Comparison of bat coronaviruses detected before and during the COVID-19 pandemic in a selected environment in the Central Province of Sri Lanka

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Introduction: Bats act as an animal reservoir for multiple viruses including coronaviruses (CoV). Since the identification of human CoV, studies on bat CoV gained prominence as bats were identified as an evolutionary source for human CoV. The recent SARS-CoV-2 has been traced to bats. Phylogenetically, the genetic identity of SARS-CoV-2 is 96.1% identical to a bat CoV strain, *Rhinolophus affinis* RaTG13. Objective: In this study, we aim to compare bat CoV detected before and after the COVID-19 pandemic in a single bat colony inhabiting a selected location.

Methods: Sampling was done from two different time points: February to March 2014 (pre-COVID-19)¹ and June to October 2022 (during-COVID-19) from the Royal Botanical Gardens in Peradeniya, a place where fruit bats *Pteropus gigantus* roost for most part of the year. Bat guano were collected once a week in the mornings by laying out polythene sheets (2m x 2m) in the afternoon of the previous day under randomly selected trees. Viral RNA was extracted to perform a conventional Pancoronavirus (PanCoV) nested RT-PCR. Selected PanCoV nested RT-PCR positive PCR products were sequenced using Sanger sequencing.

Results: Of samples collected during the COVID-19 pandemic, 44% (7/18) CoV positivity was detected in the study location. Bat guano sequenced during-COVID-19 was also the same as the genus *Betacoronavirus*, subgenus *Nobecovirus* identified pre-covid pandemic in 2014. There was no difference in the type of the betacoronaviruses detected before and during the COVID-19 pandemic in the study location.

Conclusions: It appears that pre-COVID-19 and during-COVID-19 pandemic the bat CoV diversity in the bats from the Royal Botanical Gardens in Peradeniya remained the same. The CoV was identified as Betacoronavirus belonging to the subgenus *Nobecovirus*.

Keywords: Bat coronaviruses, Virulence, COVID-19

References:

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***This abstract has been presented as a poster presentation for the 33rd ECCMID Congress, Copenhagen, Denmark in April 2023.

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