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RESEARCH AREA

The exploration and investigation of emerging infectious diseases found in nature are important for prevention and treatment. Our research area is situated within the closely intertwined fields of biology, virology, and disease ecology. Within this domain, the virological examination and molecular characterization of wildlife are the main focus. Throughout the work, the identification and understanding of diseases and the affected species are conducted based on the OneHealth concept. Therefore, our aim is to understand the interconnections between human, animal, and environmental health and to apply the results practically.

TECHNIQUES AVAILABLE IN THE LAB

We use a wide range of modern molecular biology techniques for virus identification, and genomic analysis. Virus genome sequencing with state-of-the-art next-generation sequencing technologies. These techniques are followed by bioinformatic data analysis and evolutionary phylogenetic analyses, aiding in identifying the origin, spread, and evolution of pathogens. The combination of these methods allows for a better understanding of diseases and the development of more effective treatment strategies.

SELECTED PUBLICATIONS

Lanszki, Z., Islam, Md. S., Shikder, Md. F., Sarder, Md. J. U., Khan S. A., Chowdhury, S., Islam, Md. N., Tauber, Z., Tóth, G.E., Jakab, F., Kemenesi, G., Akter, S. (2024) Snapshot study of Canine distemper virus in Bangladesh with on-site PCR detection and Nanopore sequencing. **Sci Rep 14:** 9250.

Lanszki, Z., Lanszki, J., Tóth, G. E., Cserkész, T., Csorba, G., Görföl, T., Csathó, A.I., Jakab, F., Kemenesi, G. (2022) Detection and sequence analysis of Canine morbillivirus in multiple species of the *Mustelidae* family. **BMC Vet Res 18:** 450.

Lanszki, Z., Tóth, G.E., Schütz, É., Zeghib, S., Rusvai, M., Jakab, F., Kemenesi, G. (2022) Complete genomic sequencing of canine distemper virus with nanopore technology during an epizootic event. **Sci Rep 12:** 4116.

Kemenesi, G, Tóth, G.E., Neto, M.M., Scott, S., Temperton, N., Wright, E., Mühlberger, E., Hume, A.J., Suder, E.L., Zana, B., Boldogh, S.A., Görföl, T., Estók, P., **Lanszki, Z.**, Somogyi, B.A., Nagy, Á., Pereszlényi, C., Dudás, G., Földes, F., Kurucz, K., Madai, M., Zeghib, S., Maes, P., Vanmechelen, B., Jakab F. (2022) Isolation of infectious Lloviu virus from Schreiber's bats in Hungary. **Nat Commun, 13:** 1-11.

Lanszki, Z., Lanszki, J., Tóth, G.E., Zeghib, S., Jakab, F., Kemenesi, G. (2022) Retrospective Detection and Complete Genomic Sequencing of Canine morbillivirus in Eurasian Otter (*Lutra lutra*) Using Nanopore Technology. **Viruses 14:** 1433.