

IOCVS
2nd Edition
2026
Conference

The 2nd International Online Conference on Veterinary Sciences

7-9 September 2026, online



Program and Abstract Book

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The 2nd International Online Conference on Veterinary Sciences

7–9 September 2026 | Online



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Welcome from the Chair

Dear Colleagues,

It is our great pleasure to welcome you to the **2nd International Online Conference on Veterinary Sciences (IOCVS 2026)**, which will take place online on **7–9 September 2026**. This event is organized by the open access MDPI journal Veterinary Sciences (ISSN: 2306-7381; Impact Factor: 2.7; CiteScore: 3.9).

Following the successful first edition, IOCVS 2026 returns with a sharpened focus on **global health challenges at the human–animal–environment interface**. This year's conference will highlight cutting-edge research and foster cross-disciplinary exchange through three key themes:

S1. One Health Approaches to Emerging Zoonotic Threats;
S2. Surveillance and Epidemiological Modelling at the Human–Animal–Environment Interface;
S3. Antimicrobial Resistance and Food Safety: A One Health Perspective.

Our goal is to provide an engaging platform that bridges research and practice, encourages collaboration across disciplines, and inspires innovative solutions to safeguard animal and human health alike.

We warmly invite the community to join us in shaping this exciting event. Together, let us engage in meaningful discussions, share innovative research, and address pressing global challenges at the intersection of veterinary science, public health, and environmental health.

For details on oral and poster submissions, please see the *Instructions for Authors* on the conference website.

Your support and contributions are essential to the success of this event, and we look forward to welcoming you to IOCVS 2026.



Prof. Dr. Patrick Butaye
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sciforum-188161: Comparative Metagenomic Analysis of the Viromes of *Culex pipiens*, *Aedes albopictus*, and *Anopheles maculipennis* Mosquitoes in Serbia

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Mosquitoes harbor complex viral communities dominated by insect-specific viruses, yet comparative virome data from Southeastern Europe remain limited. This study aimed to characterize and compare the viromes of three epidemiologically important mosquito taxa in Serbia: the *Culex pipiens* complex, *Aedes albopictus*, and the *Anopheles maculipennis* complex. Adult mosquitoes were collected from multiple locations across Serbia during 2024 and grouped into 50 pools according to species, sampling site, and date. Total nucleic acids were extracted and subjected to Illumina NextSeq metagenomic sequencing (2×150 bp). Bioinformatic analysis included quality filtering, host read removal, de novo assembly, taxonomic annotation using BLAST and DIAMOND, viral abundance estimation, and phylogenetic analysis of RdRp regions.

A total of 1,688 viral contigs belonging to 40 viral families and 183 viral taxa were identified. The *Culex pipiens* complex exhibited the highest virome richness (140 viral taxa), followed by *Ae. albopictus* (54 taxa) and *An. maculipennis* (24 taxa). Only nine viral species were shared among all three mosquito taxa, indicating strong host-associated virome structuring. Abundance-weighted analyses demonstrated pronounced species-specific dominance patterns, with Wuhan Mosquito Virus 6 representing the most abundant virus in both *Culex* and *Aedes* mosquitoes, whereas *Anopheles* mosquitoes displayed a more even viral community structure and the highest Shannon diversity. Several putative novel viruses were also identified. These findings provide the first comparative overview of mosquito viromes in Serbia and establish a baseline for future arbovirus surveillance and longitudinal virome monitoring.



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