



CONVENTION ON MIGRATORY SPECIES

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WILDLIFE DISEASE AND MIGRATORY SPECIES

Adopted by the Conference of the Parties at its 12th Meeting (Manila, October 2017)

Recalling Resolutions 8.27, 9.8, and 10.22 on various aspects of wildlife disease,

Acknowledging that wildlife health, livestock health, human health, and ecosystem health are interdependent and influenced by multiple factors, *inter alia*, socio-economics, sustainability of agriculture, demographics, climate and landscape changes,

Understanding the role that wildlife can play in emerging infectious diseases (EIDs) serving as either a reservoir host, temporary or periodic transmitter, or spillover/dead-end host,

Aware that diseases of wildlife are a normal cause of mortality and morbidity, and *conscious* that emerging or re-emerging diseases of wildlife can have serious implications for the status of migratory and non-migratory species, especially when populations are small and fragmented,

Noting that the increased frequency of such diseases has been linked to processes of landscape fragmentation, unsustainable land-use choices, pollution and other types of ecosystem disruption, these being, in turn, the consequences of unsustainable pressure on resources as highlighted by the Millennium Ecosystem Assessment; and *further noting* that climate change is expected to result in changes in disease distribution and emergence due to altered physiological conditions for hosts and parasites, resulting in the spread of novel micro-organisms with unpredictable consequences or the re-emergence of pathogens in new geographic locations,

Noting also that domestic animals, wild animals and humans share many pathogens, with wildlife sometimes being natural reservoirs of pathogens that can cause disease in domestic livestock, and that such pathogens have the potential significantly to affect both public health, food production, livelihoods and wider economies,

Aware that migratory species are victims and vectors of a range of contagious (e.g., viral, bacterial and fungal) diseases and some of these diseases may be transmitted to resident species, domestic stock, captive wild animals and humans. Some diseases have the potential to reduce biodiversity, especially in the case of threatened species,

Recognizing that wildlife can be a victim of diseases and there is an increase in emergence or re-emergence of diseases negatively affecting wildlife including highly pathogenic avian influenza H5N1 which causes continued mortality, and (since COP9) the spread of white-nose syndrome in bats, and the high mortalities affecting Saiga antelope (*Saiga spp.*) and Mongolian gazelle (*Procapra gutturosa*); and *highlighting* the need to understand the causes and epidemiology of these diseases and to coordinate effective and rapid responses to such events,

Recognizing that the direct effects of disease on wildlife are particularly important for small or geographically isolated populations, and that there are numerous indirect effects including lethal approaches to managing wildlife disease and their negative influence on public perception of wildlife,

Recognizing the high risk of transmission of wildlife diseases from livestock and/or humans to wildlife and vice versa in areas of growing conflicts over land and increasing habitat loss, especially in developing countries,

Acknowledging the substantial impacts of wildlife trade, both legal and illegal, on threatened and endangered species worldwide and the loss of biodiversity and food security that can result from the spread of pathogens through regional and international movements of animals and animal products,

Further acknowledging the substantial risks for wildlife, livestock and people of the wildlife trade, both legal and illegal, which can result in the spread of pathogens to previously unexposed populations through regional and international movements of animals and animal products,

Aware of the issue of outbreaks of Highly Pathogenic Avian Influenza (HPAI) (subtype H5N1), which have had major impacts on livelihoods linked to the keeping of domesticated birds (mainly poultry) and on nature conservation values (including mortality of waterbirds on at least four internationally important Ramsar sites in Eurasia, and conscious of the increasing number of countries in which HPAI has been detected following its westward spread through Eurasia,

Very conscious that, if the subtype of HPAI either genetically reassorts or adaptively mutates into a form transmissible between humans, this could have the global health, social and economic consequences of a human influenza pandemic,

Mindful, however, that the limited number of known cases of human infection with the current strain of HPAI is restricted to certain parts of Asia and have been through contact with infected poultry and none through contact with wild birds, and *recognizing* that public attitudes and support for wetland and species (particularly waterbirds) conservation and sustainable use, could be negatively affected by concerns as to the possible role of waterbirds in the spread of HPAI (subtype H5N1),

Concerned, however, that in most countries there is a significant lack of information and, in some cases, public misinformation, on important issues related to the spread of HPAI, the risks it may pose, and how to anticipate and respond to outbreaks of HPAI, and *noting* in particular the difficulties that developing countries face in assessing and responding to the threat of HPAI, especially given the significance in many of these countries of both domesticated and wild birds as the basis of rural livelihoods,

Concerned also that ill-informed responses may have unfortunate and possibly disastrous long-term consequences for conservation, especially for some of the species which are globally threatened, and already have small or localized populations and particularly those species listed in Appendix I of the Convention and in Column A, Category 1 of Table 1 of the Action Plan of the Agreement on the Conservation of African Eurasian Migratory Waterbirds (AEWA),

Noting that HPAI is considered to have been spread between countries by a number of different known vectors, including through the movement of avian livestock, cage birds and bird by-products, legal and illegal trade in birds, equipment associated with these respective industries, and movement of people, and noting that the migration of waterbirds has been suspected to be a vector as well, although direct evidence is lacking and aware that the relative significance of these different modes of spread has varied and evidence of causal links in many cases is weak or lacking,

Aware of the continued major concerns and implications of the spread of highly pathogenic avian influenza (HPAI) subtype H5N1 of Asian lineage, as reflected, inter alia, by CMS Resolution 8.27, AEWA Resolutions 3.18 and 4.15, and Ramsar Resolutions IX.23 and X.21 and the guidance annexed to the latter resolution: guidance on responding to the continued spread of highly pathogenic avian influenza H5N1; and *also aware* that national and international responses to the spread of HPAI H5N1 might provide useful models for adoption in response to the challenges of other emerging and re-emerging diseases that affect wildlife,

Welcoming the significant work of the Working Group on Wildlife Diseases of the World Organization for Animal Health (OIE) since its creation in 1994 and the recommendations and scientific publications derived from the Working Group on the surveillance and control of the most important specific wildlife diseases,

Welcoming the involvement in this issue of the Food and Agriculture Organization (FAO), the World Health Organization (WHO), and OIE, notably through the publication in May 2005 of a Global Strategy for the Progressive Control of Highly Pathogenic Avian Influenza and its implementation, inter alia, through regional Technical Cooperation Programmes on Emergency Assistance for Early Detection and Prevention of Avian Influenza,

Aware of the Convention's leading participation in various coordinating mechanisms, including the Scientific Task Force on Avian Influenza and Wild Birds_convened in late August 2005 by the Convention, which comprises representatives and observers from eleven_international organizations, namely CMS, AEWA, Ramsar Convention, FAO, WHO, Wetlands International, BirdLife International, International Council for Game and Wildlife Conservation (CIC), Royal Veterinary College, Ecohealth, and Wildlife Conservation Society (WCS), recognizing the role of the IUCN Veterinary Specialist Group and *also noting* Resolution 3.18 on Avian Influenza of AEWA and Resolution IX.25 of the Ramsar Convention on managing wetlands and waterbirds in response to highly pathogenic avian influenza,

Welcoming the international conference organized in Lyon, France, 22-27 July 2012 by the Wildlife Disease Association (WDA) and the European Wildlife Disease Association (EWDA) on Convergence in Wildlife Health,

Recalling that the Global Flyways Conference (Edinburgh 2004) called, in particular, for urgent action to assess disease risk, and establish monitoring programmes in relation to migratory waterbird movements, the trade of wild birds, and implications for human health,

Acknowledging the opportunities for information exchange provided by the Special Round-Table on the spread of HPAI held on 19 November 2005 at Nairobi, Kenya, during the 8th Conference of the Parties to the Convention on Migratory Species, and encouraged by the participation of all African and other CMS Scientific Councillors,

Acknowledging the importance of the global disease information systems WAHIS and WAHIS-Wild developed by the OIE as well as its web interface WAHID, the FAO/OIE/WHO joint mechanism Global Early Warning and Response System for Major Animal Diseases (GLEWS) and existing information systems developed by organizations such as the IUCN Wildlife Health Specialist Group, the European Union, AU-IBAR in Africa, ASEAN in Asia, SPC in the Pacific Islands and OIRSA in Central America,

Welcoming the large scope of consensus on appropriate approaches and responses to wildlife diseases which has developed among UN agencies, multilateral environmental agreements and other international organizations including OIE, reflected for example in decisions and resolutions of the Ramsar Convention, AEWA, CMS and in standards of the OIE,

Recognizing that exploration of possible scenarios of the HPAI spread, including identification of areas of higher relative risk and development of possible policy responses to outbreaks will benefit from analysis of extensive and long-term data sets relating to bird movements, waterbird counts, trade and movements of people, but noting the urgency to access and analyze such data, networks, and other information, and to fill outstanding gaps in the scientific understanding of these factors,

Recalling also that, although outbreaks of H5N1 in Hong Kong in 1997, in Japan in 2004, of H7N1 in Italy in 1999, of H7N3 in Chile in 2002 and of H7N7 in The Netherlands, Belgium and Germany in 2003 were all successfully stamped out using rigorous control and biosecurity measures, HPAI now appears to be endemic in some parts of Asia, highlighting the practical difficulties of control in countries with limited veterinary capacity,

Recognizing the potential risk of transmission of HPAI between captive birds and other animals at wetland centres and zoological gardens and wild waterbirds visiting these sites, being mindful both of animal welfare requirements and the important role such sites play in wetland communication, education and public awareness,

Recognizing also ongoing national actions and plans for monitoring habitats and bird populations for HPAI; and *also noting* that, although development of surveillance schemes and contingency planning will need to be determined nationally, there are significant benefits from international cooperation,

Aware of the outcomes of the WHO/FAO/World Bank meeting in Geneva of 7-9 November 2005 on 'Avian Influenza and human pandemic influenza' which identified the significant gap of knowledge concerning the role that wild birds might play in the spread of HPAI, *noting* the need to strengthen research and monitoring related to waterbird migration and trade in birds, as well as disease processes in wild bird populations, especially research identified by the Scientific Task Force on Avian Influenza_and Wild Birds (See Annex 1),

Recalling the outcomes of Ramsar COP 10 on the theme of 'Healthy Wetlands, Healthy People', which stressed the functional linkages between the role that wetlands play in providing ecosystem services for the support of both human and wildlife populations; and that aquatic waterbirds and other migratory species can be valuable indicators of ecosystem health,

Aware that diseases and the need for coordinated responses to them are becoming increasingly highlighted as an important issue in CMS Agreements, Memoranda and other international instruments for the conservation of migratory species, and that such coordinated surveillance and response efforts require multiple stakeholders responsible for managing the health of humans, livestock and wildlife,

Aware also of the important work of the FAO and others with regard to domestic animal health and human health, but concerned that national and international responses to wildlife health have, in many situations, yet to be acknowledged as an essential element of disease surveillance or monitoring programmes, epidemiological investigations, and/or outbreak responses,

Welcoming the development of national wildlife disease strategies by some Contracting Parties and other governments; *but also noting* that many developing countries lack functional animal health-related programmes and strategies, policies and the infrastructure needed to protect human health, agricultural and wildlife interests from endemic or introduced diseases through local movements, re-establishment programmes, or international trade,

Thanking the CMS Secretariat and the FAO Animal Health Service for their coordination of the Scientific Task Force on Avian Influenza and Wild Birds documented in document Conf. 9.25; and *also thanking* Task Force members and observers for their valuable work in maintaining coordination with respect to policies and advocacy concerning the spread of HPAI H5N1,

Recognizing the need for rapid and continued sharing of information given the potential significance of this information in terms of bird conservation and population dynamics, so as to enable or improve risk assessments and be better prepared to improve conservation of waterbirds and future management of avian disease outbreaks,

Noting that existing methods of communication between management authorities, health professionals, biologists, veterinarians and natural resource professionals could be improved in some jurisdictions and are currently inadequate to respond to the complex issues surrounding human, animal and ecosystem health,

Recalling Resolution 9.8, which called on the Secretariat and the FAO Animal Health Service to co-convene the Scientific Task Force on Wildlife and Ecosystem Health to develop guidance on responding to wildlife diseases of importance to people, domestic animals and wildlife,

Welcoming the body of work being undertaken by the Ramsar Scientific and Technical Review Panel on wetlands and health and promotion of an ecosystem approach to dealing with health, in particular the Ramsar Disease Manual on Guidelines for Assessment, Monitoring and Management of Animal Disease in Wetlands which is aimed at practical disease guidance for wetland managers and policy makers,

Further welcoming the significant work in the area of wildlife health by the IUCN Wildlife Health Specialist Group, the Working Group on Wildlife Diseases of the OIE and non-governmental agencies and organizations,

Further recalling Resolution 9.8 that requested the Secretariat and the FAO Animal Health Service to determine the relationship between the existing Scientific Task Force on Avian Influenza and Wild Birds and the Scientific Task Force on Wildlife and Ecosystem Health,

Taking note of the report from the inaugural workshop of the Scientific Task Force on Wildlife and Ecosystem Health, which took place in Beijing, China, on 27-28 June 2011, as well as the Terms of Reference and Work Plan of the Task Force included in document UNEP/CMS/ScC.17/Inf.13,

Acknowledging the proposed *Modus Operandi* for Conservation Emergencies (UNEP/CMS/Conf.10.38 and Resolution 10.2), which is envisaged to improve the rapid response to disease-related and other conservation emergencies,

Noting also that the Task Force on Wildlife and Ecosystem Health agreed to enhance research on diseases that have an impact on both domestic and migratory wildlife, and that are of greatest concern with regard to food security, sustainable livelihoods and conservation;

Further noting that the Task Force on Wildlife and Ecosystem Health agreed on a mechanism to be created for CMS Parties and FAO Member States to respond to the threat of transboundary animal health crises by reporting wildlife morbidity and mortality events,

Acknowledging the importance of existing global disease information systems coordinated between the OIE, FAO and WHO related to wildlife diseases, and the need to assure good communication and avoid unnecessary overlap in global reporting requirements,

Acknowledging that the One Health approach is increasingly gaining ground as a multidisciplinary way of addressing emerging infectious diseases, and that the concept has been endorsed by several international organizations including FAO, OIE, WHO, UNICEF and the World Bank,

Further acknowledging the need to maintain and build upon the global momentum created in response to successful eradication of rinderpest virus from animals including wild populations, and progress on control of highly pathogenic avian influenza H5N1,

Aware of the decision of AEWA (Resolution 3.6) to request the support of the CMS and other stakeholders to establish long-term funding regimes in order to develop long-term monitoring of waterbird populations *inter alia* via the International Waterbird Census and its derived outputs, and further to Ramsar Resolution VIII.38, as a means of informing a wide range of national and international conservation policies including risk assessment for HPAI, and

Noting that the CMS Working Group on Migratory Species as Vectors of Diseases established by the 12th meeting of the Scientific Council provides a means to develop responses to some of the issues highlighted by this Resolution but that integration of both wildlife and domestic animal issues is required to properly understand disease epidemiology as well as address disease transmission, control and prevention,

The Conference of the Parties to the Convention on the Conservation of Migratory Species of Wild Animals

1. Calls for fully integrated approaches, at both national and international levels, to address HPAI and other animal borne diseases by bringing ornithological, wildlife, and wetland management expertise together with those traditionally responsible for public health and zoonosis, including veterinary, agricultural, virological, epidemiological, and medical expertise;

Wild Bird information (knowledge needs)

2. In response to the issue of HPAI H5N1, given its potential significance for conservation of migratory species, and the need to be better prepared for the future management of avian disease outbreaks, calls upon Contracting Parties, non-contracting Parties, international and national organizations, in cooperation with FAO, OIE and other competent authorities in domesticated and captive birds, to support and build capacity for research (see annex) related to disease processes in migratory bird species, long-term monitoring of their movements and populations and rapid development of surveillance programmes for HPAI in populations of wild birds; and to strengthen ongoing efforts to improve, integrate and analyze existing data sets across different flyways to determine precise migratory routes, fluxes and population dynamics of species, and to disseminate the results;

Specific Instructions

- 3. *Supports* the conclusions of WHO, FAO and OIE that attempts to eliminate HPAI in wild bird populations through lethal responses such as culling are not feasible and may exacerbate the problem by causing further dispersion of infected birds;
- 4. Emphasizes that destruction or substantive modification of wetland and other habitats with the objective of reducing contact between domesticated and wild birds does not amount to wise use as urged by Article 3.1 of the Ramsar Convention and Articles 1 and 8 of the Convention on Biological Diversity, and may exacerbate the problem by causing further dispersion of infected birds;
- 5. *Calls* on Contracting Parties and urges non-contracting Parties to strictly apply internationally agreed quarantine and health standards for the cross-border transport of bird products and captive birds of all kinds and further calls for a crackdown on the illegal transport of bird products and captive birds of all kinds, both nationally and internationally;
- 6. *Suggests* that African Contracting Parties and non-contracting Parties coordinate their responses to the threats posed by the spread of HPAI through the New Partnership for Africa's Development amongst others;
- 7. Urges that hunting communities, in the framework of existing hunting activities, contribute to monitoring the spread of HPAI and co-operate actively with national authorities in the event that measures, inter alia special temporary hunting regulations are considered or put into force;

Strategic advice

- 8. *Notes* the overriding importance of enhanced biosecurity measures, including adequate farming and aquaculture standards, and the need for competent authorities to develop strategies that limit the risk of disease transmission between wild and domestic animals (through enhanced biosecurity measures) and humans;
- 9. Underlines the importance of developing and implementing national contingency or action plans related to the potential risk of disease transmission, and the need for national preparedness to respond effectively to instances of detection of HPAI in birds, notably in wetland-dependent species;
- 10. *Requests* Contracting Parties and urges non-contracting Parties to develop and implement programmes of education and public awareness on HPAI, especially aimed at actually or potentially affected stakeholders, in particular those engaged in outdoor activities and the poultry industry;
- 11. Urges the Contracting Parties to integrate wildlife, livestock, human and ecosystem health issues into a) contingency planning, b) monitoring and surveillance, c) outbreak investigations and responses to morbidity and mortality events; and d) current and future capacity building activities;

Funding Needs

- 12. Urges the Contracting Parties to:
 - a) support the establishment of an internationally or regionally coordinated wellstructured long-term monitoring and surveillance programme for migratory birds, as appropriate, to assess, inter alia, current and new disease risks, making best use of, and building on existing schemes; and
 - rapidly fill specific gaps in knowledge through provision of support to establish programmes to study migratory patterns of targeted species at flyway level (including bird-ringing/banding, colour-marking, satellite tracking and isotope study);
- 13. *Requests* the Executive Secretary to explore possibilities for establishing partnerships so as to support the development of long-term funding for monitoring schemes, including the International Waterbird Census and its derived outputs, that are relevant to the Convention's interests;
- 14. *Requests* the Executive Secretary working with the Scientific Council and in cooperation with the Scientific Task Force on Avian Influenza and Wild Birds_to approach urgently FAO, OIE and WHO in response to their call for further research into fully understanding the role of wild birds in spreading HPAI, and seek the necessary resources to perform this work;
- 15. *Further urges* Parties and international donor organizations to support the activities of the Scientific Task Force on Wildlife and Ecosystem Health, through both financial and in-kind support, and in particular for the organization of annual meetings of the Task Force;
- 16. *Calls on* Parties and international donor organizations to provide technical and financial support to assist developing countries in establishing appropriate systems of surveillance and control of wildlife diseases;

CMS Engagement

- 17. *Requests* the Executive Secretary to ensure continued leadership of the Convention in the Scientific Task Force on Avian Influenza and Wild Birds, through appropriate representatives of the Scientific Council and the Secretariat, and urges the Scientific Council, with and through the Scientific Task Force on Avian Influenza and Wild Birds, to provide relevant input on practical measures to reduce the risk of disease transmission between wild, captive and domesticated birds, to those agencies developing contingency and wetland management plans related to HPAI;
- 18. *Requests* the Executive Secretary, working with the Scientific Council and its Working Group on Migratory Species as Vectors of Diseases to make recommendations regarding the nature and extent of risks associated with other diseases in migratory species and possible areas of action to be taken by Contracting Parties in addressing this;
- 19. *Also calls* on the CMS Working Group on Migratory Species as Vectors of Diseases to become part of the broader focused Scientific Task Force on Wildlife Disease and to provide guidance related to past accomplishments and future needs;
- 20. *Requests* FAO to a) identify diseases that have an impact on both domestic and wildlife species, and that are of greatest concern in regard to food security, economics and sustainable livelihoods; and b) integrate into their "One World One Health" approach, disease and management issues that can be brought to the attention of the Scientific Task Force on Wildlife Disease for consideration and action;
- 21. Also requests the CMS Secretariat and the FAO Animal Health Service to identify the relevant members and observers that would comprise the Scientific Task Force on Wildlife and Ecosystem Health, and to determine the relationship between the existing Scientific Task Force on Avian Influenza and Wild Birds and the Scientific Task Force on Wildlife and Ecosystem Health;
- 22. *Requests* the Scientific Task Force on Wildlife and Ecosystem Health to liaise with the OIE Headquarters and the OIE Working Group on Wildlife Diseases, and with the IUCN Wildlife Health Specialist Group, so that the work and recommendations of the OIE Working Group and the IUCN Wildlife Health Specialist Group can be taken into account in the activity plan of the Scientific Task Force on Wildlife and Ecosystem Health, and to invite representatives from the OIE Headquarters and from the OIE Working Group on Wildlife Diseases, and the IUCN Wildlife Health Specialist Group, to actively participate in the Scientific Task Force particularly in the field of global wildlife disease early detection, notification and management mechanisms, and *vice versa;*
- 23. *Further welcomes* the proposal for a *Modus Operandi* for Conservation Emergencies as a mechanism to improve the rapid response to mass mortality events affecting migratory species and other conservation emergencies as outlined in Resolution 10.2;
- 24. *Encourages* the Scientific Task Force on Wildlife and Ecosystem Health to liaise with the OIE Working Group on Wildlife Diseases and other related programmes so that the work recommendations and ongoing global initiatives are well coordinated, particularly in the field of global wildlife disease surveillance, early detection, including of outbreaks of domestic livestock disease with the potential to affect wildlife, and notification;
- 25. *Encourages* the Task Force on Wildlife and Ecosystem Health to incorporate key relevant civil society organizations into the governance structure of the Task Force, at the Core Affiliate level, such that the work of the Task Force will be able to support the consensus of both governmental and non-governmental agencies and organizations focused on wildlife and ecosystem health;

Cooperation

- 26. Invites Parties to contribute voluntarily to the Wildlife Health Event Reporter (WHER) as an unofficial rapid reporting system for wildlife morbidity and mortality events in collaboration with OIE national delegates and wildlife focal points, taking fully into account the OIE WAHIS, FAO/OIE/WHO GLEWs mechanisms and existing regional information systems, and the need to complement existing communication channels, specifically OIE disease reporting and ProMed-mail;
- 27. *Calls on* Parties to collaborate with and share simultaneously information with OIE national delegates and wildlife focal points, OIE WAHIS, the IUCN Wildlife Health Specialist Group, FAO/OIE/WHO GLEWS mechanisms and existing regional information systems;
- 28. Also calls on Parties to use and promote the Ramsar Disease Manual together with guidance produced by the Task Force on Wildlife and Ecosystem Health for managing diseases of migratory animals and in cooperation with Veterinary Authorities following global standards adopted by the OIE;
- 29. *Requests* the Secretariat, in collaboration with other relevant organizations, to help in dissemination and promotion of Task Force on Wildlife and Ecosystem Health products;
- 30. *Requests* the Secretariat in collaboration with, *inter alia*, Parties, other governments, IGOs and NGOs, subject to the availability of resources, to review existing initiatives to enhance cooperation and collaboration among different conventions through national focal points;
- 31. *Requests* the Secretariat in collaboration with, *inter alia*, Parties, other governments, IGOs NGOs, subject to the availability of resources, to facilitate workshops to enhance cooperation and collaboration among different conventions through national focal points;
- 32. *Urges* Parties and *invites* other governments and donors such as the GEF to provide adequate financial support for such workshops;
- 33. *Requests* the Scientific Task Force on Wildlife and Ecosystem Health, subject to available funding, to work with the OIE Working Group on Wildlife Diseases on the development of an agreed approach to wildlife event reporting, and to communicate regularly on their combined approach to wildlife animal health issues;
- 34. *Encourages* Parties to engage in activities of the Task Force on Wildlife and Ecosystem Health including serving as National Associates, linking their organization's websites, and serving as a conduit for information-sharing;
- 35. Congratulates and thanks the members of the Scientific Task Force on Avian Influenza and Wild Birds for their unstinting efforts and output during the period 2005–2008 which have made a significant contribution to improving understanding and awareness of the causes of, and responses to, the spread of HPAI H5N1; and *requests that* the CMS Secretariat and FAO continue to act as co-convenors of the Scientific Task Force on Avian Influenza and Wild Birds with the engagement of the CMS Scientific Council, building on international activities already undertaken, and responding to new developments related to the spread of HPAI H5N1 and other subtypes as they occur;
- 36. *Endorses* the Scientific Summary of H5N1Highly Pathogenic Avian Influenza: Wildlife and Conservation Considerations prepared by the Scientific Task Force on Avian Influenza and Wild Birds and attached as Annex 2 of this resolution as similarly endorsed by AEWA Resolution 4.15 and Ramsar Resolution X.21; *calls on* other relevant bodies including FAO, UNEP and MEAs also to endorse this statement, and requests the Secretariat to ensure maximum circulation, translation and understanding of the statement;

- 37. *Encourages* the Contracting Parties to utilize, as appropriate, in relation to issues for migratory species the guidance available in Ramsar Resolution X.21: guidance on responding to the continued spread of highly pathogenic avian influenza H5N1;
- 38. *Requests* the Secretariat to report progress on the implementation of this Resolution to each meeting of the Conference of the Parties; and

Final Provisions

39. Repeals

- a) Resolution 8.27, *Migratory Species and Highly Pathogenic Avian Influenza*;
- b) Resolution 9.8, Responding to the Challenge of Emerging and Re-emerging Diseases in Migratory Species, including Highly Pathogenic Avian Influenza H5N1;
- c) Resolution 10.22, Wildlife Disease and Migratory Species.

Annex 1 to Resolution 12.6

KEY RESEARCH NEEDS RELATED TO THE SPREAD OF HIGHLY PATHOGENIC AVIAN INFLUENZA IN RELATION TO MIGRATORY BIRDS AND THEIR HABITATS

- 1. Identification and mapping of the precise nature of migration routes, including stop over sites, flux and timing for key migratory waterbirds so as to expand and/or refine existing ecological monitoring of these populations.
- 2. Clarification of virus behaviour and survival in the aquatic habitats which are waterbird breeding, staging and non-breeding (wintering) areas.
- 3. Clarification of viral incubation periods, the infectious period in birds and the symptoms affecting individual wild birds, including implications for migratory movements, as well as determining survival rates of birds and persistence of viruses in birds.
- 4. Establishment of informed assessments of the possibility of transmission between populations of wild birds and domestic flocks, including by non-waterbird species found near poultry-keeping areas.
- 5. Surveillance of the prevalence of HPAI in wild bird populations.
- 6. Development of combined risk assessments based on the known epidemiological behaviour of the virus, risks of transmission, routes and timing of migratory species, as well as known poultry and captive bird husbandry techniques.
- 7. Research on methods for improvement of farming standards and the development of strategies to limit the risk of any disease transmission between wild and domesticated birds.

SCIENTIFIC SUMMARY OF HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1: WILDLIFE AND CONSERVATION CONSIDERATIONS

Definition of avian influenza

Avian influenza is a highly contagious disease caused by influenza A viruses, affecting many species of birds. Avian influenza is classified according to disease severity into two recognised forms: low pathogenic avian influenza (LPAI) and highly pathogenic avian influenza (HPAI). LPAI viruses are generally of low virulence, while HPAI viruses are highly virulent in most poultry species resulting in nearly 100% mortality in infected domestic flocks (Center for Infectious Disease Research & Policy 2007). The natural reservoir of LPAI viruses is in wild waterbirds – most commonly in ducks, geese, swans, waders/shorebirds and gulls (Hinshaw & Webster 1982; Webster *et al.* 1992; Stallknecht & Brown 2007).

To date, influenza A viruses representing 16 haemagglutinin (HA) and nine neuraminidase (NA) subtypes have been described in wild birds and poultry throughout the world (Rohm *et al.* 1996; Fouchier *et al.* 2005). Viruses belonging to the antigenic subtypes H5 and H7, in contrast to viruses possessing other HA subtypes, may become highly pathogenic having been transmitted in low pathogenic form from wild birds to poultry and subsequently circulating in poultry populations (Senne *et al.* 1996).

Notifiable avian influenza is defined by the World Organisation for Animal Health (OIE) as "an infection of poultry caused by any influenza A virus of the H5 or H7 subtypes or by any avian influenza virus with an intravenous pathogenicity index (IVPI) greater than 1.2 (or as an alternative at least 75% mortality)" as described by the OIE's Terrestrial Animal Health Code (OIE 2008). The OIE divides notifiable avian influenza into "highly pathogenic notifiable avian influenza (HPNAI) and low pathogenicity notifiable avian influenza (LPNAI):

- HPNAI viruses have an IVPI in 6-week-old chickens greater than 1.2 or, as an alternative, cause at least 75% mortality in 4-to 8-week-old chickens infected intravenously. H5 and H7 viruses which do not have an IVPI of greater than 1.2 or cause less than 75% mortality in an intravenous lethality test should be sequenced to determine whether multiple basic amino acids are present at the cleavage site of the haemagglutinin molecule (HA0); if the amino acid motif is similar to that observed for other HPNAI isolates, the isolate being tested should be considered as HPNAI;
- LPNAI are all influenza A viruses of H5 and H7 subtype that are not HPNAI viruses" (OIE 2008).

Genesis of highly pathogenic avian influenza viruses

In wild waterbirds, LPAI viruses are a natural part of the ecosystem. They have been isolated from over 90 species of wild bird (Stallknecht & Shane 1988; Olsen *et al.* 2006; Lee 2008), and are thought to have existed alongside wild birds for millennia in balanced systems. In their natural hosts, avian influenza viruses infect the gastrointestinal tract and are shed through the cloaca; they generally do not cause disease although some behavioural anomalies have been reported, such as reduced migratory and foraging performance in Bewick's Swans *Cygnus columbianus bewickii* (van Gils *et al.* 2007). Instead, the viruses remain in evolutionary stasis as indicated by low genetic mutation rates (Gorman *et al.* 1992; Taubenberger *et al.* 2005).

When LPAI viruses are transmitted to vulnerable poultry species, only mild symptoms such as a transient decline in egg production or reduction in weight gain (Capua & Mutinelli 2001) are induced. However, where a dense poultry environment supports several cycles of infection,

the viruses may mutate, adapting to their new hosts, and for the H5 and H7 subtypes these mutations can lead to generation of a highly virulent form. Thus, HPAI viruses are essentially products of intensively farmed poultry, and their incidence has increased dramatically with the greatly enhanced volume of poultry production around the world (GRAIN 2006; Greger 2006). In the first few years of the 21st century the incidence of HPAI outbreaks has already exceeded the total number of outbreaks recorded for the entire 20th century (Greger 2006). In general, they should be viewed as something artificial, made possible by intensive poultry production techniques.

After an HPAI virus has arisen in poultry, it has the potential both to re-infect wild birds and to cause disease in various mammalian taxa. If influenza A viruses adapt inside these new hosts to become highly transmissible, there could be devastating consequences, such as the human influenza pandemics of the 20th century (Kilbourne 2006). The conditions necessary for cross-infection are provided by agricultural practices that bring together humans, poultry and other species in high densities in areas where there is also the potential for viral transmission from infected poultry, poultry products and waste to wild birds, humans and other mammals in shared wetlands and in 'wet' (live animal) markets (Shortridge 1977; Shortridge *et al.* 1977).

Highly pathogenic avian influenza H5N1 of Asian lineage (HPAI H5N1)

H5N1 HPAI of Asian lineage has infected domestic, captive and wild birds in more than 60 countries in Asia, Europe and Africa (OIE 2008). By November 2005, i.e., before widespread occurrence in western Eurasia and Africa, over 200 million domestic birds had died from the disease or been slaughtered in attempts to control its spread; the economies of the worst affected countries in southeast Asia have suffered greatly, with lost revenue estimated at over \$10 billion (Diouf 2005), and there have been serious human health consequences. By November 2008, the World Health Organisation had confirmed more than 380 human cases, over 60% of those fatal (World Health Organisation 2008).

Sporadic deaths in wild birds have been reported since 2002 and the first outbreak involving a large number of wild birds was reported in May 2005, in Qinghai province, China (Chen *et al.* 2005; Liu *et al.* 2005). Between 2002 and the present, the virus has infected a wide range of wild bird species (Olsen *et al.* 2006; USGS National Wildlife Health Center 2008; Lee 2008), but which species are important in H5N1 HPAI movement and whether the virus will become endemic and prevalent in wild bird populations is still unknown (Brown *et al.* 2006).

The virus has also infected a limited number of domestic, captive and wild mammals, including captive Tigers *Panthera tigris* and Leopards *Panthera pardus* and domestic pigs in southeast Asia, as well as domestic cats and a wild Stone Marten *Martes foina* in Germany. These cases were the result of 'spillover' infection from birds. There is no known reservoir of H5N1 HPAI virus in mammals, and there remains no sound evidence that the virus can be readily transmitted from mammal to mammal.

Emergence of H5N1 HPAI in poultry in southeast Asia (1996 – 2005)

HPAI H5N1 first received widespread recognition following a 1997 outbreak in poultry in Hong Kong, PR China with subsequent spread of the virus to humans. During that outbreak, 18 human cases were recognised and six patients died. The outbreak ended when all domestic chickens held by wholesale facilities and vendors in Hong Kong were slaughtered (Snacken 1999). A precursor to the 1997 H5N1 strain was identified in Guangdong, China, where it caused deaths in domestic geese in 1996 (Webster *et al.* 2006).

Between 1997 and 2002, different reassortments (known as genotypes) of the virus emerged, in domestic goose and duck populations, which contained the same H5 HA gene but had different internal genes (Guan *et al.* 2002; Webster *et al.* 2006).

In 2002, a single genotype emerged in Hong Kong, PR China and killed captive and wild waterbirds in nature parks there. This genotype spread to humans in Hong Kong in February 2002 (infecting two, killing one) and was the precursor to the Z genotype that later became dominant (SturmRamirez *et al.* 2004; Ellis *et al.* 2004).

Between 2003 and 2005, the Z genotype spread in an unprecedented fashion across southeast Asia, affecting domestic poultry in Vietnam, Thailand, Indonesia, Cambodia, Laos, the Republic of Korea, Japan, China and Malaysia. Later analysis showed that the H5N1 viruses that caused outbreaks in Japan and the Republic of Korea were genetically different from those in other countries (the V genotype) (Mase *et al.* 2005; Li *et al.* 2004; Webster *et al.* 2006).

In April 2005, the first major outbreak in wild birds was reported. Some 6,345 wild birds were reported dead at Lake Qinghai in central China. Species affected included Great Black-headed Gull *Larus ichthyaetus*, Bar-headed Goose *Anser indicus*, Brown-headed Gull *Larus brunnicephalus*, Great Cormorant *Phalacrocorax carbo* and Ruddy Shelduck *Tadorna ferruginea* (Chen *et al.* 2005; Liu *et al.* 2005).

Geographical spread of H5N1 HPAI out of Southeast Asia (2005 – 2006)

In July 2005, Russia reported its first outbreaks; domestic flocks were affected in six regions of western Siberia and dead wild birds were reported in the vicinities of some of these outbreaks. Kazakhstan reported its first outbreak in August 2005 in domestic birds. In the same month, 89 wild birds described as migratory species were reported infected at two lakes in Mongolia.

Europe reported its first outbreaks in October 2005 when infection was detected in domestic birds in Romania and Turkey. In the same month, Romania reported sporadic cases in wild birds as did Croatia and European parts of Russia. In November, the virus spread to domestic birds in the Ukraine, and the Middle East reported its first case: a captive flamingo in Kuwait. During December, two outbreaks were reported in European Russia in wild swans (species unreported) in regions near the Caspian Sea.

In the first half of 2006, the spread of HPAI H5N1 continued across Europe (Sabirovic *et al.* 2006; Hesterberg *et al.* 2007; Hesterberg *et al.* in press) and the Middle East and into Africa. Between January and May, infection was reported in 24 European countries with the majority of cases occurring in February and March in wild birds. During the same period, outbreaks were reported across central Asia and the Middle East, affecting domestic birds in Azerbaijan, India, Bangladesh, Pakistan, Iran and Iraq, with Azerbaijan also reporting infected wild birds. The first reported outbreak in Africa occurred in January in poultry in Nigeria, and by the end of April, eight other African nations had reported outbreaks: Burkina Faso, Cameroon, Djibouti, Egypt, Ghana, Côte d'Ivoire, Niger and Sudan (OIE 2008).

By May 2006, reports of outbreaks in Europe, the Middle East and Africa had for the most part decreased in frequency. Small numbers of cases of infection were reported in Hungary, Spain and the Ukraine in June, Pakistan and Russia in July, and one case was identified in a captive swan in Germany in August. Egypt was exceptional, continuously reporting outbreaks throughout 2006. It is also considered likely that outbreaks continued in poultry in Nigeria (UN System Influenza Coordinator & World Bank 2007).

Throughout the time H5N1 HPAI was spreading across central Asia, Europe, the Middle East and Africa, it maintained a stronghold in poultry in southeast Asia. In 2006, outbreaks were reported in Cambodia, PR China including Hong Kong, Indonesia, the Republic of Korea, Laos, Malaysia, Myanmar, Thailand and Vietnam (OIE 2008).

Period following the geographic spread westward (2007 – October 2008)

Compared with 54 countries reporting 1,470 outbreaks to the OIE in 2006, 30 countries reported 638 outbreaks in 2007 (OIE 2008). In 2007, six European countries (Poland, Hungary, Germany, the United Kingdom, Romania and the Czech Republic) reported sporadic and relatively isolated outbreaks in poultry that were quickly controlled. Outbreaks in domestic birds were also reported in European parts of Russia and in Turkey. Infected wild birds were reported in Germany, France, the United Kingdom and the Czech Republic, and birds at a rehabilitation centre were affected in Poland. In the Middle East and central Asia, poultry outbreaks occurred throughout 2007. Some 350 outbreaks were reported from Egypt and Bangladesh alone. Poultry (and in some cases captive birds) were also affected in India, Kuwait, Saudi Arabia, Pakistan, Afghanistan and Israel with most outbreaks occurring between February and April, and again between October and December. In Africa, H5N1 HPAI was reported in domestic birds in Togo, Ghana and Benin, and is considered to have become endemic in Nigeria (OIE 2008; UN System Influenza Coordinator & World Bank 2007). Again, as in 2006, poultry outbreaks continued across southeast Asia. Sporadic cases in wild birds were reported in Japan and Hong Kong, PR China. By the end of 2007, the virus was considered to be endemic in poultry in Egypt, Indonesia and Nigeria, and possibly endemic in Bangladesh and China (UN System Influenza Coordinator & World Bank 2007).

Until the end of October 2008, no new countries had reported outbreaks. Outbreaks in domestic birds were reported in Bangladesh, China, Egypt, India, Indonesia, Nigeria, Pakistan, the Republic of Korea, Russia, Turkey and Vietnam between January and July, with outbreaks in Bangladesh, Germany, Laos, Togo and Vietnam in September and October. Infected wild birds were reported in four countries: Mute Swans *Cygnus olor* and a Canada Goose *Branta canadensis* in the United Kingdom in January and February; sick and dead swans in three areas of Japan in April and May; one apparently asymptomatic Pochard *Aythya ferina* in Switzerland in March; and one dead House Crow *Corvus splendens* in Hong Kong, PR China in October. Bangladesh reported its first human case of H5N1 infection in March. China, Egypt, Indonesia and Vietnam also reported human cases in 2008.

Significant outbreaks of HPAI H5N1 in wild birds

Prior to HPAI H5N1, reports of HPAI in wild birds were very rare. The broad geographical scale and extent of the disease in wild birds is both extraordinary and unprecedented. The following table (Table 1) summarises the known major outbreaks of HPAI H5N1 in wild birds.

| Year | Month(s) | Location(s) | Description of affected birds |
|------|-----------------------|---|---|
| 2005 | April | Lake Qinghai in central China | 6,345 waterbirds, the majority of which were Great Black-headed Gulls <i>Larus ichthyaetus</i> , Bar- headed Geese <i>Anser indicus</i> and Brown- headed Gulls <i>Larus brunnicephalus</i> |
| | July | Lake Chany, Russia | Over 5000 wild birds including Pochard <i>Aythya ferina</i> , Mallard <i>Anas platyrhynchos</i> , and Teal <i>Anas crecca</i> |
| | August | Lake Erhel & Lake Khunt in Mongolia | 89 waterbirds including ducks, geese and swans |
| | October – November | Romania & Croatia | Over 180 waterbirds, mainly swans |
| 2006 | January | Coastal area in the vicinity of Baku, Azerbaijan | |
| | January – May | 23 countries in Europe including Turkey and European Russia | |
| | February | Rasht, Iran | 153 wild swans |
| | May | Multiple locations in Qinghai province, China | Over 900, mainly waterbirds, and mostly Bar-headed Geese Anser indicus |
| | May | Naqu, Tibet | Over 2,300 birds – species composition unclear but 300 infected Bar-headed Geese <i>Anser indicus</i> were reported |
| | June | Lake Khunt in Mongolia | Twelve waterbirds including swans, geese and gulls |
| | Summer | Tuva Republic, Russia | Over 3100 wild birds mainly Great Crested Grebe Podiceps cristatus |
| 2007 | June | Germany, France and the Czech Republic | Over 290, mainly waterbirds, found mostly in Germany |

Table 1: Significant known outbreaks of highly pathogenic avian influenza H5N1 in wild birds*

Numerous species of wild birds, especially waterbirds, are susceptible to infection by the H5N1 HPAI virus. Close contact between poultry and wild birds can lead to cross-infection, from poultry to wild birds and from wild birds to poultry. Additionally, species that live in and around poultry farms and human habitations may hypothetically serve as "bridge species" that could transmit the virus between poultry and wild birds either by direct contact between wild birds and poultry kept outside or by indirect contact with contaminated materials. While there is no sound evidence that wild birds have carried the virus long distances on migration (Feare & Yasué 2006), analysis of genetic sequences and other largely indirect evidence suggests that wild birds are likely to have contributed to spread (Chen *et al.* 2006; Keawcharoen *et al.* 2008; Kilpatrick *et al.* 2006; Hesterberg *et al.* 2007; Weber & Stilianakis 2007). The relative importance of different modes of infection transfer, however, is unclear in the present state of knowledge.

^{*} Data sources include OIE disease information reports, FAO, the German Friedrich-Loeffler Institute epidemiological bulletins, and Russian, Bird Disease Laboratory – dates, locations and numbers may differ slightly in other sources

Poor planning in response to development pressures has led to the increasing loss or degradation of wild ecosystems, which are the natural habitats for wild birds. This has resulted in closer contact between wild populations, domesticated birds such as chickens, ducks, geese, and other domestic fowl, and humans and has thus provided greater opportunities for the spread of HPAI H5N1 between wild and domestic birds, and thence to humans. The interplay between agriculture, animal (domestic and wild) health, human health, ecosystem health, and socio-cultural factors has been important in the emergence and spread of the virus.

Avian influenza and wetlands

Given the ecology of the natural hosts of LPAI viruses, it is unsurprising that wetlands play a major role in the natural epidemiology of avian influenza. As with many other viruses, avian influenza virions survive longer in colder water (Lu *et al.* 2003; Stallknecht *et al.* 1990), and the virus is strongly suggested to survive over winter in frozen lakes in Arctic and sub-Arctic breeding areas. Thus, as well as the waterbird hosts, these wetlands are probably permanent reservoirs of LPAI virus (Rogers *et al.* 2004; Smith *et al.* 2004) (re-)infecting waterbirds arriving from southerly areas to breed (shown in Siberia by Okazaki *et al.* 2000 and Alaska by Ito *et al.* 1995). Indeed, in some wetlands used as staging grounds by large numbers of migratory ducks, avian influenza viral particles can be readily isolated from lake water (Hinshaw *et al.* 1980).

An agricultural practice that provides ideal conditions for cross-infection and thus genetic change is used on some fish-farms in Asia: battery cages of poultry are placed directly over troughs in pigpens, which in turn are positioned over fish farms. The poultry waste feeds the pigs, the pig waste is either eaten by the fish or acts as a fertiliser for aquatic fish food, and the pond water is sometimes recycled as drinking water for the pigs and poultry (Greger 2006). These kinds of agricultural practices afford avian influenza viruses, which are spread via the faecal-oral route, an opportunity to cycle through a mammalian species, accumulating the mutations necessary to adapt to mammalian hosts. Thus, as the use of such practices increases, so does the likelihood that new influenza strains infectious to and transmissible between humans will emerge (Culliton 1990; Greger 2006).

As well as providing conditions for virus mutation and generation, agricultural practices, particularly those used on wetlands, can enhance the ability of a virus to spread. The role of Asian domestic ducks in the epidemiology of H5N1 HPAI has been closely researched and found to be central not only to the genesis of the virus (Hulse-Post *et al.* 2005; Sims 2007), but also to its spread and the maintenance of infection in several Asian countries (Shortridge & Melville 2006). Typically this has involved flocks of domestic ducks used for 'cleaning' rice paddies of unharvested grain and various pests, during which they can potentially have contact with wild ducks using the same wetlands. Detailed research (Gilbert *et al.* 2006; Songserm *et al.* 2006) in Thailand has demonstrated a strong association between the H5N1 HPAI virus and abundance of free-grazing ducks. Gilbert *et al.* (2006) concluded that in Thailand "wetlands used for double-crop rice production, where freegrazing duck feed year round in rice paddies, appear to be a critical factor in HPAI persistence and spread".

Wildlife conservation implications

Prior to H5N1HPAI, reports of HPAI in wild birds were very rare. The broad geographical scale and extent of the disease in wild birds is both extraordinary and unprecedented, and the conservation impacts of H5N1 HPAI have been significant.

It is estimated that between 5-10% of the world population of Bar-headed Goose *Anser indicus* died at Lake Qinghai, China, in spring 2005 (Chen *et al.* 2005; Liu *et al.* 2005). At least two globally threatened species have been affected: Black-necked Crane *Grus nigricollis* in China and Redbreasted Goose *Branta ruficollis* in Greece. Approximately 90% of the world population of Redbreasted Goose is confined to just five roost sites in Romania and Bulgaria,

countries that have both reported outbreaks, as also have Russia and Ukraine where they also over-winter (BirdLife International 2007).

However, the total number of wild birds known to have been affected has been small in contrast to the number of domestic birds affected, and many more wild birds die of more common avian diseases each year. Perhaps a greater threat than direct mortality has been the development of public fear about waterbirds resulting in misguided attempts to control the disease by disturbing or destroying wild birds and their habitats. Such responses are often encouraged by exaggerated or misleading messages in the media.

Currently, wildlife health problems are being created or exacerbated by unsustainable activities such as habitat loss or degradation, which facilitates closer contact between domestic and wild animals. Many advocate that to reduce risk of avian influenza and other bird diseases, there is a need to move to markedly more sustainable systems of agriculture with significantly lower intensity systems of poultry production. These need to be more biosecure, separated from wild waterbirds and their natural wetland habitats resulting in far fewer opportunities for viral cross-infection and thus pathogenetic amplification (Greger 2006). There are major animal and human health consequences (in terms of the impact on economies, food security and potential implications of a human influenza pandemic) of not strategically addressing these issues. However, to deliver such an objective in a world with an ever-growing human population and with issues of food-security in many developing countries, will be a major policy challenge.

References

- BirdLife International 2007. BirdLife statement on avian influenza. Available from <u>http://www.birdlife.org/action/science/species/avian_flu/index.html</u>.
- Brown, J.D., Stallknecht, D.E., Beck, J.R., Suarez, D.L. & Swayne, D.E. 2006. Susceptibility of North American ducks and gulls to H5N1 Highly Pathogenic Avian Influenza viruses. *Emerging Infectious Diseases* 12(11): 1663-1670.
- Capua, I. & Mutinelli, F. 2001. Low pathogenicity (LPAI) and highly pathogenic (HPAI) avian influenza in turkeys and chicken. Pp. 13-20. In: Capua, I. & Mutinelli F. (eds.). A Colour Atlas and Text on Avian Influenza. Papi Editore, Bologna, Italy.
- Center for Infectious Disease Research & Policy. 2007. Avian Influenza (Bird Flu): Agricultural and Wildlife Considerations. Available from
- http://www.cidrapforum.org/cidrap/content/influenza/avianflu/biofacts/avflu.html.
- Chen, H., Smith, G.J.D., Zhang, S.Y., Oin, K., Wang, J., Li. K.S., Webster, R.G., Peiris, J.S.M. & Guan, Y. 2005. H5N1 virus outbreak in migratory waterfowl. *Nature Online.* Available from <u>http://www.nature.com/nature/journal/vaop/ncurrent/full/nature03974.html</u>.
 - Culliton, B.J. 1990. Emerging viruses, emerging threat. Science 247: 279-280.
- Diouf, J. 2005. Address on Avian Influenza to 33rd FAO Conference. Available from http://www.fao.org/ag/againfo/subjects/avian/conf05-Al/J6651e-DG.pdf.
- Ellis, T.M., Bousfield, R.B., Bisset, L.A., Dyrting, K.C., Luk, G., Tsim, S.T., Sturm-Ramirez, K., Webster, R.G., Guan, Y., & Peiris, J.S. 2004. Investigation of outbreaks of highly pathogenic H5N1 avian influenza in waterfowl and wild birds in Hong Kong in late 2002. Avian Pathology 33(5): 492-505.
- Feare, C.J. & Yasué, M. 2006. Asymptomatic infection with highly pathogenic avian influenza H5N1 in wild birds: how sound is the evidence? *Virology Journal*. 3.96. doi:10.1186/1742-422X_3_96.
- Fouchier, R.A.M., Munster, V., Wallensten, A., Bestebroer, T.M., Herfst, S., Smith, D, Rimmelzwaan, G.F., Olsen, B. & Osterhaus, D.M.E. 2005. Characterization of a novel influenza A virus hemagglutinin subtype (H16) obtained from Black-headed Gulls. *Journal of Virology* 79: 2814-2822.
- Gilbert, M., Chaitaweesub, P., Parakamawongsa, T., Premashthira, S., Tiensin, T., Kalpravidh, W., Wagner, H. & Slingenbergh, J. 2006. Free-grazing ducks and highly pathogenic avian influenza, Thailand. *Emerging Infectious Diseases* 12(2): 227-234.
- Gorman, O.T., Bean, W.J. & Webster, R.G. 1992. Evolutionary processes in influenza viruses: divergence, rapid evolution, and stasis. *Current Topics in Microbiology and Immunology* 176: 75-97.
- GRAIN 2006. Fowl play: The poultry industry's central role in the bird flu crisis. GRAIN Briefing, February 2006. Available from <u>http://www.grain.org/briefings/?id=194</u>.
- Greger, M. 2006. Bird Flu: a virus of our own hatching. Lantern Books, New York. 465 pp.

- Guan Y, Peiris, J.S., Lipatov, A.S., Ellis, T.M., Dyrting, K.C. Krauss, S., Zhang, L.J., Webster, R.G. & Shortridge, K.F. 2002. Emergence of multiple genotypes of H5N1 avian influenza viruses in Hong Kong SAR. *Proceedings of the National Academy of Sciences* 99(13): 8950-8955.
- Hesterberg, U., Harris, K., Cook A. & Brown, I. 2007. *Annual Report. Surveillance for avian influenza in wild birds carried out by Member States. February- December 2006.* Community Reference Laboratory for avian influenza and Newcastle disease. 53 pp. Available from http://ec.europa.eu/food/animal/diseases/controlmeasures/avian/annrepres_surv_wb_02-122006_en.pdf.
- Hesterberg, U.W., Harris, K., Stroud, D.A., Guberti, V., Busani, L., Pittman, M., Piazza, V., Cook, A. & Brown, I.H. in press. Avian influenza surveillance in wild birds in the European Union in 2006. *Influenza and other respiratory diseases*.
- Hinshaw, V.S. & Webster, R.G. 1982. The natural history of influenza A viruses. In: *Basic and applied influenza research.* Beare, A.S. (ed.). CRC Press, Boca Raton, Florida. Pp. 79-104.
- Hinshaw, V.S., Webster, R.G. & Turner, B. 1980. The perpetuation of orthomyxoviruses and paramyxoviruses in Canadian waterfowl. *Canadian Journal of Microbiology* 26: 622-629.
- Hulse-Post, D.J., Sturm-Ramirez, K.M., Humberd, J., Seiler, P., Govorkova, E.A., Krauss, S., Scholtissek, C., Puthavathana, P., Buranathai, C., Nguyen, T.D., Long, H.T., Naipospos, T.S.P., Chen, H., Ellis, T.M., Guan, Y., Peiris, J.S.M. & Webster, R.G. 2005. Role of domestic ducks in the propagation and biological evolution of highly pathogenic H5N1 influenza viruses in Asia. *Proceedings of the National Academy of Sciences* 102: 10682-10687. Available from http://www.pnas.org/cgi/content/full/102/30/10682.
- Ito, T., Okazaki, K., Kawaoka, Y., Takada, A., Webster, R.G. & Kida, H. 1995. Perpetuation of influenza A viruses in Alaskan waterfowl reservoirs. *Archives of Virology* 140: 1163-1172.
- Keawcharoen, J., van Riel, D., van Amerongen, G., Bestebroer, T., Beyer, W.E., van Lavieren, R., Osterhaus, A.D.M.E., Fouchier, R.A.M. & Kuiken, T. 2008. Wild ducks as long-distance vectors of highly pathogenic avian influenza virus (H5N1). *Emerging Infectious Diseases* 14 (4): 600-607.
- Kilbourne, E.D. 2006. Influenza pandemics of the 20th century. *Emerging Infectious Diseases* 12(1): 9-14.
- Kilpatrick, M., Chmura, A.A., Gibbons, D.W., Fleischer, R.C., Marra, P.P. & Daszak, P. 2006. Predicting the global spread of H5N1 avian influenza. *Proceedings of the National Academy of Sciences* 103(15): 19368–19373. Available from <u>http://www.pnas.org/cgi/reprint/103/51/19368</u>.
- Lee, R.. 2008. Unpublished review of wild bird species reported as infected with HPAI H5N1. WWT, Slimbridge, UK.
- Li, K., Guan, S.Y., Wang, J., Smith, G.J., Xu K.M., Duan L., Rahardjo, A.P., Puthavathana, P., Buranathai, C., Nguyen, T.D., Estoepangestie, A.T., Chaisingh, A., Auewarakul, P., Long, H.T., Hanh, N.T., Webby, R.J., Poon, L.L., Chen, H., Shortridge, K.F., Yuen, K.Y., Webster, R.G. & Peiris, J.S. 2004. Genesis of a highly pathogenic and potentially pandemic H5N1 influenza virus in eastern Asia. *Nature* 430 (6996):209-213.
- Liu, J., Xiao, H., Lei, F., Zhu, Q., Qin, K., Zhang, X., Zhang, X., Zhao, D., Wang, G., Feng, Y., Ma, J., Liu, W., Wang, J. & Gao, F. 2005. Highly pathogenic H5N1 influenza virus infection in migratory birds. *Science Online*. Available from <u>http://www.sciencemag.org/cgi/content/abstract/309/5738/1206</u>.
- Lu, H., Castro, A.E., Pennick, K., Liu, J., Yang, Q., Dunn, P., Weinstock, D., & Henzler, D. 2003. Survival of avian influenza virus H7N2 in SPF chickens and their environments. *Avian Diseases* 47: 1015-1021.
- Mase, M., Tsukamoto, K., Imada, T., Imai, K., Tanimura, N., Nakamura, K., Yamamoto, Y., Hitomi, T., Kira, T., Nakai, T., Kiso, M., Horimoto, T., Kawaoka, Y. & Yamaguchi, S. 2005. Characterization of H5N1 influenza A viruses isolated during the 2003-2004 influenza outbreaks in Japan. *Virology* 332(1): 167-176.
- OIE 2008. Terrestrial Animal Health Code. Available from <u>http://www.oie.int/eng/Normes/mcode/en_sommaire.htm</u>.
- OIE 2008. Update on highly pathogenic avian influenza in animals (type H5 and H7). Available from http://www.oie.int/downld/AVIAN%20INFLUENZA/A_AI-Asia.htm.
- Okazaki, K., Takada, A., Ito, T., Imai, M., Takakuwa, H., Hatta, M., Ozaki, H., Tnizaki, T., Nagano, T., Ninomiya, A., Demenev, V.A., Tyaptirganov, M.M., Karatayeva, T.D., Yanmikova, S.S., Lvov, D.K. & Kida, H. 2000. Precursor genes of future pandemic influenza viruses are perpetuated in ducks nesting in Siberia. *Archives of Virology* 145: 885-893.
- Olsen, B., Munster, V.J., Wallensten, A., Waldenstrom, J., Osterhaus, A.D.M.E. & Fouchier, R.A.M. 2006. Global patterns of influenza a virus in wild birds. *Science* 312: 384–388.
- Rogers, S.O., Starmer, W.T., Castello, J.D. 2004. Recycling of pathogenic microbes through survival in ice. *Medical Hypotheses* 63: 773-777.
- Rohm, C., Zhou, N., Suss, J., Mackenzie, J. & Webster, R.G. 1996. Characterization of a novel influenza hemagglutinin, H15: criteria for determination of influenza A subtypes. *Virology* 217:508-516.

- Sabirovic, M., Wilesmith, J., Hall, S., Coulson, N., Landeg, F. 2006. Situation Analysis Outbreaks of HPAI H5N1 virus in Europe during 2005/2006 – An overview and commentary. DEFRA, International Animal Health Division, United Kingdom. 40 pp. Available from http://www.defra.gov.uk/animalh/diseases/monitoring/pdf/hpai-europe300606.pdf.
- Senne, D.A., Panigrahy, B., Kawaoka, Y., Pearson, J.E., Suss, J., Lipkind, M., Kida, H. & Webster, R.G. 1996. Survey of the hemagglutinin (HA) cleavage site sequence of H5 and H7 avian influenza viruses: amino acid sequence at the HA cleavage site as a marker of pathogenicity potential. *Avian Diseases* 40(2): 425-437.
- Shortridge, K.F. & Melville, D.S. 2006. Domestic poultry and migratory birds in the interspecies transmission of avian influenza viruses: a view from Hong Kong. In *Waterbirds around the world.* Eds. G.C. Boere, C.A. Galbraith & D.A. Stroud. The Stationery Office, Edinburgh, UK. Pp. 427-431.
 - Shortridge, K.F. 1997. Is China an influenza epicentre? *Chinese Medical Journal* 110: 637-641.
- Shortridge, K.F., Webster, R.G., Butterfield, W.K. & Campbell, C.H. 1977. Persistence of Hong Kong influenza virus variants in pigs. *Science* 196: 1454-1455.

Sims, L.D. 2007. Lessons learned from Asian H5N1 outbreak control. Avian Diseases 50: 174-181.

- Smith, A.W., Skilling, D.E., Castello, J.D., Rogers, S.O. 2004. Ice as a reservoir for pathogenic human viruses: specifically, caliciviruses, influenza viruses, and enteroviruses. *Medical Hypotheses* 63: 560-566.
- Snacken, R., Kendal, A.P., Haaheim, L.R. & Wood, J.M. 1999. The next influenza pandemic: lessons from Hong Kong, 1997. *Emerging Infectious Diseases* 5:195-203.
- Songserm, T., Jam-on, R., Sae-Heng, N., Meemak, N., Hulse-Post, D.J., Sturm-Ramirez, K.M., & Webster, R.J. 2006. Domestic ducks and H5N1 Influenza Epidemic, Thailand. *Emerging Infectious Diseases* 12(4): 575-581.
- Stallknecht, D.E. & Shane, S.M. 1988. Host range of avian influenza virus in free-living birds. *Veterinary Research Communications* 12: 125-141.
- Stallknecht, D.E. & Brown, J.D. 2007. Wild birds and the epidemiology of avian influenza. *Journal of Wildlife Diseases* 43(3) Supplement: S15-20.
- Stallknecht, D.E., Shane, S.M., Kearney, M.T., Zwank, P.J. 1990. Persistence of avian influenza viruses in water. *Avian Diseases* 34: 406-411.
- Sturm-Ramirez, K.M., Ellis, T., Bousfield, B., Bissett, L., Dyrting, K., Rehg, J.E., Poon, L., Guan, Y, Peiris, M.
 & Webster, R.G. 2004. Re-emerging H5N1 influenza viruses in Hong Kong in 2002 are highly pathogenic to ducks. *Journal of Virology* 78: 4892-4901.
- Taubenberger, J.K., Reid, A.H., Lourens, R.M., Wang, R., Jin, G. & Fanning, T.G. 2005. Characterization of the 1918 influenza virus polymerase genes. *Nature* 437(7060):889-93.
- UN System Influenza Coordinator & World Bank 2007. Third global progress report on responses to avian influenza and state of pandemic readiness. Available from <u>http://siteresources.worldbank.org/INTTOPAVIFLU/Resources/UN_WB_AHI_ProgressReportFinal.pdf</u>.
- USGS National Wildlife Health Center 2008. List of species affected by H5N1. Available from http://www.nwhc.usgs.gov/disease_information/avian_influenza/affected_species_chart.jsp.
- van Gils, J.A., Munster, V.J., Radersma, R., Liefhebber, D., Fouchier, R.A. & Klaasen, M. 2007. Hampered Foraging and Migratory Performance in Swans Infected with Low-Pathogenic Avian Influenza A Virus. *PLoS ONE* 2(1): e184. doi:10.1371/journal.pone.0000184.
- Weber, T.P. & Stilianakis, N.I. 2007. Ecologic immunity of avian influenza (H5N1) in migratory birds. *Emerging Infectious Diseases* 13: 1139-1143.
- Webster, R.G., Peiris, M., Chen, H. & Guan, Y. 2006. H5N1 outbreaks and enzootic influenza. *Emerging Infectious Diseases* 12(1): 3-8.
- Webster, R.G., Bean, W.J., Gorman, O.T., Chambers, T.M. & Kawaoka, Y. 1992. Evolution and ecology of Influenza A viruses. *Microbiological Reviews* 56(1): 152-179.
- World Health Organisation 2008. Cumulative Number of Confirmed Human Cases of Avian InfluenzaA/(H5N1)ReportedtoWHO.Availablefromhttp://www.who.int/csr/disease/avian_influenza/country/cases_table_2008_03_11/en/index.htmlAccessed 11 March 2008.