Implications of global climate change and migratory bird movement on the spread of - West Nile Virus and H5N1 Highly Pathogenic Avian Influenza.

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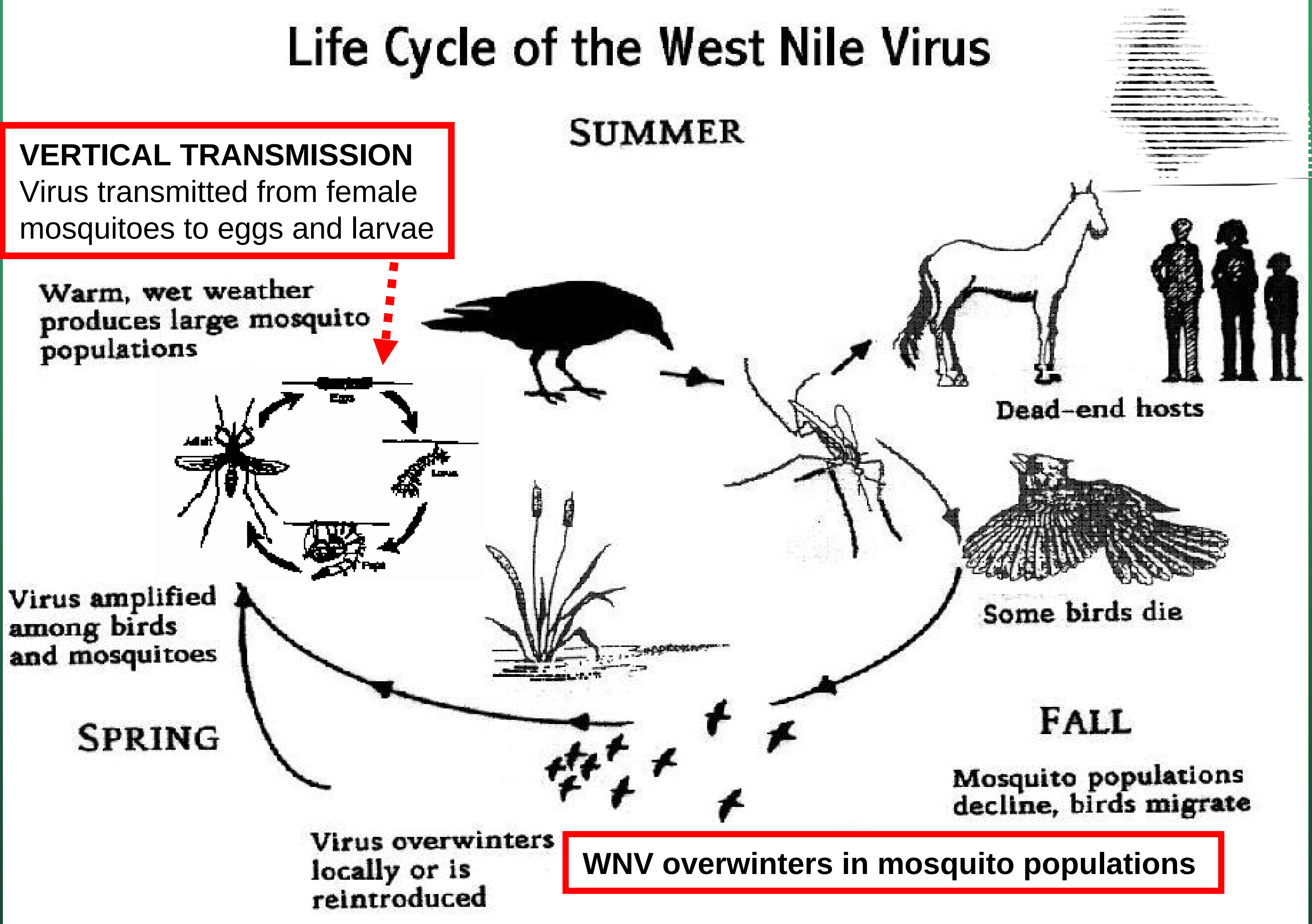
USGS science for a changing world

The challenge of forecasting the spread of zoonotic disease…….

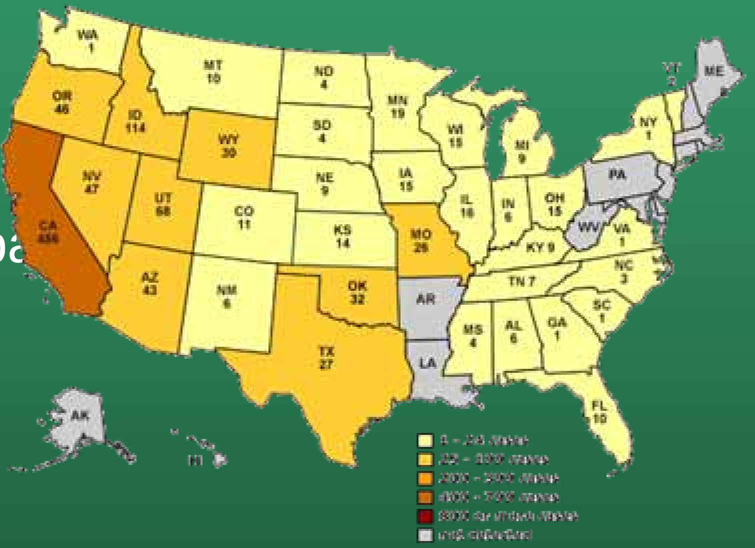
- Comparison of West Nile Virus and H5N1
- Disease Ecology and spread of WNV
- Weather/Climate and spread of WNV
- Disease Ecology and spread of H5N1 HPAI
- Weather/Climate and spread of H5N1



after http://www.warnercnr.colostate.edu/avprojects/globe/precipitation/West%20Nile%20Virus/wnvlifecycle.jpg

1999 prediction by Rappole et al.of implications of avian assisted movement of the virus

- *Rappole et al 1999*

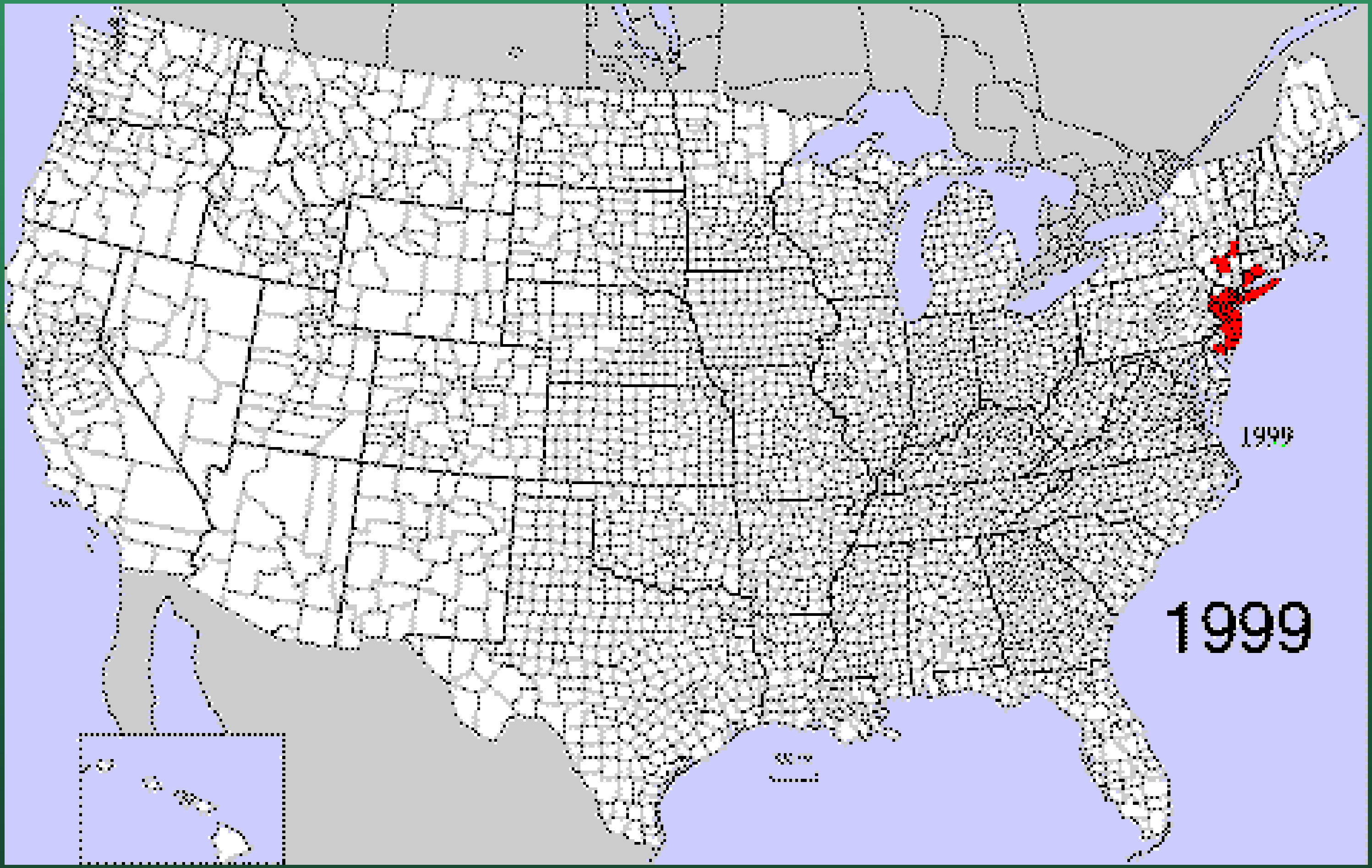


"If transovarial transmission or survival in overwintering mosquitoes were the principal means for its persistence, West Nile virus might not become established in the New World because of aggressive mosquito suppression campaigns conducted in the New York area. However, the pattern of outbreaks in southern Europe suggests that **viremic migratory birds may also contribute to movement of the virus. If so, West Nile virus has the potential to cause outbreaks throughout both temperate and tropical regions of the Western Hemisphere."**

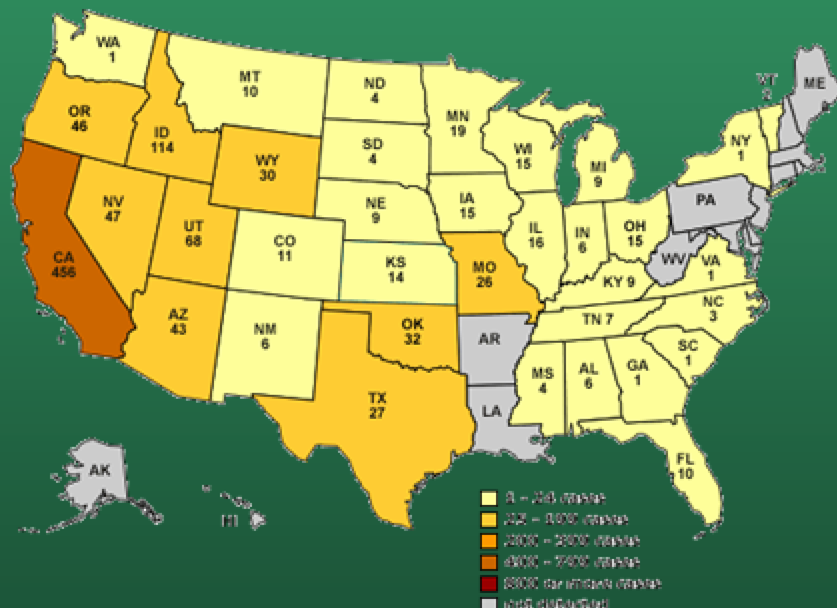
USGS

Spread of West Nile Virus in USA and Canada, 1999 – 2002

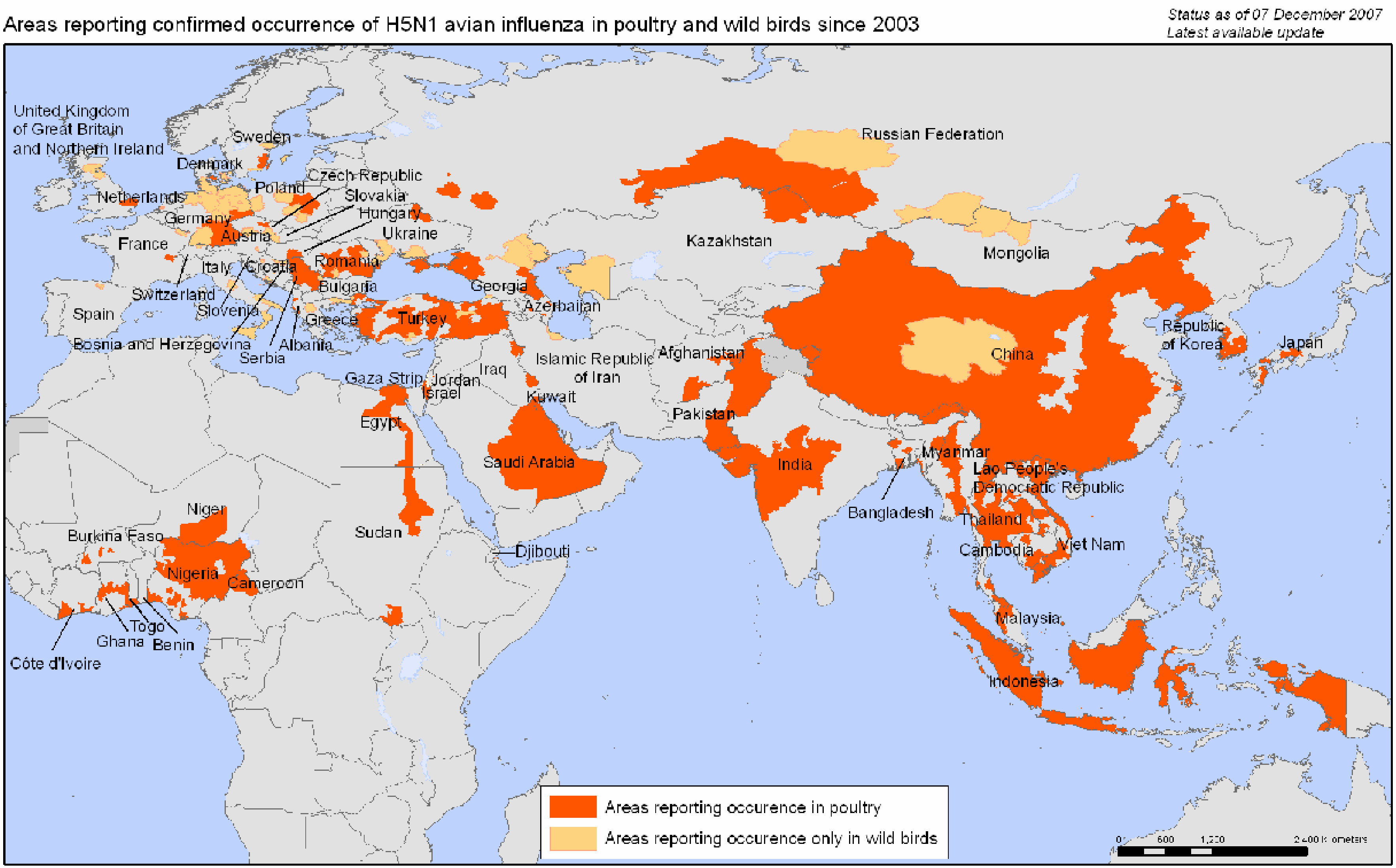
Henry V. Huang / Washington U School Medicine http://environmentalrisk.cornell.edu/WNV/Maps/HH-USCan-99-02.gif



By 2004 WNV was on the east side of the Sierra killing Sage Grouse



Geographic distribution of H5N1 HPAI



World Health Organization

The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: World Organisation for Animal Health (OIE) and national governments
Map Production: Public Health Mapping and GIS
International Health Regulations Coordination, World Health Organization

Highly Pathogenic AI - H5N1

Risk Pathways for Entry

- Poultry and poultry products
- Pet/wild bird trade
- Smuggling
- Migratory birds
- Humans

The old model for Highly Pathogenic Bird Flu dynamics in wild and domestic birds

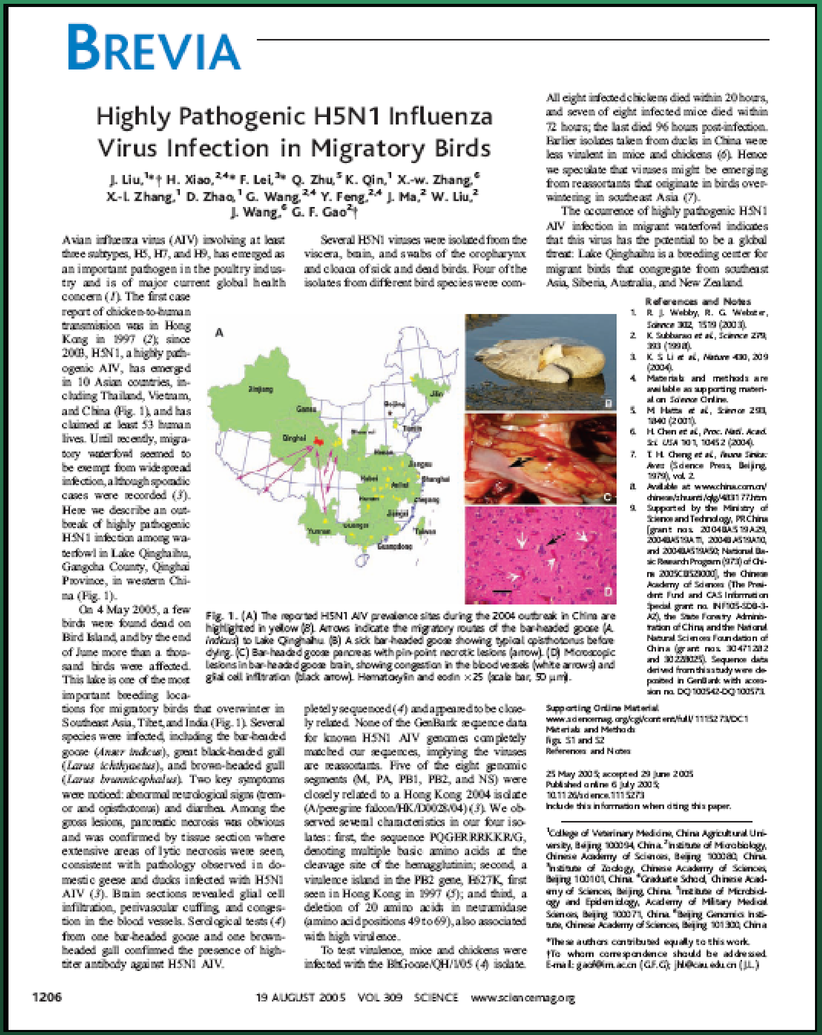
1. Wild birds transmit LPAI to farmed birds

2. Mutation into HPAI likely occurs in poultry farms

3. Wild birds are re-infected by contact with infected poultry and die

Can migratory birds carry the high pathogenic form of the H5N1 virus along migratory pathways?

Evidence of non-lethal HPAI movement by wild birds.



BREVIA

Highly Pathogenic H5N1 Influenza Virus Infection in Migratory Birds

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Avian influenza virus (AIV) involving at least three subtypes, H5, H7, and H9, has emerged as an important pathogen in the poultry industry and is of major current global health concern (1). The first case report of chicken-to-human transmission was in Hong Kong in 1997 (2); since 2003, H5N1, a highly pathogenic AIV, has emerged in 10 Asian countries, including Thailand, Vietnam, and China (Fig. 1), and has claimed at least 53 human lives. Until recently, migratory waterfowl seemed to be exempt from widespread infection, although sporadic cases were recorded (3). Here we describe an outbreak of highly pathogenic H5N1 infection among waterfowl in Lake Qinghaihu, Gangcha County, Qinghai Province, in western China (Fig. 1).

On 4 May 2005, a few birds were found dead on Bird Island, and by the end of June more than a thousand birds were affected. This lake is one of the most important breeding locations for migratory birds that overwinter in Southeast Asia, Tibet, and India (Fig. 1). Several species were infected, including the bar-headed goose (*Anser indicus*), great black-headed gull (*Larus ichthyaetus*), and brown-headed gull (*Larus brunnicephalus*). Two key symptoms were noticed: abnormal neurological signs (tremor and opisthotonus) and diarrhea. Among the gross lesions, pancreatic necrosis was obvious and was confirmed by tissue section where extensive areas of lytic necrosis were seen, consistent with pathology observed in domestic geese and ducks infected with H5N1 AIV (3). Brain sections revealed glial cell infiltration, perivascular cuffing, and congestion in the blood vessels. Serological tests (4) from one bar-headed goose and one brown-headed gull confirmed the presence of high-titer antibody against H5N1 AIV.

Several H5N1 viruses were isolated from the viscera, brain, and swabs of the oropharynx and cloaca of sick and dead birds. Four of the isolates from different bird species were completely sequenced (4) and appeared to be closely related. None of the GenBank sequence data for known H5N1 AIV genomes completely matched our sequences, implying the viruses are reassortants. Five of the eight genomic segments (M, PA, PB1, PB2, and NS) were closely related to a Hong Kong 2004 isolate (A/peregrine falcon/HK/D0028/04) (3). We observed several characteristics in our four isolates: first, the sequence PQGERRRKKR/G, denoting multiple basic amino acids at the cleavage site of the hemagglutinin; second, a virulence island in the PB2 gene, E627K, first seen in Hong Kong in 1997 (5); and third, a deletion of 20 amino acids in neuramidase (amino acid positions 49 to 69), also associated with high virulence.

To test virulence, mice and chickens were infected with the BhGoose/QH/1/05 (4) isolate. All eight infected chickens died within 20 hours, and seven of eight infected mice died within 72 hours; the last died 96 hours post-infection. Earlier isolates taken from ducks in China were less virulent in mice and chickens (6). Hence we speculate that viruses might be emerging from reassortants that originate in birds overwintering in southeast Asia (7).

The occurrence of highly pathogenic H5N1 AIV infection in migrant waterfowl indicates that this virus has the potential to be a global threat: Lake Qinghaihu is a breeding center for migrant birds that congregate from southeast Asia, Siberia, Australia, and New Zealand.

Fig. 1. (A) The reported H5N1 AIV prevalence sites during the 2004 outbreak in China are highlighted in yellow (8). Arrows indicate the migratory routes of the bar-headed goose (*A. indicus*) to Lake Qinghaihu. (B) A sick bar-headed goose showing typical opisthotonus before dying. (C) Bar-headed goose pancreas with pin-point necrotic lesions (arrow). (D) Microscopic lesions in bar-headed goose brain, showing congestion in the blood vessels (white arrows) and glial cell infiltration (black arrow). Hematoxylin and eosin ×25 (scale bar, 50 μm).

References and Notes
1. R. J. Webby, R. G. Webster, *Science* 302, 1519 (2003).
2. K. Subbarao *et al.*, *Science* 279, 393 (1998).
3. K. S. Li *et al.*, *Nature* 430, 209 (2004).
4. Materials and methods are available as supporting material on *Science* Online.
5. M. Hatta *et al.*, *Science* 293, 1840 (2001).
6. H. Chen *et al.*, *Proc. Natl. Acad. Sci. USA* 101, 10452 (2004).
7. T. H. Cheng *et al.*, *Fauna Sinica: Aves* (Science Press, Beijing, 1979), vol. 2.
8. Available at www.china.com.cn/chinese/zhuanti/qlg/403177.htm
9. Supported by the Ministry of Science and Technology, PR China [grant nos. 2004BA519A29, 2004BA519A11, 2004BA519A10, and 2004BA519A50; National Basic Research Program (973) of China 2005CB523000], the Chinese Academy of Sciences (The President Fund and CAS Information Special grant no. INF105-SDB-3-A2), the State Forestry Administration of China and the National Natural Sciences Foundation of China (grant nos. 30471282 and 30228025). Sequence data derived from this study were deposited in GenBank with accession no. DQ100542-DQ100573.

Supporting Online Material
www.sciencemag.org/cgi/content/full/1115273/DC1
Materials and Methods
Figs. S1 and S2
References and Notes

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. The presence of coexisting but genetically distinguishable avian influenza

viruses with an HP viral genotype in two cohabiting species of wild waterfowl, with evidence of non-lethal infection at least

in one species and without evidence of prior extensive circulation of the virus in domestic poultry, suggest that some strains

with a potential high pathogenicity for poultry could be maintained in a community of wild waterfowl.

Citation: Gaidet N, Cattoli G, Hammoumi S, Newman SH, Hagemeijer W, et al. (2008) Evidence of Infection by H5N2 Highly Pathogenic Avian Influenza Viruses in

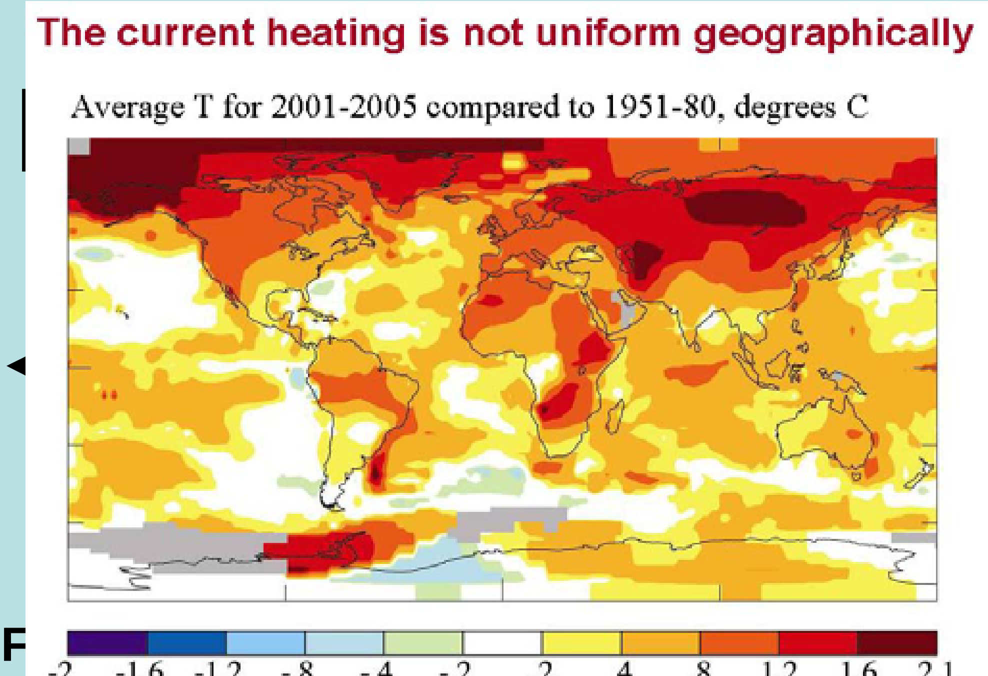
Healthy Wild Waterfowl. PLoS Pathog 4(8): e1000127. doi:10.1371/journal.ppat.1000127

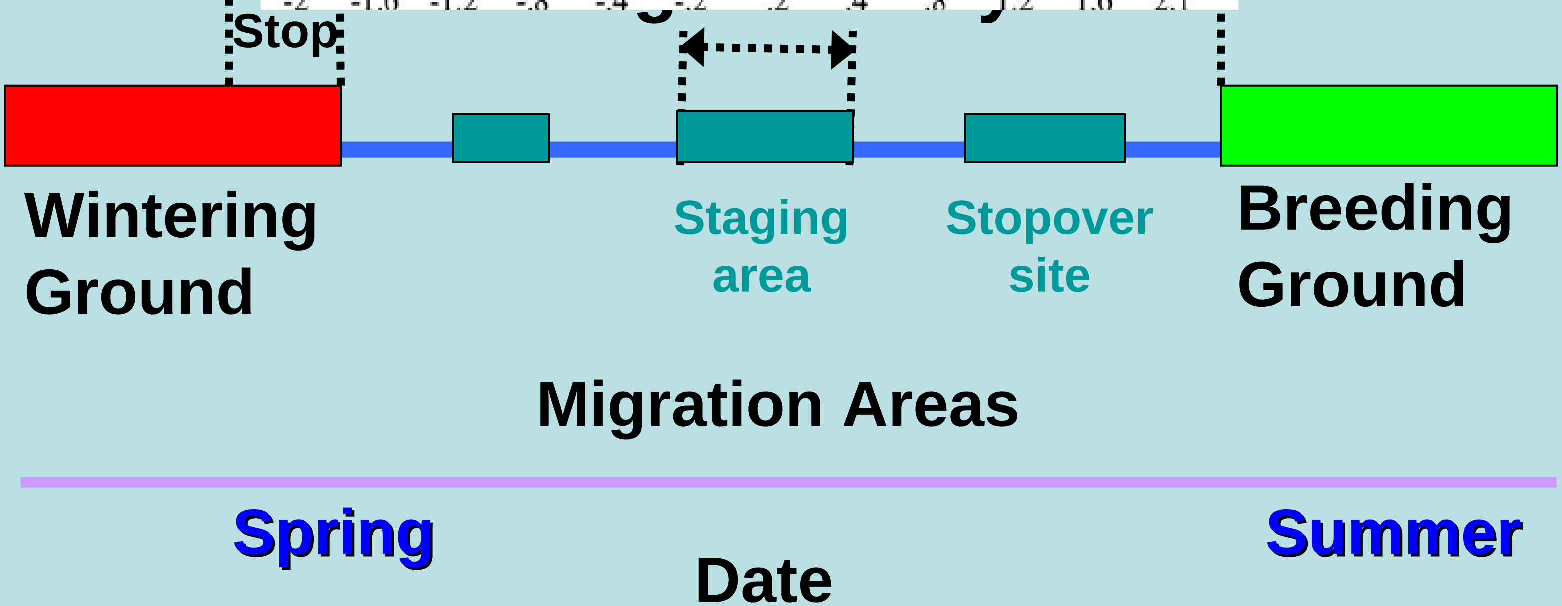
H5N1 HPAI –flu transmission

Fecal/oral route

Weather and the H5N1 Virus

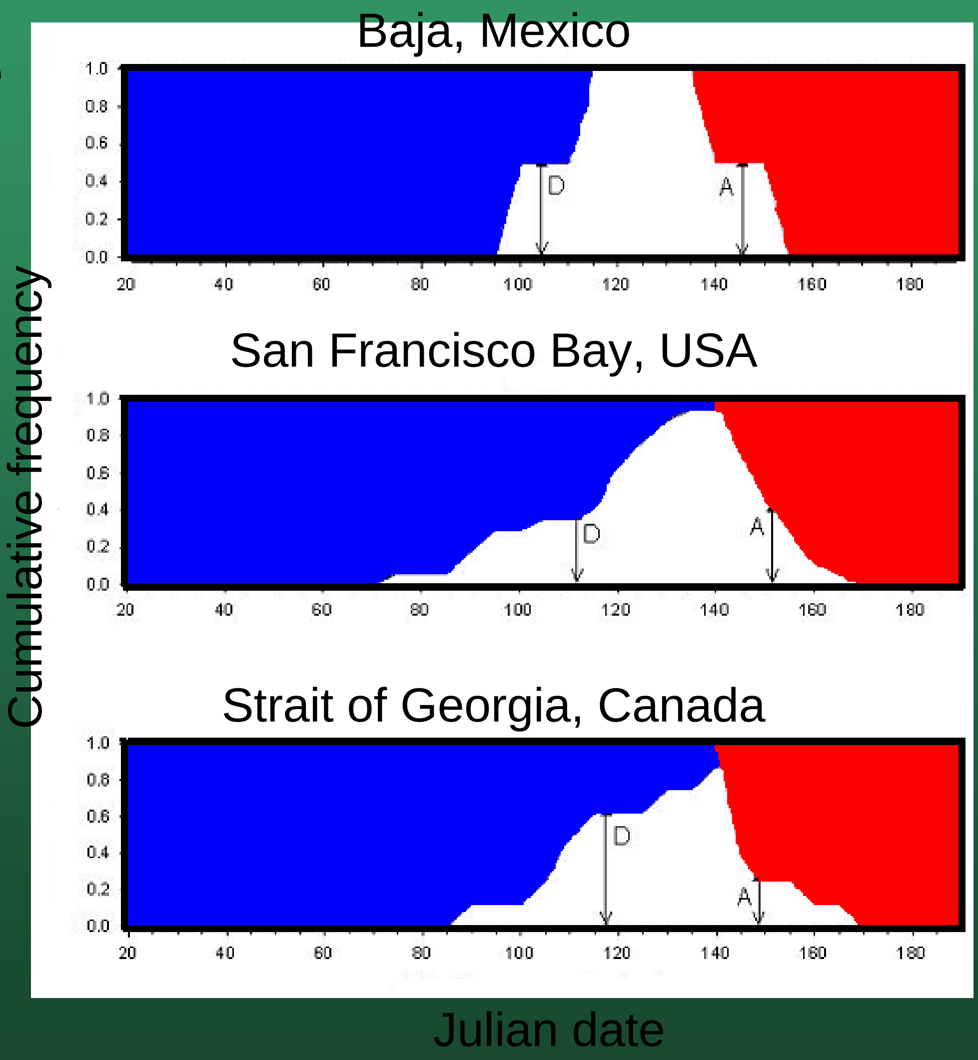
- The H5N1 avian influenza virus can survive for more than a month in bird droppings in cold weather and for nearly a week even in hot summer temperatures, the World Health Organization said on Fri 20 Jan 2006.


The current heating is not uniform geographically
Average T for 2001-2005 compared to 1951-80, degrees C
-2 -1.6 -1.2 -.8 -.4 -.2 .2 .4 .8 1.2 1.6 2.1


Stop
Wintering Ground
Staging area
Stopover site
Breeding Ground
Migration Areas
Spring
Summer
Date

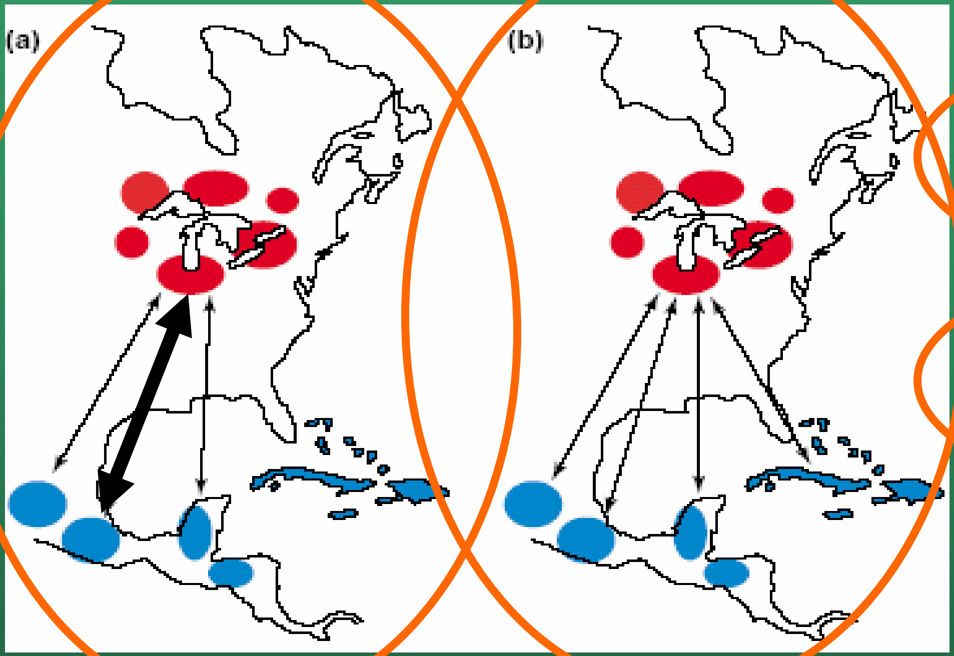
Migration Timing

<u>Example</u>: Surf scoter departure from coastal wintering areas and arrival at interior breeding areas



Wainwright and Takekawa, unpubl. data

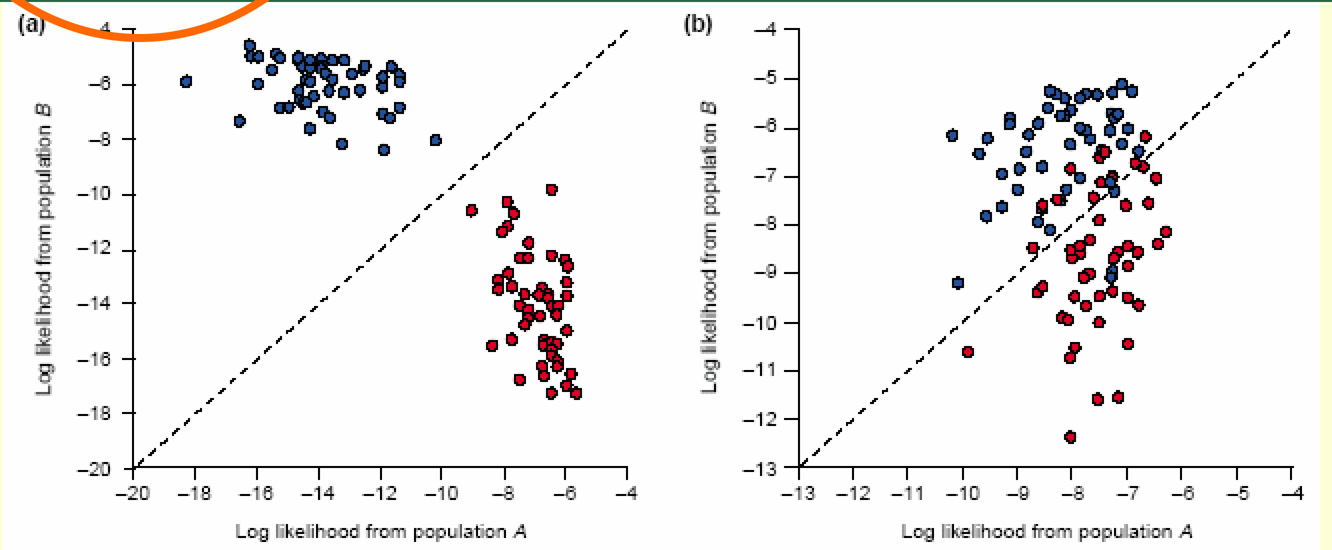
Migratory Connectivity



(a) = Strong connectivity
Most individuals from a single **breeding area** move to the same **non-breeding area**

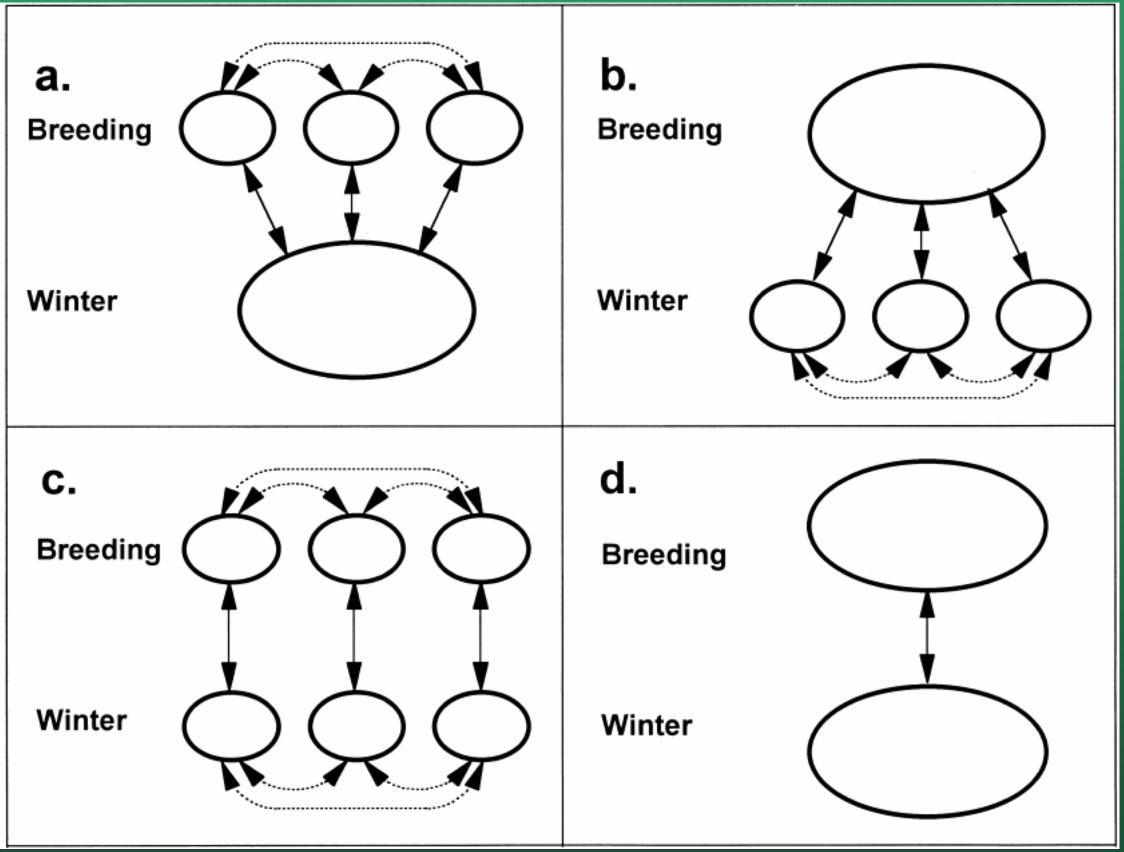
(b) = Weak connectivity
Individuals from single **breeding area** move to several **non-breeding areas**

Assignment Test



Webster et al. 2002

Population Structure

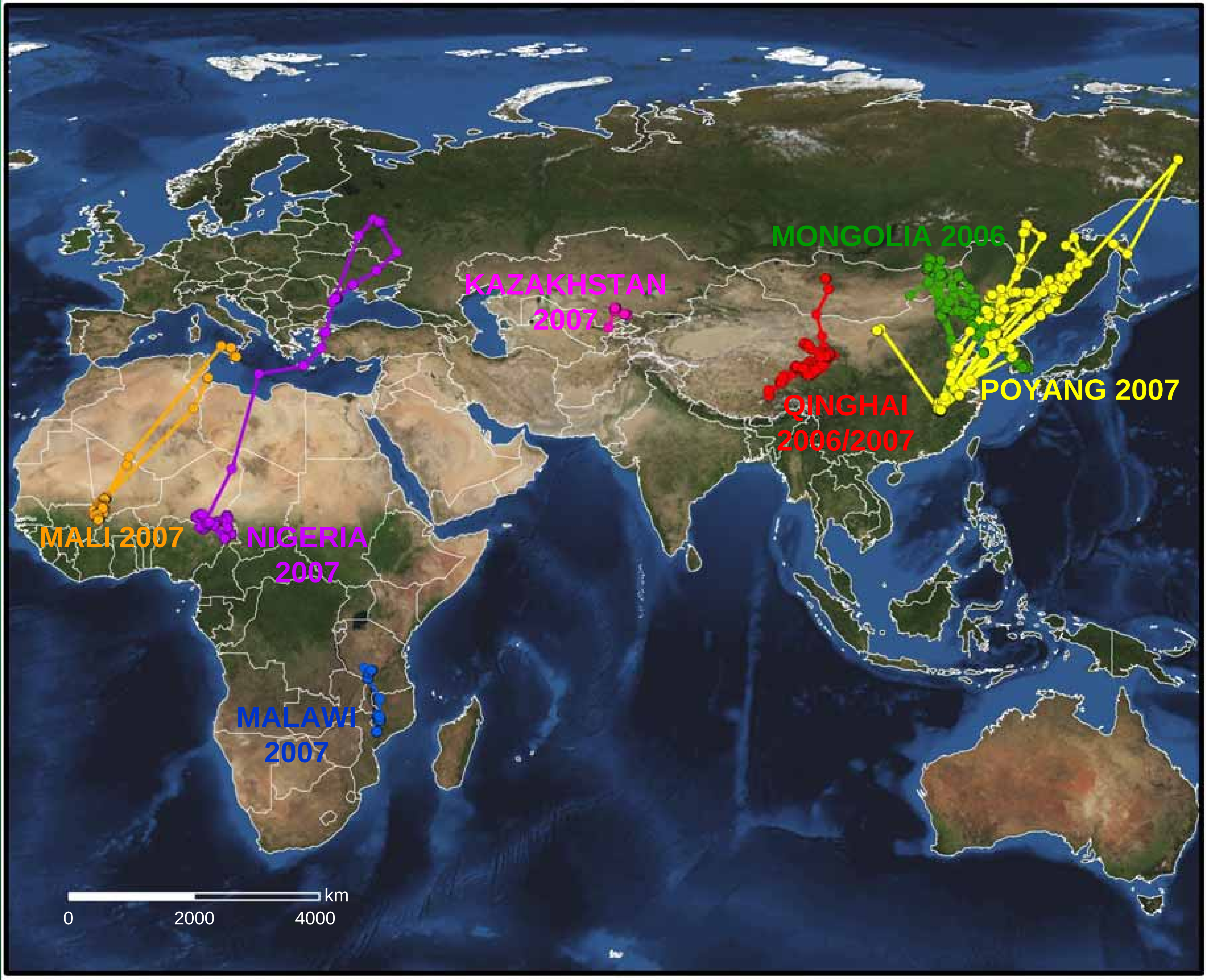


Esler 2000 – Applying Metapopulation Theory to Migratory Birds

- 4 scenarios of spatial and temporal dynamics between migratory bird breeding and wintering areas.

(a) Distinct breeding areas and winter panmixia
(b) Breeding panmixia and distinct winter areas
(c) Distinct breeding and wintering areas
(d) Unstructured – breeding and wintering panmixia

- Ovals represent geographically distinct groups, solid arrows represent migration, and dashed arrows represent dispersal.


MONGOLIA 2006
KAZAKHSTAN
2007
QINGHAI
2006/2007
POYANG 2007
MALI 2007
NIGERIA
2007
MALAWI
2007
km
0
2000
4000

Potential impacts of climate change to intercontinental bird migration

- Direct effects of weather and indirect effects on habitat
- Changes in timing of migration
- Changes in stopover locations
- Changes in length of stopovers
- Changes in species interactions during migrations
- Asynchrony of migratory clues and food supplies on breeding grounds
- Some species showing plasticity in timing of migration…. Others are not.
- Impacts may be greater on the long distance migrators

Climate comparsions – direct vs indirect effets:

- WNV – possible direct effects related drought and warmer temperatures and favorable conditions for mosquito vectors potentially favor expansion of the range WNV
- H5N1 – impacts likely indirect and related to changes in intercontinental migration of birds or changes in habitats or interactions between species

Avian Pox in Giant Petrels in the Antarctica

- In 2005 avian pox was detected for the first time in the Antarctica