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Growth Kinetics Of Bacteria Isolated From The Microbiota Of *Tussilago Farfara* L. Growing In Post-Industrial Mercury-Contaminated And Mercury Non-Contaminated Areas. *merA*[MT1] Gene Identification.

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Extended Abstract

Bioremediation is a process of environment detoxification using biological component, for example microorganisms [1]. The ability of microorganisms to survive in extremely polluted environments is one of the reasons why the environment derived samples are desired to create effective bioremediation solutions [2]. The need for implementation of bioremediation technique to heavy metal pollution is noticeable [3]. Amongst the most alarming heavy metals there is mercury. One of the sources of anthropogenic mercury contamination is industry, such like cement production [4]. One of the molecular mechanisms that enables existence in mercury-contaminated environments is based on *mer* operon genes [5]. It consists of *merR* gene encoding regulatory protein and different genes of structure [6]. One of the most important is *merA* gene encoding mercuric ion reductase [5].

Our study object were bacterial isolates from microbiota of *Tussilago farfara* L. growing in mercury-contaminated and mercury non-contaminated post-industrial areas.

Bacteria isolated from *T. farfara* L. growing in mercury-contaminated areas were cultured in standard Luria-Bertani (LB) medium with mercury concentration 0.01% (w/v) (Hg source $HgCl_2$ – 135 mg/l) and from mercury non-contaminated areas were cultured in standard LB. The growth kinetics measurements were performed for 48 hours in a microplate reader with customized shaking and incubation program with and without mercury addition. Despite the variability in *mer* operon composition, *merA* gene remains essential [5]. For this reason the *mer* operon presence in DNA isolated from analysed bacteria was checked by amplification of *merA* gene fragment in polymerase chain reaction (PCR).

Studied bacterial isolates from microbiota of *Tussilago farfara* L. growing in mercury-contaminated soil are able to grow in studied mercury concentration (0.01% (w/v)), although the lag phase is prolonged comparing to LB without Hg. *merA* gene presence was confirmed in all isolates from microbiota of *Tussilago farfara* L. growing in mercury-contaminated soil and mercury non-contaminated soil. However, isolates from mercury non-contaminated areas are unable to grow in media with mercury addition, what indicates that *merA* gene presence is not sufficient for verification of bacterial resistance in tested Hg concentration.

Studied bacterial isolates are good model for investigating mercury resistance mechanism, thanks to the tolerance to high mercury concentration and environmental origin. These results give the background for further investigation of mercury resistance mechanisms in studied bacteria and development of mercury bioremediation technique.

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