Bat flu is able to spread to humans

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MHC class II proteins mediate cross-species entry of bat influenza viruses.

Zoonotic influenza A viruses of avian origin can cause severe disease in individuals, or even global pandemics, and thus pose a threat to human populations. Waterfowl and shorebirds are believed to be the reservoir for all influenza A viruses, but this has recently been challenged by the identification of novel influenza A viruses in bats1,2.

The major bat influenza A virus envelope glycoprotein, haemagglutinin, does not bind the canonical influenza A virus receptor, sialic acid or any other glycan1,3,4, despite its high sequence and structural homology with conventional haemagglutinins. This functionally uncharacterized plasticity of the bat influenza A virus haemagglutinin means the tropism and zoonotic potential of these viruses has not been fully determined.

By using transcriptomic profiling of susceptible versus non-susceptible cells in combination with genome-wide CRISPR–Cas9 screening, authors showed that the major histocompatibility complex class II (MHC-II) human leukocyte antigen DR isotype (HLA-DR) is an essential entry determinant for bat influenza A viruses. Genetic ablation of the HLA-DR α-chain rendered cells resistant to infection by bat influenza A virus, whereas ectopic expression of the HLA-DR complex in non-susceptible cells conferred susceptibility.

Expression of MHC-II from different bat species, pigs, mice or chickens also conferred susceptibility to infection. Notably, the infection of mice with bat influenza A virus resulted in robust virus replication in the upper respiratory tract, whereas mice deficient for MHC-II were resistant. Collectively, our data identify MHC-II as a crucial entry mediator for bat influenza A viruses in multiple species, which permits a broad vertebrate tropism. (For references please visit the publication linked above).

Comment
The study found that the receptor allowing the viruses to enter their host’s cells and cause infection is shared with cells of certain livestock and humans. The study found that the virus was communicable via bat urine, feces, and saliva, making it likely that humans have been infected with the disease previously because of increasing bat-human contact. The increasing bat human contact is speculative, but bats are known to be reservoirs of Eobola virus and probably also MERS-Corona virus and SARD-Coronavirus.

Nicola Petrosillo & Eskild Petersen
ESCMID Emerging Infections Task Force - EITaF