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Exploring the epidemiology of bovine viral diarrhoea virus (BVDV) infection in beef suckler herds in two regions of Argentina: genetic variability and diagnostic implications

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Bovine Viral Diarrhoea Virus (BVDV) is highly prevalent worldwide and has a detrimental effect on the performance of beef herds. In Argentina a few reports done in the past showed prevalences between 25-90%, also, the presence of genotype 1 and 2 has been reported. In the recent decades, bovine livestock production in Argentina has undergone a remodeling process due to the expansion of land use for crop. This had an impact in marginal territories like Patagonia, where livestock existence had a significant growth, and also in traditional livestock production areas like Humid Pampa, where extensive holdings have been replaced by more intensive ones. This kind of process can have a great effect on the infectious disease dynamic. Purpose: Considering this context and the lack of up to date information, the aim of this study was to assess the prevalence of BVDV in these two regions, and to evaluate the limitations of the techniques available in the country for serological diagnostic. In addition, a survey was completed on each farm to collect information that could be associated as herd-level risk factors for the disease, analyzed by a logistic regression. Methods: Two cross-sectional studies were performed. Samples were gathered from 83(region I) and 100(region II) herds, collecting 15 and 25 samples per herd respectively, making a total of 4575 samples. The samples were evaluated by serum neutralization (SN) for the presence of antibodies against the 3 different genotypes (1a, 1b, and 2). Results: The results obtained show a prevalence of 96.34% (IC: 92.51% - 100.00%) of positive herds. The independent seropositivity against different genotypes tested was analyzed in both regions (1a, 1b,2:64-47-56.5% and 13.4-76.6-10%, respectively). Conclusions: Preliminary results when analyzing the proportions of serologically positive animals against each strain would show a different frequency distribution of genotypes between the two regions. Relevance: These results would reinforce how essential is to have current and robust epidemiological information as a starting point to design rationally control plans for BVDV for any particular region.