



ORIGINAL ARTICLE

SEROLOGICAL AND EPIZOOTIC DYNAMICS OF SWINE INFLUENZA A IN INDUSTRIAL SWINE FARMS OF UKRAINE (2021–2024)**Anatolii Kovalenko^{1*}, Jana Mojžišová Vaščinec¹, Vasil Koziiy², Nataliia Kozii², Boris Vojtek¹, Anna Ondrejková¹, Silvia Kapľavka¹, Ľuboš Korytár¹, Marián Prokeš¹, Monika Drážovská¹**¹Department of Epizootiology, Parasitology and Protection of One Health, University of Veterinary Medicine and Pharmacy in Košice, Košice, Slovakia; ²Bila Tserkva National Agrarian University, School of Veterinary Medicine, Bila Tserkva, Kiev region, Ukraine OPEN ACCESS*Correspondence: anatolii.kovalenko@uvlf.sk

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Ethical considerations: When reporting experiments on animals Observation of the ARRIVE guidelines 2.0: Updated guidelines for reporting animal research, published on July 14, 2020 (DOI: 10.1371/journal.pbio.3000410), is applied. The authors ensure that all procedures were performed in compliance with the guidelines for animal care of their institutions or with national/international guidelines.

ABSTRACT

Swine Influenza A virus (SIV-A) is a significant zoonotic pathogen with the potential to cause pandemics. In Ukraine, surveillance is crucial due to the risk of interspecies transmission between pigs and humans. SIV-A circulates within swine populations and undergoes frequent genetic changes, increasing its variability and pathogenicity. In this study, we monitored the presence of SIV-A on 92 pig farms in the Lviv and Kyiv regions during the period 2021–2024. Serological testing was performed using the IDEXX Influenza A Virus Ab Test Kit, revealing 24 seropositive farms, with a decreasing trend observed over the years. Additionally, 422 pigs from seropositive farms were tested for SIV-A using real-time RT-PCR, and the virus was detected in 59 individuals. These results suggest that while epizootic control measures were largely effective, the virus continues to circulate among susceptible animals. Continuous surveillance and timely intervention remain essential for detecting emerging subtypes and preventing potential outbreaks.

Keywords: influenza A virus; pigs; prevalence; Ukraine**INTRODUCTION**

Swine flu, or porcine influenza, is a respiratory viral infection caused by the swine influenza A virus (SIV-A) that predominantly affects pigs. This infection is important both for humans and for animals.

SIV-A was first isolated in 1930; since then, it has become endemic in pigs worldwide. The major challenge

of the disease is the big number of different subtypes and genotypes of the virus circulating among pigs worldwide [1]. The other scientists [2–5] emphasize the potential pandemic risk of circulating SIV-A. Mon et al. [6] found that the genetic diversity of SIV-A possesses zoonotic and reverse zoonotic potentials. Even though only a few hundred confirmed human cases caused by SIV-A have been

reported, Abdelwhab et al. [7] claim that a high vigilance is needed to prevent the next pandemic caused by animal influenza viruses.

The study done by Meng et al. [8] demonstrates that SIV-A may become pathogenic and transmissible by acquiring key mutations in acidic polymerase. The authors especially emphasize the possible pathogenicity development in different species of animals.

Surveillance of occupational exposure among persons working with pigs showed that up to 20.5% of humans may become seropositive, indicating the acquired human infectivity of SIV-A [9]. The authors further claim that such high infectivity enhances the possibility for viruses to acquire humans' pathogenicity and raises concerns for the possible pandemic effect.

The lack of attention to swine influenza makes it possible for the animals at exhibitions and fairs to be the spreading source of the virus. There were identified deficiencies of routine event biosecurity that may have important public and animal health consequences [10, 11]. Furthermore, the complexity of viral detection and control in exhibition swine indicates that the viruses are likely to continually re-emerge, presenting threats to human and animal health [12].

The global monitoring of swine influenza SIV-A is important for human and animal health and represents a vital 'One Health' challenge for human and veterinary medicine [13, 14]. Yet, the collective knowledge regarding the occurrence of influenza among swine is still incomplete. It is mainly due to lack and inconsistency of surveillance data on SIV-A prevalence among the world's swine populations [15]. Monitoring the viral pathogens is important for disease control and is critical from a preventive standpoint [16].

With this, the main aim of our article was to estimate the viral RNA and seropositivity prevalence of SIV-A on industrial pig farms in Ukraine.

MATERIALS AND METHODS

The study period encompasses four years (2021–2024). The pig's samples (nasal swabs and serum) came from 92 farms from the Lviv and Kyiv regions, with a total of 422 animals examined.

For the antibody detection, the IDEXX Influenza A Virus Ab Test Kit (IDEXX, USA), a blocking ELISA test that recognizes serum antibodies to any influenza A subtype of

swine influenza virus, was used. The test was performed according to the manufacturer's instructions.

For virus detection, total RNA was extracted from samples using the MagMAX Core Nucleic Acid Purification Kit (ThermoFisher Scientific, Applied Biosystems, USA) according to the manufacturer's instructions. The presence of the Influenza A virus was detected using the Kylt® Influenza A Real-Time RT-PCR Kit (Kylt®, AniCon Labor GmbH, Germany). The assay was performed following the protocol provided by the manufacturer. Reactions were run on a QuantStudio™ 5 Real-Time PCR System (Thermo Fisher Scientific, USA). Each reaction included an internal control provided with the Kylt® kit to validate RNA extraction and PCR performance.

RESULTS

In 2021, serological positivity for SIV-A was detected in 41.2% (7 seropositive farms from 17 industrial tested farms). In 2022 and 2023, the rate decreased from 26.1% (6/23) to 21.8% (7/32). In 2024, seropositivity reached 20.0% in 20 farms. Trend line of serological testing of farms among years is shown in Figure 1.

Results of virus detection are shown in Table 1. In 2021, 103 clinical samples from seven farms were analyzed, with 16.5% testing positive for SIV-A. In subsequent years, the prevalence of viral RNA detection in clinical samples remained high: 15.9% in 2022, 13.7% in 2023, and 10.2% in 2024. On average, 14% of tested samples from affected farms were positive for viral RNA, demonstrating ongoing circulation and persistence of the virus.

DISCUSSION

Analysis of data from 92 industrial pig farms over the study period confirmed a decreasing trend in the occurrence of the influenza A virus, indicating an intensification of epizootic activity during the monitoring years. Nevertheless, given that the infection rate ranged from 20% to 41.2%, our findings indicate sustained transmission of the virus among susceptible individuals. The persistent detection of viral RNA (10.2–16%) among seropositive animals underscores the heightened epizootic risk and facilitates rapid reinfection cycles within affected farms.

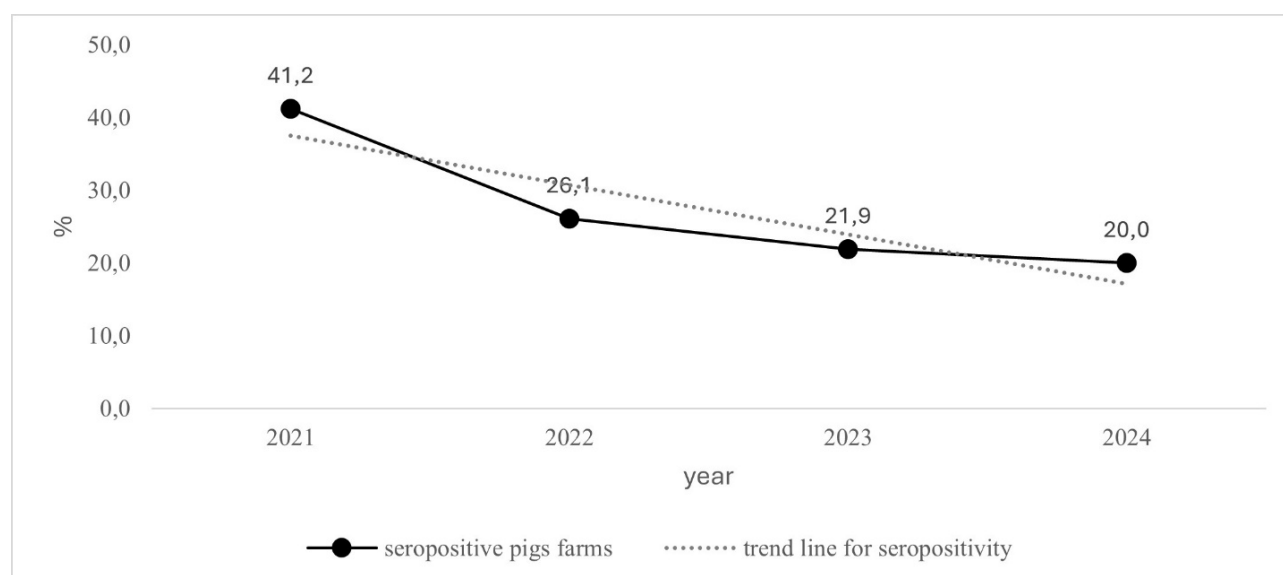


Fig. 1. Dynamics of detection of antibodies to the influenza A virus on industrial pig farms of Ukraine

Influenza viruses remain important pathogens affecting human and animal health. They have relatively low pathogenicity for swine, but in conjunction with other pathogens, the outcome can be unfavorable or even mortal [17]. It is also known that SIV-A circulates in swine populations worldwide, and has the ability for reverse zoonosis from humans to swine, and for interspecies transmission [8, 13, 14]. It was also clearly shown the rising historical drug resistance level of SIV-A around the world that is mediated by the evolution of adamantanes-resistant mutations [18]. The authors also emphasize the importance of properly monitoring the adamantanes' susceptibility of SIV-A and the necessity to draw attention to the evolution of drug-resistant H1N1 influenza variants.

Swine influenza is considered one of the most important pathogens of swine respiratory disease in Europe. This infection is primarily caused by H1N1, H1N2, and H3N2 influenza A viruses that have remained endemic in European pig populations for many years. Significant differences in the circulation of these strains occur in different regions across Europe [19].

The result of our study presents an analysis of the serological prevalence and epizootic trends of swine influenza A virus among industrial pig farms in Ukraine from 2021 to 2024. The data indicate a progressive decrease in seropositivity rates, highlighting the worsening epizootic situation and the risk of viral reassortment with potential zoonotic implications. Since the 2009 influenza pandemic caused by the A(H1N1) virus, swine populations have been recognized as important reservoirs for diverse influenza A virus lineages and reassortment events [20, 21]. In Ukraine, although systematic large-scale surveillance has been limited [22], available reports from national veterinary monitoring systems and WOAHA notifications indicate sporadic detection of swine influenza A virus in the post-pandemic period prior to 2021. Regional studies and serological surveys conducted in different parts of the country also suggest the circulation of influenza A virus among pig populations (unpublished data), though data remain fragmented and geographically heterogeneous. These limitations underscore the importance of longitudinal studies, such

Table 1. Detection of influenza A virus in animals from seropositive pig farms in Ukraine

Year	Number of samples tested	Number of positive samples	Prevalence of Influenza A virus (%)
2021	103	17	16.5
2022	63	10	15.9
2023	168	23	13.7
2024	88	9	10.2
Total	422	59	14.0

as the present work, for assessing temporal trends in seroprevalence and epizootic dynamics.

In Germany, present enzootic swine influenza viruses include several co-circulating, antigenically different viruses of each of the H1N1 and H1N2 subtypes [23]. The data obtained by Trombetta et al. [24] suggest that swine influenza viruses might have circulated in Italy as early as 2004, at least in the swine population. According to the authors, this finding highlights the importance of continuing monitoring the influenza viruses' spread in animals and humans for more detailed surveillance. Van Reeth et al. [25] suggested that SIV-A are enzootic in swine-producing regions of Western European countries, while in Central Europe SIV-A activity is low.

Bakre et al. [26] analyzed the diversity of SIV-A in nasal washes and oral fluids from commercial swine farms in the USA using influenza M qRT-PCR and hemagglutinin and neuraminidase subtyping. It was found a predominance of H1 HAs and N2 NAs in the samples examined. There were also identified HAs of the H1 alpha cluster of human novel pandemic origin. The authors claim that SIV-A surveillance can aid the understanding of viral transmission dynamics and help clarify the diversity of its human-swine interaction.

SIV-A subtypes in Brazilian commercial pig herds were studied from the year 2012 to 2019. A higher occurrence of H1N1 was observed from the year 2012 to 2015, H3N2 in 2017, and H1hu in the years 2017 to 2019. Serological data suggested a cyclical character of infection occurrence between the H3N2 and H1N1 virus subtypes over time [27]. The authors conclude that monitoring SIV-A circulation provides the relevant information for field veterinarians to apply proper and timely control measures on the sites.

The results obtained by López-Robles et al. [28] demonstrated a high circulation of strains similar to North American lineage among commercial farms in Mexico. The influenza virus H1 circulating in northwestern Mexico showed 97–100% identity among them, 89% identity with other North American strains, 88% – with strains from central Mexico, and 85% with the pandemic A/H1N1p2009 virus.

The results of another study [29] demonstrated circulation of SIV-A throughout Guatemala. The authors determined the virus's identity on commercial farms, animal health status, and age as potential risk factors associated with swine influenza virus infection and exposure. Detec-

tion of human-origin viruses in pigs leads to suggestions about a human role in the molecular epidemiology of virus influenza in swine.

Prevalence and distribution results obtained by Li et al. [30] helped to recognize the risk factors of swine influenza infection on commercial farms in China. The open access of wild birds to piggeries, the presence of wild or domestic poultry on a pig farm and no proper biosecurity measures applied to workers working on the farms were found to increase the probability of swine virus influenza in commercial pigs. The surveillance data also allowed Zhao et al. [31] to find out that the occurrences of coinfections from two or more subtypes foster their capacity to produce new viruses. The authors emphasized the need for continuous surveillance and analysis of influenza viruses.

A pilot study on influenza A viruses' prevalence in South Africa suggests that they are likely highly prevalent in the country's swine farms [32]. The authors concluded that South Africa would benefit from periodic surveillance for influenza viruses in swine farms. It was also noted the importance of education and seasonal influenza vaccine programs for the workers on swine farms.

Epidemiological features of swine influenza circulation in farm populations anticipate the continuous serological and systematic molecular surveillance to monitor the status of swine influenza virus circulating in swine populations worldwide [33–35].

The above-stated monitoring data on the prevalence of swine influenza A viruses are extremely useful for familiarizing ourselves with their spread, which makes it possible to better understand the epizootology of these infections and their ability to increase their pathogenicity and prevalence. This data makes it possible to approach the development of appropriate diagnostic and preventive measures.

CONCLUSIONS

The long-term persistence of swine influenza virus A in industrial pig farms of Ukraine poses a serious risk of viral reassortment and increased virulence, with potential zoonotic consequences. This situation is exacerbated by the lack of systematic vaccination and the uncontrolled movement of animals and humans, particularly in conflict zones. Strengthened biosecurity measures, enhanced sur-

veillance, and targeted vaccination programs are urgently needed to mitigate the threat of widespread outbreaks and potential transmission to humans. The monitoring of the prevalence of swine influenza viruses is useful not only for familiarizing oneself with their geographical distribution but also for providing a deeper understanding of the particularity of their epidemiology, spreading ability, and pathogenicity. It can improve the development and implementation of relevant preventive and control measures for the persistence of SIV-A in industrial pig farms.

Ethical Statement

This study did not require any Ethical approval.

Conflict of Interest

The authors declare no conflicts of interest.

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Generative AI Statement

Authors declare that no generative AI was used in the creation of this manuscript.

Authors' Contributions

Material preparation, data collection, results analysis and manuscript writing: A.K., V.K., and N.K.; critical review of manuscript: A.O., J.M.V., B.V., S.K., L.K., M.D., and M.P.; literature review: A.K., M.P., M.D. All authors contributed to the study revision. All authors read and approved the final manuscript.

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REFERENCES

1. Ma, W., 2020: Swine influenza virus: Current status and challenge. *Virus Res.*, 288, 198118. DOI: [10.1016/j.virus-res.2020.198118](https://doi.org/10.1016/j.virus-res.2020.198118)
2. Anderson, T. K., Chang, J., Arendsee, Z. W., Venkatesh, D., Souza, C. K., Kimble, J. B., et al., 2021: Swine influenza A viruses and the tangled relationship with humans. *Cold Spring Harb. Perspect. Med.*, 11, a038737. DOI: [10.1101/cshperspect.a038737](https://doi.org/10.1101/cshperspect.a038737)
3. Ang, L. W., Cui, L., Mak, T. M., Ng, Y., Leo, Y. S., Lee, V. J. M., Lin, R. T.-P., 2019: Differential age-specific distribution of influenza virus types and subtypes in tropical Singapore, 2011 to 2017. *J. Med. Virol.*, 91, 8, 1415–1422. DOI: [10.1002/jmv.25473](https://doi.org/10.1002/jmv.25473)
4. Kanji, J. N., Pabbaraju, K., Croxen, M., Detmer, S., Bastien, N., Li, Y., et al., 2021: Characterization of swine influenza A(H1N2) variant, Alberta, Canada, 2020. *Emerg. Infect. Dis.*, 27, 12, 3045–3051.
5. Le Sage, V., Rockey, N. C., French, A. J., McBride, R., McCarthy, K. R., Rigatti, L. H., et al., 2024: Potential pandemic risk of circulating swine H1N2 influenza viruses. *Nat. Commun.*, 15, 5025. DOI: [10.1038/s41467-024-49117-z](https://doi.org/10.1038/s41467-024-49117-z)
6. Mon, P. P., Thurain, K., Janetanakit, T., Nasamran, C., Bunnapong, N., Aye, A. M., et al. 2020: Swine influenza viruses and pandemic H1N1-2009 infection in pigs, Myanmar. *Transbound. Emerg. Dis.*, 67, 2653–2666. DOI: [10.1111/tbed.13616](https://doi.org/10.1111/tbed.13616)
7. Abdelwhab, E. M., Mettenleiter, T. C., 2023: Zoonotic animal influenza virus and potential mixing vessel hosts. *Viruses*, 15, 4, 980. DOI: [10.3390/v15040980](https://doi.org/10.3390/v15040980)
8. Meng, F., Yang, H., Qu, Z., Chen, Y., Zhang, Y., Zhang, Y., et al., 2022: A Eurasian avian-like H1N1 swine influenza reassortant virus became pathogenic and highly transmissible due to mutations in its PA gene. *Proc. Natl. Acad. Sci. USA*, 119, 34, e2203919119. DOI: [10.1073/pnas.2203919119](https://doi.org/10.1073/pnas.2203919119)
9. Sun, H., Xiao, Y., Liu, J., Wang, D., Li, F., Wang, C., et al., 2020: Prevalent Eurasian avian-like H1N1 swine influenza virus with 2009 pandemic viral genes facilitating human infection. *Proc. Natl. Acad. Sci. USA*, 117, 29, 17204–17210. DOI: [10.1073/pnas.1921186117](https://doi.org/10.1073/pnas.1921186117)
10. Bliss, N., Nelson, S. W., Nolting, J. M., Bowman, A. S., 2016: Prevalence of influenza A virus in exhibition swine during arrival at agricultural fairs. *Zoonoses Public Health*, 63, 6, 477–485. DOI: [10.1111/zph.12252](https://doi.org/10.1111/zph.12252)
11. Bliss, N., Stull, J. W., Moeller, S. J., Rajala-Schultz, P. J., Bowman, A. S., 2017: Movement patterns of exhibition

- swine and associations of influenza A virus infection with swine management practices. *J. Am. Vet. Med. Assoc.*, 251, 6, 706–713. DOI: [10.2460/javma.251.6.706](https://doi.org/10.2460/javma.251.6.706)
12. Nelson, M. I., Wentworth, D. E., Das, S. R., Sreevatsan, S., Killian, M. L., Nolting, J. M., et al., 2016: Evolutionary dynamics of influenza A viruses in US exhibition swine. *J. Infect. Dis.*, 213, 2, 173–182. DOI: [10.1093/infdis/jiv399](https://doi.org/10.1093/infdis/jiv399)
 13. Gopinath, S. C. B., Tang, T.-H., Chen, Y., Citartan, M., Tominaga, J., Lakshmipriya, T., 2014: Sensing strategies for influenza surveillance. *Biosens. Bioelectron.*, 61, 357–369. DOI: [10.1016/j.bios.2014.05.024](https://doi.org/10.1016/j.bios.2014.05.024)
 14. Mollett, B. C., Everett, H. E., van Diemen, P. M., Byrne, A. M. P., Ramsay, A., James, J., et al., 2023: JMM profile: Swine influenza A virus: a neglected virus with pandemic potential. *J. Med. Microbiol.*, 72, 1, 1–5. DOI: [10.1099/jmm.0.001623](https://doi.org/10.1099/jmm.0.001623)
 15. Detmer, S., Gramer, M., Goyal, S., Torremorell, M., Torrisson, J., 2012: Diagnostics and surveillance for swine influenza. *Curr. Top. Microbiol. Immunol.*, 370, 85–112. DOI: [10.1007/82_2012_220](https://doi.org/10.1007/82_2012_220)
 16. Graaf-Rau, A., Hennig, C., Lillie-Jaschniski, K., Koechling, M., Stadler, J., Boehmer, J., et al., 2023: Emergence of swine influenza A virus, porcine respirovirus 1 and swine orthopneumovirus in porcine respiratory disease in Germany. *Emerg. Microbes Infect.*, 12, 2, 2239938. DOI: [10.1080/22221751.2023.2239938](https://doi.org/10.1080/22221751.2023.2239938)
 17. Klivleyeva, N., Saktaganov, N., Glebova, T., Lukmanova, G., Ongarbayeva, N., Webby, R., 2024: Influenza A viruses in the swine population: ecology and geographical distribution. *Viruses*, 16, 11, 1728. DOI: [10.3390/v16111728](https://doi.org/10.3390/v16111728)
 18. He, W., Zhang, W., Yan, H., Xu, H., Xie, Y., Wu, Q., et al., 2021: Distribution and evolution of H1N1 influenza A viruses with adamantanes-resistant mutations worldwide from 1918 to 2019. *J. Med. Virol.*, 93, 6, 3473–3483. DOI: [10.1002/jmv.26670](https://doi.org/10.1002/jmv.26670)
 19. Brown, I. H., 2013: History and epidemiology of swine influenza in Europe. *Curr. Top. Microbiol. Immunol.*, 370, 133–146. DOI: [10.1007/82_2011_194](https://doi.org/10.1007/82_2011_194)
 20. Simon, G., Larsen, L. E., Dürrwald, R., Foni, E., Harder, T., Reeth, K. V., et al., 2014: European surveillance network for influenza in pigs: surveillance programs, diagnostic tools and swine influenza virus subtypes identified in 14 european countries from 2010 to 2013. *PLoS One*, 9, 12, e115815. DOI: [10.1371/journal.pone.0115815](https://doi.org/10.1371/journal.pone.0115815)
 21. Lewis, N. S., Russell, C. A., Langat, P., Anderson, T. K., Berger, K., Bielejec, F., et al., 2016: The global antigenic diversity of swine influenza A viruses. *eLife*, 5, e12217. DOI: [10.7554/eLife.12217](https://doi.org/10.7554/eLife.12217)
 22. Stegny, B. T., Rula, O. M., Muzyka, N. M., Dunaiev, Yu. K., Busol, V. O., Kolchyk, O. V., Muzyka, D. V., 2023: Risk of swine influenza for veterinary medicine and human health in Ukraine. *J. Vet. Med. Biotechnol. Biosafety*, 9, 3, 33–41. DOI: [10.36016/JVMBBS-2023-9-3-6](https://doi.org/10.36016/JVMBBS-2023-9-3-6)
 23. Zell, R., Groth, M., Krumbholz, A., Lange, J., Philipps, A., Dürrwald, R., 2020: Cocirculation of swine H1N1 influenza A virus lineages in Germany. *Viruses*, 12, 7, 762. DOI: [10.3390/v12070762](https://doi.org/10.3390/v12070762)
 24. Trombetta, C. M., Montomoli, E., Di Bartolo, I., Ostanello, F., Chiapponi, C., Marchi, S., 2022: Detection of antibodies against influenza D virus in swine veterinarians in Italy in 2004. *J. Med. Virol.*, 94, 6, 2855–2859. DOI: [10.1002/jmv.27466](https://doi.org/10.1002/jmv.27466)
 25. Van Reeth, K., Brown, I. H., Dürrwald, R., Foni, E., Labarque, G., Lenihan, P., et al., 2008: Seroprevalence of H1N1, H3N2 and H1N2 influenza viruses in pigs in seven European countries in 2002–2003. *Influenza Other Respir. Viruses*, 2, 3, 99–105. DOI: [10.1111/j.1750-2659.2008.00043.x](https://doi.org/10.1111/j.1750-2659.2008.00043.x)
 26. Bakre, A. A., Jones, L. P., Kyriakis, C. S., Hanson, J. M., Bobbitt, D. E., Bennett, H. K., et al., 2020: Molecular epidemiology and glycomics of swine influenza viruses circulating in commercial swine farms in the southeastern and midwest United States. *Vet. Microbiol.*, 251, 108914. DOI: [10.1016/j.vetmic.2020.108914](https://doi.org/10.1016/j.vetmic.2020.108914)
 27. Fraiha, A. L. S., Matos, A. C. D., Cunha, J. L. R., Santos, B. S. Á., da S., Peixoto, M. V. C., Oliveira, A. G. G., et al., 2021: Swine influenza A virus subtypes circulating in Brazilian commercial pig herds from 2012 to 2019. *Braz. J. Microbiol.*, 52, 2421–2430. DOI: [10.1007/s42770-021-00550-y](https://doi.org/10.1007/s42770-021-00550-y)
 28. López-Robles, G., Montalvo-Corral, M., Burgara-Estrella, A., Hernández, J., 2014: Serological and molecular prevalence of swine influenza virus on farms in northwestern Mexico. *Vet. Microbiol.*, 172, 323–328. DOI: [10.1016/j.vetmic.2014.05.017](https://doi.org/10.1016/j.vetmic.2014.05.017)
 29. Gonzalez-Reiche, A. S., Ramírez, A. L., Müller, M. L., Orellana, D., Sosa, S. M., Ola, P., et al., 2017: Origin, distribution, and potential risk factors associated with influenza A virus in swine in two production systems in Guatemala. *Influenza Other Respir. Viruses*, 11, 2, 182–192. DOI: [10.1111/irv.12437](https://doi.org/10.1111/irv.12437)
 30. Li, Y., Edwards, J., Wang, Y., Zhang, G., Cai, C., Zhao, M., et al., 2019: Prevalence, distribution and risk factors of farmer reported swine influenza infection in Guangdong

- Province, China. *Prev. Vet. Med.*, 167, 1–8. DOI: [10.1016/j.prevetmed.2019.03.011](https://doi.org/10.1016/j.prevetmed.2019.03.011)
31. Zhao, Y., Han, L., Chen, T., Sang, H., Ding, G., Li, Y., et al., 2022: Serological surveillance of the H1N1 and H3N2 swine influenza A virus in chinese swine between 2016 and 2021. *Biomed. Res. Int.*, 2022, 5833769, 1–8. DOI: [10.1155/2022/5833769](https://doi.org/10.1155/2022/5833769)
 32. El Zowalaty, M. E., Abdelgadir, A., Borkenhagen, L. K., Ducatez, M. F., Bailey, E. S., Gray, G. C., 2022: Influenza A viruses are likely highly prevalent in South African swine farms. *Transbound. Emerg. Dis.*, 69, 2373–2383. DOI: [10.1111/tbed.14255](https://doi.org/10.1111/tbed.14255)
 33. Baudon, E., Peyre, M., Peiris, M., Cowling, B. J., 2017: Epidemiological features of influenza circulation in swine populations: A systematic review and meta-analysis. *PLoS One*, 12, 6, e0179044. DOI: [10.1371/journal.pone.0179044](https://doi.org/10.1371/journal.pone.0179044)
 34. Senthilkumar, D., Kulkarni, D. D., Venkatesh, G., Gupta, V., Patel, P., Dixit, M., et al., 2021: Widespread prevalence of antibodies against swine influenza A (pdm H1N1 09) virus in pigs of eastern Uttar Pradesh, India. *Curr. Microbiol.*, 78, 2753–2761. DOI: [10.1007/s00284-021-02520-x](https://doi.org/10.1007/s00284-021-02520-x)
 35. Harima, H., Okuya, K., Kajihara, M., Ogawa, H., Simulundu, E., Bwalya, E., et al., 2022: Serological and molecular epidemiological study on swine influenza in Zambia. *Transbound. Emerg. Dis.*, 69, e931–e943. DOI: [10.1111/tbed.14373](https://doi.org/10.1111/tbed.14373)