

BRIEF COMMUNICATIONS

H5N1 virus outbreak in migratory waterfowl

A worrying development could help to spread this dangerous virus beyond its stronghold in southeast Asia.

The highly pathogenic H5N1 influenza virus has become endemic in poultry in southeast Asia since 2003 and constitutes a major pandemic threat to humans¹. Here we describe cases of disease caused by H5N1 and transmission of the virus among migratory geese populations in western China. This outbreak may help to spread the virus over and beyond the Himalayas and has important implications for developing control strategies.

H5N1 virus has occasionally been isolated from dead wild birds, usually within the flight range of infected poultry farms^{2,3}. In the absence of evidence that the virus is transmitted within wild bird populations or that migratory birds can carry the virus, it was possible that these birds were dead-end hosts of virus acquired from poultry. On 30 April 2005, however, an outbreak was detected in bar-headed geese (*Anser indicus*) at Qinghai Lake in western China (see supplementary information), which is a protected nature reserve with no poultry farms in the vicinity.

Initially, sick bar-headed geese were recorded on a single islet that contained about

3,000 bar-headed geese as well as some brown-headed gulls (*Larus brunnicephalus*), great black-headed gulls (*Larus ichthyaetus*) and great cormorants (*Phalacrocorax carbo*). Clinical findings included paralysis, unusual head tilt, staggering and neck thrill — all are known features of H5N1 disease in waterfowl. By 4 May, bird mortality was more than 100 a day; by 20 May, the outbreak had spread to other islets, with some 1,500 birds dead.

Overall, 90% of the dead birds were bar-headed geese, with the remainder being brown-headed gulls and great black-headed gulls. We isolated 28 H5N1 viruses from 92 cloacal, tracheal and faecal swabs from all three species, and a further 5 viruses from tissue samples from bar-headed geese. (For details of methods, see supplementary information.)

Sequence comparison revealed that the H5N1 viruses were almost identical across all gene segments. The haemagglutinin gene retains the motif of basic amino acids (QGER-RRKKR) in the connecting peptide that characterizes highly pathogenic avian flu. All Qinghai isolates had a Lys 627 mutation in the PB2 gene,

which has been associated with increased virulence in mice⁴. Phylogenetic analysis of these isolates and eight other H5N1 viruses, isolated from poultry markets in Fujian, Guangdong, Hunan and Yunnan provinces during 2005, indicated that the haemagglutinin (Fig. 1a), neuraminidase and nucleoprotein (data not shown) genes of the Qinghai viruses were closely related to the H5N1 virus A/Chicken/Shantou/4231/2003 (genotype V).

However, the other five internal genes, represented by the matrix-protein gene, were closely related to H5N1 viruses isolated from domestic poultry in southern China during 2005, represented by the virus A/Chicken/Shantou/810/2005 (genotype Z) (Fig. 1b). These viruses are therefore characterized as H5N1 genotype Z, but are clearly distinguishable from those that have caused human infection in Thailand and Vietnam (Fig. 1a, b)⁵. This indicates that the virus causing the outbreak at Qinghai Lake was a single introduction, most probably from poultry in southern China.

Qinghai Lake is an important aggregation and breeding site for bar-headed geese that are distributed over central Asia⁶. From September, they migrate southwards to Myanmar and over the Himalayas to India, returning to Qinghai around April⁶. Our findings indicate that H5N1 viruses are now being transmitted between migratory birds at the lake. Although the outbreak could burn itself out, the large migratory bird population at Qinghai Lake makes this unlikely. The viruses might also move to other migratory species that could act as carriers, remaining highly pathogenic for domestic chickens and possibly humans.

Like its precursor, A/Goose/Guangdong/1/96, the current H5N1 virus could become established in bar-headed geese. There is a danger that it might be carried along the birds' winter migration routes to densely populated areas in the south Asian subcontinent, a region that seems free of this virus, and spread along migratory flyways linked to Europe. This would vastly expand the geographical distribution of H5N1. Increased surveillance of poultry is called for because previous experience has shown that control measures become almost impossible once the virus is entrenched in poultry populations.

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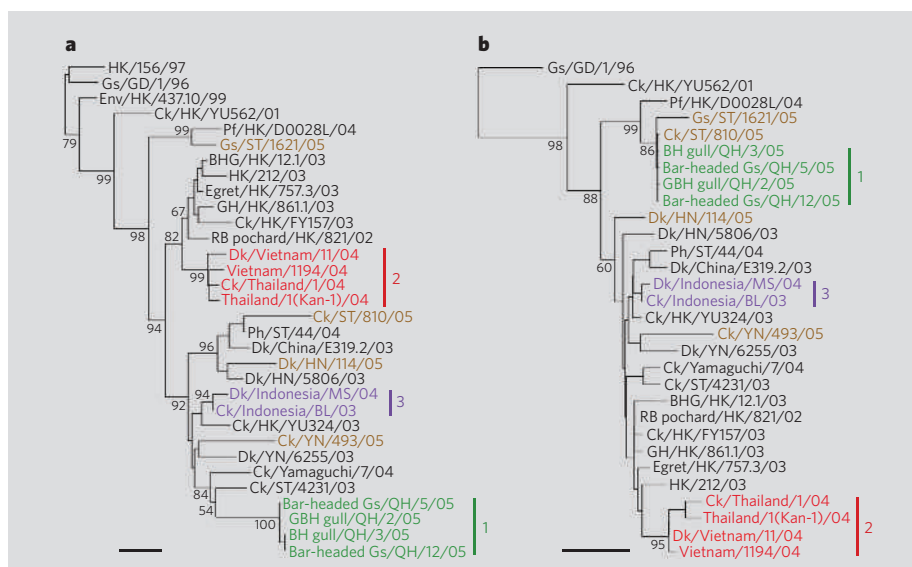


Figure 1 | H5N1 flu strains in wild birds in western China. **a, b,** Phylograms showing the genetic relationship between representative strains for **a**, the haemagglutinin gene (nucleotide positions 25–1,025; scale bar, 0.01 nucleotide changes per site), and **b**, the matrix-protein gene (nucleotide positions 91–956; scale bar, 0.01 nucleotide changes per site). Numbers at branches are bootstrap values from 1,000 replicates. Sources of isolated viruses: clade 1, Qinghai Lake; clade 2, Thailand and Vietnam; clade 3, Indonesia; viruses isolated from southern China in 2005 are shown in brown. BH gull, brown-headed gull; BHG, black-headed gull; Ck, chicken; Dk, duck; Env, environment; GBH gull, great black-headed gull; GD, Guangdong; GH, grey heron; Gs, goose; HK, Hong Kong; HN, Hunan; Pf, peregrine falcon; Ph, pheasant; RB pochard, rosy-billed pochard; ST, Shantou; YN, Yunnan. Sequences have been deposited in GenBank under accession numbers DQ095612–DQ095771.

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Supplementary information accompanies this communication on *Nature's* website.

Competing financial interests: declared none.

doi:10.1038/nature03974

Published online 6 July 2005.

CONSERVATION

Top predators and biodiversity

The charisma of top vertebrate predators is often used by conservationists as a lever for financial support^{1,2}, to raise environmental awareness^{2,3} and in planning protected areas⁴⁻⁶ — a strategy that has been criticized^{3,5,7}. Here we use information collected from five raptor species that differ widely in their diet and habitat associations to show that sites occupied by these predators are consistently associated with high biodiversity. The biodiversity at these sites is more extensive than it is at sites selected at random, or at sites occupied by species from lower down the trophic pyramid (insectivorous or herbivorous species, for example). Our results indicate that

conservation focusing on top predators can be ecologically justified because it delivers broader biodiversity benefits.

We surveyed five species of diurnal and nocturnal raptors in the Italian Alps during the breeding season: the goshawk (*Accipiter gentilis*), pygmy owl (*Glaucidium passerinum*), Tengmalm's owl (*Aegolius funereus*), tawny owl (*Strix aluco*) and scops owl (*Otus scops*) (for site locations, see supplementary information). The diversity of birds, trees and butterflies was used as a surrogate measure of biodiversity. For each raptor species, we compared the biodiversity recorded at 25 sites occupied for breeding with that at three other types of site: 25 sites randomly chosen in comparable habitat (spatial-control sites); 25 breeding sites of a randomly selected species from a lower trophic level (taxonomic-control sites A); and 25 breeding sites of a species from a lower trophic level that has specialized ecological requirements (taxonomic-control sites B). (For methods, see supplementary information.)

Compared with the three types of control site, locations occupied by top predators had greater numbers and more diversity of avian species, vulnerable avian species, butterfly species and tree species (for all raptor species and for all comparisons, $t \geq 3.14$, $P < 0.05$, except for one comparison, for which $t = 2.96$, $P < 0.07$; Fig. 1a-c). By contrast, none of the biodiversity estimates collected at sites occupied by species from lower trophic levels was higher than those collected at their associated

spatial-control sites (for all species, $t \leq 2.45$, $P \geq 0.16$; Fig. 1a-c).

We also did a simulation exercise (gap analysis^{7,8}; see supplementary information) that selects a network of protected areas by maximizing the overall level of biodiversity representation while minimizing the number of protected areas included in the network. This showed that the number of sites required to include all avian species, or all vulnerable avian species, in a hypothetical protected system was lower when using sites occupied by top predators than when using any type of control site ($t \geq 2.89$, $P \leq 0.05$). The difference between sites occupied by species from lower trophic levels and their associated spatial control sites was not significant ($t \leq 1.64$, $P \geq 0.14$).

Furthermore, the efficiency of each protected-area system (expressed as the percentage of maximum attainable biodiversity) was higher for top-predator sites than for any type of control site ($t \geq 3.97$, $P < 0.01$; Fig. 1d), whereas it did not differ between sites that were occupied by lower-trophic-level species and their associated spatial-control sites ($t \leq 1.36$, $P \geq 0.21$; Fig. 1d). On average, networks planned using lower-trophic-level species represented 72% of the maximum species richness and 76% of the maximum richness of vulnerable species in each sample, compared with 94% and 93% for networks based on the presence of top predators.

Our results are evidence of a tight association, at least in some biological systems, between apex predators and high biodiversity, which may justify the strategic economic exploitation of top-predator species on ecological grounds. More information from other systems will be needed before the powerful top predators can be dismissed from the conservation arena as unscientific tools.

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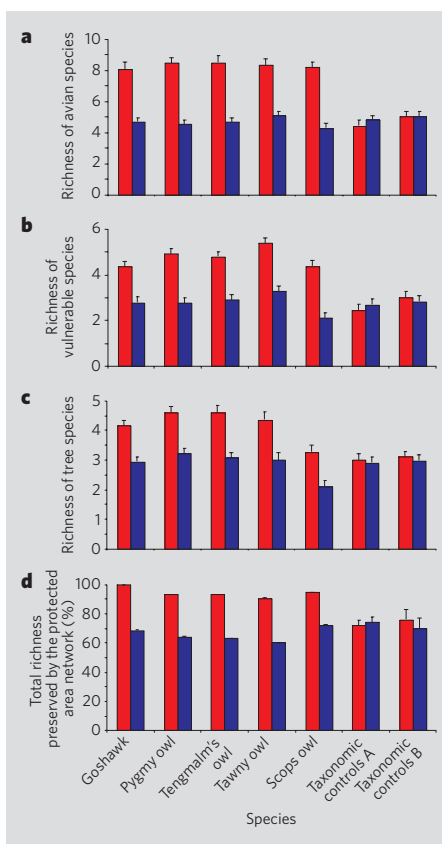


Figure 1 | Biodiversity estimates are higher at sites occupied by five top predators than at randomly selected sites or at sites occupied by species from lower trophic levels (taxonomic controls). Red bars, breeding sites; blue bars, randomly selected spatial-control sites. Values represent averages ± 1 s.e. **a**, Numbers of all avian species. **b**, Numbers of avian species classified as vulnerable. **c**, Numbers of tree species. **d**, Percentage of maximum attainable avian-species richness in a hypothetical system of protected areas, as estimated by gap analysis^{7,8}.

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Supplementary information accompanies this communication on *Nature's* website.

Competing financial interests: declared none.

doi:10.1038/436192a