Influenza A Virus in Swiss pig herds with respiratory disease: Seasonality and age dependence

J. Steiner[1, 2, 3], B. Voelkl[4], M. Mwanga[2, 3, 5, 6, 7], L. Oberholster[2,5], M. Licheri[2, 3, 5], M. F. Licheri[2, 5], R. Dijkman[2, 5], J.N. Kelly[2, 6, 7], H. Nathues[1, 2]

[1]Clinic for Swine, Department of Clinical Veterinary Medicine, Vetsuisse Faculty, University of Bern, Switzerland; [2]Multidisciplinary Center for Infectious Diseases, University of Bern, Switzerland; [3]Graduate School for Cellular and Biomedical Sciences, University of Bern, Switzerland; [4]Veterinary Public Health Institute, University of Bern, Switzerland; [5]Institute for Infectious Diseases, University of Bern, Switzerland; [6]Institute of Virology and Immunology, Bern and Mittelhäusern, Switzerland; [7]Department of Infectious Diseases and Pathobiology, Vetsuisse Faculty, University of Bern, Switzerland

https://doi.org/10.17236/sat00483

Eingereicht: 26.02.2026
Angenommen: 22.04.2026

Influenza-A-Virus in Schweizer Schweinebeständen mit Atemwegserkrankungen: Saisonalität und Altersabhängigkeit

Das Influenza-A-Virus (IAV) ist ein bedeutender Erreger von Atemwegserkrankungen bei Schweinen und stellt für Menschen ein zoonotisches Risiko dar. Während die Epidemiologie des IAV in Grossbetrieben bereits umfassend untersucht wurde, liegen aus der Schweiz – die durch kleine Bestände und begrenzte Importe lebender Schweine gekennzeichnet ist – bisher nur wenige Daten vor. Ziel dieser explorativen, landesweiten Querschnittsstudie war es, den Zusammenhang zwischen dem Nachweis von IAV auf Herdenebene und gemeldeten Atemwegserkrankungen in Schweinebeständen zu bewerten. Zusätzlich sollten Zusammenhänge aus den Bereichen Tierhaltung, Tiergesundheit und menschlicher Gesundheit untersucht werden.

Zwischen November 2023 und April 2025 wurden 25 Schweizer Schweinebestände, bei denen die Tierhalter Atemwegssymptome meldeten, untersucht. In jedem Bestand wurden fünf Nasenabstriche entnommen und mittels quantitativer PCR analysiert. Die Betriebsleiter füllten einen Fragebogen aus, und es wurden klinische Untersuchungen durchgeführt.

Insgesamt wurden 56 % (95 % KI: 37,1 – 73,3) der Bestände positiv auf IAV getestet, was mit Berichten aus anderen europäischen Ländern vergleichbar ist. Die geschätzte Nachweisrate innerhalb der Bestände betrug 49,6 % (95 % KI: 31,2 – 68,0). Ausbrüche von Atemwegserkrankungen im Zusammenhang mit dem Nachweis von IAV zeigten saisonale Schwankungen, wobei im Sommer keine positiven Bestände identifiziert wurden. Über alle Altersgruppen hinweg wiesen Schweine im Alter von 11–14 Wochen eine höhere Wahrscheinlichkeit für einen IAV-Nachweis auf,

Abstract

Influenza A virus (IAV) is an important respiratory pathogen in pigs and poses a zoonotic risk to humans in close contact. While IAV epidemiology has been extensively studied in large-scale production systems, data from Switzerland – characterized by small herds and limited live pig imports – remain scarce. This exploratory nationwide cross-sectional study aimed to assess the association between herd-level IAV detection and reported respiratory disease in pig herds, and to explore associations with husbandry-, animal-, and human health–related factors.

Between November 2023 and April 2025, 25 Swiss pig herds with caretaker-suspected respiratory symptoms were investigated. In each herd, five nasal swabs were collected and analyzed by quantitative PCR. Herd managers completed an interview, and clinical examinations were performed. Overall, 56 % (95 % CI: 37,1 – 73,3) of herds tested positive for IAV, comparable to reports from other European countries. The estimated intra-herd detection rate was 49,6 % (95 % CI: 31,2 – 68,0). Respiratory disease outbreaks associated with IAV detection showed indications of seasonal variation, with no positive herds identified during summer. Across age groups, pigs aged 11–14 weeks had a higher likelihood of IAV detection, with 15,79-fold increased odds (95 % CI: 1,50 – 860,4), although with considerable uncertainty.

The interpretation is limited by the small sample size, heterogeneous data, and reliance on single time-point qPCR detection. The results suggest that IAV detection in clinically apparent respiratory outbreaks may follow seasonal patterns in Swiss pig herds. Weaners and newly introduced fattening pigs may play a role in such respiratory outbreaks and could represent relevant targets for IAV surveillance in Switzerland. Continued monitoring and the implemenmit einer 15,79-fach erhöhten Wahrscheinlichkeit (95 % KI: 1,50 – 860,4), wenn auch mit erheblicher Unsicherheit.

Die Interpretation wird durch die geringe Stichprobengrösse, heterogene Daten und die Abhängigkeit vom qPCR-Nachweis zu einem einzigen Zeitpunkt eingeschränkt. Die Ergebnisse deuten darauf hin, dass der IAV-Nachweis bei klinisch offensichtlichen Ausbrüchen von Atemwegserkrankungen in Schweizer Schweinebeständen saisonalen Mustern folgen könnte. Absetzer und neu eingestellte Mastschweine könnten bei solchen Ausbrüchen eine Rolle spielen und stellen möglicherweise relevante Zielgruppen für die IAV-Überwachung in der Schweiz dar. Angesichts des zoonotischen Potenzials des Virus und seiner Auswirkungen auf die Gesundheit der Schweine sind eine fortgesetzte Überwachung und die Umsetzung geeigneter Bekämpfungsmassnahmen weiterhin wichtig.

Schlüsselwörter: Querschnittsstudie, Mastschweine, Nasenabstriche, Pan-IAV-qPCR, saisonale Atemwegsausbrüche, Schweinegrippe, Schweiz

tation of appropriate control measures remain important given the virus's zoonotic potential and impact on pig health.

Keywords: cross-sectional study, fattening pigs, nasal swabs, pan-IAV qPCR, seasonal respiratory out-breaks, swine influenza, Switzerland

Background

Influenza A viruses (IAV) are important respiratory pathogens circulating in pig populations worldwide, including Switzerland.[39] Their epidemiology has become increasingly complex due to the intensification of pig production systems and remains only partly understood. Humans in close contact with pigs, such as pig workers and veterinarians, are continuously exposed to a zoonotic risk.[12,23]

The circulation dynamics of IAV in pigs increased markedly in complexity following the 2009 H1N1 pandemic, as this lineage contributed to diversification of IAV clades in European pig herds.[11] Since then, IAV has remained widespread in pigs throughout Europe. A meta-analysis encompassing 42 studies estimated an overall seroprevalence of 58,7 %.[1] Clinical expression of IAV infection in pigs is highly heterogeneous,[16] ranging from acute, outbreak-like episodes characterized by high morbidity and rapid clinical resolution – occasionally complicated by severe respiratory signs due to secondary bacterial infections – to asymptomatic circulation with mild, intermittent respiratory signs in endemically infected herds.[29,40]

An increasingly important role has been attributed to endemic IAV circulation within intensive pig production systems.[14,28,33] Large production units, particularly those housing more than 3,000 pigs, appear to facilitate persistence of IAV once introduced into a herd.[26] In continuous farrow-to-finish production systems, suckling piglets and mother sows showed inconsistent occurrence of respiratory clinical signs and IAV detection.[2,18,33] Typically, an initial infection peak occurs shortly after weaning, followed by a period of low detection, with a second peak emerging towards the end of the weaning phase or beginning of the fattening period. In such enzootic settings, adequate assessment of herd-level infection status and intra-herd prevalence requires adapted sampling strategies. These include repeated longitudinal sampling, random batch-wise selection of animals, and the use of complementary diagnostic approaches such as serology and assessments of cellular immunity, to more comprehensively capture the complex epidemiological dynamics of IAV circulation.[33,39]

In finishing herds, IAV activity is often highest towards the end of the production cycle.[18] In such herds, even though clinical signs appear inconsistently, IAV infection appears to cause reduced growth performance and weight gain.[9] Understanding these complex circulation patterns is essential for improving IAV control strategies.

As a foundation for IAV control measures, studies have previously identified risk factors associated with IAV infection in pig herds.[7,10,19,20,22,27,36,37] Key drivers of infection include large herd sizes, elevated pig density on and around farms and contact interfaces with other mammals or avian species. Additionally, inadequate age-group segregation, absence of all-in/all-out management with downtime between production cycles, and shortcomings in overall hygiene practices and biosecurity implementation were important.

Swiss pig production is largely based on small herd sizes relative to other European countries[5], and biosecurity levels remain comparatively low.[3] Nevertheless, several major pig diseases, including Porcine Reproductive and Respiratory Syndrome[8], Enzootic Pneumonia[32] and *Actinobacillus pleuropneumoniae* – associated pleuropneumonia, have been successfully eliminated. Re-introductions have been prevented by minimal live pig imports and strict quarantine regulations.[6] These conditions may influence pathogen dynamics in Switzerland, where limited animal movements and specific production structures could shape patterns of disease circulation differently from those observed in neighboring countries.

Since 2001, IAV circulation in Swiss pigs has been monitored through a passive syndromic surveillance program coordinated by the Swiss Federal Food Safety and Veterinary Office (FSVO) and the Swiss Federal Office of Public Health (FOPH), in collaboration with one of the pig health services (SUISAG-SGD) and the University of Zürich.[15] Between 2010 and 2022, 375 of 674 investigated respiratory outbreaks (55,6 %) were IAV-positive. However, interpretation of these data is constrained by limited sampling (nasal swabs from only two coughing pigs per outbreak) and incomplete metadata. Phylogenetic analyses of partial HA sequences identified two closely related H1N1 clades (1C.2.1 and 1C.2.2) forming a distinct Swiss lineage, indicating largely isolated virus circulation in Swiss herds.[15] However, the lack of detailed epidemiological and sequencing data continues to hamper a comprehensive understanding of IAV dynamics in this population.

Accordingly, within a multidisciplinary consortium at the Multidisciplinary Center for Infectious Diseases, University of Bern, a nationwide cross-sectional study was performed in Swiss pig herds reporting respiratory disease. The aim was to investigate the association between IAV detection and respiratory disease in pig herds, in combination with husbandry-, animal-, and human-related predictors.

Methods

Study design and setting

An exploratory cross-sectional study of IAV detection in 25 herds across Switzerland was carried out. Herds were enrolled after field veterinarians and/or Swiss pig health services (SGD, QGS) reported clinical respiratory signs, with investigations conducted between November 2023 and April 2025. Participation required informed consent from herd managers, and no restrictions were imposed regarding herd size or production system. Herd-level data were obtained during a single on-site examination, followed by a telephone interview three months later. The study was authorized under Swiss national animal experiment number 35801. Ethical approval for human sampling was deemed unnecessary by the responsible cantonal ethics committees. Reporting followed the STROBE-Vet guidelines.[31]

Data collection

At each farm examination, a licensed veterinarian conducted a semi-structured interview with the herd manager, performed a clinical examination of the herd, and collected nasal swabs from pigs, preferentially selecting animals showing fever and/or apathy. Additionally, ten nasal swabs were taken from coughing pigs to exclude enzootic pneumonia in accordance with the Swiss Epizootics Act. Two further samples from the same coughing animals were obtained for the national swine influenza surveillance program.[15] These additional samples were analyzed separately and were not included in the present study.

The interview was based on a structured written questionnaire that was read aloud to the herd manager by the examiner. Items were developed based on previously published IAV risk factor studies[10,13,19,22,27,35,36] and informal consultation with two experts from neighboring European countries. The questionnaire addressed farm characteristics, biosecurity and hygiene practices, personnel and visitor management, and respiratory disease history in both pigs and herd managers. It was piloted with three herd managers, and minor revisions were made to improve clarity. The final German version is provided in Supplementary File S1. Responses were entered into an Access® (Microsoft Corporation, Redmond, USA) database. Following data entry, plausibility checks and missingness assessments were performed. A follow-up telephone call was conducted at least three months after the farm examination to evaluate post-sampling respiratory status, resolve implausible entries, and complete missing information.

Clinical herd assessments followed a standardized checklist focused on respiratory signs (Supplementary File S1, German). The entire herd was inspected, and coughing and sneezing indices were calculated for the sampled age group using established procedures.[25] Sneezing thresholds and fever cut-offs were defined based on field experience, as observed temperatures consistently exceeded published reference ranges.[34] Rectal temperatures were recorded in sampled pigs. Herds were classified as respiratory diseased if at least one of the following criteria was met: (i) *acute* – a maximum rectal temperature ≥ 40,5 °C in at least one sampled pig together with either a sneezing index ≥ 20 %/min in the affected group, or subjectively assessed apathy in ≥ 5 %; or (ii) *subacute* – a coughing index ≥ 2,5 %/min in the affected group, as previously described.[25]

The nasal sampling strategy was designed to maximize the likelihood of detecting IAV in herds experiencing reported respiratory disease outbreaks. Pigs exhibiting clinical signs consistent with acute infection – such as fever, apathy, and/or sneezing – were preferentially selected. Given the typically small herd sizes and frequent contact between age groups, sampling focused on the most severely affected animals, which was considered sufficient for reliable herd-level detection of IAV, if present. A sample size of five pigs per herd was determined using WinEpi (http://www.winepi.net/uk/index.htm), providing 95 % confidence of detecting IAV at the herd level, assuming an intra-herd prevalence of ≥ 50 %.

Animals were manually restrained and nasal swabs (FLOQSwab®; Copan, Brescia, Italy) were collected from one nostril following standard technique. Briefly, after cleaning the snout, the swab was advanced along the nasal septum in a dorso-caudal direction until resistance was felt, then rotated three times by 120°, pausing three seconds at each position.[38] Herd managers reporting respiratory symptoms were invited to voluntarily submit a self-collected nasal swab. All specimens were placed individually in NucleoProtect® medium (Macherey-Nagel, Düren, Germany), transported at ambient temperature, and stored at ≤ –20 °C until analysis.

Viral RNA extraction was performed at the Institute of Infectious Diseases, University of Bern, using the NucleoMag VET® kit (Macherey-Nagel GmbH & Co. KG, 52355 Düren, Germany) on a KingFisher Apex platform (Thermo Fisher Scientific, Waltham, MA, USA). Influenza A virus RNA was detected by a matrix gene–specific RT-qPCR using optimized reaction conditions.[17,24] Samples with crossing point (Cp) values < 38 were considered positive, consistent with previous studies using the same assay, in which this threshold was established to maintain high analytical specificity while retaining sensitivity for low viral loads.[14] Each run included a negative control with conservation medium.

Variables

All analyses were performed at herd level. Animal-level measurements (e.g., RT-qPCR results, rectal temperatures) were aggregated to generate herd-level indicators. The outcome was herd IAV status, defined as positive if at least one nasal swab yielded a Cp value < 38 in RT-qPCR.[14] Seven additional meta-variables were derived to further describe RT-qPCR findings but were not considered exposure variables. In total, 202 potential exposure variables were compiled from questionnaire data and clinical assessments. For clarity, these variables were grouped into four thematic domains:

Husbandry: herd size, production type, pig flow, hygiene practices, internal and external biosecurity, and personnel/visitor management.

Animal health: respiratory history reported by the herd manager, clinical findings recorded by the study veterinarian, and rectal temperature measurements aggregated to herd-level maximum and mean values.

Environment: housing characteristics, stable temperature, ventilation, and stocking density.

Human health: self-reported respiratory history of herd managers, employees, and household members.

Statistical methods

Exploratory statistical analyses comprised descriptive statistics on a cleaned dataset containing 168 predictors, followed by univariate association testing of six selected variables. All analyses were performed in R (version 4.4.2), with ChatGPT 5.2 used to support code development.

Descriptive statistics were generated for all variables to inform subsequent analyses. Factor levels with fewer than three observations were merged, and redundant variables, as well as those with zero variance or exclusively missing values, were removed. This resulted in 168 exposure variables and one binary outcome variable; eight outcome-related meta variables were retained for reference. Predictors of particular interest were presented in panels stratified by herd IAV status. Herd-level and intra-herd IAV detection rates were calculated and further stratified by sampled age group and production type. These descriptive results guided the selection of predictors for inferential testing.

Univariate associations were assessed between herd IAV status and the following exposures: age group of sampled pigs, season of sampling, reported reduced feed intake, reported human coughing, sneezing index in weaners and fattening pigs, and days since the caretaker first observed symptoms. For multi-level categorical variables (age group, season), Fisher's exact test was applied to the overall contingency table, followed by post hoc Fisher's exact tests for individual factor levels. Binary predictors (reduced feed intake, human coughing) were analyzed using Fisher's exact tests. Odds ratios and corresponding 95 % confidence intervals were calculated from contingency tables. The continuous sneezing index was evaluated using the Wilcoxon–Mann–Whitney test. All analyses were conducted on complete cases for each exposure–outcome comparison.

Results

In this cross-sectional study of 25 Swiss herds with respiratory disease, 176 exposure variables were descriptively evaluated in relation to herd IAV status. Visual exploration indicated potential seasonal patterns in IAV-associated respiratory outbreaks and an effect of the sampled age group. However, given the limited sample size, these observations should be interpreted with caution. Descriptive patterns of increased IAV detection related to personal hygiene measures, visitor management, and reports of acute respiratory signs were observed but did not reach statistical significance.

Figure 1: Overview of selected husbandry predictors stratified by pig herd Influenza A virus (IAV) status.
Bar plots and combined violin–box plots depict selected predictors across the following domains: (a) herd size, (b) general husbandry, (c) farrowing unit, (d) weaner unit, (e) fattening unit, and (f) biosecurity and personnel. IAV-positive herds are shown in red and IAV-negative herds in green. The y-axis represents the number of herds per level, while the x-axis indicates the categorical levels of each predictor.

Violin–box plots for herd size display the total number of pigs per herd. *Proximity to other pig herds* denotes a distance of < 1,000 m to the nearest pig herd. *Chicken close by* indicates that chickens are kept on the same farm. Variables describing stable occupation indicate whether an all-in/all-out system is practiced. *Cross-fostering farrowing stable* reflects the intensity of cross-fostering (1 = < 10 % of litters, 2 = 10–50 %, 3 = >50 %). Cleaning, disinfection, and drying variables indicate the frequency of implementation (TRUE = between batches; FALSE = less frequent; or ordinally coded as 1 = never, 2 = yearly, 3 = between batches). *Caretaker ppe stable* indicates whether herd managers use dedicated stable clothing. *Caretaker disease management indicates* whether a mask is worn when a caretaker suffers from respiratory disease. Di-chotomous variables are displayed with levels TRUE and FALSE; NA levels are shown only when present.

Descriptive data on exposures stratified by IAV outcome

Descriptive analyses demonstrated considerable heterogeneity within the study population, including substantial variation in production types and herd sizes. Differences in age-group structure and management practices influenced several variables and resulted in non-random patterns of missing data. Comprehensive descriptive statistics and the corresponding codebook are available on demand by contacting the corresponding author.

Within the husbandry domain, mean herd size was 703 ± 558 pigs, corresponding to 49 ± 37 sows or 503 ± 535 fattening pigs, depending on production type. The study population comprised 16 fattening herds, 3 farrow-to-finish operations, 2 breeding herds, and 4 integrated piglet-producing herds. The majority of IAV-positive herds were fattening units. On average, herds sourced pigs from 3,3 ± 3,1 different origins. No marked differences between IAV-positive and IAV-negative herds were observed for husbandry-related variables (Figure 1).

Overall, 64 % of herds reported implementing a quarantine protocol. Most farms (72 %) were located within 1,000 meters of another pig herd. Poultry was kept on 48 % of farms, although direct access of poultry to pig housing was reported in only 4 % of holdings.

In farrowing units, all-in-all-out (AIAO) management was applied in 67 % of herds. Cross-fostering involved < 10 % of litters in 44 % of herds, ≤ 50 % of litters in 22 %, and > 50 % of litters in 33 %. Farrowing areas were cleaned after each batch in 89 % of herds, disinfected at least annually in all herds, and a downtime of 24 hours between batches was reported by 78 %. In nursery units, AIAO was implemented in 40 % of herds, cleaning between batches in 80 %, annual disinfection in all herds, and ≥ 24 hours of downtime in 80 %. In contrast, for the fattening units, AIAO was used in only 17 % of herds, batch cleaning in 36 %, disinfection in 9 %, and ≥ 24 hours of downtime in 45 %.

Biosecurity assessment showed that 68 % of herds had outdoor access areas, with potential bird contact reported in 60 % and possible wild boar contact in 44 %. Bird access to indoor stable areas was noted in 40 % of herds. Herds had an average of 2,1 ± 0,7 caretakers. Dedicated stable clothing was used in 64 % of herds, 52 % reported handwashing before entering pig housing, 20 % indicated mask use when experiencing respiratory illness, and 16 % performed boot

Table 1. Clinical respiratory signs observed in study pig herds. Sneezing and coughing indices and herd-level rectal temperatures (maximum and mean) are pre-sented as means with 95% confidence intervals (CI), stratified by influenza A virus (IAV)-positive and IAV-negative herds as well as overall. Confidence intervals for means were calcu-lated using t-based estimates. The percentage of missing values (NA%) and the number of herds (n) are reported.

Clinical sign	Herd IAV status	n	NA %	Mean	95 % CI
Sneezing index (% of pigs/min)	Negative	11	18.2	2.722	[-0.814, 6.258]
	Positive	14	14.3	7.208	[-0.747, 15.164]
	All herds	25	16	5.286	[0.737, 9.835]
Coughing index (% of pigs/min)	Negative	11	18.2	5.322	[2.414, 8.231]
	Positive	14	14.3	5.097	[3.615, 6.579]
	All herds	25	16	5.193	[3.848, 6.538]
Mean herd level rectal temperature (°C)	Negative	11	0	40.055	[39.478, 40.631]
	Positive	14	14.3	39.975	[39.66, 40.29]
	All herds	25	8	40.013	[39.72, 40.306]
Maximum herd level rectal temperature(°C)	Negative	11	0	41.127	[39.158, 43.096]
	Positive	14	14.3	40.55	[40.049, 41.051]
	All herds	25	8	40.826	[39.929, 41.723]

Table 2. Detection of influenza A virus (IAV) at the pig herd level, intra-herd detection rate, and viral load (mean Cp). Herd counts per group are indicated. Percentages are point estimates. Proportion 95 % confidence intervals (CIs) use the Wilson score method; mean intra-herd detection 95 % CIs use percentile bootstrap (B = 10,000). Mean Cp 95 % CIs are based on Welch's two-sample t-test interval. CIs are reported as [lower, upper].

Metric	Herds	IAV positive herds	Estimate (%)	95 % CI
Herd-level IAV detection	25	14	56	[37.1, 73.3]
Intra-herd IAV detection	25	14	49.6	[31.2, 68.0]
Herd-level Cp-value	14	29	30.47	[28.342, 32.598]

disinfection. Caretaker contact with other pig herds was reported in 18 % of cases. Herds recorded a mean of 4,0 ± 2,6 cumulative visitor contact hours per 6 months. Among visitors, 28 % washed their hands upon entry, and 71 % had contact with other pig herds on the same day.

Within the animal health domain (Figure 2), most caretakers (60 %) reported that previous respiratory outbreaks occurred infrequently, whereas 24 % described a seasonal pattern and 16 % reported more regular episodes. Seasonal outbreaks were more commonly noted in IAV-positive herds. When stratified by sampling period, a greater proportion of herds tested IAV-positive during winter, while no positive herds were identified in summer. Caretaker-reported symptoms such as sneezing, nasal discharge, apathy, and dyspnea were less frequently noted in IAV-positive herds, whereas coughing, fever, and reduced feed intake were reported more often. In IAV-positive herds, sampling occurred on average 5,4 ± 1,7 days after the first observation of symptoms by the caretaker, compared to 10,4 ± 9,1 days in IAV-negative herds. During clinical examinations, apathy in weaners was rarely observed and occurred at similar frequencies across IAV-positive and negative fattening herds. Sneezing indices were higher in IAV-positive compared with IAV-negative herds, while coughing indices and rectal temperatures showed no apparent differences between groups (Table 1).

Within the environmental domain (Figure 3), measured parameters varied primarily with sampling season. Owing to the limited sample size, meaningful differences were apparent only in fattening units. Because IAV-positive herds were less common during summer, ventilation conditions typically associated with warmer months—higher ambient temperatures and increased airflow—were observed predominantly in IAV-negative herds.

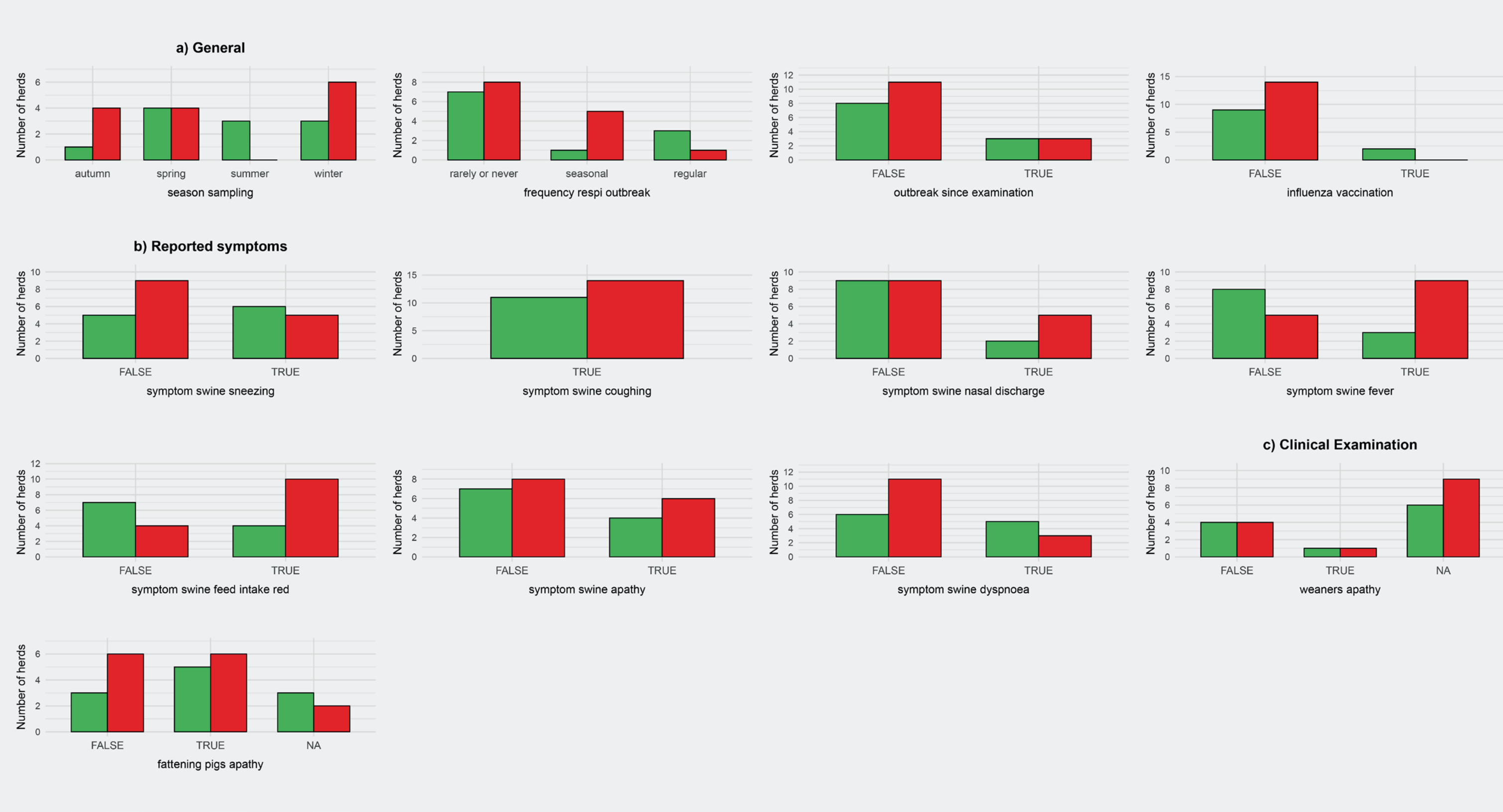

Figure 2: Overview of animal health predictors stratified by pig herd Influenza A virus (IAV) status.

Bar plots depict selected predictors across the domains of (a) general herd description, (b) clinical symptoms reported by the herd manager, and (c) clinical signs detected during examination. IAV-positive herds are shown in red and IAV-negative herds in green. The y-axis represents the number of herds per level, and the x-axis indicates the categorical levels of each predictor.

Frequency of respiratory outbreaks describes the reported frequency of respiratory disease outbreaks within the herd. *Outbreak since examination* indicates whether a respiratory disease outbreak occurred within three months after sampling. *Symptom reduced feed intake swine* indicates whether pigs were reported to have reduced feed intake. NA levels are shown only when present.

In the human health domain, respiratory symptoms among caretakers or close contacts were reported on 7 of 25 farms. These symptoms occurred less frequently in summer and followed a seasonal pattern similar to that observed in pigs.

Descriptive data on IAV detection

Overall, 56 % (14/25) of herds were IAV-positive, with a mean intra-herd detection rate of 49,6 % among positive herds (Table 2). Stratified by age group, pigs aged 11–14 weeks exhibited the highest herd-level and intra-herd detection rates, while no IAV was detected in suckling piglets (1–8 weeks) or in fatteners aged 15–18 weeks (Table 3). Detection by production type was greatest in herds containing fattening pigs (fattening and farrow-to-finish operations), although sample sizes for other production systems were limited (Table 4). Among human participants, IAV was detected in 1 of 7 symptomatic herd managers who provided nasal swabs.

Univariate association analyses of selected predictors

Univariate associations between selected exposure variables and herd IAV status were assessed, with results summarized in Table 5. Age group sampled was significantly associated with IAV detection ($p < 0,05$) yet the wide confidence intervals indicate uncertainty of this association. In particular, herds in which fattening pigs aged 11–14 weeks were sampled showed a strong association with IAV positivity, with an odds ratio (OR) of 15.79 (95 % CI: 1.50 – 860.4). Due to the small sample size, the confidence interval indicates imprecision, and this estimate should therefore be interpreted with caution. Sampling during summer approached, but did not reach, the threshold for statistical significance ($p = 0.07$). No significant associations were observed for the remaining predictors, including frequency of respiratory disease outbreaks, reported reduced feed intake or fever, the sneezing index in weaners and fattening pigs, and days since the caretaker first observed symptoms.

Discussion

This exploratory cross-sectional study assessed herd-level IAV detection in Swiss pig herds reporting respiratory disease and evaluated potential associated factors, suggesting potential age-related trends and seasonal patterns. Influenza A virus was detected in 56 % (14/25) of herds. In exploratory analyses, pigs aged 11–14 weeks showed a potential association with higher IAV detection, with an approximately 15.79-fold increase in odds (95 % CI: 1.50 – 860.4) compared with other sampled age groups.

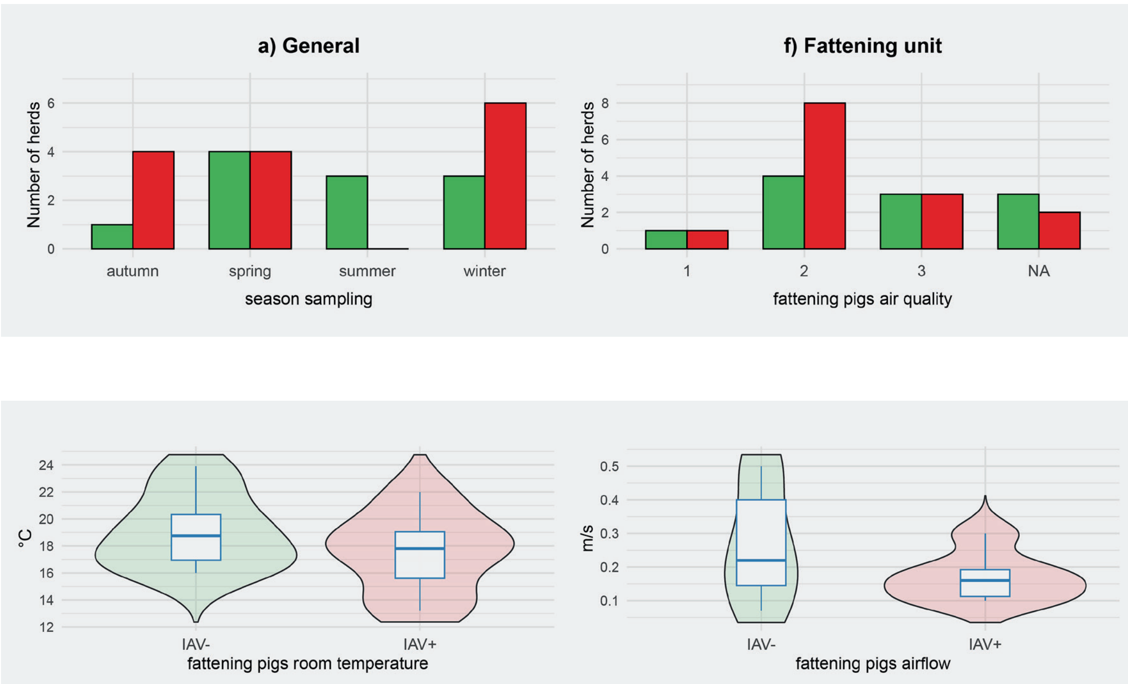

Figure 3: Overview of environmental predictors stratified by pig herd Influenza A virus (IAV)status.
Bar plots and combined violin–box plots depict selected environmental predictors in the fattening unit, and season of sampling as reference. IAV-positive herds are shown in red and IAV-negative herds in green. The y-axis represents the number of herds or the absolute ambient tem-perature (°C) and maximum airflow velocity (m/s). The x-axis indicates the season during which herds were examined or stratifies herds by IAV status.

This exploratory study offers preliminary insight into the largely uncharacterized epidemiology of IAV in Swiss pig herds. The questionnaire was developed to capture a broad spectrum of potential risk factors, enabling a structured evaluation of husbandry-, animal-, and human-related exposures, complemented by clinical assessments of pigs. In addition, the absence of strict inclusion or exclusion criteria allowed exploration of potential effects of different production systems.

Several limitations should be considered when interpreting these findings. The dataset was heterogeneous and characterized by substantial non-random missingness. Combined with the small sample size and restriction to herds with respiratory disease, the study is limited to assessing relatively strong associations in clinically apparent settings. Accordingly, results should be interpreted as exploratory and warrant confirmation in larger, adequately powered studies, including clinically inapparent herds and specifically addressing enzootic IAV circulation.

Information bias may also have affected the findings. The questionnaire underwent only limited pilot testing, and data entry was not independently verified. Farmer responses may further have been influenced by reporting constraints or reluctance to disclose potential shortcomings. Additionally, reliance on caretaker reports did not always allow sampling at the onset of clinical signs, which may have reduced the sensitivity of IAV detection. Furthermore, herd IAV status was defined solely by RT-qPCR results from nasal swabs collected at a single time point. The analyses therefore reflect associations with viral detection rather than confirmed infection status or sustained herd-level circulation.

The herd-level IAV detection rate was 56% (95% CI: 37.1 – 73.3), with an intra-herd detection rate of 49,6% (95% CI: 31.2 – 68.0). A European-wide study identified IAV in 56,6% of herds and 30,5% of samples. However, as the present study was optimized for detection rather than estimation of intra-herd prevalence – as reflected by the wide confidence intervals – these intra-herd detection rates are therefore not directly comparable.[11] Despite differences in herd structure, these figures suggest that IAV in Swiss pig herds with respiratory disease may occur at similar frequencies to those in neighboring European countries.

Biosecurity and hygiene standards in Switzerland are considered lower than the European average. However, respiratory health in Swiss pig herds benefits from the absence of several major endemic pathogens present elsewhere in Europe, and herd sizes are comparatively small, which may partly compensate for potential management-related shortcomings.[3] Herds included in this study were generally small and frequently kept additional livestock species. Quarantine procedures for newly introduced animals were not consistently applied. Moreover, a substantial proportion of farms (74%)

Table 3. Detection of influenza A virus (IAV) by age group of sampled pigs. Estimates represent the percentage of herds testing IAV-positive, with 95% confidence intervals (CI) cal-culated using the Wilson score method. Mean intra-herd detection rates and corresponding 95% CIs were estimated using percentile bootstrap resampling (B = 10,000). For each age group, the number of sampled herds and IAV-positive herds is reported. Confidence intervals are shown as [lower, upper]. "woa" denotes weeks of age.

Age group (woa)	Herds	IAV positive herds	Estimate (%)	95% CI	Intra-herd detection	95% CI
Suckling piglets (1–8)	2	0	0	[0.0, 65.8]	0	[0.0, 0.0]
Weaners (4–10)	7	3	42.9	[15.8, 75.0]	40	[11.4, 74.4]
Fatteners (11–14)	10	9	90	[59.6, 98.2]	76	[52.0, 94.0]
Fatteners (15–18)	3	0	0	[0.0, 56.1]	0	[0.0, 0.0]
Fatteners (≥19)	3	2	66.7	[20.8, 93.9]	66.7	[0.0, 100.0]

Table 4. Detection of influenza A virus (IAV) across production types. Estimates represent the percentage of herds testing IAV-positive, with 95% confidence intervals (CI) calculated us-ing the Wilson score method. Mean intra-herd detection rates and corresponding 95% CIs were estimated using percentile bootstrap resampling (B = 10,000). For each production type, the number of sampled herds and IAV-positive herds is reported. Confidence intervals are shown as [lower, upper].

Production Type	Herds	IAV positive	Estimate (%)	95% CI	Intra-herd detection	95% CI
Fattening herd	16	10	62.5	[38.6, 81.5]	53.8	[30.0, 76.2]
Farrow to finish herd	3	2	66.7	[20.8, 93.9]	66.7	[0.0, 100.0]
Breeding herd	2	0	0	[0.0, 65.8]	0	[0.0, 0.0]
Integrated piglet production	4	2	50	[15.0, 85.0]	45	[0.0, 90.0]

provided outdoor access, creating opportunities for contact with birds and wild boars. Hygiene practices among caretakers and visitors appeared suboptimal compared with European standards, reflected by limited implementation of hygiene locks, inconsistent use of dedicated clothing, and insufficient downtime following pig contact.[4,21,30] Although most herds reported using all-in/all-out management, implementation was notably weaker in fattening units. Cleaning routines and downtime between batches were broadly comparable to those described in other European settings, whereas disinfection was infrequently performed.[21] These patterns did not differ between IAV-positive and IAV-negative herds and therefore did not reveal specific risk factors; however, they highlight opportunities to strengthen overall biosecurity and preventive disease management.

Animal health findings suggested a possible seasonal occurrence of IAV in herds with clinical respiratory disease and a potential association with IAV detection in newly introduced pigs in fattening herds. Seasonal respiratory disease was more frequently reported in IAV-positive than in IAV-negative herds, and no IAV-positive herds were identified during the summer; however, these differences were not statistically significant. Across age groups, weaners and fattening pigs aged 11–14 weeks showed a potential increase in IAV detection, although this observation should be interpreted cautiously given the wide confidence intervals. Similar infection peaks towards the end of the nursery phase have been described in enzootically affected herds.[33] As herd managers predominantly reported seasonal patterns of respiratory disease, this may indicate that IAV detection in outbreak settings is influenced by seasonal factors.[39] However, concurrent secondary infections cannot be excluded as contributing factors. Unlike findings from Dutch finishing herds, peaks later in the fattening period were not observed.[18] Rather, the observed patterns were more consistent with farrow-to-finish systems. Weaners may have contributed to virus introduction into fattening units. In contrast, detection immediately after weaning occurred but was not a dominant feature. However, the wide confidence intervals prevent ruling out that these pigs may also play a major role.

Caretaker-reported clinical signs showed only weak associations with IAV detection. Apathy, fever, and reduced feed intake were reported somewhat more frequently in IAV-positive herds, whereas dyspnea was noted less often. Sneezing

Table 5. Univariate associations between selected predictors and herd influenza A virus (IAV) status. For categorical predictors, associations were assessed using Fisher's exact test and are reported as odds ratios (OR) with 95% confidence intervals (CI). Continuous variables were compared using the Wilcoxon–Mann–Whitney test. The number of herds included in each analysis (n) is indicated. Confidence intervals are reported as [lower, upper]. Asterisks (*) de-note statistically significant associations ($p < 0.05$).

Predictor	Level	n	Test	p-value	OR	95% CI
Season of sampling	All	25	Fisher exact	0.17		
	Winter	25	Fisher exact	0.68	1.95	[0.283, 16.447]
	Spring	25	Fisher exact	1.00	0.71	[0.094, 5.273]
	Summer	25	Fisher exact	0.07	0.00	[0.000, 1.759]
	Autumn	25	Fisher exact	0.34	3.80	[0.302, 216.024]
Age group	**All**	**25**	**Fisher exact**	**0.01***		
	Suckling piglets (1–8)	25	Fisher exact	0.18	0.00	[0.000, 4.082]
	Weaners (4–10)	25	Fisher exact	0.66	0.49	[0.054, 3.914]
	Fatteners (11–14)	**25**	**Fisher exact**	**0.01***	**15.79**	**[1.496, 860.365]**
	Fatteners (15–18)	25	Fisher exact	0.07	0.00	[0.000, 1.759]
	Fatteners (≥19)	25	Fisher exact	1.00	1.63	[0.074, 107.937]
Frequency of respiratory disease outbreaks	All	25	Fisher exact	0.23		
	rarely or never	25	Fisher exact	1.00	0.77	[0.109, 5.007]
	seasonal	25	Fisher exact	0.18	5.21	[0.454, 287.980]
	regular	25	Fisher exact	0.29	0.22	[0.004, 3.268]
Symptom reduced feed intake		25	Fisher exact	0.12	4.10	[0.623, 32.876]
Symptom fever		25	Fisher exact	0.11	4.5	[0.670, 39.344]
Sneezing index in weaners and fattening pigs		21	Wilcoxon Mann–Whitney	0.15		

and nasal discharge appeared to be poor indicators, likely because they are not perceived as clinically relevant by farmers, while coughing was reported in all herds and therefore lacked specificity. Clinical examinations (Table 1) were consistent with these findings, showing higher sneezing indices in IAV-positive herds, whereas coughing indices, rectal temperatures, and apathy did not differ between groups. Although these differences were not statistically significant, the overall pattern suggests that nasal swab sampling is most sensitive during the acute phase of infection, in line with current diagnostic recommendations.[39]

Seasonal variation in IAV detection among herds with respiratory disease likely affected associations with environmental predictors. During the summer, fewer herds tested IAV positive. Consequently, stable conditions typical of summer, such as higher ambient temperatures and increased ventilation rates, were therefore less common in IAV-positive herds. Therefore, no conclusions can be drawn regarding the effect of these factors on IAV detection. Seasonal patterns may also have influenced the relationship between IAV detection and influenza-like symptoms reported by caretakers in themselves. Concurrent IAV detection in pigs and their caretaker was documented only once. In the remaining cases, winter climate conditions may have contributed to concurrent but independent respiratory disease episodes in pigs and caretakers.

Conclusion

Influenza A virus was detected in Swiss pig herds with reported respiratory disease in this exploratory study at frequencies comparable to those reported in neighboring European countries. Smaller herd sizes and favorable respiratory health status in Switzerland may partly compensate for lower biosecurity and hygiene standards. Respiratory disease outbreaks associated with IAV may show seasonal patterns, with weaners and recently purchased fattening pigs potentially playing a relevant role. When nasal swabs are used for IAV detection, sampling should target time points when caretakers report clinical signs indicative of the acute phase of infection. Given the zoonotic risk of IAV and its impact on pig health and performance, implementation of targeted control measures in Swiss pig herds is warranted. Future studies should monitor herd-level IAV circulation longitudinally and aim to confirm husbandry-related risk factors in larger study populations.

Acknowledgments

We thank the pig health service teams of SUISAG-SGD and QGS, the collaborating field veterinarians, and the staff of the Swine Clinic, Vetsuisse Faculty, University of Bern, for their valuable support. We also acknowledge the Experimental Virology group at the Institute of Infectious Diseases (IFIK) and the Institute of Virology and Immunology (IVI) for their technical assistance.

ChatGPT (version 5.2, OpenAI) was used to support manuscript preparation and to assist with development of the R scripts for statistical analyses.

This study was supported by grants from the Multidisciplinary Center for Infectious Diseases (MCID), University of Bern, Switzerland, and the Swiss National Science Foundation (IZCOZ0_220329).

Le virus Influenza A dans les troupeaux porcins suisses atteints de maladies respiratoires: saisonnalité et dépendance à l’âge

Le virus Influenza A (IAV) est un agent pathogène respiratoire important chez les porcs ; il présente un risque zoonotique pour les humains en contact étroit avec eux. Alors que l’épidémiologie de l’IAV a fait l’objet d’études approfondies dans les systèmes de production à grande échelle, les données provenant de Suisse – caractérisée par de petites exploitations et des importations limitées de porcs vivants – restent rares. Cette étude transversale exploratoire à l’échelle nationale visait à évaluer le lien entre la détection de l’IAV au niveau du cheptel et les maladies respiratoires signalées dans les élevages porcins ainsi qu’à explorer les associations avec des facteurs liés à l’élevage, à la santé animale et à la santé humaine.

Virus dell’influenza A negli allevamenti suini svizzeri con patologie respiratorie: stagionalità e dipendenza dall’età

Il virus dell’influenza A (IAV) è un importante agente eziologico delle malattie respiratorie nei suini e rappresenta un rischio zoonotico per l’uomo. Sebbene l’epidemiologia dell’IAV negli allevamenti di grandi dimensioni sia già stata ampiamente studiata, in Svizzera sono finora disponibili pochi dati, visto che è caratterizzata da allevamenti di piccole dimensioni e da importazioni limitate di suini vivi.

L’obiettivo di questo studio trasversale esplorativo condotto a livello nazionale era di valutare l’associazione tra il rilevamento dell’IAV a livello di allevamento e le patologie respiratorie segnalate negli allevamenti suini. Sono state inoltre

Entre novembre 2023 et avril 2025, 25 élevages porcins suisses dans lesquels les éleveurs soupçonnaient la présence de symptômes respiratoires ont fait l'objet d'une enquête. Dans chaque élevage, cinq prélèvements nasaux ont été effectués et analysés par PCR quantitative. Les responsables ont répondu à un questionnaire et des examens cliniques ont été réalisés.

Dans l'ensemble, 56 % (IC à 95%: 37,1 – 73,3) des élevages se sont révélés positifs au virus Influenza A (IAV), un résultat comparable aux rapports d'autres pays européens. Le taux de détection intra-troupeau estimé était de 49,6 % (IC à 95%: 31,2 – 68,0).

Les foyers de maladies respiratoires associés à la détection du virus Influenza A (IAV) ont montré des signes de variation saisonnière, aucun cheptel positif n'ayant été identifié pendant l'été. Parmi les différentes tranches d'âge, les porcs âgés de 11 à 14 semaines présentaient une probabilité plus élevée de détection de l'IAV, avec une vraisemblance multipliée par 15,79 (IC à 95%: 1,50 – 860,4), bien qu'avec une incertitude considérable.

L'interprétation est limitée par la petite taille de l'échantillon, l'hétérogénéité des données et le recours à une détection par qPCR à un seul moment.

Les résultats suggèrent que la détection du virus Influenza A (IAV) lors de foyers respiratoires cliniquement apparents pourrait suivre des schémas saisonniers dans les troupeaux de porcs suisses. Les porcelets sevrés et les porcs d'engraissement nouvellement introduits pourraient jouer un rôle dans ces foyers respiratoires et constituer des cibles pertinentes pour la surveillance de l'IAV en Suisse.

Une surveillance continue et la mise en œuvre de mesures de contrôle appropriées restent importantes compte tenu du potentiel zoonotique du virus et de son impact sur la santé porcine.

Mots clés: étude transversale, porcs d'engraissement, prélèvements nasaux, pan-IAV qPCR, épidémies respiratoires saisonnières, grippe porcine, Suisse

esaminate possibili associazioni relative alla gestione degli animali, alla salute animale e alla salute umana.

Tra novembre 2023 e aprile 2025 sono stati esaminati 25 allevamenti suini svizzeri nei quali gli allevatori sospettavano la presenza di sintomi respiratori. In ciascun allevamento sono stati raccolti cinque tamponi nasali, successivamente analizzati mediante PCR quantitativa. I responsabili degli allevamenti hanno compilato un questionario e sono stati effettuati esami clinici.

Complessivamente, il 56 % degli allevamenti è risultato positivo all'IAV (IC 95 %: 37,1–73,3), un dato paragonabile a quanto riportato in altri Paesi europei. Il tasso stimato di rilevamento all'interno degli allevamenti è stato del 49,6 % (IC 95 %: 31,2–68,0).

I focolai di malattia respiratoria associati al rilevamento dell'IAV hanno mostrato variazioni stagionali e durante l'estate non è stato identificato alcun allevamento positivo. Considerando tutte le fasce d'età, i suini di età compresa tra 11 e 14 settimane presentavano una maggiore probabilità di risultare positivi all'IAV, con una probabilità 15,79 volte superiore (IC 95 %: 1,50–860,4), sebbene con un notevole grado di incertezza.

L'interpretazione dei risultati è limitata dalle ridotte dimensioni del campione, dall'eterogeneità dei dati e dalla dipendenza dal rilevamento mediante qPCR effettuato in un unico momento.

I risultati suggeriscono che il rilevamento dell'IAV durante focolai respiratori clinicamente evidenti negli allevamenti suini svizzeri potrebbe seguire un andamento stagionale. I suinetti svezzati e i suini da ingrasso di recente introduzione potrebbero svolgere un ruolo in tali focolai respiratori e rappresentare potenziali gruppi bersaglio rilevanti per la sorveglianza dell'IAV in Svizzera.

Considerato il potenziale zoonotico del virus e il suo impatto sulla salute dei suini, rimangono importanti il proseguimento della sorveglianza e l'attuazione di adeguate misure di controllo.

Parole chiave: Studio trasversale, suini da ingrasso, tamponi nasali, qPCR pan-IAV, focolai respiratori stagionali, influenza suina, Svizzera

Literaturnachweis

[1] Baudon E, Peyre M, Peiris M, Cowling BJ. 2017. Epidemiological features of influenza circulation in swine populations: a systematic review and meta-analysis. PLoS One. 12(6).

[2] Bhatta TR, et al. 2020. Infection dynamics of swine influenza virus in a Danish pig herd reveals recurrent infections with different variants of the H1N2 swine influenza A virus subtype. Viruses. 12(9).

[3] Biebaut E, et al. 2025. Large heterogeneity in biosecurity legislation in intensive pig production across Europe. Prev Vet Med. 237:106439.

[4] Boklund A, Alban L, Mortensen S, Houe H. 2004. Biosecurity in 116 Danish fattening swine herds: descriptive results and factor analysis. Prev Vet Med. 66(1–4):49–62.

[5] Bundesamt für Statistik. 2025. Landwirtschaftliche Strukturerhebung 2024.

[6] Bundesamt für Zoll und Grenzsicherheit (BAZG). 2025. Swiss-Impex.

[7] Ciuoderis-Aponte K, et al. 2022. Correction to: farm management practices, biosecurity and influenza A virus detection in swine farms: a comprehensive study in Colombia. Porcine Health Manag. 8(1):45.

[8] Corbellini LG, et al. 2006. Analysis of national serological surveys for the documentation of freedom from porcine reproductive and respiratory syndrome in Switzerland. Vet Microbiol. 118(3–4):267–273.

[9] Er C, et al. 2014. Adverse effects of influenza A(H1N1) pdm09 virus infection on growth performance of Norwegian pigs: a longitudinal study at a boar testing station. BMC Vet Res. 10(1):1–14.

[10] Fablet C, et al. 2013. Different herd-level factors associated with H1N1 or H1N2 influenza virus infections in fattening pigs. Prev Vet Med. 112(3–4):257–265.

[11] Henritzi D, et al. 2020. Surveillance of European domestic pig populations identifies an emerging reservoir of potentially zoonotic swine influenza A viruses. Cell Host Microbe. 28(4):614–627.

[12] Kessler S, et al. 2021. Influenza A viruses and zoonotic events—are we creating our own reservoirs? Viruses. 13(11):2250.

[13] Laanen M, et al. 2010. Bioveiligheid op varkensbedrijven: ontwikkeling van een online scoresysteem en de resultaten van de eerste 99 deelnemende bedrijven. Vlaams Diergeneeskd Tijdschr. 79(4):302–306.

[14] Lagan P, et al. 2024. Swine influenza A virus infection dynamics and evolution in intensive pig production systems. Virus Evol. 10(1).

[15] Lechmann J, et al. 2025. The Swiss national program for the surveillance of influenza A viruses in pigs and humans: genetic variability and zoonotic transmissions from 2010–2022. Schweiz Arch Tierheilkd. 167(11):600–616.

[16] Li Y, Robertson I. 2021. The epidemiology of swine influenza. Anim Dis. 1(1):21.

[17] Licheri M, et al. 2025. Optimized high-throughput whole-genome sequencing workflow for surveillance of influenza A virus. Genome Med. 17(1):103.

[18] Loeffen WLA, et al. 2009. Population dynamics of swine influenza virus in farrow-to-finish and specialised finishing herds in the Netherlands. Vet Microbiol. 137(1–2):45–50.

[19] López-Soria S, et al. 2010. Selected swine viral pathogens in indoor pigs in Spain: seroprevalence and farm-level characteristics. Transbound Emerg Dis. 57(3):171–179.

[20] Maes D, et al. 2000. Herd factors associated with the seroprevalences of four major respiratory pathogens in slaughter pigs from farrow-to-finish pig herds. Vet Res. 31(3):313–327.

[21] Makovska I, et al. 2024. Assessment of cleaning and disinfection practices on pig farms across ten European countries. Animals. 14(4):593.

[22] Mastin A, et al. 2011. Prevalence and risk factors for swine influenza virus infection in the English pig population. PLoS Curr. 3:RRN1209.

[23] Myers KP, et al. 2006. Are swine workers in the United States at increased risk of infection with zoonotic influenza virus? Clin Infect Dis. 42(1):14–20.

[24] Nagy A, et al. 2021. A universal RT-qPCR assay for One Health detection of influenza A viruses. PLoS One. 16(1):e0244669.

[25] Nathues H, et al. 2012. Value of the clinical examination in diagnosing enzootic pneumonia in fattening pigs. Vet J. 193(2):443–447.

[26] Pitzer VE, et al. 2016. High turnover drives prolonged persistence of influenza in managed pig herds. J R Soc Interface. 13(119).

[27] Poljak Z, et al. 2008. Prevalence of and risk factors for influenza in southern Ontario swine herds in 2001 and 2003. Can J Vet Res. 72(1):7–17.

[28] Rose N, et al. 2013. Dynamics of influenza A virus infections in permanently infected pig farms: evidence of recurrent infections, circulation of several swine influenza viruses and reassortment events. Vet Res. 44(1):72.

[29] Saade G, et al. 2020. Coinfections and their molecular consequences in the porcine respiratory tract. Vet Res. 51(1):1–19.

[30] Sahlström L, Virtanen T, Kyyrö J, Lyytikäinen T. 2014. Biosecurity on Finnish cattle, pig and sheep farms: results from a questionnaire. Prev Vet Med. 117(1):59–67.

[31] Sargeant JM, et al. 2016. Methods and processes of developing the STROBE-Vet statement. Prev Vet Med. 134:188–196.

[32] Scalisi N, et al. 2022. Seroprevalence of Mycoplasma hyopneumoniae in sows fifteen years after impl ementation of a control programme in Switzerland. Vet Microbiol. 270:109455.

[33] Schmies K, et al. 2024. Dynamics of swine influenza virus infection in weaned piglets in enzootically infected herds. Porcine Health Manag. 10(1).

[34] Sipos W, Wiener S, Entenfellner F, Sipos S. 2013. Physiological changes of rectal temperature, pulse rate and respiratory rate of pigs at different ages. Wien Tierarztl Monatsschr. 100.

[35] Stärk KDC. 2000. Epidemiological investigation of environmental risk factors on respiratory diseases in swine: a literature review. Vet J. 159(1):37–56.

[36] Suriya R, et al. 2008. Seroprevalence and risk factors for influenza A viruses in pigs in Peninsular Malaysia. Zoonoses Public Health. 55(7):342–351.

[37] Takemae N, et al. 2016. Effect of herd size on subclinical infection of swine in Vietnam with influenza A viruses. BMC Vet Res. 12(1):227.

[38] ThermoFisher Scientific, Nathues H. 2013. Guidelines for taking diagnostic samples from pigs: nasal swabs.

[39] Vincent AL, Baker KL, Van Reeth K. 2025. Influenza viruses. In: Zimmerman JJ, et al., editors. Diseases of swine. Wiley. p. 645–664.

[40] White M. 2011. Porcine respiratory disease complex (PRDC). Livestock. 16(2):40–42.

Korrespondenzadresse

Heiko Nathues
Universität Bern, Vetsuisse-Fakultät, Department für klinische Veterinärmedizin, Nutztierklinik & Multidisciplinary Center for Infectious Diseases (MCID)
Bremgartenstrasse 109 a,
CH-3012 Bern
Telefon: +41 75 500 0804
E-Mail: heiko.nathues@unibe.ch