

EPIZONE

BOOK OF ABSTRACTS

EPIZONE Annual Meeting
2026 in Bern, Switzerland,
2-4 September 2026

Hosted by



Schweizerische Eidgenossenschaft
Confédération suisse
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Institut für Virologie und Immunologie



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Welcome

Dear EPIZONE members, dear Young EPIZONE members, dear participants,

We are delighted to welcome you in Switzerland for three days of scientific exchange, discussion, and collaboration at a time when preparedness for emerging and re-emerging animal diseases has never been more important.

The ongoing spread and continuous threat of highly contagious animal and vector-borne diseases in Europe is unprecedented. Being prepared for animal health crises is more important than ever. Exchange among research experts through strong networks remains a pillar of preparedness.

The 2026 EPIZONE meeting focuses on exploring how research can better support the necessary preparations for emergencies involving highly contagious animal diseases and zoonoses within a One Health approach. In this context, preparation means understanding the mechanisms of infection transmission, developing solutions to control diseases before they impact the livestock sector, and ensuring the necessary diagnostic capacities and (novel) vaccines and vaccination strategies are developed and in place. The Young EPIZONE session looks at career pathways and provides important insights on communication research findings.

With a carefully selected range of keynote talks representing various stakeholders involved in infectious disease control, along with scientific sessions covering a wide range of topics and presentations from EPIZONE research partners on the latest advances in detection, prevention, and understanding of key pathogens, we aim to facilitate a stimulating, insightful, and collaborative meeting in the heart of Switzerland.

Thank you for being part of EPIZONE 2026.

We wish you an excellent meeting and an enjoyable stay in Bern.

Barbara and Matthijn



Barbara Wieland
Chair Local Organizing Committee, IVI



Matthijn de Boer
Coordinator of EPIZONE

Acknowledgements

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Detection of a raccoon dog and fox amdoparvovirus (variant) in domestic dogs in Serbia

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Amdoparvoviruses (family Parvoviridae, genus Amdoparvovirus) infect a wide range of carnivore hosts and are characterized by limited host specificity. Raccoon dog and fox amdoparvovirus (RFAV) has previously been reported in raccoon dogs and foxes, but natural infection of domestic dogs has not been documented. This study describes the detection and genomic characterization of an RFAV in diseased dogs with often fatal outcome in Serbia.

During March–April 2026, samples were collected from Dobermann dogs originating from a kennel in Novi Sad, Serbia, presenting with severe clinical signs and increased mortality among puppies. Following negative results for routinely investigated viral and bacterial pathogens, metagenomic sequencing was performed. Nucleic acids were extracted using the IndiSpin Pathogen Kit (Qiagen), followed by Oxford Nanopore sequencing using the Rapid Sequencing Kit V14 on a MinION platform. Sequencing reads were quality-filtered, host-derived reads were removed using the canine reference genome, and viral reads were identified using a custom DIAMOND viral database. De novo assembly was performed using Flye, followed by polishing with Medaka. Phylogenetic and comparative genomic analyses were conducted using BLAST and reference amdoparvovirus genomes.

A total of 434,220 sequencing reads were generated. Multiple amdoparvovirus-associated reads were detected in affected animals. Assembly and polishing produced a near-complete viral genome of 4,799 bp. BLAST analysis revealed approximately 97% nucleotide identity to previously described raccoon dog and fox amdoparvoviruses. Genome organization was consistent with members of the genus Amdoparvovirus, containing the characteristic non-structural and capsid protein coding regions. Phylogenetic analysis clustered the Serbian strain with RFAV strains previously reported from wildlife hosts. In addition, the molecular (PCR) detection procedure for RFAV canine strain is established.

This study reports the detection of RFAV in Dobermann breed dogs and provides genomic evidence of its close relationship to raccoon dog and fox amdoparvoviruses. The findings expand the known host range of RFAV and suggest that probably cross-species transmission between wildlife and domestic carnivores occurred. The infection is now spreading among dogs (Dobermanns) without connection to wildlife. Further investigations are ongoing to determine the prevalence, pathogenic potential, and epidemiological significance of this virus to canine populations.

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Keywords: Raccoon dog and fox amdoparvovirus (RFAV), clinical disease with often fatal outcome, dogs of Dobermann breed, metagenomic sequencing, molecular detection, whole genome sequencing, Serbia