

# HPAI outbreaks in Korea: characteristics of 3 past epidemics

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#### Introduction

Korea experienced three Highly Pathogenic Avian Influenza (HPAI) epidemics, during  $^{\circ}03/^{\circ}04$ ,  $^{\circ}06/^{\circ}07$  and  $^{\circ}08$ . During the  $^{\circ}03/^{\circ}04$  and  $^{\circ}06/^{\circ}07$  epidemics, many of the farms affected were integrated poultry farms that were infected by people, vehicles and equipment contaminated with the virus. However, in '08, additional pattern of spread was identified that involved small-scale poultry dealers and their sale of infected poultry, contaminated transportation vehicles, and contaminated loading and unloading areas at live bird markets. Here we present the major characteristics of the 3 HPAI epidemics in Korea, with an emphasis on the most recent '08 epidemic.

## Materials and Methods

Epidemiological investigations were carried out, through examination of the infected premises (IPs) and facilities, interview with farm owner and staff, review of records, trace-back and trace-forward investigations to identify possible sources and dangerous contacts, analysis of genetic and pathological characteristics, and analysis of surveillance results including wild bird surveillance.

## '03/'04 HPAI epidemic

A total of 19 outbreaks of HPAI were reported from 10 December '03 to 20 March '04 (Fig. 1, 2). The infected premises (IPs) included 10 chicken and 9 duck farms, which were located in 10 administrative areas of Shi/Gun/Gu.

All H5N1 viruses isolated during  $^{\circ}03/^{\circ}04$  were part of clade 2.2 and the homology of the HA and NA genes were between 99.3–99.9%, indicating that they were all from the same virus.

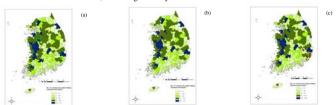


Fig. 1. Map of 3 HPAI epidemics in Korea: '03/'04 epidemic (a), '06/'07 epidemic (b) and '08 epidemic (c). Coloured circles represent outbreak areas.



Fig. 2. Epidemic curve of 3 HPAI epidemics in Korea: '03/'04 epidemic (a); '06/'07 epidemic (b) and '08 epidemic (c).

Region	Infected premises	Breed	Transmission		Source
			Most likely	2 <sup>nd</sup> most likely	1
Eumsung,	IP1	Broiler breeder	Local	Wild birds/animals	IP2
Chungbuk province	IP2	Breeder ducks	Vehicles/equipment	Wild birds/animals	IP10
	IP3	Layers	Vehicles/equipment		IP5/IP4
	IP5	Breeder ducks	Movement of poultry	People	IP2
	IP4	Breeder ducks	Local	Vehicles	IP5
Jincheon, Chungbuk province	IP10	Breeder ducks	Vehicles/equipment	People	
Icheon, Gyeonggi province	IP12	Layers	Vehicles/equipment	People	IP5/IP4
Yangju, Gyeonggi province	IP19	Layers	Vehicles/equipment		
Cheonan, Chungnam province	IP6	Breeder ducks (GPS)	Vehicles/equipment	People	IP9
	IP9	Breeder duck	Wild birds/animals	Vehicles/equipment	
	IP13	Broilers	Local	Vehicles/equipment	IP9
	IP15	Breeder ducks	People	Vehicles/equipment	IP9
	IP17	Layers	Vehicles/equipment	Wild birds/animals	
Asan, Chungnam province	IP18	Breeder ducks	Vehicles/equipment		IP15
Naju, Jeonnam province	IP8	Broiler ducks	Vehicles/equipment	People	IP6
Gyeongju, Gyeongbuk province	IP7	Layers	Local		
	IP11	Layers	Local		
Eulju, Ulsan	IP14	Korean native chicken, ducks	Vehicles/equipment	People	
Yangsan, Gyeongnam province	IP16	Layers	Vehicles/equipment	People	

# '06/'07 HPAI epidemic

A total of 7 notified outbreaks of HPAI were confirmed from 22 November '06 to 6 March '07 (Fig. 1, 2). Farms affected included 2 duck farms, 4 chicken farms and 1 quail farm, which were located in 3 provinces of Jeonbuk, Chungnam and Gyeonggi.

HPAI H5N1 viruses isolated during '06/'07 all belonged to the Qinghai-like H5N1 HPAI virus group (later grouped in clade 2.5). The homology of the HA gene between the 7 isolates were 99.1% ~ 100%. The viruses were highly pathogenic in chickens and quail while only mild symptoms were observed in ducks, which could have delayed identification of infected duck farms.

For the introduction of HPAI H5N1 to the country, migratory birds were determined to be the most likely source of introduction based on the following evidence: a. Proximity of migratory bird habitats with IPs

- b. Migration of known susceptible species from countries with HPAI outbreaks c. Seasonality of HPAI outbreaks consistent with arrival of migratory birds
- d. Isolation of H5N1 HPAI viruses from fecal samples collected from migratory bird habitats
- e. Detection of H5 antibodies in wild (migratory) ducks

Possible modes of introduction into IPs include contamination of the farm premises by people and vehicles contaminated with the virus, possibly from bird feces, and subsequent introduction into the housed birds by people with contaminated footwear.

Table 2. Possible transmission routes identified during the '06/'07 HPAI outbreaks in Korea

IP	Species	Introduction - farm	Introduction - bird house		
IP1	Broiler breeder	Wild birds, weight measurement team, manure, packaged feed delivery, egg tray	Owner, weight measurement team, bedding, bagged feed delivery, egg tray		
IP2	Broiler breeder	Wild birds, Neighboring farm, bulk feed, bedding	Owner, employee, bedding		
IP3	Quail	Wild birds, Owner, employees, bagged feed delivery,	Owner, employees, bagged feed delivery		
IP4	Breeder duck	Wild birds, Owner, employees, neighboring farm	Wild birds, owner, employees		
IP5	Layer	Wild birds, egg collection, owner, feed delivery, vet drugs, neighboring farm	Owner, employee, vet drugs		
IP6	Layer	Egg collection, feed delivery, vet drugs	Owner, employee		
IP7	Breeder duck	Employee, egg collection	Employee, egg collection		

### '08 HPAI epidemic

A total of 33 outbreaks were reported from 1 April '08 to 12 May '08 (Fig. 1, 2). The IPs included 21 chicken farms, 6 duck farms, and 6 farms rearing mixed species of poultry, which were located in 19 administrative areas of Shi/Gun/Gu. In addition, a total of 65 HPAI infected farms were identified in the control zones through various surveillance activities.

All H5N1 viruses isolated in '08 were within clade 2.3.2, belonging to a different group from the viruses isolated during the previous epidemics. This supports the view that the outbreaks in '08 we also due to a reincursion. The homology of the HA gene between 17 virus isolates representing 16 regions were 99.4%  $\sim$  100%. The '08 virus isolates were highly pathogenic in chickens, and in contrast to the previous epidemics, were pathogenic in ducks.

For the introduction into the country, the most likely source was concluded to be migratory birds based on the following evidence:

- a. Proximity of migratory bird habitats with IPs b. Migration of known susceptible species from countries with HPAI outbreaks
- c. Genetic similarity of the Korean virus isolates with those from wild swans in Japan
- d. Detection of H5 antibodies in wild (migratory) ducks

For the spread of disease among farms, movement of poultry, people, vehicles, live-bird markets and local spread was involved. Early part of the epidemic was focused in the southwest region involving mostly large scale production farms (Fig. 3). Transmission was likely due to movement of people and vehicles including those for feed delivery and movement of live poultry. Latter part of the epidemic was focused in the southeast region involving mostly small scale farms (Fig. 4). Transmission in this region was largely by small-scale poultry dealers, which involved movement of infected poultry and contaminated loading and unloading areas at traditional outdoor markets.

Table 3. Transmission routes identified during the '08 HPAI outbreaks in Korea

Factor \ Region	Seoul	Gyeonggi	Gangwon	Chungnam	Jeolla	Gyeongsang	Total
Consultant					3		3
Feed delivery		1		1	9	3	14
Market	2	- 1				5	8
Visit IP					10		10
Local					31	2	33
Feces collection					2		2
Infected bird			2		2	20	24
Removal of birds		1					1
Drug delivery						1	1
Wild birds					2		2
Total	2	3	2	1	59	31	98

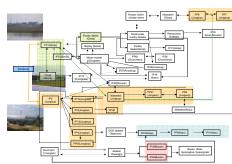


Fig. 3. Diagram of major route of transmission for southwest and middle regions of Korea

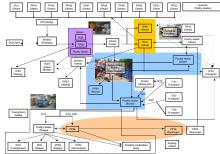


Fig. 4. Diagram of major route of transmission for southeast regions of Korea

## Conclusions

Introduction of HPAI H5N1 virus into the country was most likely by infected migratory birds for all 3 epidemics. The rapid spread of HPAI across the country in '08 was largely due to movement of poultry by small-scale poultry dealers involving traditional markets. This was in contrast to the previous HPAI outbreaks, which were largely due to farm to farm spread through indirect contact. The findings demonstrates the importance of on-farm bio-security measures, in particular for footwear, and the increased need for control measures for movement of poultry by small-scale poultry dealers.

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