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EVALUATION OF BIOFILM FORMATION AND BIOFILM-ASSOCIATED GENES DISTRIBUTION IN CLINICAL ISOLATES OF OPPORTUNISTIC PATHOGEN STENOTROPHOMONAS MALTOPHILIA

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One of the biggest health problems in recent years is bacterial multidrug resistance to antibiotics. Almost 5 million deaths were associated with drug-resistant infections in 2019 and it is estimated that by 2050 this number will increase to 10 million per year [1]. *Stenotrophomonas maltophilia* is one of the rising multidrug-resistant opportunistic pathogens that has a mortality rate of up to 37.5% [2]. Infections caused by this pathogen are difficult to treat because of its multidrug resistance phenotype and ability to form biofilms [3]. Bacterial biofilms are complex microbial communities encased in extracellular polymeric substances [4]. This structure produced by bacteria helps them adhere to surfaces and protects them from unfavourable conditions (e.g. desiccation, antibiotics, immune system). *S. maltophilia* is a genetically diverse species and its ability to form biofilms can highly vary [5], therefore it is important to determine the biofilm-forming capability of *S. maltophilia* isolates collected from various sources.

This study aimed to evaluate biofilm formation and biofilm-associated gene distribution in 44 clinical isolates of *S. maltophilia* received from patients of Vilnius university hospital Santaros klinikos. Biofilm formation at 37 °C temperature was evaluated using crystal violet dye assay [5]. Gene prevalence in isolates was evaluated by performing PCR with gene-specific primers and visualizing results using agarose gel electrophoresis.

This study found that all analysed *S. maltophilia* isolates were able to form biofilms. Out of 44 analysed isolates, 14% were weak biofilm producers, 36% were moderate biofilm producers, and 50% were strong biofilm producers. The analysed biofilm-associated genes were highly abundant in all clinical isolates but could not be associated with biofilm production levels. This indicates that differences in gene expression could be responsible for the intensity of biofilm formation.

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