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# Substrate Inhibition Kinetics Models for Fitting the Growth Rate of *Stenotrophomonas maltophilia* on Methyl Orange

Aisami Abubakar[1]*

[1]Department of Biochemistry, Faculty of Science, Gombe State University, P.M.B 127, Tudun Wada, Gombe, Gombe State, Nigeria.

**ABSTRACT**
Substrate inhibition is a common phenomenon in the biodegradation of xenobiotic compounds, especially dyes, where high concentrations of substrate inhibit the microbial growth and degradation activity. These inhibitory effects are not described by the classical Monod kinetics and therefore other models of substrate inhibition such as Haldane, Luong, Teissier, Aiba, Edwards, Yano, Han-Levenspiel, and Webb models have been developed. In the present study, the growth kinetics of methyl orange (MO)-degrading *Stenotrophomonas maltophilia* were investigated using various substrate inhibition models, particularly the Webb model. The model fitting indicated that the Webb model was the best model to describe the relationship between specific growth rate and MO concentration. The fitted parameters were $\mu_{max}$ = 2.274 $h^{-1}$, $K_s$ = -288.599 mg/L, $K_i$ = 6370.331 mg/L and $K$ = 6.643. However, the negative $K_s$ and the excessively large $K_i$ were biologically unrealistic, indicating that the parameters were poorly identifiable and the parameter estimation was unstable. These limitations were probably due to the small dataset, limited data points within the inhibition region, and strong parameter correlation during nonlinear regression. The estimated actual maximum specific growth rate from the experimental growth curve was 0.0186 $h^{-1}$ at 124.865 mg/L MO. The Webb model provided a reasonable fit to the observed growth pattern, but fitted parameters should be treated with caution. The findings underscore the importance of evaluating multiple inhibition models and critically assessing the realism of parameters when modelling microbial degradation of inhibitory xenobiotic compounds. The output of curve fitting interpolation should not be considered the true value, and the user should be duly informed of this as the true $\mu_{max}$ should be the point at which the slope's gradient becomes zero; in this instance, the value was 0.0186 $h^{-1}$ at 124.865 mg/L of MO.

**KEYWORDS:** Substrate Inhibition Kinetics, Nonlinear regression, Methyl orange, *Stenotrophomonas maltophilia*, Webb model

**SDG Keywords**: SDG 6 Clean water and sanitation; SDG 12 Responsible consumption and production; SDG 9 Industry, innovation and infrastructure

## INTRODUCTION

Various industrial processes utilize diverse synthetic dyes. Methyl orange is an azo dye sulphonated (Guo et al., 2014; Sharmila et al., 2015). The chemical structure is shown in Fig. 1. In methyl orange the azo group (-N—N-) is the chromophore and responsible for orange colour. It also serves as a laboratory indicator. The dye is reported to be carcinogenic by the United States Environmental Agencies (USEPA) and other major environmental law enforcement organizations and dangerous pollutants. Wastewater contaminated with detergent, dye, suspended solid, aldehyde, additive, non-biodegradable, heavy metal, and insoluble material have the potential to pollute the water bodies into which it is drained.

One of the most sustainable pollution remediation is bioremediation, which is the process of removal of pollutants (such as heavy metals, hydrocarbons and dyes) from soil, water and other environments using living or dead microorganisms (Harun et al., 2024; Ivshina et al., 2024; Muhammad et al., 2024; Zhang et al., 2024). It has been reported in literature that several bacterial strains such as bacteria, fungi and yeasts have the capability to degrade azo dyes. Bacteria are used more often than fungi, algae and plants for bioremediation because they reproduce quickly and can survive in a range of habitats under adverse conditions. Azo dyes can be mineralized or converted to water and carbon dioxide by bacteria (Aisami et al., 2023; Harun et al., 2023; Ishaya et al., 2023; Pradhan et al., 2023). Methyl orange (MO) is an azo dye widely used in textile and allied industries, and several bacterial species have demonstrated promising potential for its biodegradation. Haque et al. showed that *Aeromonas hydrophila* degraded methyl orange up to 90% under optimized conditions (Haque et al., 2024). Similarly, Yang et al. reported the ability of *Stenotrophomonas acidaminiphila* to degrade about 95% of the dye which shows its effectiveness in azo dye bioremediation (Yang et al., 2011). Al-Ansari et al. (2022) also demonstrates that *Enterobacter aerogenes* ES014 removes up to 75% of methyl orange from polluted wastewater. Also, Masarbo et al. (2018) reported that *Kerstersia* sp. decolorize and mineralize methyl orange up to 96%. Another example-*Stenotrophomonas maltophilia*, has been reported to biodegrade methyl orange effectively under a wide range of environmental conditions . Moreover, the biofilms formed by plant growth-promoting rhizobacteria (PGPR) have shown decolorization efficiencies above 99% and analytical studies have confirmed the degradation of methyl orange into less toxic metabolites.

Synergistic metabolic interactions among mixed bacterial consortia have also been demonstrated to be better than individual strains in decolorizing and detoxifying azo dyes leading to enhanced performance. Collectively, these findings indicate bacterial biodegradation as an eco-friendly and economical approach for the treatment of dye-contaminated industrial effluents. The presence of dyes in water at low concentrations can have adverse environmental consequences because of their carcinogenic nature. Hence, methyl orange dye containing wastewater needs to be properly treated before discharge (Du et al., 2014; Elavarasi & Priya, 2015; Guo et al., 2014; Islam et al., 2018; Shariati-Rad et al., 2014; Sharmila et al., 2015; Yu et al., 2011).

Many conventional methods such as physio-chemical (ion exchange, membrane separation, adsorption, etc.), chemical (UV/H2O2, Fenton, ozonation, advanced oxidation, etc.), and biological methods are available to degrade methyl orange dye (Du et al., 2014; Guo et al., 2014; Shariati-Rad et al., 2014). These techniques are effective in the removal of dyes but are limited by their high cost, energy requirements and generation of secondary pollutants. Therefore, it is needed for sustainable, cost-effective and effective ways for treatment of waste water from textile industries. Without accessibility to quantitative experimental data, it is not possible to build biological transformation processes and then optimize those processes. Several various mathematical models have been proposed in order to explain the metabolic characteristics of compounds when those chemicals are exposed to either pure cultures of microorganisms or wild populations of microorganisms. The relationship between the substrate concentration ($S$) and the specific growth rate ($\mu_{max}$) of a microbial colony is an important tool in biotechnology. The Monod equation is a typical tool that is used to characterize the relationship between growth and the rate of substrate consumption (Kiviharju et al., 2006; Shokrollahzadeh et al., 2007).

When a substrate, on the other hand, acts as an inhibitor of its own biodegradation, the original Monod model is rendered completely useless. In its place, the development of novel constant-carrying derivatives has taken place in order to facilitate substrate-related changes. The Haldane model is one that is used to represent substrate inhibition of growth or degradation rate, and it may be found in a wide variety of published works. Even though it has been demonstrated that alternative models are more accurate when taking into account a large number of substrate-inhibiting compounds all at once, such as phenol, this model is still widely employed. To illustrate this point, the Haldane model is not the only one currently available (Arif et al., 2013), In addition to the model, there have been numerous models that have been shown to be superior such as Luong (Hamitouche et al., 2012; Nickzad et al., 2012) and Edward (Saravanan et al., 2009). As a result of this, the Haldane may be rendered obsolete in some circumstances as a result of the utilization of the more extensive models that are currently available.

It is not recommended to make haphazard use of the Haldane model without first doing exhaustive statistical analysis and attempting to fit other models to previously collected data on rate of growth or degradation. In this study, we continue the work by further modeling the influence of substrate or phenol on the growth rate of the bacterium by using different substrate inhibition kinetic models. Several mathematical models have been proposed to account for the metabolic biotransformation of xenobiotics by microorganisms. The relationship between substrate concentration ($S$) and maximum specific growth rate (μmax) of a microbial population is an important tool in biotechnology. The Monod equation is a widely used expression to describe the relationship between growth and substrate consumption rate (Guha & Jaffé, 1996; Ibrahim et al., 2016; Mpongwana et al., 2020; Sniegowski et al., 2009). However, the original Monod model is of no use whatsoever if a substrate is an inhibitor of its own biodegradation. In its place, novel constant-carrying derivatives have been developed in order to allow such substrate-related changes.

The Haldane model is a model for substrate inhibition of growth or degradation rate. It is found in a wide variety of published works. Although it has been demonstrated that alternative models are more accurate when a large number of substrate-inhibiting compounds are considered simultaneously (e.g. dyes), this model is still widely used. For example, the Haldane model is not the only model currently available (Lodha et al., 2007; Manogaran et al., 2017; Mpongwana et al., 2020; Nandi et al., 2020), in addition to the model, many models have been demonstrated to be better such as Luong, Yano, Teissier (or Tessier or Tessier-Edward), Webb, Aiba and Edward (Muloiwa et al., 2020). Because of this, the Haldane may become obsolete in some situations due to usage of the more comprehensive models that are currently available. It is not recommended to use the Haldane model ad hoc without first conducting exhaustive statistical analysis and attempting to fit other models to previously collected data on rate of growth or degradation. In this work we extend this work by modelling the effect of substrate or Methyl orange on the growth rate of *Stenotrophomonas maltophilia* using different substrate inhibition kinetic models.

## MATERIALS AND METHODS

Data of Figure 3. from growth of an *Stenotrophomonas maltophilia*on (Mishra et al., 2024)were processed with the software Webplotdigitizer 2.5 (Rohatgi, 2017, 2018). It changes the scanned image to a digital form. It is used by a large number of scholars and is recognized for the accuracy it provides (Burda et al., 2017; Cicala et al., 2023; Drevon et al., 2017; Mani et al., 2018; Sandi et al., 2023). **Table 1** summarizes the ten models for inhibition kinetics.

### Data fit

The inhibition curves were fitted by CurveExpert Professional software (Version 1.6, www.curveexpert.net) with different growth models using non-linear regression with the Marquardt algorithm.



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**Table 1**. Various mathematical models developed for degradation kinetics involving substrate inhibition of the dye.

| Author | Degradation Rate | Author |
|---|---|---|
| Monod | $\frac{\mu_{max}S}{S+K_s}$ | (Monod, 1949) |
| Haldane | $\frac{\mu_{max}S}{S+K_s+\left(\frac{S^2}{K_i}\right)}$ | (Boon & Laudelout, 1962) |
| Teissier | $\mu_{max}\left(1-exp\left(-\frac{S}{K_i}\right)-exp\left(\frac{S}{K_s}\right)\right)$ | (Teissier, 1942) |
| Aiba | $\mu_{max}\frac{S}{K_s+S}exp\left(-\frac{S}{K_i}\right)$ | (Aiba et al., 1968) |
| Yano and Koga | $\frac{\mu_{max}S}{S+K_s+\left(\frac{S^2}{K_i}\right)\left(1+\frac{S}{K}\right)}$ | (Yano & Koga, 1969) |
| Han and Levenspiel | $\mu_{max}\left(1-\left(\frac{S}{S_m}\right)\right)^n\left(\frac{S}{S+K_s\left(1-\left(\frac{S}{S_m}\right)\right)^m}\right)$ | (Han & Levenspiel, 1988) |
| Luong | $\mu_{max}\frac{S}{S+K_s}\left(1-\left(\frac{S}{S_m}\right)\right)^n$ | (Luong, 1987) |
| Moser | $\frac{\mu_{max}s^n}{K_s+s^n}$ | (Moser, 1985) |
| Webb | $\frac{\mu_{max}S\left(1+\frac{S}{K}\right)}{S+K_s+\frac{S^2}{K_i}}$ | (Webb, 1963) |
| Hinshelwood | $\mu_{max}\frac{S}{K_s+S}(1-K_pP)$ | (Hinshelwood, 1946) |

Note:
$\mu_{max}$ maximal specific growth rate
$K_s$ half saturation constant
$K_i$ inhibition constant
$S_m$ maximal concentration of substrate tolerated
$K_p$ product inhibition constant
m, n, K curve parameters
$S$ substrate concentration
$p$ product concentration

**Error function or statistical analysis**

To find the best model the following statistical discriminatory or error function tests were utilized and include corrected Akaike Information Criterion (AICc), root-mean-squared error (RMSE), adjusted coefficient of determination ($R^2$), Bias Factor (BF), Accuracy Factor (AF), Marquardt's percent standard deviation (MPSD), and Bayesian Information Criterion. O*bi* and P*di* are the expected and observed values, $n$ is the total number of observations, and $p$ is the total number of model parameters (Allamin et al., 2023).

RMSE was calculated based on the following formula;

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n}(Pd_i-Ob_i)^2}{n-p}} \quad \text{(Eqn. 1)}$$

BF and AF were calculated based on the following formula;

$$Bias\ factor = 10\left(\sum_{i=1}^{n} log\frac{(Pd_i/Ob_i)}{n}\right) \quad \text{(Eqn. 2)}$$

$$Accuracy\ factor = 10\left(\sum_{i=1}^{n} log\frac{|(Pd_i/Ob_i)|}{n}\right) \quad \text{(Eqn. 3)}$$

AICc was calculated based on the following formula;

$$AICc = 2p + n\ln\left(\frac{RSS}{n}\right) + \frac{2(p+1)+2(p+2)}{n-p-2} \quad \text{(Eqn. 4)}$$

BIC was calculated based on the following formula;

$$BIC = n\ln\left(\frac{RSS}{n}\right) + k\ln(n) \quad \text{(Eqn. 5)}$$

HQC was calculated based on the following formula;

$$HQC = nIn\left(\frac{RSS}{n}\right) + 2k\ln(\ln n) \quad \text{(Eqn. 6)}$$

Adjusted coefficient of determination ($R^2$) was calculated based on the following formula;

$$Adjusted\ (R^2) = 1 - \frac{RMS}{S_Y^2} \quad \text{(Eqn. 7)}$$

$$Adjusted\ (R^2) = 1 - \frac{(1-R^2)(n-1)}{(n-p-1)} \quad \text{(Eqn. 8)}$$

MPSD was calculated based on the following formula;

$$MPSD = 100\sqrt{\frac{1}{n-p}\sum_{i=1}^{n}\left(\frac{Ob_i-Pd_i}{Ob_i}\right)^2} \quad \text{(Eqn. 9)}$$

## RESULTS AND DISCUSSION

In this study, the specific maximum growth rate on MO ($\mu_m$) was first obtained using the no lag modified logistics model (**Fig. 1**). The results of the RMSE, AICc, adjusted$R^2$, F-test, and bias and accuracy factor comparisons demonstrate that the Webb model is the most accurate and precise of the kinetic models considered (**Table 2**). The resultant fittings (**Figs 2** to **11**) demonstrate satisfactory fit except for the Monod and Yano models.

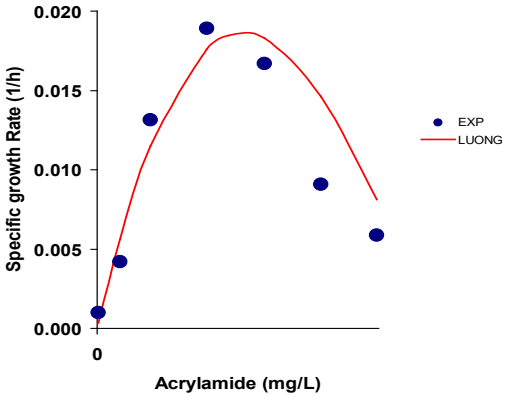



**Fig 1.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the Luong model.

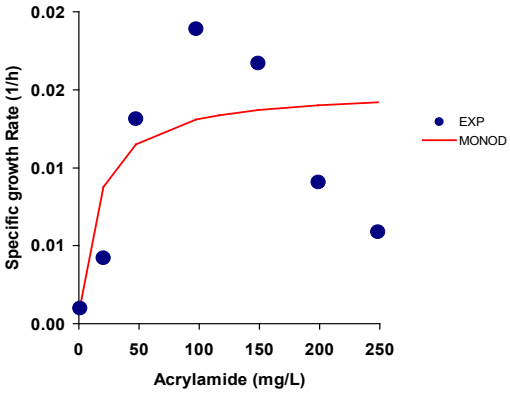



**Fig 2.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the Monod model.



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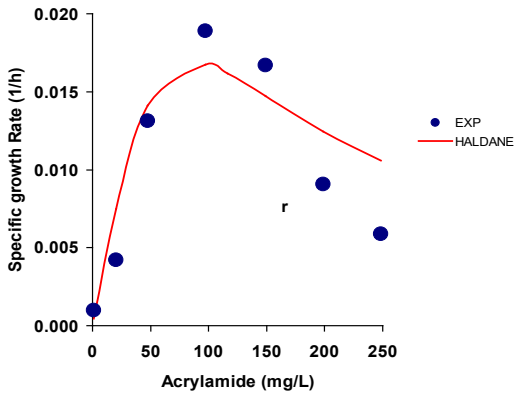



**Fig 3.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the Haldane model.

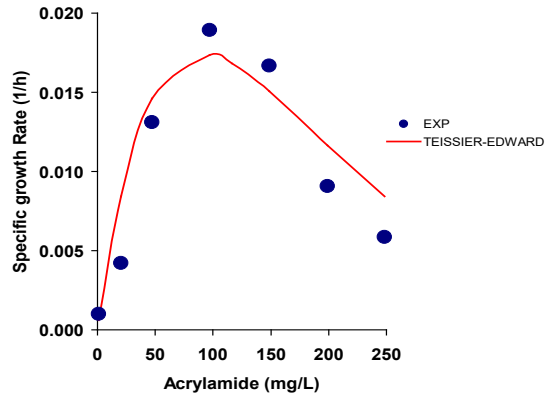



**Fig 4.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the model of Teissier.

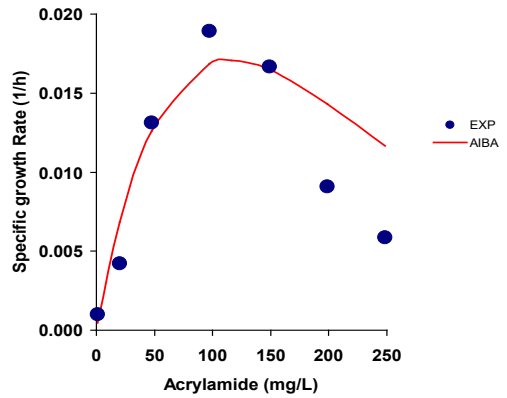



**Fig 5.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the model of Aiba.

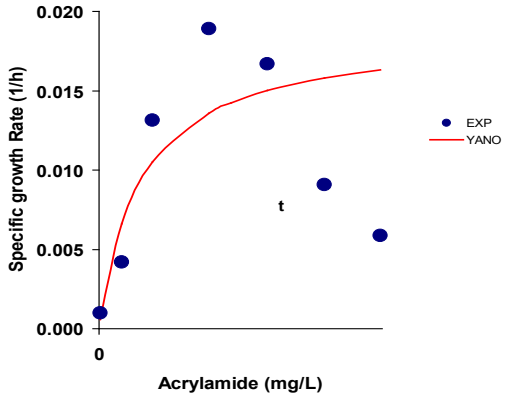



**Fig 6.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the model of Yano and Koga.

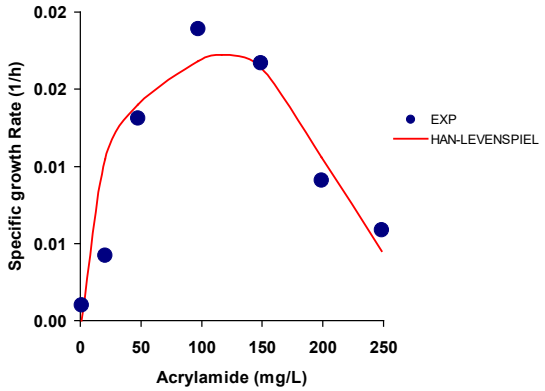



**Fig 7.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the model of Han and Levenspiel.

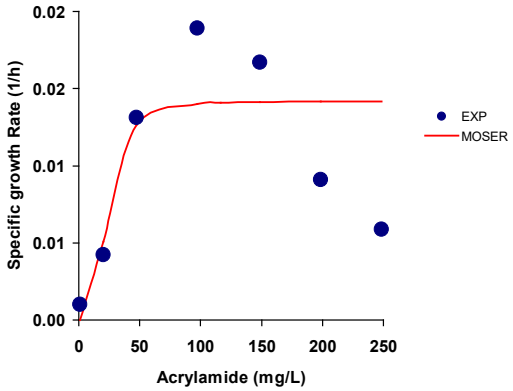



**Fig 8.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the model of Moser.



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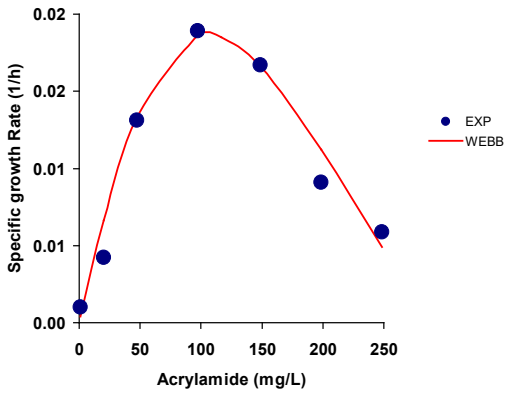



**Fig 9.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the model of Webb.

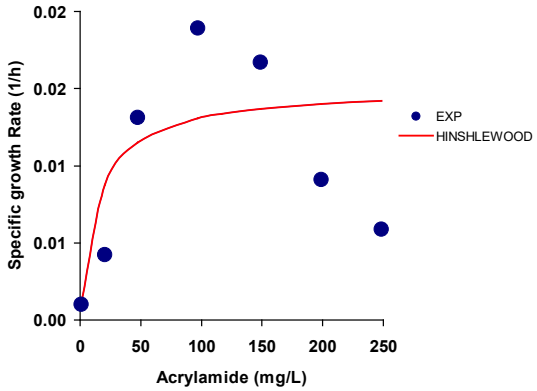



**Fig 10.** Growth rate data of *Stenotrophomonas maltophilia* fitted with respect to MO concentration using the model of Hinshelwood.

From the Webb model, the maximum specific growth rate ($\mu_{max}$) was 2.274 $h^{-1}$, the substrate inhibition constant ($K_i$) was 6370.331 mg/L, and the inhibition parameter ($K$) was 6.643 (**Table 3**). However, the negative $K_s$ value (-288.599 mg/L) is biologically unrealistic indicating poor parameter estimation and possible model instability. These discrepancies may be due to the low number of data points, the low concentrations of substrate in the inhibition region, the high variability of the data and the strong correlation of the fitted parameters. The reason may be due to all of the above since all of the lesser ranked models also gave a wide range of confidence interval. The too high value for Ki also indicates a poor characterization of substrate inhibition. Therefore, even if the model is acceptable in fitting the data, the estimated parameters should be interpreted with caution.

The output of curve fitting interpolation should not be considered the true value, and the user should be duly informed of this as the true $\mu_{max}$ should be the point at which the slope's gradient becomes zero; in this instance, the true $\mu_{max}$ should be the point at which the slope's gradient becomes zero and was 0.0186 $h^{-1}$ at 124.865 mg/L of MO. The equation for the Webb model using the values obtained from the fitting is as follows;

$$\mu = \frac{2.274 \cdot S\left(1+\frac{S}{6.643}\right)}{S-288.599+6370.331+\frac{S^2}{6.643}} \quad \text{(Eqn. 10)}$$

**Table 3**. Parameter of the Webb model.

| Parameter | unit | value |
|---|---|---|
| $\mu_{max}$ | $h^{-1}$ | 2.274 |
| $K_s$ | mg/L | -288.599 |
| $K_i$ | mg/L | 6370.331 |
| $K$ | unitless | 6.643 |

Models like Luong's, Teissier's, and Hans Levenspiel's have been developed to account for the occurrences in which the growth rate approaches zero at very high substrate concentrations where the earlier Monod model could not be used (Saravanan et al., 2008). Overly high concentrations of substrates can have toxic and repressive effects on microbes, stunting their growth. Much of the current use of the Haldane model for modelling the effect of toxic xenobiotics to xenobiotic-degrading bacteria centres predominantly to MO-degrading microorganisms (Agarry et al., 2009; Bai et al., 2007; Basak et al., 2014; Ding et al., 2014; Kotturi et al., 1991; Liu et al., 2013; Long et al., 2010; Mohanty & Jena, 2017). This is followed by Teissier (Agarry et al., 2008, 2008; Agarry & Solomon, 2008; Begum & Radha, 2011; Halmi et al., 2014). It appears that other models were found to be less reported and the reason for this is that in numerous cases only the Haldane model was utilized to model the effect of MO on the growth or degradation rate of microorganisms on MO.

**Table 2.** Statistical analysis of the various fitting models.

| Model | *p* | RMSE | R2 | adR2 | MPSD | AICc | BIC | HQC | BF | AF |
|---|---|---|---|---|---|---|---|---|---|---|
| Luong | 4 | 0.0033 | 0.8613 | 0.6763 | 25.635 | -49.047 | -88.730 | -91.191 | 1.078 | 1.160 |
| Yano | 4 | 0.0056 | 0.4045 | -0.3895 | 49.906 | -40.533 | -80.215 | -82.676 | 1.073 | 1.382 |
| Tessier-Edward | 3 | 0.0029 | 0.8072 | 0.6626 | 20.479 | -69.739 | -90.834 | -92.680 | 1.044 | 1.145 |
| Aiba | 3 | 0.0031 | 0.7924 | 0.6368 | 29.340 | -68.715 | -89.810 | -91.656 | 1.106 | 1.203 |
| Haldane | 3 | 0.0031 | 0.7664 | 0.5913 | 27.371 | -68.832 | -89.927 | -91.773 | 1.065 | 1.199 |
| Monod | 2 | 0.0048 | 0.0158 | -0.3779 | 40.722 | -71.794 | -83.635 | -84.865 | 1.026 | 1.355 |
| Han and Levenspiel | 5 | 0.0043 | 0.7928 | 0.2748 | 23.062 | 11.138 | -84.465 | -87.541 | 0.959 | 1.102 |
| Moser | 3 | 0.0044 | 0.5390 | 0.1932 | 40.421 | -63.338 | -84.433 | -86.279 | 1.060 | 1.315 |
| Hinshelwood | 4 | 0.0059 | 0.0158 | -1.2965 | 49.874 | -39.794 | -79.476 | -81.937 | 1.026 | 1.355 |
| Webb | 4 | 0.0019 | 0.9565 | 0.8985 | 14.356 | -58.131 | -97.813 | -100.274 | 0.993 | 1.066 |

Note:
*p* no of parameters
RMSE Root Mean Square Error
AdjR$^2$ Adjusted Coefficient of determination
BF Bias factor
AF Accuracy factor
n.a. not available


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In 1930, Haldane presented his model, now known as the Haldane model (Haldane, 1930). The model is thought of as a development of the Monod model. The model includes a third constant, $K_i$, to account for substrate concentration-dependent inhibition of the specific growth rate. The substrate concentration at which the specific growth rate is half the maximum growth rate absent inhibition is equal to the inhibition constant or $K_s$. Hazardous substrate may slow an organism's specific growth rate at high substrate concentrations. The model can deal with both hazardous and non-hazardous substrates. The Haldane model's strength lies in its ability to characterize all stages of the kinetics of growth rate. The Haldane model was widely utilized because it well described growth rate at both low and high substrate concentration. Before the Haldane model became widely used, the classical Monod model was the most often utilized model.

The Monod model was originally developed by Jacques Monod in 1942 (Monod, 1949) to describe the correlation between specific growth rate and specific substrate consumption rate in a bioreactor. The Michaelis-Menten equation and the Monod equation look very similar, but they are based on theory (rather than observation). The Monod equation for the specific growth rate can be expressed in terms of constants, similar to the Michaelis-Menten formula for enzyme kinetics. To account for the occurrences in which the growth rate approaches zero at very high substrate concentrations where the earlier Monod model could not be used, models such as those of Luong, Teissier and Hans Levenspiel have been developed. Excess substrate concentrations may have toxic and repressive effects on microbes, thus retarding their growth. Most of the current applications of the Haldane model for modeling the effect of toxic xenobiotics on xenobiotic-degrading bacteria have been concentrated mainly on microorganisms that degrade dyes (Beydilli & Pavlostathis, 2007; Inan Beydilli & Pavlostathis, 2005; Sonwani et al., 2021; Srinivasan et al., 2011; Yu et al., 2015). Next is Teissier (Agarry et al., 2008; Agarry & Solomon, 2008; Gharibzahedi et al., 2013; Kiviharju et al., 2006; Sack et al., 2011; Singh et al., 2008). Other models were less reported and the reason is that in many cases only the Haldane model was used to model the effect of MO on the growth or degradation rate of microorganisms on dyes.

In many xenobiotics or hazardous compounds, bioremediation works; toxic substrates that inhibit bacterial growth and consumption of substrates mean that the Monod models will not be useful, and other substrate inhibition models are needed. The Webb model is one of the most popular models for substrate inhibition since it has an additional parameter for inhibition and can describe more complex patterns of microbial growth at high substrate concentrations more precisely than simple models (Agarry & Solomon, 2008; Jahan et al., 2008; Muloiwa et al., 2020; Sahoo et al., 2011; Singh et al., 2008). It has been successfully applied to biodegradation of dyes and other xenobiotic compounds, where inhibitory effects are important at high pollutant concentrations. In the study of phthalate biodegradation by *Gordonia* sp., the Webb model was found to fit better than the conventional inhibition models (Kanaujiya et al., 2023). Because it can account for both phases of growth promotion and inhibition, it is particularly suitable for applications in wastewater treatment and bioremediation of recalcitrant pollutants. Webb model is a modified version of the Haldane model, describing $\mu$ as a function of S only. In the phenol degradation studies, the Webb model was the best model describing the substrate inhibition kinetics to *Acinetobacter* sp. compared to other rmodels including Haldane (Nandi et al., 2020).

## CONCLUSION

The results of this study show the importance of using substrate inhibition kinetic models for the studies of the biodegradation of inhibitory xenobiotic compounds such as methyl orange. The Webb model was the best statistically fitting model to the growth data of Stenotrophomonas maltophilia among the models evaluated and supported its usefulness for describing complex growth-inhibition behavior. However, some fitted parameters (negative Ks value and very high Ki value) were biologically unrealistic, which indicates poor parameter estimation and uncertainty due to lack of sufficient experimental data. The findings indicate that better statistics do not necessarily mean biologically meaningful parameters. The maximum growth rate obtained experimentally, 0.0186 $h^{-1}$ at 124.865 mg/L MO, is probably a more realistic estimate of microbial performance than the fitted $\mu_{max}$ value. Future work should involve more data points especially in the region of substrate inhibition and multiple inhibition models should be compared to select the most appropriate kinetic description. This approach will increase the model certainty and improve the prediction of microbial dye biodegradation processes for environmental remediation applications.

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In the preparation of this work, the authors used generative AI technologies solely for the purpose of language editing and refinement. All authors reviewed and edited the content. The authors are responsible for the contents of the publication.

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***Abbreviations:***

| | |
|---|---|
| MO | Methyl Orange |
| *p* | no of parameters |
| RMSE | Root Mean Square Error |
| $AdjR^2$ | Adjusted Coefficient of determination |
| BF | Bias factor |
| AF | Accuracy factor |

**** Corresponding author.***

Abubakar Aisami
Department of Biochemistry, Faculty of Science,
Gombe State University,
P.M.B 127, Tudun Wada,
Gombe, Gombe State,
Nigeria.
Email: aaisami@gsu.edu.ng

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