

# IDENTIFICATION OF BIOFILM FORMATION FACTORS IN CLINICAL METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) ISOLATES

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is a significant pathogen capable of forming biofilms, which enhance its resistance to antibiotics and host immune responses [1]. Various genes regulate biofilm formation, including *fnbA*, *fnbB*, *clfA*, *icaD*, *icaR*, *spa*, and *bap* [2]. The aim of this study was to evaluate the relationship between biofilm formation strength and the presence of biofilm-associated genes in clinical MRSA isolates. Understanding the prevalence and combination of these genes in clinical isolates can provide insights into MRSA biofilm development and its potential impact on pathogenicity.

This study analyzed the biofilm-associated genes (*fnbA*, *fnbB*, *clfA*, *icaD*, *icaR*, *spa*, *bap*) in 95 clinical MRSA isolates from two hospitals in Vilnius, using PCR. Isolates were categorized as strong or moderate biofilm formers based on a quantitative biofilm assay using microtiter plates method. The optical density of the stained biofilms was measured spectrophotometrically to determine the biofilm formation strength. The most frequent genes and their combinations were identified, and their distributions among the biofilm-forming groups were statistically assessed.

All the MRSA isolates demonstrated the ability to form biofilms. 72% produced strong biofilms and 28% produced moderate biofilms. The most prevalent genes in the isolates were *fnbA* (94.74%), *icaR* (96.84%), and *icaD* (84.21%). The *spa* gene was present in all the MRSA clinical isolates (100%), suggesting its ubiquitous role in these strains. *bap* was absent in all the isolates. Statistical analysis revealed no significant differences in the prevalence of individual genes between the two biofilm-forming groups ( $p > 0.05$ ). The most common gene combination, detected in 44% of all isolates, included *icaD*, *spa*, *fnbA*, *clfA* and *icaR*. While gene combinations did not significantly differ between strong and moderate biofilm formers ( $p > 0.05$ ), one specific combination (*icaD*, *fnbA*, *fnbB*, *clfA*, *icaR* and *spa*), which included all the investigated genes, was found exclusively in strong biofilm formers (5.89%).

This study identified the dominant genetic profile of the biofilm-forming MRSA isolates. All the tested genes were present only in strong biofilm producers, suggesting that an expanded genetic repertoire may enhance biofilm formation. Further research is required to identify additional biofilm-associated genes.