

# Prevalence of BRD-related viral pathogens in the upper respiratory tract of Swiss veal calves

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## Background

- Respiratory disease is the main indication for antimicrobial treatment in Swiss veal calves
- Viral pathogens can cause or enhance the onset of respiratory disease
- Current prevalence estimates are lacking. They help to increase the epidemiological understanding of circulating viruses

## Objectives

- To estimate the prevalence of viruses known to infect the respiratory tract
- To analyze risk factors for isolation of viruses
- To suggest mitigation measures on veal calf farms
- To eventually reduce respiratory disease and antimicrobial treatment

## Results

Prevalence of viruses at calf-level and risk factors were:

- Bovine coronavirus (BoCV) **53.5%**;
- Limited group size in young calves associated with lower prevalence of BoCV than increased group size
- Bovine parainfluenza-3 (BPI3V) **3.3%**
- Bovine respiratory syncytial virus (BRSV) **2.1%**
- Influenza C/D virus (IC/DV) **0.0%/4.4%**

## Conclusions and Outlook

- Overall prevalence of pathogenic viruses (BPI3V and BRSV) were low at the time of the study, and lower compared to others
- Epidemiological significance of high prevalence of BoCV remains unclear
- IDV as newly emerging virus in cattle also circulates in CH



Fig. 1: Procedure of nasopharyngeal swab sampling in a young Swiss veal calf ( $\leq 100$  days of age).

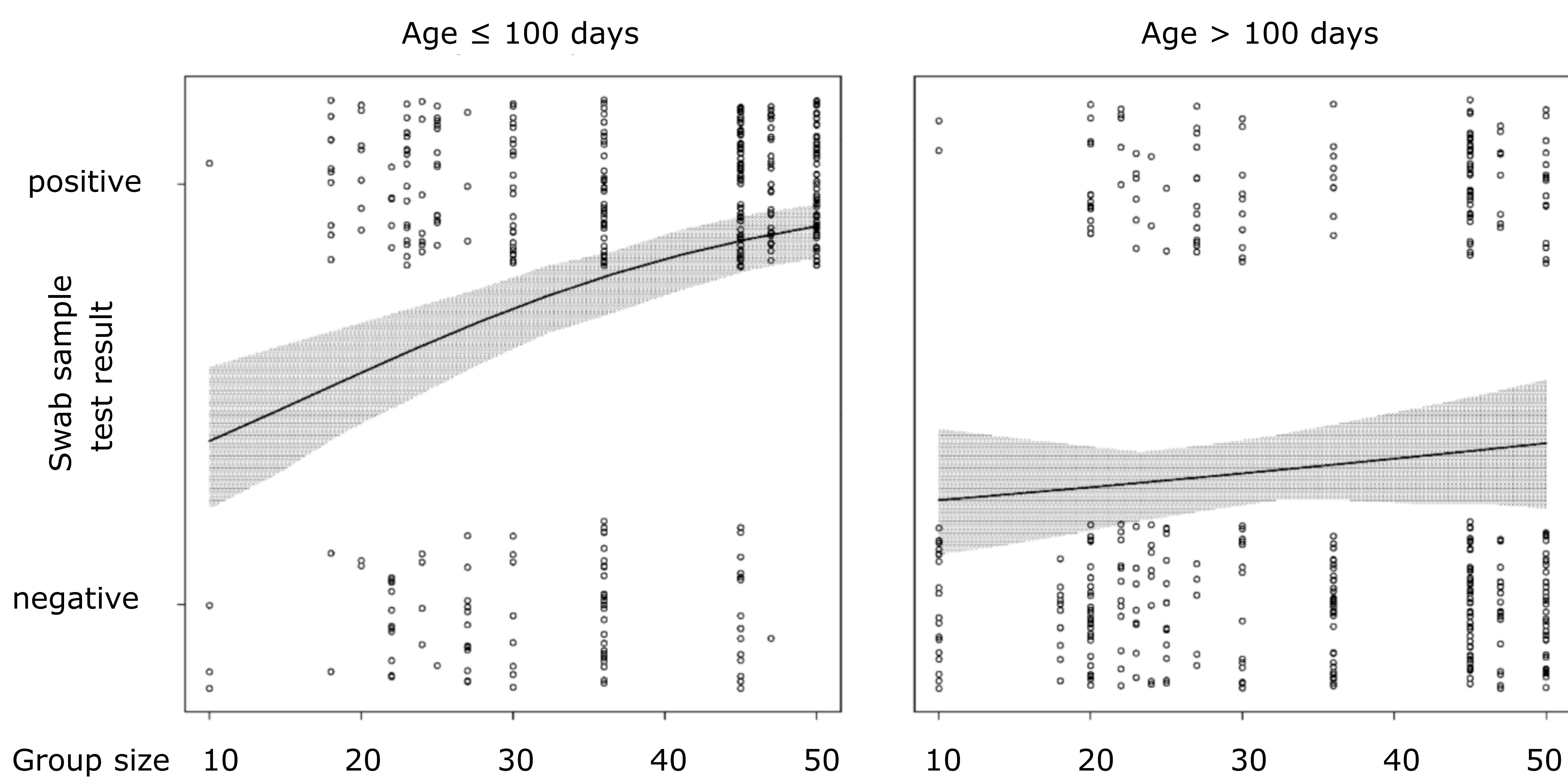


Fig. 2: Probability of positive nasopharyngeal swab sample of bovine coronavirus, dependent of mean group size and age. In small groups at a young age, calves were less likely to carry BoCV.

## Materials and Methods

Calves were enrolled on farms which were followed in the frame of other research projects not aiming at investigating viruses. In this convenience population, the following farm characteristics were observed (purchased calves 94.1%, birth farms per ten calves 3.3, vaccination at the farm level 77.2%, median number of calves fattened per year 63.8, mean farm mortality 5.1). A total of 764 samples of 4492 were screened. Samples were taken with sterile swabs and viral RNA was detected using qRT-PCR using described primers (Boxus 2005, Hortwood 2011, Kishimoto 2017, Zhang 2018, Holwerda 2019). For risk factor analysis, redundant variables were removed, and candidate variables for multivariate logistic regression were selected through repeated elastic net technique to avoid selection of univariable models and p-values. To account for farm and animal effects, individual calf identification nested within farms was added as a random intercept term.

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