Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Blood transfusion linked to vCJD death

The death of a man in the UK who had received blood from a donor incubating variant Creutzfeldt-Jakob disease (vCJD) is the first case of "possible transmission" of the disease in blood. The man, who died from vCJD in autumn 2003, had been given blood in 1996 from an apparently healthy donor who developed the disease 3 years later and died.

The transfusion took place before the introduction of precautions against the unknown risk of vCJD, such as leucodepletion and the sourcing of plasma from the USA instead of the UK. Since 1997, blood donation records of all cases of "probable vCJD" diagnosed by the UK National CJD Surveillance Unit have been checked and any identified blood stocks destroyed. All 15 patients who received blood from people who subsequently developed vCJD (ten before leucodepletion was introduced) have been contacted.

First US case of BSE

On Dec 25, 2003, the first case of bovine spongiform encephalopathy (BSE) in the USA was confirmed in a cow slaughtered on Dec 9. The animal, from a farm in Washington state, was one of a herd of 82 cows imported in 2001 from Canada, where a case of BSE was confirmed in May 2003. The cow, aged 6 years when slaughtered, would have been born before feed bans were implemented in North America (in August 1997). In the UK, BSE has been transmitted to human beings through consumption of infected beef products, causing variant Creutzfeldt-Jakob disease.

There is no test to detect the vCJD prion in blood, so donated blood cannot be screened for the infective agent. The UK National Blood Service says, "It is important to balance the unknown risk of contracting vCJD through a blood transfusion against the risk of a patient not receiving the blood transfusion they require".

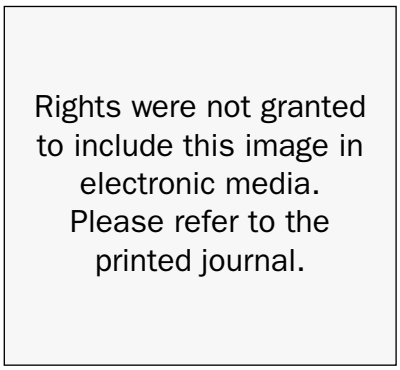
In October 2003 the Advisory Committee on the Microbiological Safety of Blood and Tissues advised the UK government that excluding blood-transfusion recipients from donating blood "would have a damaging effect on blood supplies". UK Health Secretary John Reid has asked the committee to consider what further precautionary measures could be taken without adversely affecting the safety and supply of blood. Regional and hypotensive anaesthetic techniques, salvage, and reinfusion of red cells lost during surgery, and the use of antifibrinolytic drugs are being increasingly used to reduce reliance on transfusion. Some experts predicted a huge epidemic of vCJD, but so far only 143 cases have been identified in the UK, and the number of new cases has fallen in each of the past 3 years.

Dorothy Bonn

SARS: an amalgam of avian and mammalian viruses?

Researchers studying the evolution of the severe acute respiratory syndrome (SARS) coronavirus claim that it may be an amalgam of two different viruses, one from birds and the other from mammals. They also suggest that the two viruses came together at a spot in a gene that determines the virulence of the virus and host preference.

John Stavrinides and David Guttman from the University of Toronto, Canada, did a detailed phylogenetic analysis of the genes that make up the SARS coronavirus genome and compared the sequences of the proteins encoded by these genes with the same genes in all other known coronaviruses (avian, feline, canine, porcine, murine, and human). Analysis of two (matrix [M] and nucleocapsid [N]) of the four virus proteins supported a descent from an avian-like coronavirus ancestor. The phylogeny of another protein (PP1ab replicative polyprotein) was markedly different from that of the M and N proteins and indicated that it originated from a mammalian-like ancestral virus. A fourth, host-determining, protein called surface-spike glycoprotein (S) was seen to be a mosaic originating from avian and mammal coronaviruses, the authors report in the *Journal of Virology* (2004; **78:** 76–82).



AP Photo/Tom Uhlman

Feline unwell?

In the SARS genome, the S gene is sandwiched between PP1ab on one side and M and N on the other, determining the human-receptor-binding site. "We propose that a recombination event likely occurred within the S gene. [Since] the S protein is responsible for host specificity, this event may have been the critical step in the switch to a human host and the subsequent emergence of this new pathogen", say Stavrinides and Guttman.

According to David Mindell, University of Michigan in Ann Arbor, USA, this work "provides evidence indicating recombination among different coronavirus lineages". However, he added that even though recombination "does provide a mechanism for adaptive change among viruses, there is . . . no evidence linking any particular recombination event to the recent emergence of SARS in humans". Speaking at a meeting of the Royal Society, London, UK, on January 13, Eddie Holmes (Oxford University, UK) said that "If recombination has occurred, it's so ancient it's irrelevent to SARS emergence". Both the paper's authors and Mindell agree that an accurate identification of the zoonotic source will require extensive sampling of coronaviruses from a broad range of hosts.

Xavier Bosch