Journal for Research in Applied Sciences and Biotechnology

www.jrasb.com

ISSN: 2583-4053

Volume-3 Issue-5 || October 2024 || PP. 101-106

https://doi.org/10.55544/jrasb.3.5.12

Influenza A as a True Zoonotic Pathogen: Transmission through Reservoir Hosts

Neyazi Ghulam Rabani[1], Khaidarov Saken[2], Mohammad Hamid Mohammadi[3], Mukhlis Hujatullah[4] and Taibullah Modaqeq[5]

[1]Associate Professor, Department of Biology, Education Faculty, Badakhshan University, Badakhshan, AFGHANISTAN.
[2]Associate Professor, Department of Biology, Kazakh National University, Kazakhstan, AFGHANISTAN.
[3]Associate Professor, Department of Biology, Daikundi University, AFGHANISTAN.
[4]Associate Professor, Department of Biology, Zabul University, Zabul, AFGHANISTAN
[5]Associate Professor, Department of Chemistry, Baghlan University, Baghlan, AFGHANISTAN.

[2]Corresponding Author: logicalmind1984@mail.ru

ORCiD

https://orcid.org/0000-0001-7770-8427

www.jrasb.com || Vol. 3 No. 5 (2024): October Issue

Received: 13-10-2024	**Revised:** 16-10-2024	**Accepted:** 24-10-2024

ABSTRACT

Influenza A virus (IAV) represents a considerable global health threat due to its rapid mutation rates and broad host range, facilitating cross-species transmission and enabling the virus to evade immune defenses. This review explores the molecular mechanisms underlying IAV's pathogenicity, focusing on its zoonotic potential through reservoir hosts, such as wild birds and swine. The virus's ability to undergo antigenic shift and drift allows it to continually adapt to new hosts and environments, posing challenges for control and treatment. Current antiviral therapies are limited by the emergence of resistant strains, underscoring the necessity for innovative vaccine development and treatment strategies. By examining IAV's molecular evolution, immune evasion tactics, and transmission dynamics, this review highlights the critical need for enhanced surveillance, improved therapeutic options, and international cooperation to mitigate future outbreaks. A deeper understanding of these processes is essential to inform public health efforts and combat the persistent threat of IAV.

Keywords- Zoonotic transmission, zoonotic pathogen, Reservoir hosts, Cross-species adaptation, Viral reassortment.

I. INTRODUCTION

Influenza IAVs are members of the Orthomyxoviridae virus family (Palese and Shaw, 2007 reviewed). The surface antigens neuraminidase (NA or N) and haemagglutinin (HA or H) are used to subtype them. Nine kinds of NA and sixteen subtypes of HA have been identified in birds thus far, which are the host species for most IAV strains. IAVs are distinguished by an RNA genome segmented and arranged into eight ribonucleoprotein (RNP) units per virion, each of which can encode up to eleven proteins.[1] Influenza A viruses are classified into subtypes based on the antigenic properties of the external glycoproteins haemagglutinin (HA) and neuraminidase (NA). The HA and NA are very important for the induction of an antibody response in the host, but they are also highly variable while the “internal” proteins like the nucleoprotein (NP) and matrix (M) proteins are more conserved between different influenza A viruses. Sixteen antigenically different HA (H1-H16) and 9 different NA (N1-N9) have been recognized so far, and their combination designates the subtype of the virus. Influenza viruses are genetically unstable, and the reader is referred for a detailed overview of antigenic drift and

Journal for Research in Applied Sciences and Biotechnology

www.jrasb.com

ISSN: 2583-4053

Volume-3 Issue-5 || October 2024 || PP. 101-106

https://doi.org/10.55544/jrasb.3.5.12

shift mechanisms.[2] Interspecies transmission of influenza A viruses has occurred occasionally, mainly from 250 aquatic birds to mammalian species. Marine mammals and horses have been shown to acquire 251 influenza A viruses from avian origin. [3] The method of spread of avian influenza viruses to mammals remains unresolved but could be either airborne or waterborne. In this report, we will consider recent examples of interspecies transmission of influenza A viruses and the possible prevention of the emergence of the next human pandemic, which is considered imminent. [4]

II. ECOLOGICAL AND EVOLUTIONARY DYNAMICS OF INFLUENZA A VIRUS

From an evolutionary perspective, more is known, and more sequence data about influenza viruses have been generated than any other group of pathogens. These data have provided a general understanding of the extent and structure of virus genetic diversity, the evolutionary processes that gave rise to it, from where influenza viruses originate, and the mutations that underpin host adaptation, antigenic drift, and antiviral resistance. We also know much about how human influenza viruses spread and evolve seasonally. Human influenza A virus was the focus of the first large-scale pathogen genome-sequencing projects. Moreover, the reservoirs of influenza A viruses are traditionally considered to be waterbirds of the orders Anseriformes (ducks) and Charadriiformes (shorebirds, gulls); these animals are commonly infected, reaching prevalence levels of >20% in the autumn migration season. [5] The influenza viruses of domestic poultry, mammals, and humans have all evolved directly or indirectly from influenza viruses in the aquatic bird reservoirs. The processes involved in influenza virus evolution are acquiring mutations, reassortment, and, less frequently, nonhomologous recombination. The negative sense RNA genome of the influenza virus has no proof-reading mechanism during replication and is extremely error-prone, giving rise to a high mutation rate. [6] Also, many RNA viruses' ecological and evolutionary dynamics have been increasingly well described over the last several decades, yet the factors driving their dynamics are still poorly understood. One approach towards identifying key factors is by formulating mathematical models that, when analyzed analytically or simulated, yield quantitative predictions of the case dynamics and the evolutionary dynamics of the viral population.[7] Traditional approaches to studying IAV evolutionary dynamics have typically focused on single subtypes (e.g., H3N2, H3N8, or H5N1) or analyses restricted to coarse geographical scales comparing data from one continent to data from another. However, to identify geographical variations in IAV evolution across a spectrum of subtypes, a more comprehensive approach was needed to compare data from individual countries. [8]

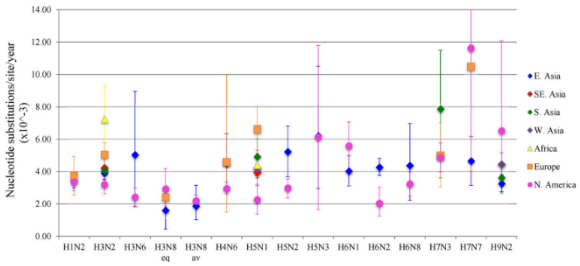

Diagram -1 Evolutionary rates of influenza A virus subtypes by region. Evolutionary rates (substitutions per site per year x103) and 95% highest-probability density (HPD) values of the HA gene for 14 high-priority IAV subtypes from multiple world regions (East [E.] Asia, Southeast [SE.] Asia, South [S.] Asia, West [W.] Asia, Europe, Africa, and North [N.] America) from 2000 to 2011. Up to 500 sequences per region were used in the analysis. H3N8 eq and H3N8 av refer to equine and avian strains of H3N8, respectively. (https://doi.org/10.1128/JVI.01100-15)

III. ANIMAL RESERVOIRS OF INFLUENZA A VIRUS

a. Wild Birds as Primary Reservoirs

Influenza A viruses have been isolated from many species, including humans, pigs, horses, mink, felids, marine mammals, and a wide range of domestic birds, but wildfowl and shorebirds are thought to form the virus reservoir in nature. LPAI (Low et al.) viruses have been isolated from at least 105 wild bird species of 26 families (Table 1). All influenza virus subtypes and most HA/NA combinations have been detected in the bird reservoir and poultry, whereas relatively few have been detected in other species. Although many wild bird species may harbor influenza viruses, birds of wetlands and aquatic environments such as the Anseriformes (particularly ducks, geese, and swans) and Charadriiformes (particularly gulls, terns, and waders) constitute the major natural LPAI virus reservoir. Anseriformes and Charadriiformes are distributed globally, except for the most arid regions worldwide. Also, Extensive surveillance studies of wild ducks in the Northern Hemisphere have revealed high LPAI virus prevalence primarily in juvenile— presumably immunologically naive—birds with a peak in early fall before southbound migration. In North America, the prevalence falls from È60% in ducks sampled at marshalling sites close to the Canadian breeding areas in early fall, to 0.4 to 2% at the wintering grounds in the southern U.S.A., and È0.25% on the ducks' return to the breeding grounds in spring. Similar patterns have been observed in Northern Europe, but influenza virus detection during spring migration can be significantly higher, up to 6.5%. Surveillance of the nesting grounds of ducks in Siberia before winter migration revealed the presence of influenza virusesinupto8%ofbirds. [9] the natural reservoir of influenza A viruses is birds;

ISSN: 2583-4053

Volume-3 Issue-5 || October 2024 || PP. 101-106

https://doi.org/10.55544/jrasb.3.5.12

consequently, many are known as avian influenza viruses. These viruses naturally infect the intestinal tract of wild birds, and as expected in coevolved host-parasite systems, they usually cause asymptomatic infections in their natural hosts. [10] The 16 hemagglutinin (HA) and nine neuraminidase (NA) subtypes in wild bird species are perpetuated in the nonpathogenic or low pathogenic states. After transmission from wild birds to domestic poultry, two subtypes, H5 and H7, are unique in having the capacity of acquiring high pathogenicity (HP) with the systemic spread and induction of neurologic signs and death. [11] Therefore, patterns of viral spread and subsequent risk posed by wild bird viruses remain unpredictable. Methodological advances present an opportunity for large-scale assessment of spatiotemporal patterns of viral movement between migrating bird populations.[12]

Table 1: Prevalence of influenza A virus in wild birds. Influenza virus prevalence in specific species is given only if tests on 9500 birds have been reported; lower numbers in individual species are included in the total. See (5) for additional comments and original data. Of the 36 species of ducks, 28,955 were dabbling ducks and 1011 wereivingducks, with influenza virus prevalence of 0.1 and 1.6%, respectively.

Family	Species	Sampled	Positive	
			(*n*)	(%)
Ducks	36 species	34,503	3275	9.5
	Mallard (*Anas platyrhynchos*)	15,250	1965	12.9
	Northern Pintail (*Anas acuta*)	3,036	340	11.2
	Blue-winged Teal (*Anas discors*)	1,914	220	11.5
	Common Teal (*Anas crecca*)	1,314	52	4.0
	Eurasian Wigeon (*Anas penelope*)	1,023	8	0.8
	Wood Duck (*Aix sponsa*)	926	20	2.2
	Common Shelduck (*Tadorna tadorna*)	881	57	6.5
	American Black Duck (*Anas rubripes*)	717	130	18.1
	Green-winged Teal (*Anas carolinensis*)	707	28	4.0
	Gadwall (*Anas strepera*)	687	10	1.5
	Spot-billed Duck (*Anas poecilorhyncha*)	574	21	3.7
Geese	8 species	4,806	47	1.0
	Canada Goose (*Branta canadensis*)	2,273	19	0.8
	Greylag Goose (*Anser anser*)	977	11	1.1
	White-fronted Goose (*Anser albifrons*)	596	13	2.2
Swans	3 species	5,009	94	1.9
	Tundra Swan (*Cygnus columbianus*)	2,137	60	2.8
	Mute Swan (*Cygnus olor*)	1,597	20	1.3
	Whooping Swan (*Cygnus cygnus*)	930	14	1.5
Gulls	9 species	14,505	199	1.4
	Ring-billed gull (*Larus delawarensis*)	6,966	136	2.0
	Black-tailed Gull (*Larus crassirostris*)	1,726	17	1.0
	Black-headed Gull (*Larus ridibundus*)	770	17	2.2
	Herring Gull (*Larus argentatus*)	768	11	1.4
	Mew Gull (*Larus canus*)	595	0	0.0
Terns	9 species	2,521	24	0.9
	Common Tern (*Sterna hirundo*)	961	16	1.7
Waders	10 species	2,637	21	0.8
Rails	3 species	1,962	27	1.4
	Eurasian Coot (*Fulica atra*)	1,861	23	1.2
Petrels	5 species	1,416	4	0.3
	Wedge-tailed Shearwater (*Puffinus pacificus*)	794	4	0.5
Cormorants	1 species	4,500	18	0.4
	Great Cormorant (*Phalacrocorax carbo*)	4,500	18	0.4

b. Domestic Poultry:

Globally, avian influenza is one of the most potent zoonotic diseases affecting poultry, but some strains can also potentially affect wildlife and human health.[13] India reported outbreaks of the highly pathogenic avian influenza (HPAI) H5N1 in poultry in the states of Maharashtra, Gujarat, Madhya Pradesh in the western region and in Manipur, West Bengal, Tripura and Assam in the Eastern and North Eastern region during the period spanning from 2006 to 2011. [14] Thousands of migratory birds that migrate long distances yearly stop to breed and drink in Poyang Lake and Donating Lake, where the AIV is very active. Since 2013, there have been H7N9, H10N8, and other cases in Nanchang City. Epidemiological investigations show that most of the cases have had a history of poultry contact or were exposed to live poultry markets (LPMs) before the onset of illness.[15]

c. Mammalian Hosts:

Phylogenetic evidence strongly suggests that all mammalian influenza A virus lineages originally derive from avian influenza A viruses after initial cross-species transmission of the viruses from birds to mammals. Until the emergence of highly pathogenic avian influenza virus (AIV) H5N1, cross-species transmission of low pathogenic AIV (LPAIV) from birds to mammals was infrequently reported, and for only a limited number of animal species. Such transmission typically results in outbreaks of severe respiratory disease. Since 2003, highly pathogenic AIV (HPAIV) of subtype H5N1 has been transmitted to a wide range of non-human mammalian species. They cause fatal respiratory and extra-respiratory infections with no or limited mammal-to-mammal transmission. [16] also, Repeated introductions of avian H5N1 influenza viruses into the human population have resulted in more than 380 reported cases of severe disease since 2003. Greater than half of these cases have been fatal, highlighting the extreme pathogenicity of H5N1 influenza in humans. Furthermore, clinical specimens collected from infected patients have detected high viral loads. [17] Influenza virus was first recognized as a viral agent causing respiratory disease in pigs in 1918 (Koen, 1919; Shope, 1931). The pig plays an important role in influenza ecology because it supports the replication of influenza viruses from avian, swine, and human species. The pig has both a2-3 and a2-6 linkages on the glycocalyx of epithelial cells lining the pig respiratory tract that serve as receptors for avian and mammalian influenza A viruses, respectively (Ito et al., 1998). These receptors and the possibility of dual infections can result in the generation of new reassort and strains.[18] Based on the close genetic relatedness of influenza viruses isolated from marine mammals and wild birds, it has been hypothesized that wild birds are the main source of influenza infection in marine mammals. Contact between marine mammals and wild birds at hauling-out sites or when feeding on the same food resources, i.e., fish or krill species, can facilitate cross-species transmission of avian influenza viruses (AIV). The role of marine mammals as hosts or carriers of potential zoonotic pathogens such as highly pathogenic AIV is an issue which needs further analyzed. Nevertheless, the migration of seals and other marine mammals may play a key role in spreading AIV from one continent to another.[19] More than 300,000 marine mammals, including California sea lions (CSL), Steller sea lions, Northern and Guadalupe fur seals, Pacific harbor seals (PHS), and northern elephant seals (NES), live in the eastern North Pacific Ocean and molt and birth along mainland and island coastlines of California.

Journal for Research in Applied Sciences and Biotechnology

www.jrasb.com

ISSN: 2583-4053

Volume-3 Issue-5 || October 2024 || PP. 101-106

https://doi.org/10.55544/jrasb.3.5.12

Pinnipeds in California are in contact with influenza virus reservoirs, including avian and mammalian hosts. [20] additionally In Florida in January 2004 respiratory disease was noticed in 22 racing greyhound dogs. Clinically, a mild respiratory syndrome consisting of moderate fever and coughing in 14 dogs was distinguishable from eight cases of severe hemorrhagic tracheitis, bronchopneumonia, pleuritis, and signs of vasculitis associated with high fever and an ultimately fatal course. An influenza A virus of subtype H3N8 was isolated from lung tissue homogenates of these cases.[21]

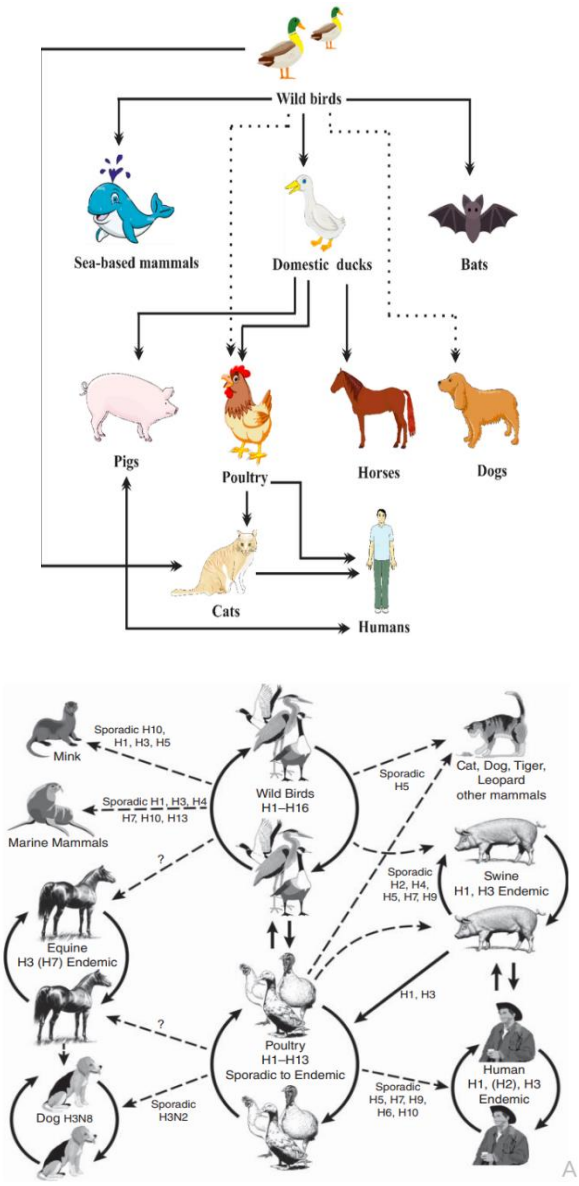

Fig1.1 Diagrammatic representation of the source and movement of influenza A viruses or their genes within avian and mammalian ecological and epidemiological situations (updated from [160]). H = hemagglutinin subtype, ( ) = subtype previously common but no longer circulating. Source: K. Carter, University of Georgia, and D. Swayne, USDA/ARS.

IV. MECHANISMS OF TRANSMISSION BETWEEN RESERVOIR HOSTS AND HUMANS

Wild aquatic birds are considered the reservoir for all subtypes of influenza A viruses, with most infections thought to be inapparent [1]. Bird-to-bird and bird-to-mammal transmission may result in the establishment of influenza viruses in new hosts, with some possibly evolving into highly pathogenic avian influenza (HPAI) viruses in poultry and pandemic influenza viruses in humans [2]. Outbreaks of HPAI H5N1 virus in wild birds have been associated with mortality. However, reports that apparently healthy wild birds are infected with HPAI H5N1 substantiate concerns that birds may distribute this virus during migration. [23] A schematic layout of the room used for the transmission studies is presented that the rooms were mechanically ventilated, and the air was HEPA filtered at the intake and the exhaust. Briefly, the infected and contact animals were placed close to each other in two different cages (with rubber coated floors) to study the indirect transmission of H3N2 TR viruses between swine (large white breed) and specific pathogen free (SPF) turkeys. The direction of the air current was always from the infected animals' side to the contact animals' side. The animals received a virus titer of 107 TCID50 contained in 0.5 ml, and the contact animals were placed in the same room close to the infected animals at one day post inoculation (1 DPI). Nasal swabs from pigs and tracheal swabs from turkeys were collected daily, maintained in Brain Heart Infusion (BHI) media, and directly used for RNA extractions. Contact animals were always handled first. [22]

V. CASE STUDIES AND OUTBREAKS LINKED TO RESERVOIR HOSTS

A particular subtype of influenza A virus, highly pathogenic avian influenza (HPAI) virus H5N1, is transmitted by contact with infected birds. It is epizootic in many bird populations, especially in Southeast Asia. Clade 2.2 of the virus has spread globally, including Europe, the Middle East and Africa after first appearing in Asia in 2005. The spatial spread of H5N1 avian influenza and long-term persistence of the virus in some regions has enormously impacted the poultry industry. It presents a serious threat to the health of humans and migratory birds. It has been 17 years since the first case in geese of H5N1 avian influenza was discovered in Hong Kong in 1996. As of 19 May 2013, H5N1 has caused 628 human cases of influenza in 15 different countries, with 374 deaths.[24] also, the National Reference Lab for Poultry Diseases (NRLPD) at the Animal Sciences Institute, National Agricultural Research Center,

ISSN: 2583-4053

Volume-3 Issue-5 || October 2024 || PP. 101-106

https://doi.org/10.55544/jrasb.3.5.12

Islamabad, Pakistan, confirmed the first case of HPAI H5N1 in a commercial layer flock in February 2006 from the northern part of the country. Afterward, the infection spread to other parts of the country, infecting different poultry populations, including commercial broilers, breeders, layers, backyard poultry, and other domesticated wild birds. Subsequently, outbreaks of antigenically related viruses were reported among wild and migratory birds, backyard poultry, and commercial poultry during 2007 and 2008. The only area continuously hit by the HPAI outbreaks during 2006–08 was Abbottabad.[25] in other hand an outbreak of novel A/H7N9 influenza virus infections rapidly unfolded in Eastern China, with the first laboratory-confirmed case identified in Shanghai on 31 March 2013 and a total of 132 laboratory-confirmed cases and 38 fatalities reported as of 3 June 2013 [1,2]. Although the number of new A/H7N9 cases has stalled since early May 2013, several features of this virus have heightened concerns for its pandemic potential and prompted an intense public health response from the Chinese authorities and international health organizations.[26]

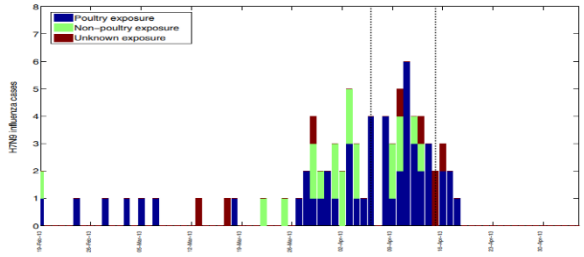

Diagram 2: Temporal incidence of laboratory-confirmed A/H7N9 influenza in the provinces of Shanghai and Zhejiang according to date of symptoms onset (n = 78). Vertical dashed lines indicate the timing of the preemptive live bird market closure in Shanghai (6 April) and Zhejiang (15 April), respectively. Cases are color coded by exposure history.

VI. CONCLUSION

Influenzas virus remains a major public health concern due to its ability to cross species barriers and its rapid evolutionary dynamics. Despite advancements in treatment and prevention, the virus's high mutation rate and zoonotic potential allow it to persist and adapt, often evading immune defenses and antiviral drugs. Effective control of IAV requires an integrated approach that includes continuous global surveillance, novel antiviral strategies, and enhanced vaccine development to provide broader protection. Addressing these challenges will necessitate collaboration among researchers, public health officials, and policymakers. Future research can better predict and mitigate zoonotic spillovers by focusing on the virus's ecological and evolutionary dynamics. As new strains emerge, a proactive stance on research and biosecurity measures will be essential to prevent widespread transmission and minimize future pandemics' health and economic impacts. Continued investment in innovative technologies and international cooperation is crucial to combat the evolving threat of the influenza A virus.

REFERENCES

[1] Schmolke, Mirco, and Adolfo García-Sastre. "Evasion of innate and adaptive immune responses by influenza A virus." *Cellular microbiology* 12.7 (2010): 873-880. https://doi.org/10.1111/j.1462-5822.2010.01475.x

[2] Van Reeth, Kristen. "Avian and swine influenza viruses: our current understanding of the zoonotic risk." *Veterinary research* 38.2 (2007): https://doi.org/10.1051/vetres:2006062

[3] Kalthoff, Donata, Anja Globig, and Martin Beer. "(Highly pathogenic) avian influenza as a zoonotic agent." *Veterinary microbiology* 140.3-4 (2010): 237-245. https://doi.org/10.1016/j.vetmic.2009.08.022

[4] Plowright, R., Parrish, C., McCallum, H. *et al.* Pathways to zoonotic spillover. *Nat Rev Microbiol* 15, 502–510 (2017). https://doi.org/10.1038/nrmicro.2017.45

[5] Wille, Michelle, and Edward C. Holmes. "The ecology and evolution of influenza viruses." *Cold Spring Harbor perspectives in medicine* 10.7 (2020): a038489. https://doi.org/10.1101/cshperspect.a038489

[6] Yoon, S. W., Webby, R. J., & Webster, R. G. (2014). Evolution and ecology of influenza A viruses. *Influenza pathogenesis and control-volume I*, 359-375. https://doi.org/10.1007/978-3-319-07207-6_12

[7] Koelle K, Khatri P, Kamradt M, Kepler TB. A two-tiered model for simulating the ecological and evolutionary dynamics of rapidly evolving viruses, with an application to influenza. J R Soc Interface. 2010 Sep 6;7(50):1257-74. doi: 10.1098/rsif.2010.0007. Epub 2010 Mar 24. PMID: 20335193; PMCID: PMC2894885. https://doi.org/10.1098/rsif.2010.0007

[8] Rejmanek, Daniel, et al. "Evolutionary dynamics and global diversity of influenza A virus." *Journal of Virology* 89.21 (2015): 10993-11001. https://doi.org/10.1128/JVI.01100-15

[9] Olsen, B., Munster, V. J., Wallenstein, A., Waldenström, J., Osterhaus, A. D., & Fouchier, R. A. (2006). Global patterns of influenza A virus in wild birds. *science*, *312*(5772), 384-388. https://doi.org/10.1126/science.1122438

[10] Causey, Douglas, and Scott V. Edwards. "Ecology of avian influenza virus in birds." *The Journal of Infectious*

ISSN: 2583-4053
Volume-3 Issue-5 || October 2024 || PP. 101-106
https://doi.org/10.55544/jrasb.3.5.12

Diseases 197.Supplement_1 (2008): S29-S33. https://doi.org/10.1086/524956

[11] Krauss, Scott, and Robert G. Webster. "Avian influenza virus surveillance and wild birds: past and present." *Avian diseases* 54.s1 (2010): 394-398. https://doi.org/10.1637/8703-031609-Review.1

[12] Bahl, Justin, et al. "Influenza A virus migration and persistence in North American wild birds." *PLoS Pathogens* 9.8 (2013): e1003570. https://doi.org/10.1371/journal.ppat.1003570

[13] Brugh, Max, and Daryl C. Johnson. "Epidemiology of avian influenza in domestic poultry." *Avian Diseases* 47 (2003): 177-186.

[14] Pawar, S.D., Kale, S.D., Rawankar, A.S. *et al*. Avian influenza surveillance reveals presence of low pathogenic avian influenza viruses in poultry during 2009-2011 in the West Bengal State, India. *Virol J* **9**, 151 (2012). https://doi.org/10.1186/1743-422X-9-151

[15] Guo, J., Song, W., Ni, X. *et al.* Pathogen change of avian influenza virus in the live poultry market before and after vaccination of poultry in southern China. *Virol J* **18**, 213 (2021). https://doi.org/10.1186/s12985-021-01683-0

[16] Reparent LA, Rimmel Zwaan GF, Kuiken T. Avian influenza viruses in mammals. Rev Sci Tech. 2009 Apr;28(1):137-59. https://doi.org/10.20506/rst.28.1.1876

[17] Ito, Toshihiro, and Yoshihiro Kawaoka. "Host-range barrier of influenza A viruses." *Veterinary microbiology* 74.1-2 (2000): 71-75. https://doi.org/10.1016/S0378-1135(00)00167

[18] orremorell, M., Allerson, M., Corzo, C., Diaz, A. and Gramer, M. (2012), Transmission of Influenza A Virus in Pigs. Transboundary and Emerging Diseases, 59: 68-84. https://doi.org/10.1111/j.1865-1682.2011.01300.x

[19] Fereidouni, Sasan, et al. "Influenza virus infection of marine mammals." *Eco Health* 13 (2016): 161-170. https://doi.org/10.1007/s10393-016-1109-9

[20] Plancarte M, Kovalenko G, Baldassano J, Ramírez AL, Carrillo S, et al. (2023) Human influenza A virus H1N1 in marine mammals in California, 2019. PLOS ONE 18(3): e0283049. https://doi.org/10.1371/journal.pone.0283049

[21] Harder, Timm C., and Thomas W. Vahlenkamp. "Influenza virus infections in dogs and cats." *Veterinary immunology and immunopathology* 134.1-2 (2010): 54-60. https://doi.org/10.1007/s10393-016-1109-9

[22] Yassine, H.M., Al-Natour, M.Q., Lee, CW. *et al.* Interspecies and intraspecies transmission of triple reassortant H3N2 influenza A viruses. *Virol J* **4**, 129 (2007). https://doi.org/10.1186/1743-422X-4-129

[23] Ip, H.S., Flint, P.L., Franson, J.C. *et al.* Prevalence of Influenza A viruses in wild migratory birds in Alaska: Patterns of variation in detection at a crossroads of intercontinental flyways. *Virol J* **5**, 71 (2008). https://doi.org/10.1186/1743-422X-5-7

[24] Tian, H., Cui, Y., Dong, L. *et al.* Spatial, temporal and genetic dynamics of highly pathogenic avian influenza A (H5N1) virus in China. *BMC Infect Dis* **15**, 54 (2015). https://doi.org/10.1186/s12879-015-0770-x

[25] Siddique, N., Naeem, K., Abbas, M.A. *et al.* Sequence and phylogenetic analysis of highly pathogenic avian influenza H5N1 viruses isolated during 2006–2008 outbreaks in Pakistan reveals genetic diversity. *Virol J* **9**, 300 (2012). https://doi.org/10.1186/1743-422X-9-300

[26] Chowell, G., Simonsen, L., Towers, S. *et al.* Transmission potential of influenza A/H7N9, February to May 2013, China. *BMC Med* **11**, 214 (2013). https://doi.org/10.1186/1741-7015-11-214