

mortality from recently emerged diseases varies, ranging from less than 200 people thus far for H5N1 avian influenza to about 20 million for AIDS. Livestock production has been negatively affected by the direct mortality of animals from emerging infections and depopulation policies to protect the safety of international trade and to control the spread of pathogens. The environmental impact of emerging infections is of special concern for endangered wild animal populations, which can be pushed to the brink of extinction by such events. Animals, and particularly wild animals, are thought to be the source of more than 70% of all emerging infections (Philos Trans R Soc London B 356: 983). Understanding how some infectious agents have breached the barriers that normally limit this interspecies transmission is important. However, these barriers are poorly characterised. The host species barrier for infection can be defined as an interaction of factors that collectively limits the transmission of an infection from one host species (the donor species) to another (the recipient species) (Science 312: 394). Such limiting factors may occur at different levels, of which the functional components are organism, tissue, and cell. At the organism level, barriers limiting contact between two host species, and thus preventing transmission of an infection, may be geographical, environmental, or behavioural. Because of the rapid growth of both human populations and their consumption patterns, these barriers are often breached. Even if two host species share the same geographical area and habitat, pathogen transmission may not occur due to behavioural restrictions. At the tissue level, an emerging pathogen, in particular a virus, needs to gain access to the appropriate tissue or tissues in order to replicate. First it must invade the host through a portal of entry. It may then remain localised and replicate in a tissue near the original portal of entry, or may generate a systemic infection, using various pathways to spread to more distant target tissues in the host. Release of progeny virus from the infected host typically occurs through dissemination by respiratory, enteric, or urogenital secretions, or by an arthropod vector that has ingested blood from a viremic host. There are barriers at each stage of this process that may prevent the virus from developing a productive infection. At the cellular level, a virus needs to enter, replicate in, and exit from the appropriate cell type, simultaneously dealing with any host response to infection. Understanding how a pathogen is able to breach the constraints of the host species barrier and become established in a new host species will help us to detect and control the emergence of zoonotic infections.

S391 The domestic animal revolution and influenza

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In humans, influenza A virus causes yearly seasonal influenza epidemics of respiratory disease resulting in high morbidity. There are many different subtypes of influenza virus which are characterised according to two surface structures – the hemagglutinin (H1–H16) and neuraminidase (N1–N9). These subtypes have the ability to recombine, thereby creating new variants, for example H5N1. If a subtype that humans have not encountered starts to spread it can result in a pandemic. Pandemic outbreaks have occurred at irregular intervals and have had a devastating impact on mankind. The Spanish influenza pandemic of 1918 is thought to have killed about 50 million people. In particular dabbling ducks are believed to constitute the main reservoir for influenza A virus. In ducks, the virus causes sub-clinical gastrointestinal infection. By a meta-analysis on all published screening data of wild birds and data from a four-year screening of ducks caught and sampled in Sweden we found that the prevalence of influenza A virus in the western Eurasian duck population shows a different temporal pattern compared to North America. The prevalence in western Eurasian ducks is high from August to December and also rises in the spring. These findings are of importance for the understanding of how influenza virus is perpetuated in nature. Of concern is the presence of H5 and H7 subtypes that are prone to change into highly pathogenic variants in poultry. Many of the strains isolated in our study are prototypes that have caused influenza outbreaks in poultry in Europe during recent years. This indicates that wild bird surveillance for influenza A virus can be of value as a sentinel system to prevent outbreaks in domestic poultry.

A result of the domestic animal revolution is that there has never before in history been so much poultry as today. This fact, in combination with a growing number of humans, creates an arena where domestic animals, humans and finally zoonotic pathogens can interact. Influenza A virus is the ultimate actor in this play where some subtypes may change into highly pathogenic forms. These may be transmitted directly to man. Another worrying scenario is that an avian influenza virus will reassort with a circulating human influenza. A genetic trait might then readily go from the human to the bird virus so that avian influenza acquires the capacity to pass from person to person. With this risk in mind, it would be advisable to consider any method to reduce the probability of this happening. Contingency planning should take into account the known evolutionary potential of animal viruses and other pathogens to adapt to the environment of humans and domestic animals.

S392 Wildlife hosts of SARS-coronavirus and related viruses

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Severe acute respiratory syndrome (SARS) represents the first pandemic transmissible disease of previously unknown aetiology in the 21st century. The pandemic started in November 2002 in Guangdong, China and was brought under control in July 2003, after it had spread to 33 countries on 5 continents resulting in more than 8000 infections and close to 800 deaths. The outbreak was caused by a newly emerged coronavirus, now known as the SARS coronavirus (SARS-CoV). A closely related virus was detected in masked palm civets from a live animal market in Guangdong during the outbreaks. In late 2003 and early 2004, sporadic outbreaks were reported in the same region of China where the 2002/3 outbreaks originated. This time, civets were identified as the direct source of the virus responsible for human infections. However, a large-scale survey in China failed to find any evidence of infection of farmed or wild civets with SARS-CoV. It appears that the infection of civets was limited to animals present in the live animal markets only. The role of civets as a natural reservoir of SARS-CoV was hence never confirmed. Molecular epidemiological studies revealed that the viruses responsible for the 2003/4 outbreaks were not the same as those isolated during the 2002/3 outbreaks, indicating independent species-crossing events. These findings indicate that a SARS epidemic may recur in the future and that SARS-like coronaviruses (SARS-like-CoVs) originating from different reservoir host populations may lead to epidemics at different times and in different regions depending on the distribution of the reservoirs and transmitting hosts. This notion was supported by the later discovery of a group of diverse SARS-like-CoVs in bats. At least five different SARS-like coronaviruses have been identified in different species of horseshoe bats in the genus *Rhinolophus*. Sequences of four complete genomes were determined and the overall nucleotide sequence identity between bat SARS-like coronaviruses and SARS-CoV was 87–92%. Although the exact host species for the SARS-CoV has not been identified, the great genetic diversity of bat coronaviruses highly suggests that a different horseshoe bat or a closely related bat species is the most likely natural reservoir of the SARS-CoV responsible for the 2002–2004 outbreaks.

S393 Bats: important hosts of emerging viruses

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Bats (order Chiroptera, suborders Megachiroptera and Microchiroptera) are abundant, diverse, and geographically widespread. Bats represent about 20% of the approximately 4,600 species of mammals. The megachiropterans include 166 species and the microchiropterans 759 species. Bats provide us with resources but their importance is minimised and many of their populations and species are at risk, even threatened or endangered. Some of their characteristics (what they eat, whether they are colonial or solitary, how their populations are structured, that they can fly, that they migrate seasonally and may move daily, that they enter torpor and/or hibernate, that they are able to live for many years, that they have peculiar roosting behaviours, that they can echolocate, and that they have various virus susceptibilities) make them