Tracking antimicrobial resistance in diverse ecological niches - one health perspective (TRACE)

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Principal Investigator: Dr. Ina Gajić, Faculty of Medicine, University of Belgrade

Participant from IMGGE: Dr. Radmila Novaković

The rise of antimicrobial resistance (AMR) has become a global public health crisis. The AMR evolvability is mainly influenced by the flow of bacteria, antimicrobial resistance genes (ARGs), and active antimicrobials through hospital settings, farm animals, and water sources. Thus, the One Health approach (OHA) is best suited to address the existing and emerging threats of AMR, particularly in multidrug-resistant (MDR) Gram-negative bacteria (GNB) as global priority AMR pathogens widely distributed in three interconnected sectors.

Molecular characterization of MDR GNB isolated from human, animal, and water samples (≥300) will be done by multilocus sequence typing and whole-genome sequencing, while the long- and short-reads-based metagenomics will be applied to assess bacterial diversity and resistomes of animal and water samples. Post-sequencing analyses aimed at extracting phylogenetic and functional information will be performed by advanced bioinformatic tools.

Hence, the "One health genomics" to tackle AMR will be adopted for the first time in Serbia, a South-Eastern European country with a substantial burden of AMR in clinical settings. Besides, the Project will bring progress beyond the state-of-the-art in genomic analyses, enabling the detection of emerging MDR GNB clones and their potential for further spread.

The scientific impact is reflected in obtaining a comprehensive and multidisciplinary insight into the molecular diversity and spread of relevant MDR GNB. The long-term impact will be the development of a research basis for rational public health practices, which will primarily be directed to strengthening national capacities to address AMR towards OHA.

The expected results of the Project will be an in-depth insight into the clonal complexes and genetic relatedness of the circulating MDR GNB, their transmission routes and point sources, and the assessment of the selective pressure of antibiotics on ARGs and bacterial communities in Serbian cities.