

Metagenomic Analysis of Viruses in Bat Fecal Samples from Moscow Region Reveals the Whole Genome Sequences of Mastadenovirus and Alphacoronavirus

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Due to the current epidemiological situation caused by the pandemic of COVID-19 the study of virus diversity in bats as a potential source of zoonotic diseases is crucially important. Our previous study based on genus specific PCR-using *Coronaviridae* specific primers and following high throughput sequencing revealed the presence of several types of coronaviruses. In this study we performed the whole genome sequencing for the samples which were positive for *Coronaviridae* in order to get more information about viral communities in bat fecal samples. Fecal samples from bat species (*Pippistrellus nathusii*, *Nyctalus noctula*, *Myotis brandtii*, *Myotis daubentonii*) were collected in 2015 in the Moscow region and stored in RNA later. RNA extraction using Viral RNA Mini Kit (QiaGen), library preparation using NEBNext Ultra II Directional RNA Library Prep Kit for Illumina (NEB) and HTS on Illumina HiSeq platform was performed. Metagenomic data was obtained using FastQC, trimmomatic 0.38 and SPAdes 3.13 for genome assembly, taxonomy of resulting contigs was identified by the BLASTn. For 8 bat fecal samples positive for *Coronaviridae* we performed the whole genome sequencing and metagenomic analysis. In one sample we detected the complete genome (37915 bp) with 74,66% nucleic identity to *Mastadenovirus sp. isolate WA3301* from a *Nyctalus noctula*, in the other sample from *Pippistrellus nathusii* we found the complete genome sequence with 82 % nucleotide identity to *Bat alphacoronavirus isolate BtCoV/020_16/M.dau/FIN/2016* (28,245 bp). Whereas, as we've reported the presence of *Alphacoronavirus* before, this is the first time when we detect the whole genome of *Mastadenovirus*. The fact that the material was obtained from bats which nest next to human and domestic animals our findings might give better understanding the potential risk of the cross-species transmission and virus migration in bats from Moscow Region.

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