Summary

Viral enteropathies pose a challenge for veterinary medicine specialists and racing pigeon breeders, being a serious health problem especially of young birds with incompletely developed immune system and exposed to stress associated with first trainings and races. Viruses present in the gastrointestinal tract of pigeons are poorly understood, and literature offers virtually no evidence on their enteropathogenic effect. Direct proof of the pathogenicity of these viruses is not possible to achieve due to lack of developed methodology for laboratory cultivation of most of them. This study was aimed at determining which viruses that are associated with enteropathies inhabit the gastrointestinal tract of pigeons, and which of them may be associated with the occurrence of gastrointestinal disease. To achieve this, genetic material (both DNA and RNA) extracted from 153 cloacal swab samples collected from young racing pigeons of different health status (study group - birds exhibiting signs of enteropathy [n = 90], control group – asymptomatic birds [n = 63]) was subjected to metagenomic analyses using methods such as sequencing by synthesis on an Illumina sequencer and nanopore sequencing. The obtained genomic sequences of viruses suspected of possible involvement in causing enteropathy were subjected to bioinformatics analyses, including phylogenetic analysis. Then, using the nucleotide sequences of the viruses obtained in this study and downloaded from the NCBI GenBank database, primers and probes for TaqMan qPCR and ddPCR techniques were designed for quantitative analysis (calculation of the number of copies) of genetic material of each virus present in the samples. Metagenomic analysis resulted in acquisition of 19 complete or nearly complete genomic sequences of viruses from *Astroviridae, Picornaviridae, Coronaviridae*, *Parvoviridae* and *Adenoviridae* families and *Rotavirus* genus, including 5 sequences of viruses likely belonging to new species and 3 sequences of possibly recombinant viruses. The quantitative analysis revealed that the aforementioned viruses are present in pigeons regardless of their health status, while pigeon rotavirus A was presumably responsible for causing enteropathy in the examined pigeons, with both the difference in prevalence ($p = 0.0001$) and the difference of amount of genetic material ($p = 0.0050$) between the study and control group highly statistically significant. This study is of high cognitive value, and its results indicate the relevance of conducting further studies to better understand the composition of the pigeon virome in order to track viral infections in this species.

Keywords: enteropathy, viruses, metagenomics, bioinformatic analysis