

Emergency surveillance for novel influenza A(H7N9) virus in domestic poultry, feral pigeons and other wild birds in Bhutan

T. Tenzin ^{(1)*}, S. Tenzin ⁽¹⁾, D. Tshering ⁽¹⁾, K. Lhamo ⁽¹⁾, P.B. Rai ⁽¹⁾,
N. Dahal ⁽²⁾ & K. Dukpa ⁽¹⁾

(1) National Centre for Animal Health, Department of Livestock, Serbithang, Post Box 155, Thimphu, Bhutan

(2) Animal Health Division, Department of Livestock, Post Box 113, Thimphu, Bhutan

*Corresponding author: tenzinvp@gmail.com; tenzin.tenzin@yahoo.co.uk

Summary

Following the March 2013 outbreak of novel avian influenza A(H7N9) virus in humans and the subsequent isolation of the virus from chickens, ducks and pigeons in the People's Republic of China, concerns were raised that the H7N9 virus would spread beyond China through the poultry value chain linking to a number of bordering countries. For this reason, a rapid emergency surveillance exercise took place in Bhutan between May and July 2013 with the objective of determining whether influenza A(H7N9) virus was silently circulating in domestic poultry and wild birds in Bhutan. A total of 1,716 oropharyngeal, tracheal and cloacal swabs together with faecal droppings were collected from poultry, wild birds and feral pigeons throughout the country; these samples included 150 that had been previously collected for surveillance of influenza A(H5N1) virus. Overall, 733 of the samples were tested. A QIAamp[®] Viral RNA Mini K kit was used to extract viral RNA from a mix of oropharyngeal, tracheal and cloacal swabs and faecal droppings. The matrix gene of avian influenza type A virus was detected using a specific real-time quantitative reverse-transcription polymerase chain reaction (RT-PCR) assay, and positive samples were further tested in RT-PCR for simultaneous detection of the H7 and N9 genes. Among the 733 samples tested, 46 (26 prospective, 20 retrospective) were confirmed positive for influenza A, a prevalence of 6.3% (95% CI: 4.6 to 8.3). The influenza A-positive samples were from areas in the south of Bhutan that had experienced previous outbreaks of highly pathogenic influenza A(H5N1). None of the samples tested positive for H7N9 strains, providing evidence that influenza A(H7N9) virus was not present in the sampled population. A risk-based approach for surveillance of influenza A(H7N9) and H5N1 is recommended in Bhutan, based on the epidemiology of the disease in China and other countries in South and Southeast Asia.

Keywords

Bhutan – Emergency surveillance – Novel avian influenza A(H7N9) virus – Poultry – Wild bird.

Introduction

On 31 March 2013, in accordance with the International Health Regulations (1), the authorities of the People's Republic of China notified the World Health Organization (WHO) of three human cases of infection with a novel influenza A(H7N9) virus in eastern China (Shanghai, Anhui Province). Following that report, H7N9 was the subject of increasing global attention because of the growing number of new cases, accompanied by a relatively high mortality

rate, in other provinces in China (2, 3). By 31 May 2013, a total of 132 laboratory-confirmed human cases, of which 39 were fatal, had been reported from eight provinces (1). A further two cases were reported in July. In October the same year the disease re-emerged with a second wave of human cases reported from a number of provinces in China (4, 5, 6). At the same time, H7N9 virus was laboratory-confirmed in poultry. Environmental samples and epidemiological and virological studies have shown that human infection appears to be associated with exposure

to live poultry or contaminated environments, including markets where live poultry are sold (1, 7, 8, 9, 10). Thus, the human H7N9 virus has been identified as the product of reassortment of viruses of avian origin (10). Another important feature of this novel influenza virus is that it shows low pathogenicity in wild birds and domestic poultry, infection resulting only in subclinical or mild disease. This is important, because potentially there could be a silent widespread epizootic in China and its neighbouring countries (2). The emergence and discovery of this novel influenza A(H7N9) virus in humans and poultry is of major public health significance and raises many global public health concerns (1, 2, 3, 11).

As an immediate first step, the Food and Agriculture Organization of the United Nations (FAO) initiated and funded emergency surveillance in China and other high-risk countries in South and Southeast Asia with the explicit aim of determining how widely the virus had spread outside the infected provinces/municipalities in China and how far it had spread in neighbouring at-risk countries (12). The information from these studies was expected to be used to strengthen future medium- to long-term surveillance strategies in the region and to monitor incursion and spread of the virus into uninfected areas (12). Bhutan, with other countries in Southeast (China, Vietnam, Cambodia, the Lao People's Democratic Republic (Lao PDR), Indonesia, Myanmar) and South (Bangladesh, Nepal) Asia, was considered to be at high risk for the spread of this novel influenza A(H7N9) virus because of its geographical proximity to China, the presence of bird migration pathways and the possibility that spread might occur from neighbouring countries through trade in poultry and/or poultry products (12).

Possible scenarios for the introduction of this novel avian influenza H7N9 virus into Bhutan are:

- imported human cases
- detection of cases in migratory birds but not in poultry or humans
- detection of cases in migratory birds and poultry but not in humans
- detection of cases in migratory birds, poultry and humans.

It was concluded, therefore, that there was a definite risk of incursion of virus into Bhutan and, for this reason, guidelines for surveillance and contingency plans for each of the possible scenarios of introduction were developed.

In February 2010, Bhutan experienced its first outbreak of the highly pathogenic avian influenza (H5N1) virus in backyard poultry farms in the south-west of the country,

close to the Indian state of West Bengal (13, 14). Up to January 2014, at least seven district-level outbreaks were reported in six districts of Bhutan. All the outbreaks were quickly controlled through stamping-out procedures and no human cases of H5N1 were reported, but the outbreaks had a serious economic impact on poultry farmers and on the government (14). The emergence of novel influenza A(H7N9) virus in China heightened public health concern in Bhutan and emergency surveillance was recommended.

The main objective of the emergency surveillance programme was to determine whether H7N9 virus was circulating in domestic poultry and wild birds, including feral pigeons, in Bhutan, and how widely the virus had spread outside the current infection foci in China. The information would be used to strengthen Bhutan's capacity for laboratory and clinical surveillance.

Materials and methods

Between May and July 2013, a total of 1,716 oropharyngeal, tracheal and cloacal samples from domestic poultry in backyards and commercial farms, together with fresh faecal droppings of feral pigeons and other wild birds, were collected from carefully selected high-risk villages in 15 districts of Bhutan (Fig. 1, Table I). A risk-based surveillance approach was adopted by selecting villages/sites that were known to have had outbreaks of highly pathogenic avian influenza (HPAI) (H5N1), and to have a relatively high density of poultry with increased human activity, and/or were habitat areas for migratory birds. The surveillance strategy was designed to provide 95% confidence that infection would be detected at a prevalence of 0.04% in an estimated poultry population of 0.2 million using a test with 100% sensitivity and specificity. To fulfil these requirements 1,490 samples were needed. To allow for any damage and wastage of samples during shipment to the laboratory or at the time of processing, a total of 1,716 samples were collected by the sampling team. The 82 selected villages/sites had similar poultry populations and an average of 21 samples was collected at each one. Systematic random sampling, based on the approximate estimated poultry population in each village/site, was used until the required numbers of samples were collected. Samples from wild birds were taken randomly from sites close to or in contact with domestic poultry.

All samples were transported to the National Centre for Animal Health at Thimphu, with strict maintenance of the cold chain, and were stored at -80°C . For logistical reasons and because of time constraints, only 583 of the prospectively collected samples were tested in polymerase chain reaction (PCR) assay. To determine whether the novel virus had already been circulating silently in the poultry

Table I
Overall prevalence of influenza A virus in poultry and wild bird species in Bhutan

District	Number of samples tested			Number of influenza A positives			% Prevalence (95% CI) ^(c)
	Wild birds ^(a)	Poultry ^(b)	Total	Wild birds	Poultry	Total	
<i>Prospectively collected samples:</i>							
Chukha	93	75	168	11	5	16	9.5 (5.9–15)
Dagana	21	14	35	0	1	1	2.8 (0.5–15)
Samtse	36	43	79	2	2	4	5.1 (1.9–12.3)
Sarpang	45	32	77	5	0	5	6.5 (2.8–14.3)
Haa	6	16	22				
Paro	15	15	30				
Punakha	2	3	5				
Samdrup Jongkhar	23	6	29				
Bumthang	12	5	17				
Thimphu	38	10	48				
Trashigang	4	7	11				
Trashiyangtse	2	6	8				
Trongsa	9	9	18				
Tsirang	11	16	27				
Wangdue	2	7	9				
Total	319	264	583	18	8	26	4.5 (3.1–6.5)
<i>Retrospective samples:</i>							
Chukha	27	28	55	6	4	10	18.2 (10.2–30.3)
Samtse	15	17	32	0	5	5	15.6 (6.9–31.7)
Sarpang	15	15	30	1	4	5	16.6 (7.3–33.6)
Dagana	4	2	6				
Punakha	3	1	4				
Samdrup Jongkhar	11	1	12				
Bumthang	2	0	2				
Thimphu	0	2	2				
Trashiyangtse	1	0	1				
Tsirang	4	1	5				
Wangdue	1	0	1				
Total	83	67	150	7	13	20	13.3 (8.8–19.7)

a) Includes crows, feral pigeons and other wild birds

b) Includes chickens, ducks and geese

c) Influenza A-positive samples per 100 samples tested

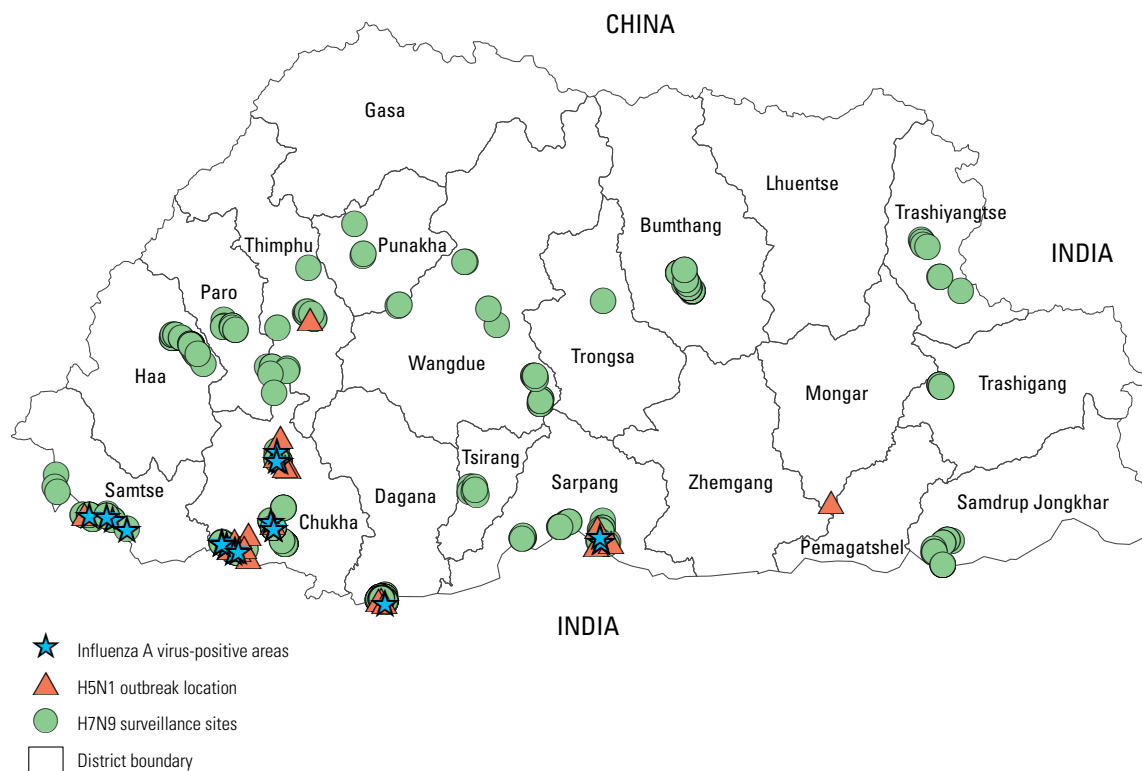


Fig. 1
Influenza A(H7N9) emergency surveillance sampling sites, A(H5N1) outbreak areas (February 2010 to January 2013) and areas of avian influenza A virus-positive poultry and wild birds in Bhutan

and wild bird population prior to the first report of the first outbreak in China (Table I), a further 150 stored samples previously collected from poultry and wild birds between January and May 2013 for HPAI (H5N1) surveillance were tested for avian influenza virus and strain H7N9. Thus, a total of 733 samples (583 prospective, 150 retrospective) were tested on the assumption that they might be influenza positive, based on details of when, where and from which species they were collected.

The RNA was extracted from a mix of oropharyngeal, tracheal and cloacal swabs and faecal droppings using a QIAamp® Viral RNA Mini Kit (Qiagen, GmbH, Hilden, Germany) according to the manufacturer's instructions. A manual centrifugation method was used. Samples were amplified using a Superscript® III Platinum® One-step quantitative reverse-transcription PCR (qRT-PCR) Kit (Invitrogen, Carlsbad, California, USA) in a Bio-Rad IQ™5 multiplex real-time PCR system for the detection of type A avian influenza viruses by targeting the matrix gene. Primers and probes were supplied by the Australian Animal Health Laboratory (AAHL) of the Commonwealth Scientific and Industrial Research Organisation (CSIRO) in Geelong, Australia: forward primer 5'-AGATGAGYCTTCTAACCGAGGTCG-3', reverse primer 5'-TGCAAANACATCYTCAAGTCTCTG-3' and probe

5'-FAM-TTTGTATTACGCTCACCGTGCCCA-BHQ1-3'. Samples that tested positive for avian influenza virus were used for further H7 subtype identification in a Superscript® III Platinum® One-step qRT-PCR Kit and an FLI H7 real-time RT-PCR kit (AAHL, CSIRO): forward primer 5'-AYAGAATACAGATWGACCCAGT-3', reverse primer 5'-TAGTGCACYGCATGTTTCCA-3' and probe 5'-FAM-TGGTTTAGCTTCGGGGCATCATG-BHQ1-3'. Since none of the samples tested positive for the H7 strain, no further testing was carried out to identify N9 strains.

Results and discussion

Of the 733 samples tested, 46 (6.3%, 95% CI 4.6 to 8.3) were positive for influenza type A virus: 26 of 583 prospectively collected samples (4.5%, 95% CI 2.9 to 6.5); 20 of 150 retrospectively collected samples (13.3%, 95% CI 8.3 to 20). None of the samples tested positive for the H7 strain, indicating that the novel avian influenza A(H7N9) virus was not circulating in the sampled population in Bhutan in July 2013 (Table I).

Similar surveillance findings have been reported in Southeast (Vietnam, Cambodia, Lao PDR, Myanmar, Indonesia) and South (Bangladesh, Nepal) Asian countries where influenza

A has been detected but not the novel H7N9 strains (FAO, unpublished reports). This provides some reassurance that A(H7N9) virus is not circulating in poultry and wild birds beyond China, although imported human cases have been reported in Malaysia, Hong Kong and Chinese Taipei (15, 16, 17). Nevertheless, vigilance and targeted surveillance are recommended, particularly during the winter, as previous outbreaks of A(H5N1) in Bhutan have occurred between December and February (13, 14) and because there were reports of a second wave of A(H7N9) human cases in China after October 2013 (5). The FAO and WHO have also warned of a rising number of human cases and have called on countries neighbouring China to exercise increased vigilance and strengthen preparedness for A(H7N9) and other avian influenza viruses, such as A(H5N1) (11). Although Bhutan has been carrying out surveillance for H5N1 virus in domestic poultry, water fowl, and wild and migratory birds following outbreaks in Bhutan and neighbouring countries, there was no testing for influenza A(H7N9) prior to the present study, which was the first emergency surveillance study on novel influenza A(H7N9) virus in Bhutan. With the establishment and strengthening of laboratory diagnostic facilities in Bhutan, it is expected that surveillance and preparedness for avian influenza incursions will be enhanced.

The influenza A-positive samples in this study, both prospectively and retrospectively collected, were from the four districts in the south of Bhutan (Samtse, Chukha, Sarpang, Dagana) that had reported outbreaks of influenza A(H5N1) between February 2010 and January 2013 (Fig. 1). This could be an indication of the establishment and adaptation of the virus to the local environmental conditions in these high-risk areas. Chukha district (Fig. 1, Table I) reported the highest prevalence of influenza A and also reported outbreaks of HPAI (H5N1) for the four consecutive years 2010 to 2013 (12, 13). Influenza A viruses were detected in all bird species tested (poultry, feral pigeons, wild birds). Risk-based surveillance is recommended in this area of Bhutan to detect circulating influenza A(H7N9) virus and other influenza strains in poultry and wild birds and, ultimately, to prevent infection in humans.

Conclusions

Tests on 150 samples from poultry and wild birds collected between January and May 2013 and 583 samples collected between May and July 2013 were all negative for avian influenza A(H7N9). If avian influenza A(H7N9) infection was present in Bhutan at the time of sampling it is 95% certain that the prevalence of infection was below 0.04%.

Poultry in areas of Bhutan that had previously recorded outbreaks of HPAI (H5N1) tested positive for influenza A virus. In acknowledging that incursion of virus into the country could occur at any time, a risk-based approach to serological and virological surveillance for A(H7N9) is recommended in Bhutan. The disease situation in China and other countries in South and Southeast Asia should be monitored on an ongoing basis and testing for influenza A(H5N1) should be carried out, particularly during winter months.

Contingency plans for responding to any possible incursion of virus into the country should be prepared.

Acknowledgements

The authors thank the FAO Regional Office for Asia and the Pacific in Bangkok for funding support (OSRO/GLO/302/USA) for the emergency surveillance in Bhutan. The field veterinary officials and laboratory technicians are also acknowledged for their assistance during the emergency surveillance and sampling.

Surveillance d'urgence d'un nouveau virus influenza A(H7N9) chez les volailles domestiques, les pigeons retournés à l'état sauvage et l'avifaune au Bhoutan

T. Tenzin, S. Tenzin, D. Tshering, K. Lhamo, P.B. Rai, N. Dahal & K. Dukpa

Résumé

La survenue en mars 2013 d'un foyer d'infection humaine dû au nouveau virus de l'influenza aviaire A(H7N9) et l'isolement ultérieur de ce virus chez des poulets, des canards et des pigeons en Chine ont fait prendre conscience du risque de propagation du virus H7N9 en dehors de la Chine via la filière de production de volailles qui a des ramifications dans plusieurs pays frontaliers. Le Bhoutan a donc décidé de conduire immédiatement un exercice de surveillance d'urgence, qui s'est déroulé de mai à juillet 2013 pour détecter une éventuelle circulation à bas bruit du virus A(H7N9) dans les populations de volailles domestiques et d'oiseaux sauvages du pays. Dans ce cadre, 1 716 écouvillons oropharyngés, trachéaux et cloacaux ont été prélevés sur des volailles, des oiseaux sauvages et des pigeons retournés à l'état sauvage dans tout le pays ; parmi ces échantillons figuraient 150 prélèvements collectés antérieurement à des fins de surveillance du virus influenza A(H5N1). En tout, 733 de ces écouvillons ont été testés. L'ARN viral présent dans un mélange d'écouvillons oropharyngés, trachéaux et cloacaux et de fèces a été extrait au moyen du kit de diagnostic QIAamp[®] Viral RNA Mini Kit. Le gène de la matrice du virus de l'influenza aviaire de type A a été détecté au moyen d'une amplification en chaîne par polymérase en temps réel couplée à une transcription inverse qRP-PCR ; les échantillons positifs à ce test ont ensuite été soumis à une nouvelle qRP-PCR visant cette fois-ci à détecter simultanément les gènes spécifiques des virus H7 et N9. Au total, la présence du virus de type A a été décelée dans 46 des 733 échantillons testés (soit 26 prélèvements prospectifs et 20 prélèvements rétrospectifs) ce qui représente une prévalence de 6,3 % (intervalle de confiance à 95 % compris entre 4,6 et 8,3). Les échantillons positifs provenaient de diverses zones méridionales du Bhoutan ayant déjà enregistré des foyers d'influenza aviaire hautement pathogène dus au virus A(H5N1) dans le passé. Aucun échantillon ne contenait la souche H7N9, ce qui démontre l'absence du virus influenza A(H7N9) dans la population prélevée. En se basant sur l'épidémiologie de la maladie en Chine et dans d'autres pays d'Asie du Sud et du Sud-Est, les auteurs préconisent d'exercer une surveillance des virus influenza A(H7N9) et H5N1 au Bhoutan, axée sur le risque.

Mots-clés

Avifaune – Bhoutan – Nouveau virus de l'influenza A(H7N9) – Surveillance d'urgence – Volailles.



Vigilancia de emergencia de un nuevo virus de la influenza A(H7N9) en aves de corral, palomas silvestres y otras aves salvajes de Bután

T. Tenzin, S. Tenzin, D. Tshering, K. Lhamo, P.B. Rai, N. Dahal & K. Dukpa

Resumen

A raíz del brote en seres humanos provocado en marzo de 2013 por un nuevo virus de la influenza aviar A(H7N9), y tras el subsiguiente aislamiento de ese agente en pollos, patos y palomas chinos, cundió la inquietud de que el virus H7N9 pudiera extenderse fuera del país a través de la cadena de valor de productos aviares que liga a China con una serie de países limítrofes. Por este motivo, entre mayo y julio de 2013 se instituyó en Bután un proceso de vigilancia rápida de emergencia que tenía por finalidad determinar si el virus de la influenza A(H7N9) circulaba de modo silencioso en la población de aves salvajes y de corral del país. Para ello se obtuvieron en todo el territorio nacional un total de 1.716 hisopados orofaríngeos, traqueales y cloacales, así como muestras de deyecciones, de aves de corral, aves salvajes y palomas silvestres. También se incluyeron 150 muestras extraídas anteriormente con fines de vigilancia del virus de la influenza A(H5N1). En total se analizaron 733 de esas muestras. Empleando el estuche comercial QIAamp[®] Viral RNA Mini Kit se extrajo ARN vírico de una mezcla de las muestras orofaríngeas, traqueales, cloacales y fecales. Para detectar el gen matriz del virus de la influenza aviar de tipo A se utilizó una técnica específica de reacción en cadena de la polimerasa con transcripción inversa en tiempo real qRT-PCR, y las muestras positivas se analizaron nuevamente con la técnica de qRT-PCR para la detección simultánea de los genes H7 y N9. De las 733 muestras analizadas, se confirmó la positividad para la influenza A de 46 de ellas (26 prospectivamente, 20 retrospectivamente), lo que supone una prevalencia del 6,3% (intervalo de confianza al 95%: 4,6 a 8,3). Las muestras positivas para la influenza A procedían de zonas del sur de Bután que anteriormente habían sufrido brotes de influenza altamente patógena A(H5N1). Ninguna de las muestras resultó positiva para cepas H7N9, lo que demuestra que el virus de la influenza A(H7N9) no estaba presente en la población muestreada. Atendiendo a la epidemiología de la enfermedad en China y otros países de Asia meridional y sudoriental, los autores preconizan un método basado en el grado de riesgo para vigilar la presencia en Bután de la influenza A(H7N9) y H5N1.

Palabras clave

Ave de corral – Ave salvaje – Bután – Nuevo virus de la influenza aviar A(H7N9) – Vigilancia de emergencia.



References

- World Health Organization (WHO) (2013). – Overview of the emergence and characteristics of the avian influenza A(H7N9) virus, 31 May 2013. WHO, Geneva. Available at: www.who.int/influenza/human_animal_interface/influenza_h7n9/WHO_H7N9_review_31May13.pdf?ua=1 (accessed on 10 June 2013).
- Uyeki T.M. & Cox N.J. (2013). – Global concerns regarding novel influenza A(H7N9) virus infections. *N. Engl. J. Med.*, **368** (20), 1862–1864. doi:10.1056/NEJMp1304661.
- Gao H.-N., Lu H.-Z., Cao B., Du B., Shang H., Gan J.-H., Lu S.-H., Yang Y.-D., Fang Q., Shen Y.-Z., Xi X.-M., Gu Q., Zhou X.-M., Qu H.-P., Yan Z., Li F.-M., Zhao W., Gao Z.-C., Wang G.-F., Ruan L.-X., Wang W.-H., Ye J., Cao H.-F., Li X.-W., Zhang W.-H., Fang X.-C., He J., Liang W.-F., Xie J., Zeng M., Wu X.-Z., Li J., Xia Q., Jin Z.-C., Chen Q., Tang C., Zhang Z.-Y., Hou B.-M., Feng Z.-X., Sheng J.-F., Zhong N.-S. & Li L.-J. (2013). – Clinical findings in 111 cases of influenza A(H7N9) virus infection. *N. Engl. J. Med.*, **368** (24), 2277–2285. doi:10.1056/NEJMoa1305584.
- Chen E., Chen Y., Fu L., Chen Z., Gong Z., Mao H., Wang D., Ni M.Y., Wu P., Yu Z., He T., Li Z., Gao J., Liu S., Shu Y., Cowling B.J., Xia S. & Yu H. (2013). – Human infection with avian influenza A(H7N9) virus re-emerges in China in winter 2013. *Eurosurveillance*, **18** (43), pii=20616. Available at: www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20616 (accessed on 11 November 2013).
- World Health Organization (WHO) (2014). – WHO risk assessment: human infections with avian influenza A(H7N9) virus (21 January 2014). WHO, Geneva. Available at: www.who.int/influenza/human_animal_interface/RiskAssessment_H7N9_21Jan14.pdf?ua=1 (accessed on 24 January 2013).
- World Health Organization (WHO) (2013). – Number of confirmed human cases of avian influenza A(H7N9) reported to WHO. Report 10: Data in WHO/HQ as of 25 October 2013. WHO, Geneva. Available at: www.who.int/influenza/human_animal_interface/influenza_h7n9/10u_ReportWebH7N9Number.pdf?ua=1 (accessed on 30 November 2013).
- Chen Y., Liang W., Yang S., Wu N., Gao H., Sheng J., Yao H., Wo J., Fang Q., Cui D., Li Y., Yao X., Zhang Y., Wu H., Zheng S., Diao H., Xia S., Zhang Y., Chan K., Tsoi H.-W., Teng J.L.-L., Song W., Wang P., Lau S.-Y., Zheng M., Chan J.F.-W., To K.K.-W., Chen H., Li L. & Yuen K.Y.-Y. (2013). – Human infections with the emerging avian influenza A H7N9 virus from wet market poultry: clinical analysis and characterisation of viral genome. *Lancet*, **381** (9881), 1916–1925.
- Li Q., Zhou L., Zhou M., Chen Z., Li F., Wu H., Xiang N., Chen E., Tang F., Wang D., Meng L., Hong Z., Tu W., Cao Y., Li L., Ding F., Liu B., Wang M., Xie R., Gao R., Li X., Bai T., Zou S., He J., Hu J., Xu Y., Chai C., Wang S., Gao Y., Jin L., Zhang Y., Luo H., Yu H., He J., Li Q., Wang X., Gao L., Pang X., Liu G., Yan Y., Yuan H., Shu Y., Yang W., Wang Y., Wu F., Uyeki T.M. & Feng Z. (2014). – Epidemiology of human infections with avian influenza A(H7N9) virus in China. *N. Engl. J. Med.*, **370** (6), 520–532. doi:10.1056/NEJMoa1304617.
- Shi J.Z., Deng G.H., Liu P.H., Zhou J.P., Guan L.Z., Li W.H., Li X.Y., Guo J., Wang G.J., Fan J., Wang J.L., Li Y.Y., Jiang Y.P., Liu L.L., Tian G.B., Li C.J. & Chen H.L. (2013). – Isolation and characterization of H7N9 viruses from live poultry markets: implication of the source of current H7N9 infection in humans. *Chin. Sci. Bull.*, **58** (16), 1857–1863.
- Gao R., Cao B., Hu Y., Feng Z., Wang D., Hu W., Chen J., Jie Z., Qiu H., Xu K., Xu X., Lu H., Zhu W., Gao Z., Xiang N., Shen Y., He Z., Gu Y., Zhang Z., Yang Y., Zhao X., Zhou L., Li X., Zou S., Zhang Y., Li X., Yang L., Guo J., Dong J., Li Q., Dong L., Zhu Y., Bai T., Wang S., Hao P., Yang W., Zhang Y., Han J., Yu H., Li D., Gao G.F., Wu G., Wang Y., Yuan Z. & Shu Y. (2013). – Human infection with a novel avian-origin influenza A(H7N9) virus. *N. Engl. J. Med.*, **368** (20), 1888–1897. doi:10.1056/NEJMoa1304459.
- Food and Agriculture Organization of the United Nations (FAO) (2014). – News article: Human cases of influenza A(H7N9) on the rise in southern and eastern China. FAO, Rome. Available at: www.fao.org/news/story/en/item/212599/icode/ (accessed on 24 January 2014).
- Food and Agriculture Organization of the United Nations (FAO) (2013). – Emergency surveillance response to avian influenza A(H7N9) in China and high risk countries. OSRO/GLO/302/USA (Project document). FAO, Rome.
- Dubey S.C., Dahal N., Nagarajan S., Tosh C., Murugkar H.V., Rinzin K., Sharma B., Jain R., Katare M., Patil S., Khandia R., Syed Z., Tripathi S., Behera P., Kumar M., Kulkarni D.D. & Krishna L. (2012). – Isolation and characterization of influenza A virus (subtype H5N1) that caused the first highly pathogenic avian influenza outbreak in chickens in Bhutan. *Vet. Microbiol.*, **155** (1), 100–105.
- Tenzin T., Dukpa K., Tshering Y. & Thapa L. (2013). – Status of notifiable animal diseases in Bhutan, 1996–2012. *Animal Health Bulletin No. 1*. National Centre for Animal Health, Thimphu, Bhutan, 20–22.
- World Health Organization (WHO) (2014). – Human infection with avian influenza A(H7N9) virus – update, February. WHO, Geneva. Available at: www.who.int/csr/don/2014_02_17/en/ (accessed on 5 July 2014).
- World Health Organization (WHO) (2014). – Human infection with avian influenza A(H7N9) virus – update, April. WHO, Geneva. Available at: www.who.int/csr/don/2014_06_27_avian_influenza/en/ (accessed on 5 July 2014).
- Center for Infectious Disease Research and Policy (CIDRAP) (2014). – China, Hong Kong report four more H7N9 cases. CIDRAP, Minneapolis. Available at: www.cidrap.umn.edu/news-perspective/2014/04/china-hong-kong-report-four-more-h7n9-cases (accessed on 5 July 2014).