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Selection of best fitting mathematical model to analyse the anthracene degradation ability of *Bacillus velezensis*

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Living things frequently come into contact with a wide range of harmful pollutants, including polyaromatic hydrocarbons (PAHs) like anthracene, which are highly carcinogenic and genotoxic. Microbial degradation is the most promising approach for removing anthracene from the environment, using microorganisms to transform it into nontoxic compounds, rather than using physical and chemical methods. The study aimed to assess the kinetic approach in anthracene degradation by *Bacillus velezensis*, isolated from the phyllosphere of leaf samples. Leaf samples (*Ixora chinensis*, *Ervatamia divaricate*, and *Plumeria sp.*) were collected by using random sampling techniques from the most polluted urban areas (Maradana, Orugodawatta, Pettah, Panchikawatta, Sapugaskanda, and Colombo Fort) in Sri Lanka. Then, in vitro, anthracene degradation patterns were analysed using HPLC analysis at different anthracene concentrations (100 ppm, 200 ppm, 300ppm, 400 ppm, 500 ppm, and 600 ppm) as a model of limited substrates while monitoring the growth patterns based on fluctuations in dry cell biomass. Anthracene was completely degraded in six days of incubation for low initial anthracene concentrations. Dry cell biomass and degradation percentages were measured with time for different initial liquid substrate concentrations of PAHs. The specific growth rates and degradation rates were calculated. The study used box plot analysis to identify and eliminate outliers from 65 data points, ensuring the validity and reliability of the findings. After eliminating four outliers, 61 usable data points were obtained, and the ANOVA was used to compare average specific growth rates between anthracene concentration groups, revealing all specific growth rates were statistically significant. The kinetic parameters of anthracene degradation were analysed by using various models including, Monod's, Haldane's, Wayman and Tseng's models because they focused on their convergence with experimental data. The models were evaluated by determining the parameter's significant value, Root Mean Square Error (RMSE), and the Adj.R² value. Among these models, Wayman and Tseng's model demonstrated the better fit for the experiment with Adj.R²- 0.95191 and RMSE – 0.0019. The experimental kinetics data of anthracene degradation closely followed Wayman and Tseng's model, indicating that this model provided an accurate representation of the interaction between the PAH substrate (anthracene) and the growth kinetics of the microorganisms. The half saturation constant K_s , the maximum specific growth rate μ_{max} , the threshold substrate concentration S_θ , and the inhibition coefficient i were defined as Wayman and Tseng's model parameters and were estimated in their numerical values.

Keywords: *Bacillus velezensis*, Biodegradation, Kinetics, Substrate inhibition, Toxicity, Wayman and Tseng's model