Surveillance for H_5N_1 Highly Pathogenic Avian Influenza in Wild Birds in Thailand

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Introduction

There have been four outbreaks of avian influenza H_5N_1, known as Highly Pathogenic Avian Influenza (HPAI), in poultry in Thailand between 2004–2006(1). The outbreaks occurred in different locations in over 50 provinces (2). As a result, national disease surveillance programs for HPAI were conducted by the Government of Thailand with the aim of surveying and monitoring viral persistence in both poultry and wild bird populations. The national surveillance program in poultry, known as the "X-ray survey", was launched by the Department of Livestock Development (DLD) at the end of September 2004 with the aim to provide active surveillance for HPAI H_5N_1 throughout the country (3).

Materials and Methods

Wild bird surveillance programs for HPAI have been conducted in Thailand since January 2004 by the Department of National Parks, Wildlife and Plant Conservation (DNWPC) (4) and the Monitoring and Surveillance Center for Zoonotic Diseases in Wildlife and Exotic Animals, Faculty of Veterinary Science, Mahidol University (VSMU). Thus, some samples and specimens in this study were collected and submitted from DNWPC via their wild bird surveillance program, while others were from the active surveillance program, a result of cooperation between Mahidol University and DNWPC.

Samples were collected from wild birds using various methods including mist netting, baiting and netting, trapping, manual catching, or scarified by shooting. Samples were also collected from wild bird carcasses or from fresh faecal material beneath roosting sites. Samples collected included tracheal (or choanal) and cloacal swabs, serum and faeces from live birds and whole carcasses. Swab specimens from the same bird species collected at the same location and time were pooled (up to four individuals per tube) and then tested as a single sample. Specimens were tested by virus culture in MDCK cells and then haemagglutination tests (HA) with confirmation by conventional reverse transcribed PCR tests (RT-PCR), using universal primer (5) for reverses transcription and using specific primers (6) to detect H5 (7), N1(8), and M gene (9,10). Some samples were also tested by real-time RT-PCR that was described by Spackman et al (11). Disease surveillance data was analyzed using the SPSS program (SPSS 13.0 for Windows).

Results and Discussion

The study revealed that the prevalence of infection with H_5N_1 in wild birds was low (0.8% with 95% confidence intervals 0.6%, 1.0%, out of 5,246 pooled samples). The yearly prevalence varied considerably over this period with a peak of 2.7% (with 95%CI 1.4, 4.1) in 2004, 0.5% (with 95%CI 0.3, 0.8) and 0.6% (with 95%CI 0.3, 1.0) in 2005 and 2006 respectively. During this period twelve species of wild birds were positive for H_5N_1 virus infection (Table1). Infected wild bird samples were only found in provinces where poultry outbreaks had occurred. Detection of H_5N_1 virus infection in wild birds was reported up to three years after control of the /poultry outbreaks in the provinces where outbreaks occurred.

Table 1: Number of wild bird samples positive and negative for HPAI H_5N_1

Wild bird species	Number of positive samples		
	Positive	Total	% Positive (95% CI)
Asian Open-bill stork	17	937	1.8 (1.0, 2.7)
Rock Pigeon	13	953	1.4 (0.6, 2.1)
Tree Sparrow	3	697	0.4 (0.0, 0.9)
Common Myna	1	184	0.5 (0.0, 1.6)
Heron species*	1	145	0.7 (0.0, 2.0)
Dove species*	1	51	2.0 (0.0, 5.8)
Brown-headed Gull	1	49	2.0 (0.0, 6.0)
Duck species*	1	29	3.4 (0.0, 10.1)
Asian Pied Starling	1	15	6.7 (0.0, 19.3)
Kentish Plover	1	4	25.0 (0.0, 67.4)
Common Koel	1	3	33.3 (0.0, 86.7)
Black Drongo	1	3	33.3 (0.0, 86.7)

* indicates that genus and species level were not reported in field data records.

Other results from the surveillance program demonstrated that there was no significant difference between prevalence of waterfowl and non waterfowl groups (p=0.5); specimens from carcasses were significantly more likely to be positive than swabs ($p<0.0001$); specimens from dead birds were significantly more likely to be HPAI H_5N_1 positive than those from live birds with a healthy appearance ($p<0.0001$); some wild bird species were less susceptible to the virus than others as there were some positive samples from apparently healthy wild birds, and the H_5N_1 virus was shown to be mainly circulating in wild bird populations in areas where domestic poultry outbreaks had occurred. The HPAI H_5N_1 outbreaks in wild birds were significantly higher in winter which is similar to the poultry outbreaks.

Conclusion

For a complete understanding of the mechanisms of persistence and ongoing transmission of the H_5N_1 virus in Thailand, and the role played by natural reservoirs further investigation into the transmission pathways involving wild birds and domestic poultry will be required.

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Biographical sketch

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