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Towards
the veterinary
diagnostics
of the
future

Main topic : Surveillance and control of emerging diseases

Georgian Bats as carriers for pathogens with zoonotic potential

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Background: In the last decades two largest outbreaks of emerging infection disease including the SARS-CoV-2 and Ebola virus outbreaks have implicated bats as their primary source. Epidemics of emerging infectious diseases are on the rise; novel coronavirus strain SARS-CoV-2 has resulted in the biggest quarantine in human history. We decided to detect high consequence viral coronaviruses, Ukraine and Georgia;

Methods: A total of 94 bats, four different species captured in 2022, from two locations in western and eastern Georgia were tested for presence of CoV (Anal swabs and fecal samples) by one step RT-PCR. Pan-coronavirus RT-PCR screening assay was performed using highly conserved RbRp gene primers. RT-PCR positive coronavirus amplicons were purified and sequenced on Seqstudio Genetic Analyzer. Sequences were analyzed using Genius Prime version 2020.2.1.

Results: Sequence analysis demonstrated 97- 99.0% identity 4 different type of coronavirus available at NCBI database. As a result, 19 (20%) bats were positive for Coronavirus, Betacoronavirus (n=4), Decacovirus (n=6), Sarbecovirus (n=5), Myotacovirus (n=1) Endemic species that were identified with a higher prevalence of CoV are from Rhinolophus Eurialle and Myotis Blithy collected in Tskaltubo, west Georgia.

Conclusion: The identification of diverse CoV pathogen strains in Georgian bats, highlighted that bats may play important role in maintaining those agents in nature. Further research will help develop spillover risk models, and pilot community outreach tools with the goal of reducing the threat of future bat-CoV emergence in Georgia.