structural protein 4 gene. First-round primers were AlphaF1 (GenBank accession no. NC004162, nt 6942–6961, 5′-CSATGATGAARTC HGGHATG-3′) and AlphaR (nt 7121–7141, 5′-CTATTTAGGACCRC CGTASAG-3′). Second-round primers were AlphaF2 (nt 7480–7501) (5′-TGGNTBAAYATGGAGGTIAAG-3′) and AlphaR. Sequencing of the second-round product identified the virus. A 339-bp fragment (GenBank accession no. DQ678928) had 97% identity with the African prototype strain S27 isolated in Tanzania (Tanganyika) in 1953 (AF369024) and 100% identity with viral sequences from Reunion Island in 2006 (DQ443544).

Knowledge of distant epidemics aids clinical recognition of infections not commonly seen in Australia. Websites and electronic bulletins (e.g., Promed) are a conduit of information. On the basis of this case-patient, those in Australia became more aware of the chikungunya virus epidemics affecting the islands of the southwestern Indian Ocean.

Laboratory diagnosis of chikungunya virus infection is usually serologic. However, alphavirus infections not endemic to Australia are unlikely to be diagnosed serologically because specific assays are generally available only for those viruses known to circulate in Australia. Because viremia of alphaviruses is brief, success of RT-PCR depends on early admission and clinical recognition of infection (*6*).

Rapid establishment of a definitive diagnosis had substantial benefits that included management of the febrile patient, reduced need for further investigations, and better prognosis. Infection caused by an introduced arbovirus may have important public health implications in Australia. Because immunity in the Australian population is unlikely, consideration must be given to the potential for transmission of the virus to caregivers and the local community. chikungunya virus is commonly spread by mosquitoes of the genera *Aedes*, including *Aedes aegypti*, *Ae. furcifer-taylori*, *Ae. luteocephalus*, *Ae. albopictus*, and *Ae. dalzieli* (*7*). The Australian Ross River and Barmah Forest alphaviruses are spread by many species of *Aedes* and *Culex* (*8*). Because some local species could transmit chikungunya virus, necessary steps should be taken to ensure containment when a patient is viremic.

This case highlights the potential for exotic viruses to be introduced into Australia by visitors or returning travelers and the utility of molecular testing for their rapid detection. The generic nature of the RT-PCR enabled detection of an alphavirus with subsequent specific identification by sequencing. Rapid identification and differentiation in a public health setting minimized the potential for spread of the virus.

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Avian Influenza A (H5N1) Age Distribution in Humans

To the Editor: A total of 229 confirmed human cases of avian influenza A (H5N1) were reported to the World Health Organization (WHO) from 10 countries of Africa, Asia, and Europe in the 30 months leading up to July 4, 2006 (*1*). WHO has highlighted the skewed age distribution of these confirmed cases toward children and young adults, with relatively few cases in older age categories (*2*). An explanation for this age bias is currently lacking, although a range of behavioral, biological, demographic, and data-related factors may account for the observed pattern (*2*,*3*).

To determine whether the statistical parameters of the case distribution can shed any light on the issue, we reviewed the age profile of patients with confirmed avian influenza A

(H5N1) included in WHO's Situation Updates—Avian Influenza archive (January 13, 2004–May 18, 2006) (*4*). We supplemented our review with case information from an additional WHO source (*5*); to allow for the age structure of reporting countries, we accessed age-specific population estimates for 2005 from the Population Division of the United Nations Secretariat (*6*).

For the period under review, age-related information was available for 169 case-patients with WHO-confirmed human avian influenza A (H5N1) in 10 countries. Information for an additional 47 confirmed case-patients, reported to WHO from Vietnam (n = 39) and Turkey (n = 8), could not be ascertained from the published sources. The mean age of the 169 sample case-patients (77 males and 92 females) was 19.8 years (median 18.0; range 0.3–75.0). Age distribution was as follows: 0–9 years, 26.0%; 10–19 years, 29.0%; 20–29 years, 23.1%; 30–39 years, 16.0%; and ≥40 years, 5.9%. Estimated age-specific case rates per million population were 0.15 (0–9 years), 0.15 (10–19 years), 0.13 (20–29 years), 0.08 (30–39 years), and 0.02 (≥40 years).

Box-and-whisker plots (*7*) (Figure) illustrate the skewed nature of the age distribution of cases by sex (A), year of report (B), and patient outcome (C); the third quartiles of the distributions (Q_3, defined by the box tops) demarcate an age band (30–35 years) above which proportionally few cases (<10%) occurred. The country-level analysis in plot D yields similar findings, although interpretation is limited by the small numbers of cases (<10) in some countries (Azerbaijan, Cambodia, Djibouti, Iraq, and Turkey).

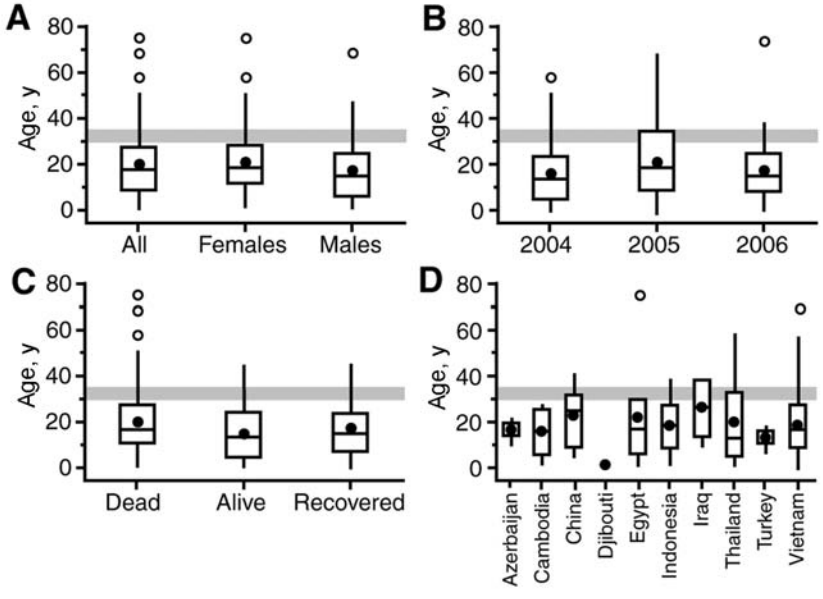

Figure. Age distribution of patients with confirmed cases of avian influenza (H5N1), December 2003–May 2006 (*4,5*). Box-and-whisker plots show the age distribution of patients by A) sex; B) year of report, C) patient outcome, and D) country. The horizontal line and bullet mark in each box give the median and mean age of cases, respectively. Variability in age is shown by plotting the first and third quartiles (Q_1 and Q_3) of the ages as the outer limits of the shaded box. Whiskers encompass all ages that satisfy the criteria $Q_1 – 1.5(Q_3 – Q_1)$ (lower limit) and $Q_3 + 1.5(Q_3 – Q_1)$ (upper limit). Points beyond the whiskers denote outliers. Panel C data are based on the recorded status of patients according to World Health Organization sources, with the category "alive" formed to include patients who were last reported as hospitalized or discharged. The age band 30–35 years is marked on each graph for reference.

Examination of case-patients in the 30- to 39-year age category showed a pronounced "front-loading" effect, with 21 case-patients 30–35 years of age and only 6 case-patients 36–39 years of age.

Subject to multiple selection biases in the identification and reporting of WHO-confirmed human cases of avian influenza A (H5N1) (*2*), our analysis yields 3 noteworthy observations: 1) case counts and case rates suggest similar levels of disease activity in the age categories 0–9, 10–19, and 20–29 years; 2) few cases have occurred above the age band of 30–35 years; and 3) the skewed distribution of cases toward children and young adults transcends sex, reporting period, patient outcome, geographic location, and, by implication, local cultural and demographic determinants.

Behavioral factors increase the risk for exposure in younger persons and have been proposed as 1 determinant of the age distribution of confirmed human cases of avian influenza A (H5N1) (*2*). However, the possible role of biologic (immunologic and genetic) and other factors has yet to be determined (*3*). Such factors may include an age-related bias in case recognition, in which clinical suspicion about the cause of respiratory disease in older persons is lower. Alternatively, we suggest that the 3 observations listed above are consistent with a biological model of geographically widespread immunity to avian influenza A (H5N1) in persons born before 1969, i.e., ≈35 years before the onset of the currently recognized panzootic in domestic poultry. Such a model would account for the similar rates of disease activity in younger age categories, the sudden and pronounced reduction of cases in patients >30–35 years of age, and the age skew that transcends the sociocultural and demographic contexts of countries and continents.

The results of broad serologic surveys for antibodies to influenza A

(H5N1) virus, suggestive of a cohort effect or otherwise, have yet to be published, although anecdotal reports of completed surveys point to a lack of widespread human infection with the virus (*8*). Current evidence indicates that pandemic influenza of humans since 1918 has been restricted to 3 influenza A virus subtypes: H1 (1918–57 and 1977–present); H2 (1957–68); and H3 (1968–present) (*9*,*10*). If an element of immunity to avian influenza A (H5N1) does exist in older populations, its possible association with geographically widespread (intercontinental) influenza A events before the late 1960s merits further investigation.

The work described has been undertaken as part of a program of research entitled Historical Geography of Emerging and Re-Emerging Epidemics, 1850–2000, funded by the History of Medicine Committee of the Wellcome Trust.

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Toxoplasma gondii, Brazil

To the Editor: Recently, Jones et al. reported that past pregnancies increased risk for recent *Toxoplasma gondii* infection in Brazil (*1*). They did not, however, control for age. Previous seroepidemiologic studies have shown that age is a main confounding variable in analysis of risk factors for toxoplasmosis (*2*). Age can explain why mothers with more children are at higher risk for toxoplasmosis; the longer persons live in areas with high toxoplasmosis prevalence, the higher their risk for infection.

Also not explored were drinking water–related factors. Our recent study of pregnant women in Quindio, Colombia, found factors that explained attributable risk percent for infection to be eating rare meat (0.26%) and having contact with a cat <6 months of age (0.19%) (*3*). Drinking bottled water was more significantly protective for the group that did not consume undercooked or raw meat (odds ratio 0.06, 95% confidence interval 0.006–0.560, p = 0.008). We think that drinking water–related factors could explain up to 50% of toxoplasmosis infections in our region.

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In response: We thank Dr Gomez-Marin for his letter regarding our article on recently acquired *Toxoplasma gondii* infection in Brazil (*1*). Dr Gomez-Marin states that perhaps age could account for our finding that having had children was a risk factor for recent *T. gondii* infection among women. Studies have shown that age is a risk factor for prevalent *T. gondii* infection; i.e., infection prevalence increases with age (*2*). However, age is not necessarily a risk factor for recent (incident) infection.