Influenza Risk Assessment Tool (IRAT) - Virus Report

Prepared by the CDC Influenza Division

North American Highly Pathogenic Avian Influenza A(H7N9)

Virus Strain: A/chicken/Tennessee/17-007147-2/2017

Date of Evaluation: October 2017

Introduction

Human infections with novel influenza A viruses that originate in animals are rare and the risk of such infections overall to humans is generally low. Sporadic infections with novel influenza A viruses do occur, but typically in situations where individuals are exposed to infected animals through direct or close contact. The IRAT is used to examine multiple attributes of novel influenza A viruses that have not gained the ability to spread among humans to assess their potential to acquire this ability and the consequent potential public health impact.

Situation

In March 2017, the U.S. Department of Agriculture (USDA) reported the detection of a highly pathogenic avian influenza (HPAI) A(H7N9) virus in 2 commercial poultry flocks in Tennessee. Full genome sequence analysis indicated that all eight gene segments of the virus were of North American wild bird lineage and genetically distinct from the lineage of influenza A(H7N9) viruses infecting poultry and humans in China since 2013. The outbreak investigation revealed that a related North American low pathogenic avian influenza A(H7N9) was circulating in poultry prior to the detection of the HPAI A(H7N9) [1].

In October 2017, the CDC assessed the pandemic potential of a representative strain of HPAI A(H7N9) virus from the described outbreak using the Influenza Risk Assessment Tool (IRAT).

IRAT Evaluation

Influenza subject matter experts (SMEs) from the CDC, USDA, and FDA were asked to evaluate influenza A/chicken/Tennessee/17-007147-2/2017 using ten risk elements defined in the IRAT. Each SME scored 1 to 3 elements based on their particular areas of expertise. The point estimate scores for each risk element were averaged, multiplied by predetermined weights, and summed to give an aggregate score for each of the two IRAT risk questions related to potential risk for emergence in humans and potential public health impact if the virus gained the ability to spread efficiently human to human [2].

The summary average risk score was 2.8 for the virus to achieve sustained human-to-human transmission (Table 1), placing the virus in the low risk category. The average risk score for the virus to significantly impact public health if it were to achieve sustained human-to-human transmission was 3.5 (Table 2) and was between the low to low-moderate risk range. Overall, the virus is categorized in the low risk range.

Some variability was seen among SME point estimate scores in the risk elements of Genomic Variation, Infections in Animals, and Disease Severity and Pathogenesis indicating some differences in interpretation of the available data. A sensitivity analysis using the highest scores received in each of these three specific elements resulted in an adjusted emergence score of 3.0 and potential impact score of 4.0, indicating that the overall scores would still categorize this virus in the low risk range.

Table 1-Estimated Risk of Emergence

Risk Element	Weight (W)	Risk Score (RS)	W x RS
Human Infections	0.2929	1.71	0.50
Transmission in Lab Animals	0.1929	1.80	0.35
Receptor Binding	0.1429	1.75	0.25
Population Immunity	0.1096	8.50	0.93
Infections in Animals	0.0846	3.33	0.28
Genomic Variation	0.0646	3.80	0.25
Antigenic Relatedness	0.0479	2.75	0.13
Global Distribution in Animals	0.0336	1.67	0.06
Disease Severity & Pathogenesis	0.0211	2.57	0.05
Antiviral/Treatment Options	0.0100	2.00	0.02
Total			2.82

Table 2-Estimated Potential Public Health Impact

Risk Element	Weight (W)	Risk Score (RS)	W x RS
Disease Severity & Pathogenesis	0.2929	2.57	0.75
Population Immunity	0.1929	8.50	1.64
Human Infections	0.1429	1.71	0.24
Antiviral/Treatment Options	0.1096	2.00	0.22
Antigenic Relatedness	0.0846	2.80	0.23
Receptor Binding	0.0646	1.75	0.11
Genomic Variation	0.0479	3.80	0.18
Transmission in Lab Animals	0.0336	1.80	0.06
Global Distribution in Animals	0.0211	1.70	0.04
Infections in Animals	0.0100	3.00	0.03
Total			3.51

A low risk of emergence score was influenced by low scores in the top weighted risk elements. Specifically, there were no human infections, inefficient transmission in laboratory animal model testing, and an avian receptor binding preference for this virus. Humans are not expected to have immunity to this virus, which results in a high individual score for population immunity risk, but this factor alone is not sufficient to raise the aggregate emergence risk score out of the low risk category. Similarly, when answering the IRAT question of risk of potential public health impact, the top weighted risk elements scored relatively low, although the population immunity score had a slightly greater effect due to its higher relative importance raising the score above 3 to 3.5.

Individual Risk Element Summaries

Human Infections: There were no reports of human infection with this virus, resulting in a risk score in the lower range.

Transmission in Laboratory Animals: In ferret studies, this virus did not transmit between animals in the direct contact model and did not replicate to a high titer [3]. Results suggest low risk to humans.

Receptor Binding: Sequence analysis reveals no known markers associated with adaptation to mammalian receptors. Similar to other avian influenza viruses that preferentially bind to α2,3–linked sialic acid. Receptor studies with recombinant hemagglutinin revealed strict avian receptor preference.

Population Immunity: Although no specific serological studies are available, the overall population immunity to this virus is expected to be very low, raising the risk score to a high level for this element.

Infections in Animals: The virus was associated with a limited outbreak in 2 related flocks and was eradicated. There is no evidence of the virus infecting mammals. It does not appear to be associated with sustained transmission in wild birds [1].

Genomic variation: The virus is closely related in all gene segments to viruses circulating in wild birds. Evidence of reassortment involves only closely related viruses. The virus acquired a multibasic cleavage site linked to high pathogenicity in poultry [4].

Antigenic relatedness: This virus was well inhibited in hemagglutination inhibition testing with candidate vaccine viruses.

Global Distribution in Animals: This virus was found in only one management system (commercial poultry); spread was contained and the virus eradicated.

Disease Severity & Pathogenesis: No human illness was observed. Experimental animal models showed mild illness and no extra-pulmonary spread in ferrets [3].

Antivirals and Treatment Options: No known markers of neuraminidase resistance are present.

Comparison to other Viruses Scored with IRAT

The scores for the emergence risk and potential public health impact for the HPAI A/chicken/Tennessee/17-007147-2/2017 were plotted along with a selection of other viruses previously scored using the IRAT (Figure 1). The HPAI A(H7N9) virus aligns with other North American lineage avian viruses in a category of low risk. Viruses with higher IRAT risk scores are included for comparison.

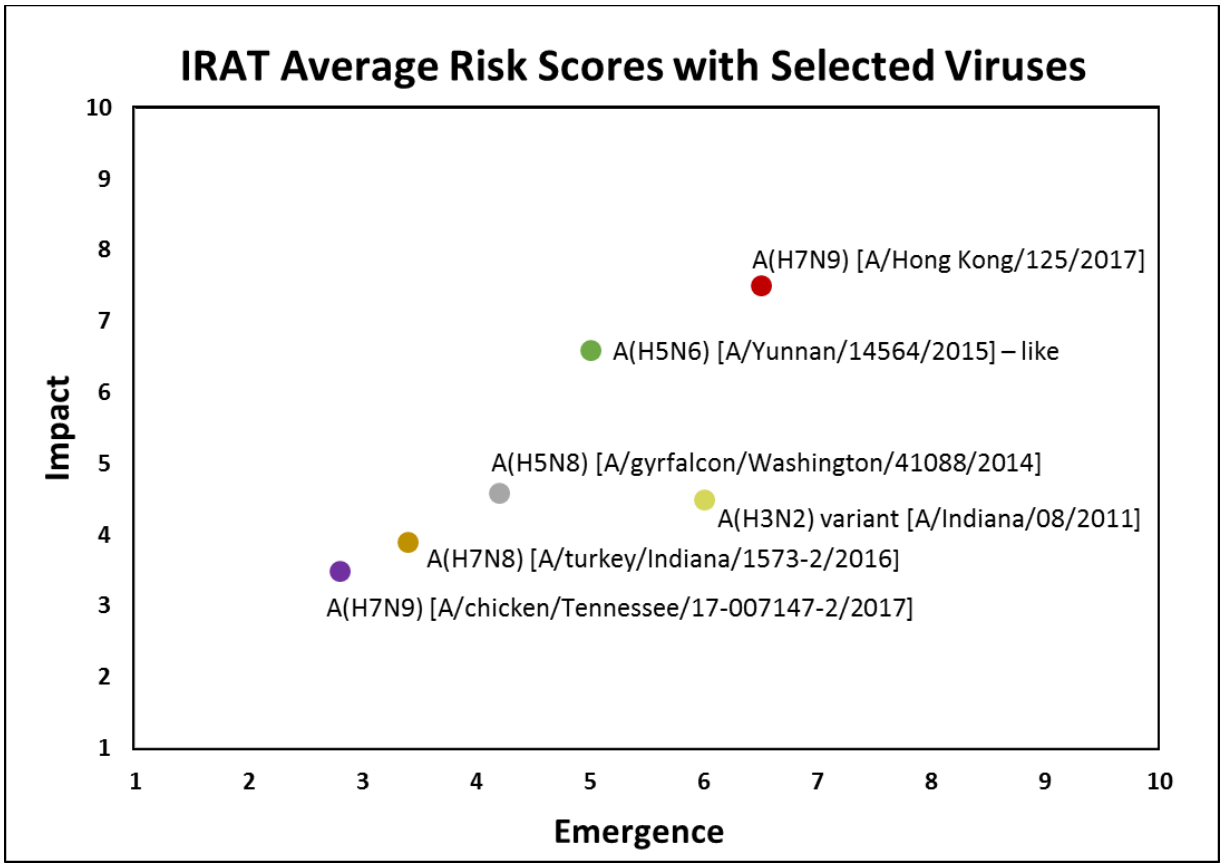

Figure 1: Average IRAT scores for HPAI A/chicken/Tennessee/17-007147-2/2017 plotted by emergence score and impact score. Additional viruses scored using IRAT are displayed for comparison.

Note: IRAT results were generated using information and data known to influenza subject matter experts at the time of the evaluation. Subsequent findings may raise or lower the overall risk scores associated with the virus.

References

1. USDA-APHIS (2017). Epidemiologic and other analyses of HPAI/LPAI affected poultry flocks: June 26, 2017 Report. USDA:APHIS:VS:STAS:Center for Epidemiology and Animal Health. Fort Collins, CO. June 2017. Doc #391.0317 V2. 39 pgs.
2. Trock SC, Burke SA, Cox NJ. Development of a framework for assessing influenza virus pandemic risk. Emerg Infect Dis. 2015;21:1372–8. http://dx.doi.org/10.3201/eid2108.141086
3. Belser JA, Brock N, Sun X, Jones J, Zanders N, Hodges E, et al. Mammalian pathogenesis and transmission of avian influenza A(H7N9) viruses, Tennessee, USA, 2017. Emerg Infect Dis. 2018 Jan 24(1): 149-152. http://doi.org/10.3201/eid2401.171574 [Note: manuscript was in preparation during IRAT evaluation, but available to IRAT SMEs for use in virus scoring]
4. Lee D, Torchetti MK, Killian M, Berhane Y, Swayne DE. Highly Pathogenic Avian Influenza A(H7N9) Virus, Tennessee, USA, March 2017. Emerg Infect Dis. 2017;23(11):1860-1863. https://dx.doi.org/10.3201/eid2311.171013 [Note: manuscript was in preparation during IRAT evaluation, but available to IRAT SMEs for use in virus scoring]