VACCIREVIEW

Avian influenza A(H9N2) virus transmission across chicken production and distribution networks, Vietnam

Bibliography

Hennessey M, Hoang Thi T, Raghwani J, Kim Y, Pham HTT, Nguyen TH, Nguyen HQ, Lynton-Jenkins JG, Banyard AC, Brown IH, James J, Lewis T, Lewis NS, Pfeiffer D, Tomley F, Blake D, Pham Thi N, Conan A, Bui VN, Fournié G. Avian influenza A(H9N2) virus transmission across chicken production and distribution networks, Vietnam. Emerg Infect Dis. 2026;32(2):259-264.

Summary

This cross-sectional study investigated avian influenza A(H9N2) and H5N1 virus circulation in chickens across 50 farms and 52 distribution facilities (retail and wholesale markets, small slaughter points, and industrial slaughterhouses) in four provinces of northern Vietnam between March 2021 and March 2022. A total of 1,682 chickens were sampled using oropharyngeal and cloacal swabs, which were screened by real-time RT-PCR for influenza A and subtyped for H5 and H9; positive H9 samples with low cycle thresholds underwent whole-genome sequencing and Bayesian phylogenetic analysis. Only one H5-positive chicken was detected, but H9N2 infection was found in 11.7% of all sampled birds, with markedly higher prevalence in distribution facilities (especially informal slaughter points and retail markets) than on farms. Bayesian hierarchical models showed that bird-level H9N2 prevalence increased several-fold along the production and distribution network, with the highest levels in small slaughter points and evidence that supplying area and trading practices strongly influenced contamination. Phylogenetic analysis assigned all viruses to clade B4.71, revealed limited overall genetic diversity but multiple co-circulating lineages, frequent reassortment, and no strong geographic structure, indicating extensive viral mixing along the network. The authors conclude that risk mitigation and surveillance must address the entire production–distribution chain, not only live bird markets and formal slaughterhouses, prioritizing informal slaughter points and retail markets where viral amplification appears greatest.

Comment

This work illustrates how endemic avian influenza viruses, such as H9N2 in poultry, can silently spread and mix genetically across dense production and trade networks, generating reassort ant strains with pandemic potential. Because such networks facilitate continual viral evolution and occasional spillover to humans, avian influenza remains a plausible source of future influenza pandemics.

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