Surveillance Studies for Influenza A viruses at the Human-Animal Interface in South Africa

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The findings of the present study suggest that **influenza A viruses** are **likely prevalent** in South African **swine** farms. The study shows that avian IAV are also present in the **South African wild migratory** bird population, emphasizing the need for more **extensive surveillance** studies to determine the South African avian **influenza gene pool** and relevant local host species.

Abstract Reference

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BACKGROUND

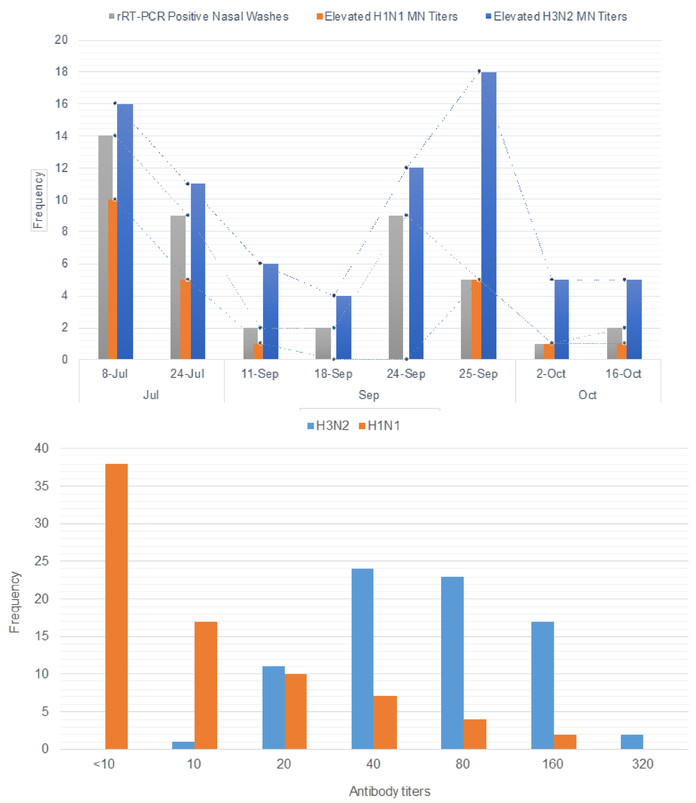
Highly pathogenic avian influenza (HPAI) H5 viruses continue to be a devastating threat to the poultry industry and an incipient threat to humans with a low level of infection that cause over 50% deaths of infected persons. Since 1997 the HPAI H5 virus has continued to spread and evolve. Since 2004, the HPAI H5 virus has spread to many countries worldwide and has been responsible for destruction of many millions of birds. Wild birds are often blamed for dispersal of HPAI H5 viruses, but definitive proof is often lacking. Much of our knowledge on avian influenza viruses is based on surveillance studies in wild migrating birds. While these studies have been extensive over the last decades, our knowledge is still far from complete, because many surveillance studies have been limited in geographical locations, species, sample types, and timing. Rapid growth of South Africa's animal production industries has the potential to increase zoonotic pathogen emergence. We aim to achieve this goal by initiating sampling efforts in South Africa, which is geographically situated on the convergence of the East Atlantic, East Africa-West Asia and Mediterranean/Black Sea migratory flyways. We conducted this One Health study in South Africa. We sought to employ molecular and serological laboratory analyses to obtain evidence that influenza A viruses may cross the species barrier between animals and man. As sparse surveillance has been conducted, we partnered with animal production industries and wildlife biologists in conducting pathogen surveillance at the human-animal interface.

METHODS

Samples (n=1,311) were collected from swine (51 oral secretions), swine workers (84 nasal washes and 78 sera), chicken and geese (119 swabs), waterfowl (*Anseriformes* and *Charadriformes*, 550 swabs) other avian species (381 swabs from non-waterfowl and 48 swabs from raptors) in these pilots during 2017 and 2018 from different locations in KwaZulu-Natal Province in South Africa. Swine workers were surveyed for details on animal exposure and work behavior to identify possible risk factors for serological evidence of animal pathogen infection. All animal samples and human nasal washes were screened for the presence of influenza A viruses using qRT-PCR, virus isolation, and nucleotide sequencing. Avian IAV-positive samples were further screened for the presence of H5, H7 and H9 viruses. Human sera were screened for influenza virus antibodies using microneutralization assays against two swine influenza viruses, A/SW/Iowa/73(H1N1) and A/SW/TX/1/98(H3N2).

RESULTS

Add info hereAmong 84 human nasal washes and 51 swine oral secretion specimens, 44 (52.4%) and 6 (11.8%) had molecular evidence of influenza A virus. Microneutralization assays with enrolled workers' sera against swine H1N1 and H3N2 viruses revealed a high prevalence of elevated antibodies, but cross-reactivity due to immunity against human H1N1 and H3N2 viruses is likely. Multivariate risk factor analysis showed that male workers from the age-group quartile 23–32 years, who self-reported a recent history of exposure to someone with influenza disease and seldom use of personal protective equipment were at highest risk of molecular detection of influenza A virus. A total of 14 samples from 11 birds of prey (45.8% of all sampled birds) were IAV positive. Five out of 24 birds (20.8%) were positive for IAV RNA in duplicate testing, albeit at low concentrations. Among raptor samples, three out of 24 birds (12.5%) were positive for IAVs with viral RNA detected in both cloacal and oropharyngeal swabs. One IAV-positive sample was also positive for H5 subtype (4.1%); all other samples were H5, H7 and H9 negative. All samples from raptors were NDV negative.



CONCLUSIONS

These pilot study data suggest that IAV are likely prevalent in South African swine farms. The study shows that avian IAV are also present in the South African wild migratory bird population, emphasizing the need for more extensive surveillance studies to determine the South African avian influenza gene pool and relevant local host species. The country would benefit from periodic surveillance for novel influenza viruses in swine farms as well as education and seasonal influenza vaccine programs for swine workers. Overall, our results support the development of more intensive and expanded influenza and other emerging virus studies in raptor species, migratory waterfowl, swine and humans. The present findings are of scientific importance and these will contribute to our better understanding of the ecology and mobility of influenza viruses and other pathogens among different animal hosts and humans.

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MORE INFORMATION / REFERENCES

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