more complicated than was previously thought, because parasitism seems to have evolved as part of an existing system of cooperative breeding, rather than the other way around. Intriguingly, the same single factor of high levels of nest predation drives both behaviours. Cooperative breeding is favoured over solitary nesting (in which a single female and her mate care for the nest) because of predator pressure[4].

The idea that genetic relatedness between individuals can affect the evolution of social interactions has had a central role in our understanding of cooperative breeding in many species, and some models[2,3] suggest that kinship might also have a role in the evolution of brood parasitism. A brood parasite might actively target kin to increase the survival of host eggs by buffering their predation risk as a result of adding parasite eggs[11], or hosts might accept eggs of non-nesting kin because that is the parasite's only opportunity to reproduce[12]. Parasitism might, therefore, sometimes have a cooperative aspect, blurring the distinction between cooperative breeding and parasitism when kin are involved. However, Riehl and Strong show that kinship does not play a part in the parasitism of *C. major*, because the relatedness of the hosts and parasites was not greater than that in the general population. This meant that the authors could focus on the evolution of nesting tactics without having to consider the influence of kinship.

Why specific *C. major* females pursue parasitism is unknown. The observation that individual females consistently used this tactic each time their nest failed, whereas others did not, suggests that there might be a heritable basis. Alternatively, parasitism might be shaped by other factors, such as development, learning or physiology. Perhaps certain females consistently provide less parental care than others in cooperatively breeding nests, and therefore have more resources in reserve for parasitic egg laying if their nest is destroyed. Another possibility is that some females avoid parasitism and reserve resources to meet the higher demand for parental care in their own future nests. Quantifying the costs of parental care and the energetic demands of egg laying would help to shed light on this. Following these behaviours across the entire lifetimes of *C. major* could determine whether the benefits of parasitism across breeding seasons found in this study scale up to benefits in lifetime reproductive success in this fascinating species. ■

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VIROLOGY

Receptor bats for the next flu pandemic

How bat influenza viruses infect cells has been unclear. The discovery that they bind to a cell receptor that is present in many different species raises concerns about their potential risk to humans. SEE LETTER P.109

WENDY S. BARCLAY

Bats are excellent hosts for viruses: they are numerous, accounting for 20% of all mammals on Earth, and prolific, existing in colonies of up to 20 million individuals. Bats harbour dangerous pathogens that can spread to domestic animals and humans. Ebola, SARS and Nipah viruses have all crossed from bats to humans, either directly or through intermediate hosts[1]. The discovery in 2012 (ref. 2) that bats harbour influenza A viruses was alarming, because flu viruses are notoriously adept at crossing from animals into humans and causing pandemics that have devastating consequences[3]. Karakus *et al.*[4] show on page 109 that bat flu viruses infect animals using a host cell receptor that is highly similar across species. The findings are a key step towards quantifying the risk to human and animal health that is posed by flu viruses residing in bats.

Wild birds are the natural reservoir of most influenza A viruses. Avian flu viruses infect birds by binding to sialic acid receptors on the host cells (Fig. 1). The cells that line the human respiratory tract also display sialic acid receptors, but these are slightly different from the receptors in birds. Avian flu viruses can acquire the capacity to pass through the air between humans when they undergo mutations in haemagglutinin, a glycoprotein, which forms the spikes on the virus particle that interact with the sialic acid receptors on host cells. The requirement for optimal receptor binding is a major barrier to infection between species that saves us from frequent flu pandemics originating from birds[3].

Until the discovery of bat flu viruses, all known influenza A viruses used sialic acid receptors to infect their hosts. It was a huge surprise when studies revealed that bat flu viruses did not use sialic acid receptors to

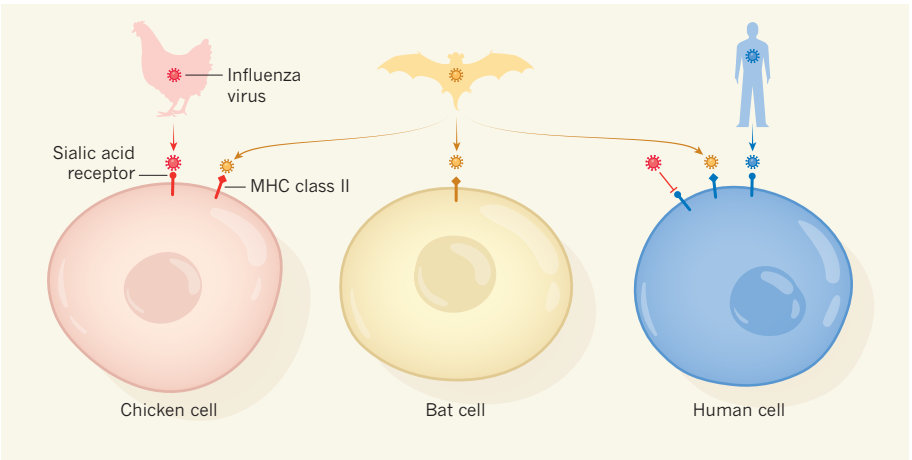

Figure 1 | Infection by influenza viruses. Karakus *et al.*[4] report that the bat flu virus can use a protein complex known as major histocompatibility complex (MHC) class II from different species as a receptor by which to enter cells and infect the host. This contrasts with avian and human flu viruses, which bind to sialic acid receptors on cells. The avian virus does not efficiently use the human sialic acid receptor, and so does not easily infect human cells.

enter cells, and the hunt was on to identify their receptor.

Given that the elusive receptor had been suggested to be made of protein[5], the authors developed two genetic approaches to search for it. One approach was to compare total gene expression in cells that were either resistant or susceptible to infection by an artificial virus bearing the bat flu haemagglutinin at its surface. This led to the identification of messenger RNAs encoding cell-surface proteins that were differentially expressed in resistant and susceptible cells. The second approach was to use the CRISPR gene-editing technique to mutate genes in susceptible cells to prevent these genes from being expressed, and then identify those whose loss of expression prevented the artificial virus from entering. Both approaches led to the same conclusion: the bat flu virus entered host cells by the binding of viral haemagglutinin to a protein complex known as major histocompatibility complex (MHC) class II.

MHC class II proteins are an important component of the immune system. Each complex is composed of one α-chain and one β-chain. The complex displays 'foreign' molecules, such as those from invading bacteria and viruses, at the surface of specialized immune cells — a process called antigen presentation. The foreign molecules are then recognized by other cells that develop an immune response against the infectious agent.

Notably, Karakus *et al.* observed that MHC class II proteins from humans, mice, pigs and chickens all functioned as receptors for bat virus haemagglutinin when expressed in human cells. This finding shows that receptor differences are unlikely to pose a barrier against infection by bat flu viruses between species (Fig. 1). Moreover, it suggests that farm animals might be a possible route by which the newly identified flu virus could pass from bats, with which people have infrequent contact, into the human population. This route is reminiscent of that taken by avian flu viruses when they give rise to human pandemics.

The ability of the bat flu virus to use MHC class II proteins from such a broad range of species is perhaps at first surprising. However, chicken MHC class II α-chains are similar to one type of mammalian α-chain[6], and such similarities might provide clues to which molecular domains of the receptor are directly involved in its interactions with the virus haemagglutinin.

The identity of this viral receptor raises several questions. Does receptor choice confer an evolutionary advantage? Hijacking MHC class II as a receptor might allow the virus to evade immune surveillance in infected bats. Indeed, MHC class II proteins are the means by which the Epstein–Barr virus infects certain human immune cells, and binding of the virus to the receptor impairs the immune system's ability to respond[7]. Many viruses interfere with the expression of, or destroy, their receptors to stop other virus particles from sticking to cells they have just infected and enable their onward spread. Other flu viruses use another spike protein, called neuraminidase, to remove sialic acid receptors from infected cells. Neuraminidase is present in bat flu viruses, but its function is unclear.

Receptor use often determines which cells and tissues a virus can infect. MHC class II proteins are usually thought of as occurring on immune cells, but Karakus *et al.* show that bat flu viruses infect mice through MHC class II molecules expressed on epithelial cells that line the upper airways. Whether epithelial cells are the target for infection in the natural host is difficult to establish but relevant to address, because infection of particular tissues in bats might affect the likelihood of animal-to-human transmission.

Interestingly, viruses that spread readily between bat species are also more likely to spread to humans[8]. Virus excretion in saliva, urine or faeces might make transmission to humans easier than an airborne route. Of note, the expression levels of MHC class II proteins in the respiratory epithelium are usually low, but they increase under certain circumstances, such as during viral infections[9]. Infection with other viruses could thus affect the susceptibility to flu of people or animals exposed to infected bats.

The likelihood of bat viruses spilling over to other species is also influenced by factors such as the bats' geographical distribution and the exposure of the recipient hosts to the animals[1]. We lack surveillance data to tell us how widely distributed bat flu viruses are, and whether they are carried by bat species with which humans or domestic animals have close contact. Given that receptor use does not seem to be host-restricted[4], and that the enzyme responsible for replicating the bat flu virus seems to function well in human cells[2], the lack of human infections by bat flu so far might be due solely to lack of opportunity. ■

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QUANTUM PHYSICS

Quantum-information scrambling validated

The delocalization of information in interacting quantum systems seems to play a key part in their evolution. A method has been developed that could enable the dynamics of this process to be directly probed in experiments. SEE LETTER P.61

JONATHAN HOME

Quantum correlations that spread between parts of a many-body system are intrinsically linked to the system's evolution towards thermal equilibrium, in a process called thermalization. Measuring these correlations is challenging, because of the need to filter relevant information from the huge amount that is present, without the measurement being mimicked or corrupted by the presence of noise. On page 61, Landsman *et al.*[1] demonstrate that quantum teleportation of a single quantum bit (qubit) can provide direct evidence of dynamics that lead to correlations between all the components of a three-body system. This approach could be a powerful tool for characterizing future many-body quantum simulators — controllable quantum systems that can be used to model other quantum systems.

When physical systems interact, information is distributed between them. In general, this process leads to correlations between the systems. In the case of quantum-mechanical interactions, the correlated systems are said to be entangled; the information cannot subsequently be retrieved from any single system, but is shared across the whole composite array. As a result, if we were to look at only a local region (such as a single system), we would conclude that the interactions have caused any initial information to be lost. This effect is connected to the progression