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THE EFFECT OF POOLING TWO DIFFERENT TYPES OF SAMPLES TO DETECT TYPE 1 PRRS VIRUS ON PRE-WEANING PIGLETS IN AN ENDEMIC POSITIVE HERD AND PRACTICAL IMPLICATIONS

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Introduction

Most of the time, breeding herd stability against PRRSv is assessed by sampling 30 due-to-wean piglets in a farrowing batch and pooling the samples by five to test them with a RT-qPCR test. The aim of this study was to compare the capacity to detect PRRSv in pre-weaning piglets using 2 different types of samples per litter and pooling them by five.

Material and methods

One PRRS positive and not vaccinated farrow-to-finish farm was selected. 80 litters of four nonconsecutive batches were sampled. In each litter, a piglet's serum and a collective oral fluid (cOF) collected with a cotton rope were taken. RT-qPCR (Labofarm, Loudéac, France) was performed for both samples, testing them individually and pooled by five.

To assess the pooling, we compared the result of each pooled sample to the individual results of the samples constituting this pool, for serum and cOF respectively. Individual analyses at pool level (IAPL) were considered positive if at least one of the samples was positive.

Results

22 pools are analysed. 12 IAPL of serum and 12 of cOF are positive. Sensitivities are 67% (95% CI 35%, 90%) and 58% (28%, 85%) for pooled serum samples and cOF, respectively. The positivity of each pooled sample is correlated with the number of individual positive samples in the pool. Ct values of pooled sera range from 24.8 to 36.3. Ct values of pooled cOF range from 35.1 to 39.4. Three out the four batches are positive and PRRSv is detected by both pooled sera and pooled cOF.

Conclusion

The sensitivity after pooling, albeit lowered, is sufficient at batch level for both sera and cOF samples. Ct values of pooled blood and cOF samples are too high for sequencing, which could be a limitation when the diagnosis is done in a MLV vaccinated herd.