ones.

## Results

From a total of 529 cows analyzed, 114 (21.5%) were seropositive, and 24 herds (85.7%) had at least one seropositive animal. Within the seropositive herds the seroprevalence was 26.85% (range: 6.06-69.2%). The antibody-age plot for all herds combined showed that seroprevalence clearly increased with age, and no seropositive animals were observed within the younger group (<2 years old) in 26 (92.85%) of the herds. Three variables, namely, age, cow origin and number of seropositive cows within the herd, remained associated with seropositivity (Table 1). No significant two-factor interactions were found. Risk for abortion did not increase when cows were seropositive to both BVDV and NC as compared with that for cows being only NC seropositive (Table 2).