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INVESTIGATION OF BIOFILM FORMATION IN THREE WARDS OF PERADENIYA TEACHING HOSPITAL AND COMPUTATIONAL PREDICTION OF ANTI-BIOFILM DRUGS

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Biofilm formation in healthcare settings presents a significant challenge due to its role in antibiotic resistance and persistent infections. This study investigated biofilm formation in clinical isolates from the surgical, medical, and psychiatric wards of the Peradeniya Teaching Hospital, employing three distinct detection methods: The Test Tube Method, Congo Red Agar (CRA) Method, and Tissue Culture Plate (TCP) Method. The Test Tube Method enabled qualitative assessment of biofilm production, while the CRA Method utilised Brain Heart Infusion (BHI) agar supplemented with Congo Red dye to differentiate biofilm producers visually, which formed characteristic black, dry colonies. The TCP Method provided a quantitative analysis of biofilm biomass using crystal violet staining and spectrophotometric absorbance at 630 nm. Scanning electron microscopy further confirmed the presence of dense biofilm matrices in high biofilm-forming samples, particularly from surgical and medical wards. In contrast, samples from the psychiatric ward showed significantly lower biofilm production. These differences correlated with variations in patient demographics, hygiene practices, and antibiotic exposure. In the computational component of the study, machine learning models, including Random Forest (RF), Support Vector Machine (SVM), and Artificial Neural Network (ANN), were implemented using KNIME software to predict biofilm-inhibitory potential among 200 antibiotics, based on a training dataset of 23 known inhibitors. All models identified ceftazidime as a promising anti-biofilm agent, demonstrating strong activity against single-species biofilms. However, its reduced efficacy in mixed-species communities highlighted the increased resistance and complexity of polymicrobial biofilms. The RF and SVM models achieved prediction accuracy of 86.04%, while the ANN model achieved 83.33%. This integrative study underscores the value of combining experimental assays with computational prediction to advance the discovery of effective anti-biofilm agents. It also emphasises the need for novel strategies tailored to overcome the resilience of complex, hospital-acquired biofilms.

Keywords: Antibiotic resistance, Biofilm, Drug prediction, KNIME, Machine learning