# Summary

Bats are increasingly recognized to harbor a wide range of viruses and in most instances these viruses appear to establish long term persistence in these animals. Amongst the 60 viral species reported to be associated with bats, 59 are RNA viruses, which are potentially important in the generation of emerging and re-emerging infections in humans. They are the reservoir of a number of human zoonotic diseases including Nipah, Ebola and SARS. Severe acute respiratory syndrome (SARS) has been described by the World Health Organization (WHO) as the first, serious and readily transmissible disease to emerge in the 21st century which caused over 770 deaths in seven months.

The cause of SARS has been conclusively identified as a previously unknown coronavirus. Masked palm civets have been identified as the intermediate host while the definitive hosts may be the horseshoe bats (genus *Rhinolophus*).

Until now, all the studies on bat coronaviruses have been confined to Hong Kong and Mainland China. In Sri Lanka over 1/3 of mammalian species are bats, most of which roost in human dwellings or in close contact with humans. Therefore we initiated a study to determine the species and the phylogenetic relationships of coronaviruses and astroviruses by genetic analysis of several species of Sri Lankan bats. We also wanted to see any possible relationship between ectoparasites of bats and coronaviruses.

During the study period, 10 species of bats from 12 locations were screened. This included 7 species of microchiropetans (*Rhinolophus rouxii, Hipposideros lankadiva, H. speoris, H. ater, M. schreibersii, Megadema spasma, Taphozous melanopogon)* and 3 megachiropteran species (*Pteropus giganteus, Cynopterus sphinx, Rousettus leschenaulti)*. The roosting sites of bats included 3 caves, one mine, four buildings, two open roosts of Flying foxes and two mist nettings. Bats were also screened for the presence of ectoparasites.

During the study, 367 individuals representing all species of bats (except *P. giganteus,*) were screened for parasites. Parasites were recorded from *R. leschenaulti*, *M. spasma*, *H. speoris*, *H. ater*, *R. rouxii* and *M. schreibersii*. No parasites were recorded for *T. melanopogon, H. lankadiva* and *C. sphinx*. The ectoparasites recorded were from seven families; Nycteribiidae (Bat Flies),

Streblidae (Bat Flies), Trombiculidae (Mites), Spinturnicidae (Mites), Ixoididae (Ticks), Argasidae (Ticks) and Ischnopsyllidae (Fleas). Nycteribiidae and Spinturnicidae were the most abundant families from which, bat parasites were recorded

With the pan-coronavirus and pan-astrovirus RT-PCR assays, two coronavirus positives and 14 astrovirus positives were detected from the samples. Coronaviruses were found only from *M.* schreibersii captured from Wavulgalge. The astroviruses were found from *R. rouxii, H. ater, H. speoris, M. spasma, M. schreibersii, H. lankadiva* and *R. leschenaulti.* Viruses were not recorded at all from *C. sphinx, P. giganteus* and *Taphozous melanopogon*. We also did not find any significant association between the presence of parasites and presence of viruses.

The astroviruses recorded from Sri Lankan bats separate into two main groups. All microchiropterans into one and those recorded from the fruit eating bat, *R. leschenaulti* into the other. The astrovirus recorded from *R. leschenaulti* from Wavulgalge (SL99 F- Figure 3.7) differed from the astroviruses recorded from all other microchiropteran bats. This astrovirus is clustered among the astrovirus recorded from other major groups of mammals such as dolphins, sealions and cheetah and showed a unique relationship to typical human astroviruses. Moreover, no astrovirus from a bat species relating to any other group of mammal has previously been recorded. These findings are likely to provide new insights into evolution of astroviruses and reinforce the role of bats as a reservoir of viruses with potential to pose a zoonotic threat to human health.

This is the first record of the presence of viruses in a Sri Lankan bat population. Our findings of novel coronaviruses and astroviruses in bats in Sri Lanka provide information on the ecology of these viruses in bats in this country. When integrated with similar studies of bats in other contries, these results would also provide a wider picture on the ecology of the viruses in nature. The remarkably high prevalence and presence of novel astrovirus relating to those recorded in humans found within a relatively small geographic area highlight the need for study in other species of bats and in a more broader scale.