

Prevalence survey and spatial analysis of bovine herpesvirus

Miranda, I.C.S., Hein, H.E., Costa, E.F., Machado, G., Neto, W.S., Marks, F.S., Almeida, L.L., Canal, C.W. and Corbellini, L.G., Universidade Federal do Rio Grande do Sul, Brazil; lgcorbellini@hotmail.com

Bovine herpesvirus (BoHV) is an important pathogen of cattle that has worldwide distribution. Infection can cause substantial economic losses due reproductive failures and increased calf mortality. The identification of infected herds is commonly based on the detection of BoHV-specific antibodies in sera or milk samples. The aim of this study was to estimate the herd prevalence of BoHV in dairy herds and to evaluate the viral dissemination with spatial scan statistic. The target population was composed by 1,656 semi-intensive dairy herds in southern Brazil from which 300 were randomly sampled. Sample size was calculated considering an absolute precision of 5%, expected herd prevalence of 58%, and 95% confidence level. Samples of bulk milk tank were collected from those herds to determine antibody levels against BoHV by a commercial ELISA test. SaTScan 9.1 software with Bernoulli model was used to detect areas of significantly high rates of BoHV infection. The software has a circular window, variable in size and position in a given study region, and each circle is a possible candidate cluster. This window was set in maximum radius of 10 km and an upper limit of 50% of the population at risk. From the 300 samples, 12 were excluded due to inconclusive results. The prevalence of BoHV antibodies in bulk milk tank was 27.1% (CI 95%: 22.5%-33.3%). There were observed one most likely cluster ($P=0.099$) and five secondary clusters ($P\geq 0.675$). The most likely cluster had 8.91 km radius window with all 5 herds positive, when only 1.38 positive herds were expected. The moderate prevalence of BoHV and the presence of clusters of positive herds suggest the relation between cases and possible viral dissemination among them due to proximity. Disease clusters may occur either because herds share common risk factors or via transmission between herds through the movement of infected animals.