

**A Bayesian model for herd prevalence estimate of Newcastle disease virus**

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Newcastle disease virus (NDV) is the etiological agent of Newcastle disease (ND) and can infect domestic and wild birds. It can cause an acute and highly contagious viral disease. Infected birds can transport the virus over long distances and immune carriers can shed the virus indefinitely. Epidemiological data on NDV is scarce in Brazil. The aim of this study is to detect the presence of NDV in backyard flocks in the main wintering site for migratory birds in southern Brazil. The target population comprised all the domiciles raising poultry within 3.5 km around the main wetlands in the region (n=131). Sample size was designed to detect with 95% probability an infected flock with a herd-level prevalence (HP) of 5% (n1=48). Within each flock a fixed number of 9 (n2) birds were randomly selected. Considering an average test sensitivity (TSE=90%) and test specificity (TSP=93%) of a real-time reverse transcriptase PCR (RRT-PCR) applied in tracheal and cloacal swab and a within-herd prevalence of 30%, the average herd sensitivity (HSE) and herd specificity (HSP) were 96% and 76% respectively. A Bayesian model was developed to estimate herd-level prevalence using an uninformed prior with a HP likely to range from 0% to 25%. A binomial distribution was used as likelihood function considering the numbers domiciles infected, sampling size (n=48), HSE, HSP and HP. The posterior distribution for prevalence was normalized using a general function provided in [@risk](#). Ten thousand iterations were used. A total of 411 birds were sampled from 48 domiciles. All swabs were negative in RRT-PCR. The mean HP estimated by the model was 2.1%; the cumulative distribution showed that there is approximately 95% probability that the HP is less than 6.1%. Results suggest that if the NDV is present the prevalence is probably low.