

in association with Serbian Society of Microbiology

30 June - 2 July

2022 • Serbia

ELECTRONIC ABSTRACT BOOK



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We thank the pharmaceutical, lab and biomedical industry partners from Serbia, the South East Europe region and worldwide for their recognition of the importance of the event, their participation and their support.

We hope that you enjoyed the content and all the other aspects of the Conference. If you missed anything, you can catch up by watching the recordings, presentations or have a detailed look at the posters.

We warmly wish you health, love and happiness and are looking forward to the new encounters, coming up next: FEMS 2023 Congress in Hamburg, FEMS 2024 Conference in Tallinn and numerous events of the SSM in Serbia and South East Europe region.

Sincerely · · · · ·



Hilay hoppi-Scott

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Blisasecup

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FEMS Director of Events and Internationalization



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Vice-President of Serbian Society of Microbiology



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800 / FAECAL POLLUTION AS POTENTIAL DRIVER OF ANTIBIOTIC RESISTANCE GENES IN THE DANUBE RIVER

05

Keywords: River, Antimicrobial resistance, Faecal pollution, nan

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Human-induced antimicrobial resistance is an emerging concern in aquatic environments. Faecal pollution sources represent potential propagation pathways, however large-scale quantitative studies in whole river systems are missing. In the course of the Joint Danube Survey, the Danube River was investigated for the fourth time in summer 2019 from its headwaters to the delta. Microbial-faecal pollution patterns and the occurrence of selected antibiotic resistance genes (ARGs) were studied. Subsequently, a one-year time series analysis at selected relevant sites allowed to assess temporal variability.

The intestinal bacterium Escherichia coli was quantified according to standard cultivation methods as indicator for total faecal pollution. In general, longitudinal patterns of faecal pollution showed a comparable picture to previous Joint Danube Surveys, with low to moderate pollution in the upper reaches (Germany, Austria) and critical to strong pollution in the middle and lower sections, especially in Serbia. Genetic microbial source tracking methods, determined via quantitative PCR, allowed us to define human faecal pollution as dominant pollution source along the whole Danube. This trend could be generally confirmed during the annual sampling campaign. To estimate the potential of permanent colonialization of faecal microorganisms within the Danube River ecosystem, biofilms as potential reservoirs were studied along the course of the entire river. Here, E.coli were ubiquitously present but highly variable. Ongoing analyses on the occurrence and quantity of selected ARGs will identify hotspots of antimicrobial resistance and their relationship to faecal pollution along the Danube River and thereby contribute to guide future monitoring and management strategies.

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