

Ecological surveillance of bat coronaviruses in Sarawak, Malaysian Borneo

ABSTRACT

Objective: Coronaviruses (CoVs) are natural commensals of bats. Two subgenera, namely Sarbecoviruses and Merbecoviruses have a high zoonotic potential and have been associated with three separate spillover events in the past 2 decades, making surveillance of bat-CoVs crucial for the prevention of the next epidemic. The study was aimed to elucidate the presence of coronavirus in fresh bat guano sampled from Wind Cave Nature Reserve (WCNR) in Sarawak, Malaysian Borneo. Samples collected were placed into viral transport medium, transported on ice within the collection day, and preserved at – 80 °C. Nucleic acid was extracted using the column method and screened using consensus PCR primers targeting the RNA-dependent RNA polymerase (RdRp) gene. Amplicons were sequenced bidirectionally using the Sanger method. Phylogenetic tree with maximum-likelihood bootstrap and Bayesian posterior probability were constructed. Results: CoV-RNA was detected in ten specimens (47.6%, n =21). Six alphacoronavirus and four beta coronaviruses were identified. The bat-CoVs can be phylogenetically grouped into four novel clades which are closely related to Decacovirus-1 and Decacovirus-2, Sarbeco virus, and an unclassified CoV. CoVs lineages unique to the Island of Borneo were discovered in Sarawak, Malaysia, with one of them closely related to Sarbecovirus. All of them are distant from currently known human coronaviruses.