Influenza A H7N9 Update

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June 20, 2013



Recognition of a Novel Influenza A H7N9

- On 31 March 2013, the China Health and Family Planning Commission notified WHO of three cases of human infection with influenza A(H7N9)^{1,2}
- Cases were from:
 - Shanghai Municipality (2 cases)
 - Anhui Province (1 case)
- All three cases presented with respiratory tract infection with progression to severe pneumonia and breathing difficulties
- Two deaths, one in critical condition

Initial H7N9 Cases in China



Initial H7N9 Cases in China



Around 575 million people, 45% of China, 8% of World

Cases of Influenza A H7N9 As of June 20, 2013

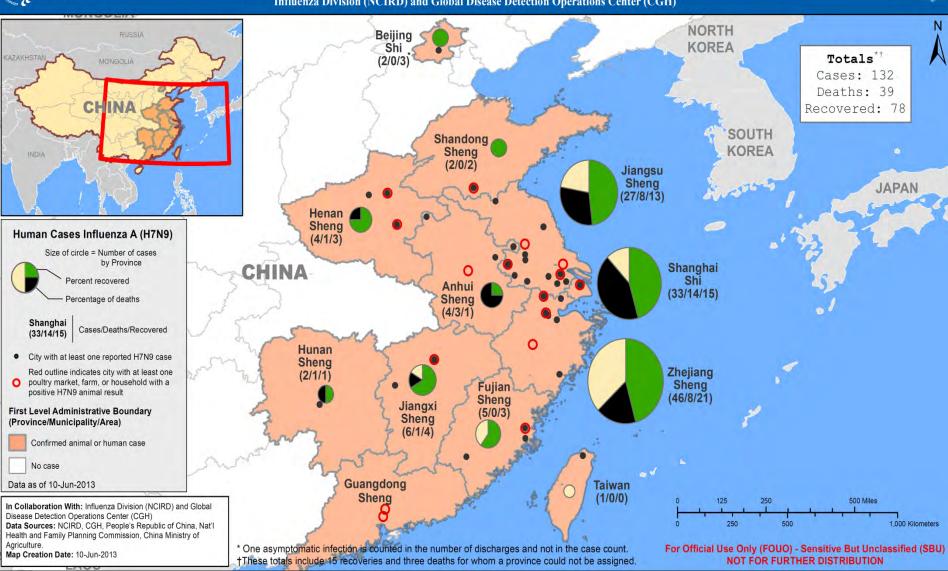
- 132 lab-confirmed cases
 - 127 (96%) hospitalized
 - 78 (59%) recovered
 - 39 (30%) dead
 - 77% exposure to live animals, mostly chickens and ducks
- Cases diagnosed in 8 provinces, 2 municipalities, and Taiwan
- 5 lab-confirmed clusters, H-H transmission possible
- 1 lab-confirmed asymptomatic infection
- >2,000 contacts followed
 - Only two were lab-confirmed positive infections
- US Suspect Cases: 67, all negative



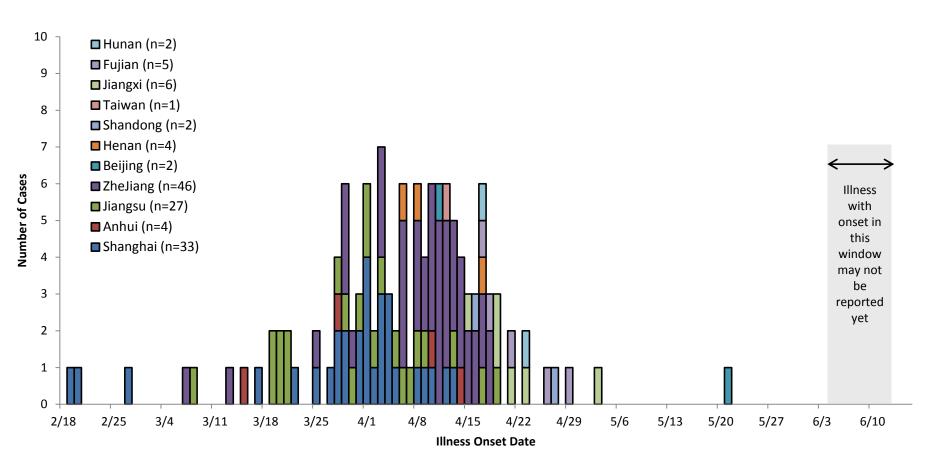
Confirmed Cases and Deaths from Avian Influenza A (H7N9), China - 2013 10-Jun-2013

SITUATION AWARENESS GIS GRASP

Influenza Division (NCIRD) and Global Disease Detection Operations Center (CGH)



Epidemic Curve of Avian Influenza A (H7N9) Virus Cases by Onset of Illness Date and Province, Municipality, or Area, 18 Feb – 13 Jun 2013 (N=132)



Demographic Information Confirmed Cases – China

Predominantly severe disease in older men with underlying conditions

	Hospitalized Cases (N=52)	Discharged Cases ¹ (N=49)	Fatal Cases ² (N=28)	Total (N=129)
Age, n (%)				
0-17 years	0 (0)	6 (12)	0 (0)	6 (5)
18-34 years	1 (2)	7 (14)	2 (7)	10 (8)
35-59 years	20 (38)	18 (37)	6 (21)	44 (34)
60-74 years	22 (42)	10 (20)	10 (36)	42 (33)
>= 75 years	9 (17)	8 (16)	10 (36)	27 (21)
Sex, n (%)				
Male	36 (69)	37 (76)	20 (71)	93 (72)
Female	16 (31)	12 (24)	8 (29)	36 (28)
Severe infection, n (%)	51 (98)	32 (65)	28 (100)	111 (86)
Underlying health conditions, n (%)				
Yes	7 (100)	4 (100)	7 (88)	18 (95)
No	0 (0)	0 (0)	1 (12)	1 (5)

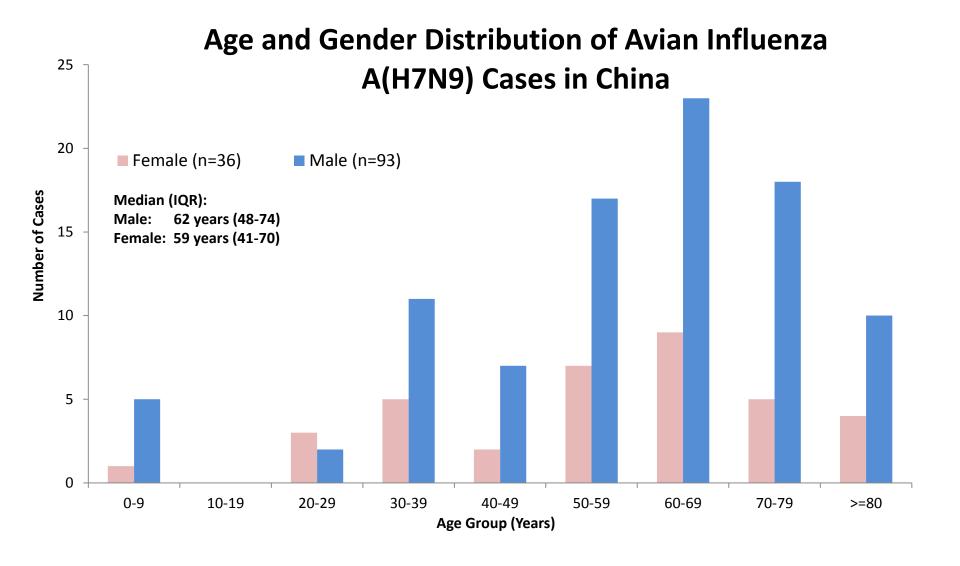
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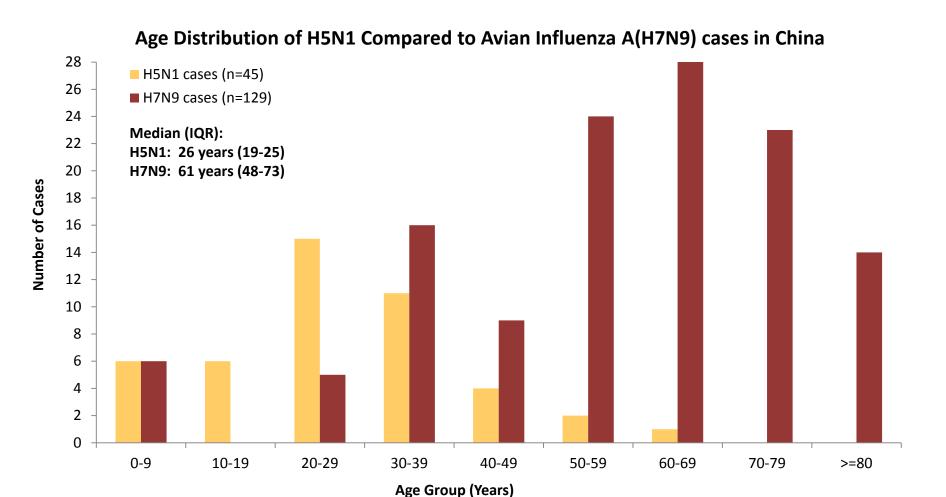
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¹Includes 2 pregnant women ²data not available for all reported cases

Prior human illness due to H7 has been mild (conjunctivitis), and only one death





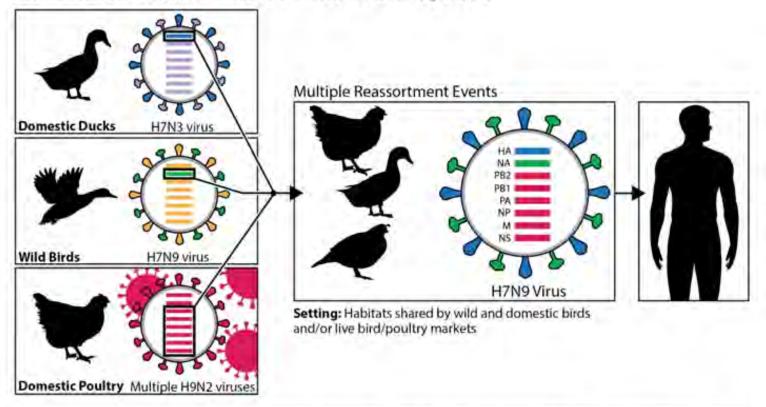
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Laboratory Investigation

- 19 partial or complete genetic sequences posted
 - All 8 genes are from avian origin
- Genetic changes in the sequences are present that have been associated with adaptations leading to:
 - Enhanced virus binding to mammalian respiratory cells
 - Enhanced replication in mammalian respiratory cells
 - Increased severity of infection
- Antiviral Susceptibility
 - Overall, susceptible to oseltamivir and zanamivir
 - One virus shows resistance to oseltamivir and zanamivir, clinical relevance is unknown
 - Resistant to amantadine and rimantadine

Genetic Evolution of H7N9 Virus in China, 2013



The eight internal genes of the H7N9 virus are closely related to avian influenza viruses found in domestic ducks, wild birds and domestic poultry in Asia. The virus likely emerged from "reassortment," a process in which two or more influenza viruses co-infect a single host and exchange genes. This can result in the creation of a new influenza virus. Experts think multiple reassortment events led to the creation of the H7N9 virus. These events may have occurred in habitats shared by will and domestic birds and/or in live bird/poultry markets, where different species of birds are bought and sold for food. As the above diagram shows, the H7N9 virus likely obtained its HA (hemagglutinin) gene from domestic ducks, its NA (neuraminidase) gene from wild birds, and its six remaining internal genes from multiple related H9N2 influenza viruses in domestic poultry.



Laboratory Investigation Serology and Vaccine Development

Serologic Studies

- Studies using the HAI and MN assays and serum from individuals vaccinated with the 2012-13 seasonal trivalent inactivated influenza vaccine show no existing cross-reactive antibodies to H7N9 either before or after vaccination in young children, adult and older adults.
- Preliminary results of NHANES sera collected from the general US population in 2010 suggest there are very little to no pre-existing cross-reactive antibodies against H7N9 in all age groups tested (6-80+ yrs)

Laboratory Investigation Serology and Vaccine Development

- Sera from individuals that had received 2 doses of a Eurasian lineage H7N7 LAIV and one dose of Eurasian H7N7 inactivated vaccine (LAIV prime and inactivated vaccine boost) showed good cross-reactivity for the H7N9 virus.
- Candidate H7N9 vaccine viruses have been developed and provided to vaccine manufacturers
- A clinical trial of inactivated, non-adjuvanted, vaccine is planned
- Decisions for stockpiling H7 vaccine are under discussion

Animal Investigation



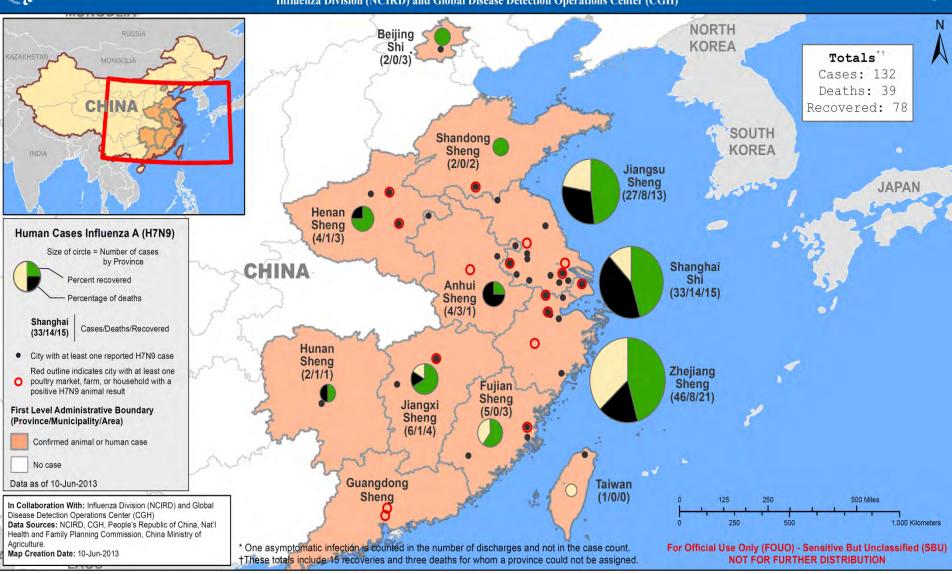
- While humans have severe disease, testing indicates:
 - Chickens and quail show <u>NO</u> signs of illness, but
 - Birds are shedding virus well
- H7N9 has been confirmed in:
 - Chickens, ducks, pigeons (feral and captive), and environmental specimens
 - Live bird markets
 - >4,000 swine have been tested in China, and are reported negative
- In the US, ongoing surveillance has not identified H7N9 viruses in tested birds



Confirmed Cases and Deaths from Avian Influenza A (H7N9), China – 2013 10-Jun-2013

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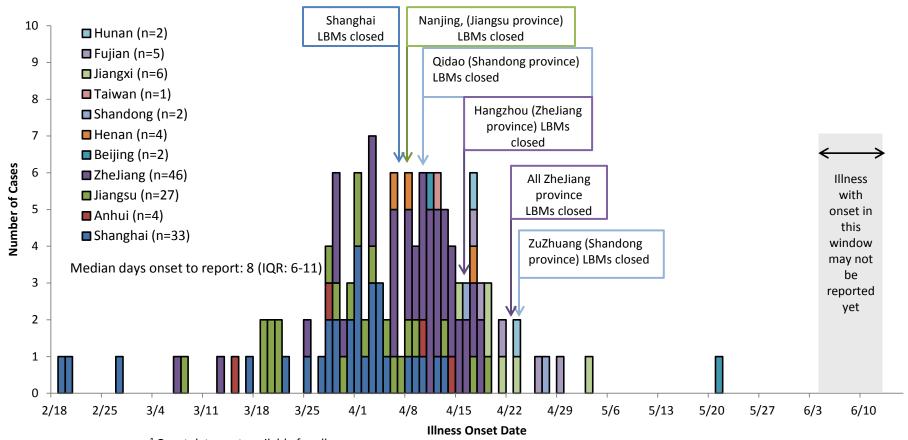
Shanghai Live Bird Markets







Epi-Curve of Avian Influenza A (H7N9) Virus Cases by Onset of Illness Date and Province, Municipality, or Area, 18 Feb – 13 Jun 2013 (N=132)



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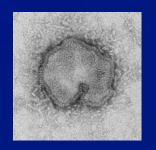
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Conclusions

- Recognition and response has been faster and more transparent than in the past
- Public Health Concerns Persist
 - High severity of illness
 - Genetic changes in H7N9 associated with mammalian adaptation and transmission
 - Birds may shed virus without symptoms
 - Challenge for control efforts
 - Ongoing surveillance in animals is needed
- No new H7N9 cases with onset after May 21, 2013
 - Effect of live bird market closure? Seasonal factors? Will cases recur in the fall?
 - No evidence of sustained human to human spread
 - Ongoing surveillance in humans is needed
 - Vaccines being developed and evaluated



Questions? Daniel Jernigan, MD MPH dbj0@cdc.gov



Acknowledgements

CDC, Atlanta

Danielle Iuliano

Marc-Alain Widdowson

Lyn Finelli

Joseph Bresee

Ann Moen

Jackie Katz

Min Levine

Terry Tumpey

Elise Lockamy

Sue Trock

Ruben Donis

CDC, Atlanta

Julie Villanueva

Larisa Gubareva

James Stevens

Todd Davis

Xu Xiyan

Steve Lindstrom

Michael Shaw

Nancy Cox

Steve Redd

Sonja Rasmussen

...and many others

Chinese Center for Disease Control and

Prevention, Beijing

Tom Gomez

US Department of Agriculture

Div Global Migration and Quarantine,

NCEZID, CDC

Div State and Local Readiness,

OPHPR, CDC

Immunization Services Division, NCIRD,

CDC

