THE CONTRIBUTION OF *MET* REGION FROM PLASMID PA81 FROM BACTERIUM *ACHROMOBACTER XYLOSOXIDANS* A8 TO HEAVY METAL RESISTANCE

PŘÍSPĚVEK GENŮ *MET* Z PLASMIDU PA81 BAKTERIE *ACHROMOBACTER XYLOSOXIDANS* A8 K RESISTENCI K IONTŮM TĚŽKÝCH KOVŮ

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Abstract:
Gram-negative soil bacterium *Achromobacter xylosoxidans* A8 hosts a 92,5-kb plasmid pA81. The analysis of nucleotide sequence revealed that the plasmid harbors a *met* region consisting of seven genes *metTDYRAB*. The homology searches suggested identities of encoded gene products as (i) putative membrane protein from Pb^{2+}/Fe^{2+} family of transporters (*metT* gene), (ii) transporter of Cation-Diffusion Facilitator family (*metD*), (iii) steroldesaturase (*metY*), (iv) member of MerR family of metal-responsive transcriptional activators/repressors (*metR*), (v) efflux P1-ATPase (*metA*), (vi) putative membrane lipoprotein (*metB*) along with its cognate (vii) prolipoprotein signal peptidase (*metC*). In order to study the metalloresistance phenotype, which would be determined by the individual *met* genes, vectors based on pBla were constructed. These allowed constitutive expression of the individual *met* genes in *E. coli* GG48. The clones expressing the *metA* gene showed increased metalloresistance, as compared with a strain harboring pBla vector alone. Moreover, expression of *metA* reduced the accumulation of Cd^{2+} and Zn^{2+}. Taken together, these data attest that MetA is a functional transporter of CPx-ATPase subfamily. When expressed in *E. coli*, remaining *met* genes did not exert any phenotype that would suggest their functionality in metalloresistance.

Keywords:
Bacterial metalloresistance, protein transportes, heavy metals