BACTERIAL HEAVY METAL TRANSPORTERS AND THEIR POTENTIAL FOR USE IN PHYTOREMEDIATIONS

BAKTERIÁLNÍ TRANSPORTÉRY TĚŽKÝCH KOVŮ A JEJICH POTENCIÁL VYUŽITÍ VE FYTOREMEDIAČNÍCH TECHNOLOGIÍCH

Jáchym Šuman[1)], Pavel Kotrba[1)], Martina Nováková[1,2)], Martina Macková[1,2)], Tomáš Macek[1,2)]

1) Department of Biochemistry and Microbiology, Faculty of Food and Biochemical Technology, Institute of Chemical Technology Prague, Technicka 3, 166 28 Prague, Czech Republic, e-mail: sumanj@vscht.cz

2) Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences, IOCB & ICT Joint Laboratory, Flemingovo n. 2, 166 10 Prague, Czech Republic, e-mail: sumanj@vscht.cz

Abstract:

The work was focused on the study of bacterial *metA*, *metTs* and *pbrT* genes encoding for heavy metal ions transporters. *MetA* and *metTs* genes are originally localized on pA81 megaplasmid in Gramnegative soil bacterium *Achromobacter xylosoxidans* A8 and they encode for P1-ATPase transporting Cd^{2+}/Zn^{2+} ions from cytoplasm to periplasm and putative heavy metal transporter, respectively. *PbrT* gene constitutes *pbr* determinant carried by multi-metalloresistant bacterium *Cupriavidus metallidurans* CH34 and it encodes for transmembrane protein transporting Pb^{2+} ions from periplasm of bacterial cell to cytoplasm of bacterial cell. In order to reveal their phenotypical effect in eukaryotic model a set of plasmids enabling constitutive expression of *met* and *pbrT* genes in yeasts was constructed. It was demonstrated, that constitutive expression of *metA* gene in *Saccharomyces cerevisiae* strain DTY168 (Cd^{2+}/Pb^{2+}-hypersensitive strain) increases Cd^{2+} sensitivity of transformed cells. According to preliminary results, *metA* and *metTs* expression also increases intracellular Cd/Zn accumulation. Subcellular localization of *met* and *pbrT* protein products was also studied. A set of expression plasmids carrying *met* and *pbrT* coding sequences in 3‘-fusion with green fluorescent protein (eGFP) gene was prepared. Using fluorescent microscopy it was demonstrated that proteins expressed from all three fusion genes localize in cytoplasmic membrane and tonoplast of *S. cerevisiae* cells.

Keywords:

Heavy metals, bacterial metalloresistance, heavy metal transporters, *Saccharomyces cerevisiae*, genetically modified organisms, bioremediation