

Studies on the Genetic Diversity and Origin of Viruses in Animals

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The majority of emerging viral infections which represent a significant threat to human health, as exemplified by Ebola hemorrhagic fever, pandemic influenza virus infection and the Middle East respiratory syndrome (MERS), are zoonoses which cause serious diseases when pathogens harbored by natural animal reservoirs are transmitted to humans. In order to prepare for the future emergence of zoonoses, it is imperative to gather evidence regarding pathogens carried by wildlife as a preemptive measure against future potential pandemics. We have conducted such epidemiological research on wildlife in Zambia and Indonesia.

We have isolated a novel herpesvirus, phylogenetically related to human herpes simplex virus 1 (HSV-1), from an Indonesian pteropodid bat. Experimental infection of this bat-derived herpesvirus caused a lethal infection in mice with multifocal hepatic necrosis. Serological and PCR screening revealed that fruit bats infected with the herpesvirus are widely distributed in Indonesia [1].

We have performed RT-PCR screening for paramyxoviruses in wildlife. The genome of human parainfluenza virus type 3 (HPIV3), a major cause of lower respiratory tract infection, was identified from wild baboons in Zambia, indicating that wild nonhuman primates are susceptible to HPIV3 infection. In addition, we detected a number of novel paramyxoviruses from pteropodid bats, rodents and shrews and revealed extensive genetic diversity of paramyxoviruses [2].

We have also applied viral metagenomics approaches to pathogen discovery. Metagenomic analysis of the shrew enteric virome identified a novel parvovirus, which is related to the emerging human parvovirus, human bufavirus. We subsequently identified animal bufaviruses related to human bufavirus from pteropodid bats and non-human primates as well as shrews, highlighting the prevalence and genetic diversity of bufaviruses in wildlife [3]. Recombination analyses suggested that the recent ancestor of the bat bufavirus might have emerged from interspecies transmissions with genetic recombination events.

These studies deepen our knowledge regarding the genetic diversity and evolution of viral pathogens and provide an evidence base to contribute to preemptive measures against the threat of zoonoses.

References

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- [3] Sasaki M. *et al.*: Distinct lineages of bufavirus in wild shrews and nonhuman primates. *Emerg Infect Dis* 21(7): 1230-1233 (2015).