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Assessment of individual and population-based sampling for detection of Influenza A virus RNA in breeding swine herds

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ARTICLE INFO	A B S T R A C T
<i>Keywords:</i> Breeding herd Swine IAV Sample type Surveillance	This study compared the probability of influenza A virus (IAV) ribonucleic acid (RNA) detection between selected individual and population-based samples in breeding herds. A 3500-sow breeding herd was sampled for matched sets ($n = 57$) of family oral fluids (FOF), udder wipes, sow nasal wipes, individual piglet nasal wipes, and drinker wipes and tested by reverse transcription real-time polymerase chain reaction (RT-rtPCR) for IAV RNA detection. Overall, 57.9% (33/57) of FOF samples, 49.1% (28/57) of udder wipes, 28.1% (16/57) of sow nasal wipes, 15.8% (9/57) of drinker wipes and 66.6% (38/57) of the individual piglet nasal wipes tested positive for IAV RNA. FOF had a kappa value of 0.81, a near-perfect agreement compared to individual piglet nasal wipes. Udder wipes revealed a kappa value of 0.65, a substantial agreement with individual piglet nasal wipes. The other sample types had a fair agreement with individual piglet nasal wipes (kappa values <0.28). These results validate FOF as an efficient alternative population-based sample type for IAV surveillance in the breeding herd. The proportion of positive piglets within litter by room A had 91% positivity (20/22), room B had 70% (17/24), and room C had 9% (1/11) positivity. The findings also highlight the importance of testing different farrowing rooms in the same breeding herd to strengthen IAV surveillance.

Video to this article can be found online at https://doi.org/10.1016/j.sctalk.2024.100362.

Figures and tables

Table 1

Test performance measures for sample types tested for IAV RNA detection by RT-rtPCR.

	Reference sample type Positive	Reference sample type Negative
The sample type tested positive	True positive (TP)	False positive (FP)
The sample type tested negative	False negative (FN)	True negative (TN)

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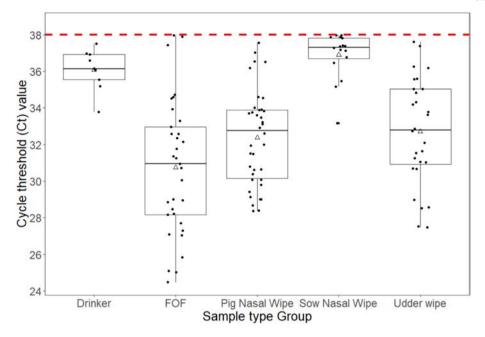


Fig. 1. Boxplots display the distribution of Ct values for each sample type, with the mean of each group represented by a triangular marker in the boxplot. Individual positive samples are denoted by black dots on the plot, and the red dashed line indicates the RT-rtPCR Ct value (Ct 38) used to classify a sample as positive. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

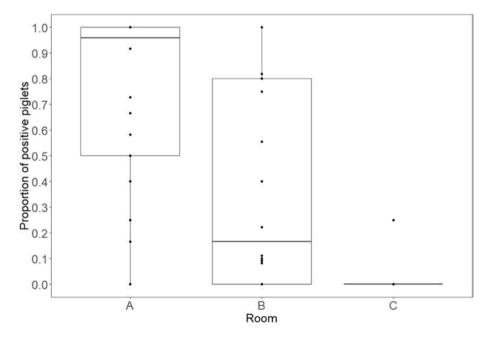


Fig. 2. The proportion of RT-rtPCR-positive piglets within a litter by room. Each room is represented by a letter (A, B, C). Each black dot represents the proportion of positive piglets within litter by room.

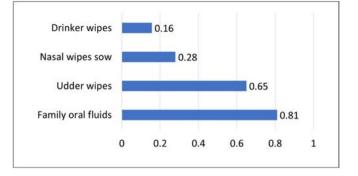


Fig. 3. Kappa agreement using piglet nasal wipes as a reference.

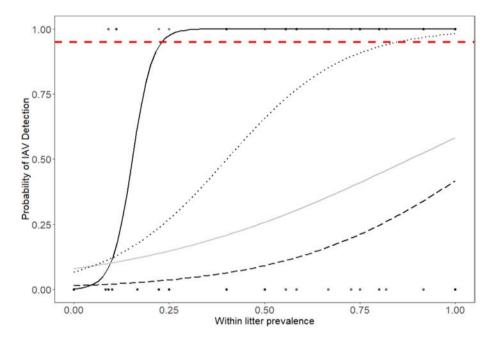
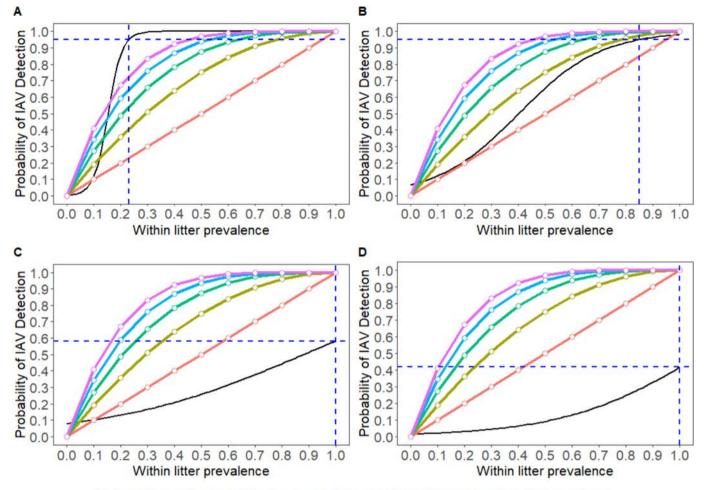


Fig. 4. The probability of IAV RNA detection is delineated according to within-litter prevalence and by sample type. A continuous solid black line denotes FOF. A dotted black line depicts udder wipes (UW). Sow nasal wipes (SNW) are represented by a solid gray line, and a long-dashed black line characterizes Drinker wipes (DW). Additionally, the red dashed line on the graph signifies the probability of IAV RNA detection at a 95% confidence level. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)



Specimen ∾ Nasal wipe 1 piglet 🗢 Nasal wipe 2 piglets 🗢 Nasal wipe 3 piglets 🗢 Nasal wipe 4 piglets ∾ Nasal wipe 5 piglets

Fig. 5. The figure portrays the Influenza A Virus (IAV) probability of detection within litter prevalence concerning the number 1 to 5 piglet nasal wipes. Fig. A illustrates the probability of IAV detection for Family Oral Fluids (FOF) and nasal wipes. In Fig. B, the probability of IAV detection is delineated for udder wipes and nasal wipes. Fig. C presents the probability of IAV detection for drinker wipes and nasal wipes. The blue dashed line in Figs. A and B represents the probability of IAV detection a 100% within-litter prevalence. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

CRediT authorship contribution statement

D.C.A. Moraes: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. P.C. Gauger: Writing – review & editing, Validation, Resources, Methodology, Investigation, Conceptualization. O.H. Osemeke: Writing – review & editing, Methodology, Formal analysis, Conceptualization. I.F. Machado: Writing – review & editing, Resources, Methodology, G. Cezar: Writing – review & editing, Resources, Methodology, Investigation. R. Paiva: Writing – review & editing, Resources. M. Mil-Homens: Writing – review & editing, Resources. M.N. Almeida: Writing – review & editing, Methodology. A. Ramirez: Writing – review & editing. G.S. Silva: Writing – review & editing, Supervision, Methodology, Investigation, Formal analysis, Data curation. D.C.L. Linhares: Writing – review & editing, Resources, Project administration, Funding acquisition, Conceptualization.

Data availability

Data will be made available on request.

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Declaration of interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Further reading

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Dr. Moraes obtained his DVM at the State University of Londrina, Brazil. In 2016, he obtained his Master's in Business Administration at ESALQ, University of Sao Paulo, Brazil. In 2020, he obtained a Master of Science at the State University. In 2022, he obtained a Master of Science at the State at Iowa State University. He worked as a swine veterinarian for 8 years in a technical and commercial position in the swine industry in Brazil. Dr. Moraes is also a Real Pork Scholar from the National Pork Board cohort that started Fall of 2023. His current research interests include the influenza A virus's ecology in the swine population, surveillance, diagnostics, and macroepidemiology.