Exploring the copper-detoxification mechanisms of wild-type Pseudomonas strains as a potential tool for metal-polluted environments remediation

SpT-07-3

O. Havryliuk[I], L.M. Pérez[II], F. Correa-Fiz[III], V. Hovorukha[I,IV], G. Gladka[I], R. Mariychuk[V], T. Tzanov[II], O. Tashyrev[I,IV]

[I]Department of Extremophilic Microorganisms Biology, Zabolotny Institute of Microbiology and Virology, National Academy of Sciences of Ukraine, 03143, Kyiv, Ukraine, [II]Grup de Biotecnologia Molecular i Industrial, Department of Chemical Engineering, Universitat Politècnica de Catalunya, Rambla Sant Nebridi 22, 08222, Terrassa (Barcelona), Spain, [III]IRTA, Programa de Sanitat Animal. Centre de Recerca en Sanitat Animal (CReSA), Campus de la Universitat Autònoma de Barcelona (UAB), 08193, Bellaterra (Barcelona), Spain, [IV]Institute of Environmental Engineering and Biotechnology, University of Opole, 45-040, Opole, Poland, [V]Department of Ecology, Faculty of Humanities and Natural Sciences, University of Presov, 08116, Presov, Slovakia

Understanding the physiological adaptation of metal-resistant bacteria and the mechanisms involved in metal detoxification can help in the development of new biotechnologies for environmental bioremediation. The copper-resistant *Pseudomonas lactis* UKR1 strain, previously isolated from Ukrainian soil (Kyiv region), exhibits great potential for use in the remediation of metal-polluted environments. In a previous study, we found that the UKR1 genome contains several genes related to copper (Cu) resistance and metal detoxification [1]. Therefore, the aim of this work is to describe the biochemical, physiological, and molecular adaptation of UKR1 exposed to moderate levels of Cu (250 ppm) by analyzing the growth rate, biofilm-forming ability, cellular levels of reactive oxygen species, and metal-resistance gene expression. Strain UKR1 showed no growth difference in the presence of Cu compared to the control condition. In addition, the copA, copB, copC, and copD genes were detected in the genome of this bacteria by end-point PCR. Later, the expression of copA and copB genes was quantitated by RT-qPCR as a response to metal stress. Obtained results show that Cu presence induced the expression of copA gene, which is related to the physiological adaptation of the bacteria to metal toxicity. CopA groups of genes encode for copper-resistant proteins that mediate metal sequestration in the bacterial periplasm, thus playing an important role in the resistance of UKR1 to Cu. Moreover, the level of intracellular ROS in the Cu-exposed bacteria as well as the biofilm-forming ability increased at 250 ppm Cu presence. Further studies including other metal resistance genes and their products, as well as a more comprehensive analysis by using advanced high-throughput methods (e.g., RNAseq), will deepen knowledge of the molecular mechanisms underlying Cu resistance in the wild-type UKR1 strain. Previously published in: [1] Havryliuk O et al. (2020) Curr Res Microb Sci 1, 44-52