

A global initiative on sharing avian flu data

The global spread of the H5N1 avian influenza virus has already extensively damaged economies worldwide and food safety in developing countries. The spread of infection to new ecosystems results in adaptation of the virus to new hosts, including humans, which amplifies the potential for a flu pandemic. Because it is recognized that avian influenza viruses may be the progenitors of the next human pandemic virus, their genetic evolution should be tracked in detail and promptly investigated.

The full support of the international scientific community is therefore urgently needed to understand better the spread and evolution of the virus, and the determinants of its transmissibility and pathogenicity in humans. This in turn demands that scientists with different fields of expertise have full access to comprehensive genetic-sequence, clinical and epidemiological data from both animal and human virus isolates.

Several countries and international agencies have recently taken steps to improve sharing of influenza data¹⁻⁴, following the initiative of leading veterinary virologists in the field of avian influenza. The current level of collection and sharing of data is inadequate, however, given the magnitude of the threat. We propose to expand and complement existing efforts with the creation of a global consortium — the Global Initiative on Sharing Avian Influenza Data (GISAID; <http://gisaid.org>) — that would foster international sharing of avian influenza isolates and data.

Scientists participating in the GISAID consortium would agree to share their sequence data, to analyse the findings jointly and to publish the results collaboratively. Data would be deposited in the three publicly available databases participating in the International Sequence Database Collaboration (EMBL, DDBJ and GenBank) as soon as possible after analysis and validation, with a maximum delay of six months. The six-month deadline for data release is expected to become shorter as the consortium gains experience and works out its operating procedures.

GISAID's policies for rapid and complete data release are modelled on those established for community resource projects. These policies have successfully been employed previously, for example by the International HapMap Project (www.hapmap.org) — a project to map, and make freely available, data on DNA sequence variations in the human genome.

The GISAID consortium will be comprised of scientists from around the world working in the fields of animal and human virology,

epidemiology and bioinformatics, as well as experts in intellectual-property issues. An international panel of distinguished scientists will be formed to govern the charter and to advise the consortium.

As an international collaborative effort, GISAID offers many benefits to the world as a whole, as well as to individual scientists and to groups participating in the consortium. It would encourage valuable collaboration among researchers in industrialized countries and in the developing countries that are hit hardest by avian influenza. It would also attract international attention to the need for increased funding and technical assistance to help affected countries build comprehensive and sustained disease-surveillance programmes.

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||A full list of signatories to this letter as of 23 August 2006 is available as supplementary information at [[url to come](#)]

1. *Nature* **441**, 1028 (2006).
2. OFFLU Keeps its Pace on Global Sharing Virus Samples *Press Release* (OIE/FAO Network of Expertise on Avian Influenza, 21 July 2006); available at <http://www.offlu.net/portals/0/pdf/Press.pdf>
3. Rukmantara, Tb. A. Bird Flu Data Now Open to All *The Jakarta Post* (4 August 2006); available at <http://www.thejakartapost.com/yesterdaydetail.asp?fileid=20060804.H07>
4. CDC and APHL Make Influenza Virus Sequence Data Publicly Accessible *Press Release* (Centers for Disease Control and Prevention, Atlanta, Georgia, 22 August 2006); available at <http://www.cdc.gov/od/oc/media/pressrel/r060822.htm>