CAS Center for Influenza Research and Early-warning (CASCIRE)

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1. AIVs have not obtained the human-to-human transmissibility, and human AIV infections mainly caused by the direct contact to the diseased poultry or virus contaminated environments, e.g. live poultry markets (LPMs).

2. The novel AIVs or viral genes always originate from wild birds and transmitted by wild birds and poultry.
Constant surveillance is currently the best way to predict and identify emerging AIVs that pose a potential threat to public health.
H5N6 infected human case was identified in China

May, 2014

A total of 21 human H5N6 infected cases have been reported. 14/21 (66.7%) died.
H5N6 AIVs transmitted by wild birds

H5N6 has been transmitted into China, Japan, South Korea, Greek, Netherlands, England by migratory birds.

So, H5N6 poses a high risk to public health in the world.
The reason of the biggest outbreak of human H7N9 infections in Wave 5

The broad distribution and genetic diversity of H7N9 with mammalian adaptation and drug-resistance mutations contributed the shark increased human infections in Wave 5.

Journal of Virology. 2018
Emerging Microbes & Infection. 2019
Our Mission on Finding Emerging Viruses

Novel: Totivirus

AIV: H1, H2, H3, H4, H6, H11, H5N1, H5N6, H5N8, H7N9, H7N4, H7N3, H10N8

CoV: SADS-CoV, SVV, Flu-D

AIV: H5N1, HP-H7N9, H5N6, H5N8

Novel: Astrovirus

AIV: LP-H7N9, HP-H7N9, ZIKV, YFV, RVFV, CHIKV, DENV 1-3, VZV, PIV 1-2, ADV

Novel virus emerging in animals and humans

Gene evolution
Epidemiology
Pathogenesis
Vaccine and drug
CAS President's International Fellowship Initiative (PIFI)

- Category A: PIFI for Distinguished Scientists
- Category B: PIFI for Visiting Scientists
- Category C: PIFI for Postdoctoral Researchers
- Category D: CAS-TWAS President's Fellowship for international PhD students

CAS-TWAS: the Chinese Academy of Sciences (CAS) and The World Academy of Sciences (TWAS)
Welcome to CASCIRE

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Conclusion

H5N6 has gradually replaced H5N1 to become a dominant subtype in China.

- H5N6 is mainly spread and流行在家禽中, 但已在野鸟中分离发现;
- H5N8 is mainly spread in wild birds, and has not yet caused outbreaks in domestic poultry;
- H5N8 follows the migration of wild birds and can spread worldwide. H5N6 has the possibility of spreading in the world with wild birds;
- H5N6 and H5N8 AIV HA belong to the Clade2.3.4.4, both with a waterfowl origin virus NA(N6/N8) and LPAIV (internal gene) recombination generated.

Clade2.3.4.4 H5N6 and H5N8 are the main types of AIV流行的目前.

Risk of infection to human should not be ignored!!