ABSTRACT

Biofilm formation is one of the most common bacterial survival strategies. Majority of bacterial species are able to form these three-dimensional structures, including pathogens like *Mycobacterium tuberculosis*. Representatives of *Mycobacterium* genus widely occur in the nature, although they can cause serious problems when they appear in medical equipment and artificial replacements of the human body.

Non-pathogenic *Mycobacterium smegmatis mc*^{2} *155* was used as a model organism in our experiments. We investigated morphology of the three- and six-day-old colonies (in fact biofilms) on agar and agar covered with cellophane using Stereo microscope and Scanning Electron Microscope. We found that a type of surface as well as a carbon source has a great influence on the morphology of the *M. smegmatis* colonies. We isolated proteomes from the agar and cellophane cultures and from planktonic culture. Two-dimensional electrophoresis was used as the main proteomic method. Proteomic data were analyzed using PDQuest software. Then the sets of proteins detected by qualitative and quantitative analyses were compared using Venn diagrams. As a result, we recognized 7 unique proteins that might be specific for recognition and adhesion of bacteria to the cellophane, no unique protein in agar proteome and 46 unique proteins that might be specific for submerged growth in liquid culture. Quantitative analysis revealed only 3 proteins with different expression in all proteomes. These results show that morphological changes are associated with changes in proteome. Expression of new unique proteins rather than the changes in expression of those present in all conditions seems to play a key role in adapting to different types of cultivation.

Key words: *Mycobacterium smegmatis*, *Mycobacterium tuberculosis,* biofilm, colony morphology, carbon source, two-dimensional electrophoresis, SEM, proteome.