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Phenol degradation using an immobilized Bacillus cereus–PVA–alginate system: Process optimization, kinetic modeling, and repeated-batch performance

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Abstract

Phenol removal from wastewater remains a challenge because of the toxicity of this compound and its effects on aquatic systems. Physical and chemical treatments have been used for this purpose, but they may require high energy consumption and chemical reagents. In this work, *Bacillus cereus* cells were immobilized in a polyvinyl alcohol (PVA)–sodium alginate matrix, and their ability to degrade phenol was evaluated at concentrations of 500, 750, and 1000 mg/L. Degradation efficiencies of 99.78, 99.88, and 99.89% were obtained, respectively. The immobilized cells were reused for 13 cycles and maintained degradation efficiencies above 97% at the three concentrations. When the degradation percentages obtained in each cycle were added, cumulative values higher than 1200% were reached. Phenol concentration and number of reuse cycles were analyzed using response surface methodology. The model identified 737.37 mg/L phenol at 13 cycles and 997.14 mg/L phenol at 12.99 cycles as the conditions with the highest cumulative degradation responses, with predicted values of 1286.86 and 1283.00%, respectively. During experimental validation, the corresponding values were 1279.40 and 1288.82%, which were close to those predicted by the model. The validation data were also fitted to the Haldane–Andrews model. The estimated (Ki) values were 715.21 and 835.58 mg/L, the (Ks) values were 30.76 and 25.65 mg/L, and the μ_{max} values were 0.37 and 0.42, with (R^2) values of 0.99 and 0.97, respectively. Overall, immobilization in PVA–sodium alginate allowed *Bacillus cereus* cells to maintain their phenol-degrading activity during repeated use.

1. Introduction

Wastewater discharge is one of the main threats to human health and the environment because wastewater effluents may contain pollutants capable of compromising the ecological balance, even at low concentrations (Honda & Suzuki, 2020). Phenol is one such pollutant and has been reported to pose a risk to aquatic ecosystems at concentrations ranging from 5 to 25 mg/L (Biswas et al., 2020). In humans, ingestion of 1.0 g of phenol may cause acute toxicity, while prolonged exposure has been associated with mutagenic and carcinogenic effects (Zou et al., 2025).

Physical, chemical, and biological methods, as well as combinations of these approaches, have been used to remove phenol from wastewater (Pal, 2017 a,b,c). Although some physical and chemical treatments can achieve high removal efficiencies, their application may be limited by high energy requirements, operating costs, and the use of chemical reagents (Villegas et al., 2016). Biological treatment represents a potentially more sustainable alternative in which microorganisms, including yeasts, fungi, microalgae, and bacteria, act as phenol-degrading agents (Karatay & Dönmez, 2014; Karimi & Hassanshahian, 2016; Ke et al., 2018; Singh et al., 2021). Some microorganisms can use phenol as their sole source of carbon and energy and tolerate relatively high phenol concentrations (Bai et al., 2021; Pal, 2017a). They are also tolerant to their high toxicity; therefore, they can degrade high concentrations of phenol (Chris Felshia *et al*., 2017). Their ease of cultivation and comparatively low generation of secondary pollutants make them attractive, low-cost tools for wastewater treatment (Bai et al., 2021; Kotresha & Vidyasagar, 2017). Immobilization has therefore been explored as a strategy to improve the stability, recovery, and reuse of microbial cells through physical methods, such as adsorption, entrapment, and encapsulation, or chemical methods, such as covalent binding and cross-linking (Bouabidi et al., 2019; Hou *et a.l*, 2024; Wadhawan et al., 2026) .

Although microorganisms can be immobilized using different physical and chemical methods, each technique has specific advantages and limitations. Adsorption is relatively simple to perform; however, the weak interactions between the cells and the support may result in cell detachment (Nogina et al., 2020). Similarly, cells immobilized by entrapment may gradually leak from the polymeric matrix (Ma et al., 2020). Covalent binding and cross-linking provide stronger interactions between the cells and the support, but the chemical reactions and cross-linking agents used during immobilization, such as glutaraldehyde and bisacrylamide, may negatively affect cell viability or metabolic activity (Brickerstaf, 1996; Eş et al., 2015; Sirisha and Jain, 2016). In contrast, encapsulation surrounds the cells within a polymeric matrix, reducing the probability of cell leakage while allowing the diffusion of substrates, nutrients, and oxygen between the reaction medium and the immobilized biomass (Ruan et al., 2018).

The selection of suitable support is a critical step in microbial cell immobilization. Immobilization supports can generally be classified as organic or inorganic materials. Common organic supports include agar, agarose, cellulose, chitosan, alginate, carrageenan, gelatin, pectin, polyvinyl alcohol, polypropylene, polyethylene, polyacrylamide, polyurethane, and acrylamide, whereas inorganic supports include zeolite, silica, clay, glass, activated carbon, and ceramics (Thakur & Thakur, 2018).

Organic supports are commonly selected because many of them have low toxicity, are economical, can be regenerated, and are compatible with microorganisms (Bouabidi et al., 2019). For example, alginate and polyvinyl alcohol also have good gel-forming properties and high mechanical resistance, respectively (El-Naas et al., 2013; Jiang et al., 2013; Paisio et al., 2016). These materials can be used individually, combined with each other, or mixed with other supports. Their use has allowed bacteria from the genera *Acinetobacter*, *Bacillus*,

Glutamicibacter, *Providencia*, *Pseudomonas*, *Rhodococcus*, and *Sphingomonas* to be reused over several treatment cycles and to degrade higher phenol concentrations (Escobedo et al., 2022).

In this work, *Bacillus cereus* cells were immobilized in a polyvinyl alcohol (PVA)–sodium alginate matrix to evaluate phenol removal and the reuse of the system in successive batch cycles. The effects of initial phenol concentration and number of reuse cycles on cumulative phenol removal were analyzed using response surface methodology. Finally, the Haldane–Andrews model was applied to estimate the kinetic parameters associated with microbial growth and substrate inhibition under the validated process conditions.

2. Materials and methods

2.1 Microorganism and growth conditions

Bacillus cereus used in this study was isolated from a donated activated sludge sample and was selected as the microorganism showing the highest tolerance to phenol. *Bacillus cereus* was inoculated in Erlenmeyer flasks containing 50 ml of minimal salt medium (MSM) consisting of 500 mg/L of $\mathrm{NaNO_3}$, 650 mg/L of $\mathrm{K_2HPO_4}$, 170 mg/L of $\mathrm{KH_2PO_4}$, 100 mg/L of $\mathrm{MgSO_4}$, 200 mg/L of yeast extract and 575 mg/L phenol. The cultures were incubated at pH 7.0, 37°C and 180 rpm on an orbital shaker.

2.2 Immobilization technique by encapsulation of *Bacillus cereus* cells.

The *Bacillus cereus* biomass produced in Erlenmeyer flasks containing MSM was encapsulated in PVA-sodium alginate matrix using boric acid as the cross-linking agent. PVA and sodium alginate solutions were prepared at concentrations of 10.5% and 1.5%, respectively, and at a 1:1 volume ratio. The resulting mixture was inoculated with *Bacillus cereus* and added dropwise to a 3.5% boric acid solution containing 2.0% $\mathrm{Ca(OH)_2}$, previously adjusted to pH 7.0. The resulting beads were maintained in the cross-linking solution for 60 min, collected, and washed with sterile water.

2.3 Kinetics of phenol degradation by the immobilized *Bacillus cereus*-PVA-Sodium alginate system.

The immobilized *Bacillus cereus*-PVA-sodium alginate system was inoculated in 250 mL Erlenmeyer flasks containing 50 mL of MSM. Three initial phenol concentrations were evaluated: 500, 750, and 1000 mg/L. The experiments were conducted at 37°C, 180 rpm, and pH 7.0. Samples were collected at 4-h intervals until phenol removal was complete. All experiments were performed in duplicate.

2.4 Reusability of the *Bacillus cereus*-PVA-Sodium alginate immobilization system.

The *Bacillus cereus*-PVA-sodium alginate system was reused in repeated-batch phenol degradation experiments. After complete phenol removal, the MSM was decanted and replaced with fresh sterile medium to initiate a new cycle. This procedure was repeated for consecutive cycles under the same experimental conditions.

2.5 Experimental design and optimization of phenol degradation processes.

A two-factor experimental design was used, considering phenol concentration (X_1) and number of reuse cycles (X_2), resulting in a total of 78 experimental observations. Table 1 presents the levels of both factors and the response variable (Y), defined as cumulative phenol removal performance. Optimization was performed using response surface methodology and the optimization tool in Minitab version 19. The optimal process conditions were determined by maximizing the composite desirability function. The predicted optimal conditions were subsequently validated experimentally.

Table 1
Variables used in full factorial design

Factor	Variable	Level
X_1	Phenol concentration, (mg/L)	500 750 100
X_2	Reuse cycles	13

2.6 Kinetic parameters of the phenol degradation process.

The Haldane–Andrews kinetic model (Haldane, 1965) was used to describe phenol degradation by immobilized Bacillus cereus cells. Experimental data obtained during process validation were fitted to the model shown in Eq. 1, where S_0 represented the initial substrate

concentration ($mg.L^{-1}$), K_s is the substrate affinity constant ($mg.L^{-1}$), K_i is the substrate inhibition constant ($mg.L^{-1}$) and μ_{max} is the maximum growth rate (h^{-1}). These kinetic parameters were estimated using Excel Solver and the nonlinear evolutionary algorithm. The model was solved numerically using Euler's method, as shown in Eq. 2, where (y) represents the new predicted value, (x) is the estimated slope, and (h) is the step size.

$$\text{Haldane } (\mu): \mu_{\max} \frac{S_0}{K_s + S_0 + \frac{S_0^2}{K_i}} \quad \text{(Eq. 1)}$$

$$\text{Euler}: \ y_{i+1} = y_i + f(x_i, y_i) * h \quad \text{(Eq. 2)}$$

2.7 Analytical methods

Phenol removal from MSM by the immobilized *Bacillus cereus*–PVA–sodium alginate system was quantified using the Folin–Ciocalteu colorimetric method (Bray & Thorpe, 1954).

Biomass released into the reaction medium was estimated by protein quantification using the Bradford method. A 1-mL sample of the bacterial suspension was centrifuged at 10,000 rpm for 20 min, and the supernatant was discarded. Subsequently, 500 µL of [reagent] was added to the pellet. The samples were heated for 10 min and centrifuged again at 10,000 rpm for 20 min. Finally, 200 µL of the supernatant was mixed with 1 mL of Bradford reagent, and absorbance was measured at 595 nm (Bradford, 1976).

3. Results and discussion

3.1 Biomass production and Immobilization efficiency of *Bacillus cereus*

The amount of biomass produced from *Bacillus cereus* was 0.97 g. It should be noted that this amount of biomass was obtained from 9 Erlenmeyer flasks of 250 ml containing 50 ml of MSM and 575 mg/L phenol, which is the standard substrate concentration for the *Bacillus cereus* growth. According to the Bradford method, 0.89 g of the produced biomass was immobilized in the PVA–sodium alginate matrix, corresponding to an immobilization efficiency greater than 91%.

3.2 Phenol degradation kinetics by the *Bacillus cereus*-PVA-sodium alginate immobilization system.

Bacillus cereus cells immobilized in the PVA–sodium alginate system were able to achieve nearly complete degradation of phenol at initial concentrations of 500, 750, and 1000 mg/L. As shown in Fig. 1, the degradation percentages obtained with immobilized *Bacillus cereus* cells were 99.78, 99.88, and 99.89% within 36, 42, and 46 h, respectively. In comparison, free-cell controls degraded the same phenol concentrations by 98.05, 99.66, and 99.21% within 18, 22, and 44 h, respectively. Nevertheless, after adaptation to the conditions and composition of the medium, the immobilized cells were able to degrade 500, 750, and 1000 mg/L phenol within 5, 8 and 15 h, respectively.

The phenol degradation performance obtained in the present study was compared with that reported for other bacterial strains and immobilization systems. Table 2 summarizes microorganisms, immobilization supports, initial phenol concentrations, degradation efficiencies, and treatment times reported in previous studies.

Table 2
Phenol degradation by immobilized bacteria immobilized on organic and inorganic supports and their reuse.

Bacteria	Support	Method	Degraded phenol / Reaction time ($\varvec{mg.L^{-1}/h}$)	Repeated cycles (N°)	Reference
Bacillus sp.	Carbonaceous alginate gel	Encapsulation	1600/96	5	Ke et al., (2018)
Bacillus cereus	Calcium alginate	Encapsulation	200/20	20	Banerjee & Ghoshal, (2016)
Bacillus thuringiensis	Sodium alginate	Encapsulation	700/120	7	Ereqat et al., (2018)
Acinetobacter sp	Polyvinyl alcohol	Encapsulation	600/24	10	Jiang et al., (2012)
Acinetobacter sp.	Sodium alginate	Entrapment	1000/72	4	Paisio et al., (2016)
Acinetobacter baumannii	Calcium alginate	Encapsulation	200/20	5	Yadzir et al., (2016)
Rhodococcus sp.	Sodium alginate-bamboo charcoal-chitosan	Entrapment	2000/108	4	Ma et al., (2020)
Pseudomonas putida	Silica – alginate	Encapsulation	700/120	3	Shim et al., (2014)
Sphingomonas sp.	Polyvinyl alcohol - Sodium alginate - Kaolin	Encapsulation	200/22	16	Ruan et al., (2018)
Pseudarthrobacter phenanthrenivorans Sphe3	Calcium alginate	Encapsulation	1000/192	5	Asimakoula et al., (2023)

As shown in Table 2, Yadzir et al. (2016) reported that immobilized *Acinetobacter baumannii* cells degraded 400 mg/L phenol within 44 h, which was longer than the time required by immobilized *Bacillus cereus* cells to degrade 500 mg/L phenol in the present study. Other microorganisms, such as *Bacillus thuringiensis* and Pseudomonas putida, immobilized in sodium alginate and alginate–silica, respectively, required 120 h to degrade 700 mg/L phenol (Ereqat et al., 2018; Shim et al., 2014). Therefore, compared with these microorganisms, the immobilized *Bacillus cereus* cells used in the present study required shorter treatment times to degrade higher phenol concentrations.

3.3 Reusability of the *B. cereus*-PVA-Sodium alginate immobilization system.

Repeated use of *Bacillus cereus* cells immobilized in PVA–sodium alginate resulted in a gradual increase in phenol degradation. After 13 cycles, the cumulative degradation percentage was higher than 1200% for the three phenol concentrations tested: 500, 750, and 1000 mg/L. This value was calculated by adding the degradation percentage obtained in each cycle.

As the Bacillus cereus cells encapsulated in PVA–sodium alginate were reused over successive cycles, their phenol degradation performance became more remarkable compared with that of free cells. As shown in Fig. 2, the encapsulated *Bacillus cereus* cells were reused for 13 cycles at initial phenol concentrations of 500, 750, and 1000 mg/L. The degradation time decreased as the number of cycles reused increased. During the first cycle, the encapsulated cells degraded more than 97% of 500 mg/L phenol within 36 h. By the second cycle, the same degradation efficiency was achieved in less than half of the initial treatment time, and by cycle 13, the treatment time had decreased to only 5 h. From cycle 1 to cycle 13, the removal efficiency for 500 mg/L phenol remained above 97%, with residual phenol concentrations below 15 mg/L.

During the first cycle, the immobilized *Bacillus cereus* cells degraded more than 98% of phenol at initial concentrations of 750 and 1000 mg/L within 42 and 46 h, respectively. This degradation efficiency was maintained during the following 12 cycles. During cycle 13, the immobilized cells degraded to 750 and 1000 mg/L phenol within 12 and 15 h, respectively. In both cases, the residual phenol concentrations were below 10 mg/L. These results are attributed to the protection provided to *Bacillus cereus* cells within the PVA–sodium

alginate matrix. According to Ereqat et al. (2018), bacterial cell immobilization improves phenol degradation because free cells may be unable to degrade high phenol concentrations within short treatment periods. In addition, immobilization facilitates cell recovery and reuse, whereas the reuse of free cells is more difficult. Previous studies have reported that immobilization is an effective alternative for improving the degradation activity of different bacterial genera. Table 2 presents a comparison of the bacterial strains, immobilization materials, phenol concentrations, degradation times, and numbers of reuse cycles reported in previous studies. Banerjee and Ghoshal (2016) indicated that sodium alginate is a highly resistant matrix. When used as an immobilization support for *Bacillus cereus*, the microorganism could be reused for 20 consecutive cycles for the degradation of 200 mg/L phenol. Similar results were reported by Ruan et al. (2018), who used sodium alginate in combination with PVA and kaolin as the matrix to immobilize *Sphingomonas* sp. The immobilized system was reused for 16 consecutive cycles for the degradation of 200 mg/L phenol. Alginate is one of the most widely used materials for bacterial immobilization (Ereqat et al., 2018; Paisio et al., 2016; Yadzir et al., 2016) and, when used in conjunction with other materials, acquires outstanding properties (Ma et al., 2020).

One of the most common combinations is alginate with PVA, a synthetic polymer with high mechanical strength and porosity that allows substrates and oxygen to diffuse through the matrix and reach the immobilized biomass, thereby supporting the degradation process (Wang et al., 2020a; El-Naas et al., 2013). Whatever polymeric material is used as a support for bacterial immobilization, it is important that it is stable and resistant to environmental perturbations to avoid rupture of the polymeric matrix, which may lead to cell release and exposure to the reaction medium (Ereqat et al., 2018). In this study, it is important to note that less than 27% of the total cells initially immobilized in PVA–alginate were released into the reaction medium (data not shown). This result allowed the almost complete degradation of phenol at concentrations of 500, 750, and 1000 mg/L. Therefore, it can be said that the *Bacillus cereus* system immobilized in PVA–alginate is viable for phenol degradation. However, it is necessary to improve the stability of the polymers to maintain a higher percentage of cells immobilized in the polymer matrix and allow their reuse for a longer period.

3.4 Optimization and experimental validation of the phenol degradation process using RSM

By analyzing the experimental data, the optimal conditions of the phenol degradation process were determined. The optimization solutions are shown in Table 3.

Table 3
Experimentally obtained responses at various conditions used in RSM optimization

Implemented solutions	Factor		Response
	X1	X2	Y
1	737.374	13.0000	1286.86
2	997.147	12.9992	1283.00
3	750.000	7.7982	771.91
4	999.288	4.4475	436.57
5	500.514	4.4300	436.57

RSM: response surface methodology; X1: phenol concentration (mg/L); X2: reuse cycles; Y: phenol degradation process yield (%).

The relationship between the factors (X1 and X2) and the response (Y) is represented by Eq. 3.

$$Y = -25.91 + 0.0808\ X_1 + 98.241\ X_2 - 0.000057\ X_1{}^* X_1 + 0.0267\ X_2{}^* X_2 + 0.000265\ X_1{}^* X_2 \quad \text{(Eq. 3)}$$

The model showed a high coefficient of determination (R^2) of 99.9982% and an adjusted coefficient of determination (R^2adj) of 99.9981%, indicating good agreement between the experimental and predicted values.

According to the experimental model, the optimum conditions for phenol degradation by immobilized *Bacillus cereus* were phenol concentrations of 737.37 and 997.14 mg/L and 13 and 12.99 reuse cycles, respectively. The concentration of 737.37 mg/L showed higher performance (Table 3).

The summary of the ANOVA is given in Table 4. The model was significant ($p < 0.05$), showing that it adequately represented the experimental data. The linear terms of X_1 and X_2 were also significant for phenol degradation ($p < 0.05$).

Table 4
ANOVA for the optimization model

Source	Sum of squares	df	Mean square	F value	P value
Model	10662576	5	2132515	281376.92	0.000
Lineal	10662345	2	5331173	703427.03	0.000
X_1	25	1	25	3.36	0.071
X_2	10662320	1	10662320	1406850.71	0.000
Square	228	2	114	15.05	0.000
X_1*X_1	220	1	220	28.96	0.000
X_2*X_2	9	1	9	1.13	0.292
Interaction of 2 factors	3	1	3	0.42	0.518
X_1*X_2	3	1	3	0.42	0.518
Error	546	72	8		
Lack of Fit	125	33	4	0.35	0.999
Pure Error	420	39	11		
Total	10663122	77			
ANOVA: Analysis of variance					

The quadratic model was validated by performing experiments with immobilized *Bacillus cereus* at phenol concentrations of 737.37 and 997.14 mg/L for 13 repeated cycles. Temperature, pH, and agitation were maintained at 37°C, 7.0, and 180 rpm, respectively.

Under these conditions, the cumulative degradation values predicted by the experimental design were 1286.86 and 1283.00% for phenol concentrations of 737.37 and 997.14 mg/L, respectively (Table 3). The values obtained experimentally were 1279.40 and 1288.82%, respectively (data not shown graphically). The comparison between the predicted and experimental values showed good agreement, supporting the validity of the model.

3.6 Kinetic parameters of the validated phenol degradation process.

Immobilization of *Bacillus cereus* in PVA–alginate improved its operational performance during phenol degradation over repeated cycles. The Haldane–Andrews model was used to determine kinetic parameters associated with substrate inhibition (Ki), substrate affinity (Ks), and the maximum specific growth rate (μ_{max}). Table 5 presents the kinetic parameters estimated by nonlinear regression using the evolutionary algorithm.

Table 5
Phenol degradation kinetics parameters using different bacteria at different substrate concentrations.

Immobilized bacterial cells	Kinetic parameters				Concentration range	Reference
	μmax (h^{-1})	Ks (mg/L)	Ki (mg/L)	R^2	(mg/L)	
R. eutropha	0.36	40.48	181.90	0.98	574.00	Nickzad et al., (2012)
P. aeruginosa	0,60	234.00	394.00	-	1200.00	Hasana & Jabeen, 2015
B. subtilis	1.80	206.00	520.00	-	1200.00	Hasana & Jabeen, (2015)
B. lichenformis	0.02	58.40	1619.26	-	2000.00	Chris Felshia et al., (2017)
G. nicotianae	0.37	20.29	268.10	0.98	1117.00	Duraisamy et al., (2020)
B.cereus	0.37	30.76	715.21	0.99	737.37	This studio
B.cereus	0.42	25.65	835.58	0.97	997.14	This studio

As reported in previous studies, the Haldane model is useful for describing microbial growth under substrate-inhibitory conditions, in which the specific growth and degradation rates decrease as substrate concentration increases (Jiang et al 2017). Although various microorganisms, such as bacteria of the genera Pseudomonas and Bacillus, have a high affinity for phenol (K_s), they may also be inhibited as the substrate concentration increases. Hasan and Jabeen (2015) studied the degradation of 1200 mg/L phenol by immobilizing *Pseudomonas aeruginosa* and *Bacillus subtilis*. The kinetic results showed that the highest (Ki) value, 520 mg/L, was obtained for the Bacillus subtilis strain, indicating a higher level of substrate tolerance than the other strain. Similarly, Chris et al. (2017) reported that Bacillus licheniformis was able to tolerate high phenol concentrations of up to 2000 mg/L, with a (Ki) value of 1619.26 mg/L. *Ralstonia eutropha* and *Glutamicibacter nicotianae* have also been reported to degrade 574 and 1117 mg/L phenol, respectively; their degradation activity decreased at 181.90 and 268.10 mg/L, respectively (Nickzad et al., 2012; Duraisamy et al., 2020).

Figure 3a and Fig. 3b show the relationship between the specific growth rate of immobilized *Bacillus cereus* and phenol concentrations of 737.37 and 997.14 mg/L, respectively. The Haldane–Andrews model showed a good fit to the experimental cell-growth data. The estimated kinetic parameters were Ki values of 715.21 and 835.58 mg/L, Ks values of 30.76 and 25.65 mg/L, and μ_{max} values of 0.37 and 0.42 h^{-1} with R^2 values of 0.99 and 0.97, respectively. These results showed that the immobilized Bacillus cereus strain exhibited high tolerance to the phenol concentrations evaluated.

4. Conclusions

Compared with free cells, Bacillus cereus cells immobilized in PVA–sodium alginate showed greater efficiency in the degradation of high phenol concentrations, considering that the immobilized cells were reused over several consecutive cycles. Response surface methodology was successfully applied to optimize the process, and the fitted model showed good agreement between the predicted and experimental values obtained during validation. In addition, the Haldane–Andrews model was used to determine the kinetic parameters of the process, indicating that immobilized cells may experience substrate inhibition when exposed to high phenol concentrations.

Declarations

Competing Interests

The authors have no relevant financial or non-financial interests to disclose.

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Author Contribution

G.E.-M. performed the experimental work and collected the data. J.U.H.-B. contributed to the experimental procedures, statistical analysis, and mathematical modeling. N.B. contributed to the microbiological methodology, process design, interpretation of results, and manuscript review and editing. M.P.L.-E. was responsible for the conceptualization and supervision of the research project, as well as manuscript writing, review, and editing. All authors reviewed and approved the final version of the manuscript.

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Figures

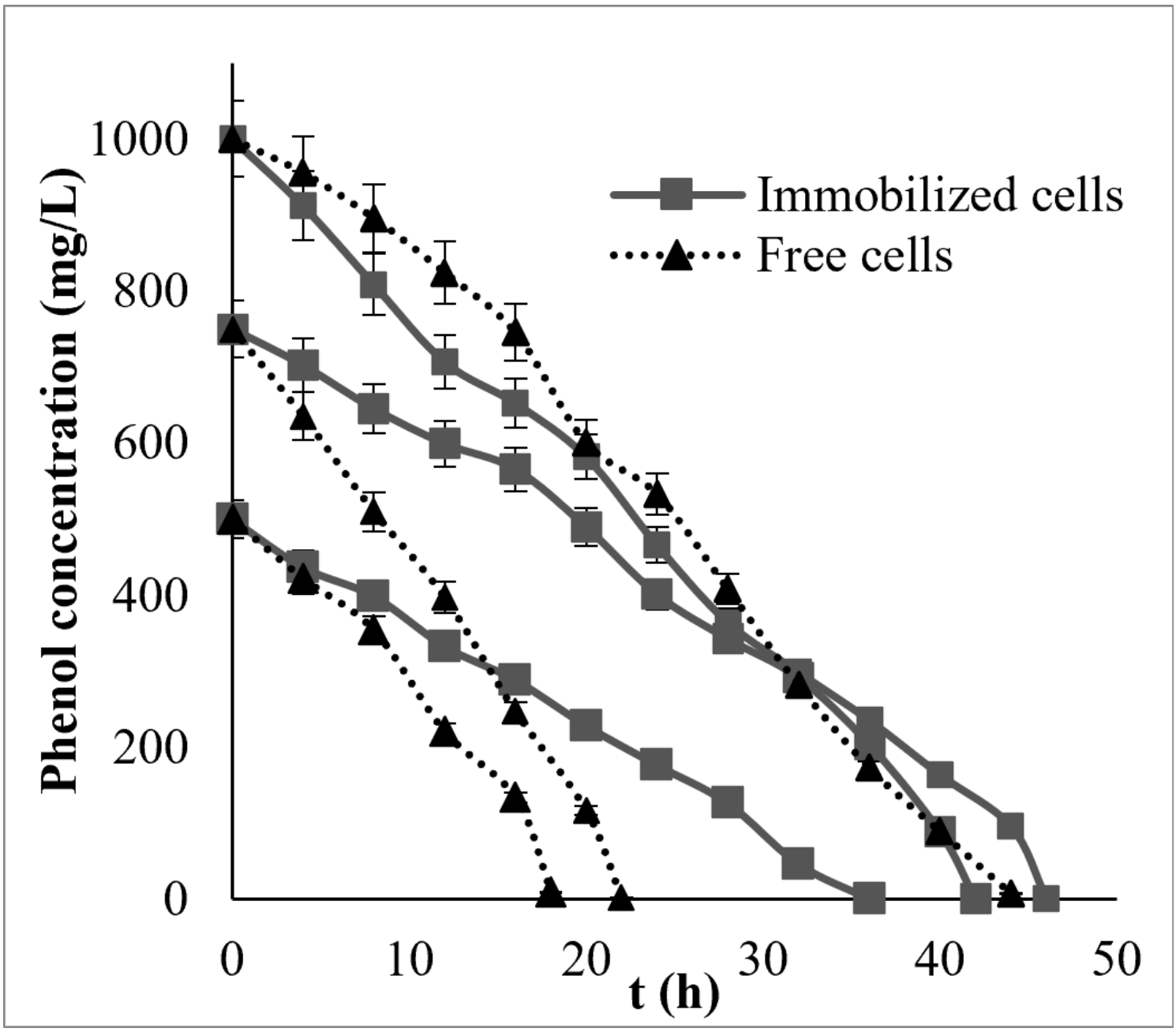
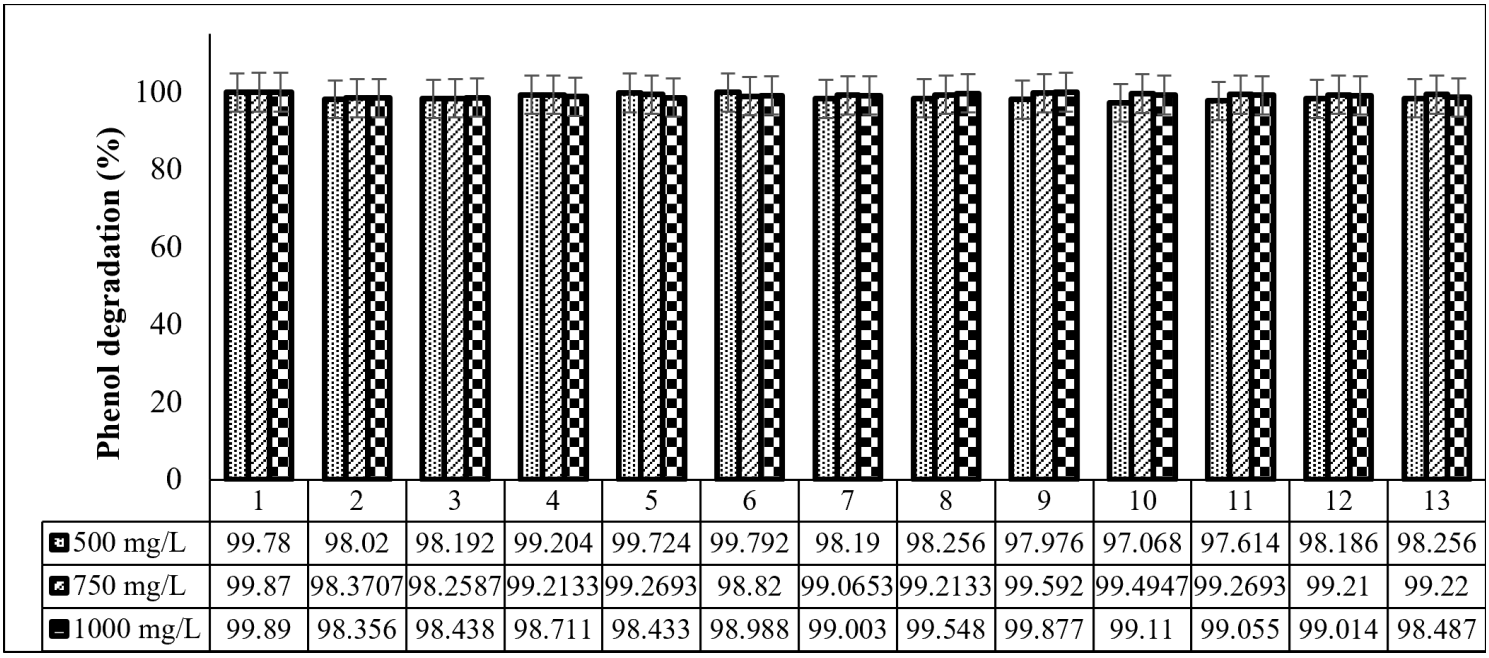


Figure 1

Degradation trajectories of free and immobilized cells



	1	2	3	4	5	6	7	8	9	10	11	12	13
500 mg/L	99.78	98.02	98.192	99.204	99.724	99.792	98.19	98.256	97.976	97.068	97.614	98.186	98.256
750 mg/L	99.87	98.3707	98.2587	99.2133	99.2693	98.82	99.0653	99.2133	99.592	99.4947	99.2693	99.21	99.22
1000 mg/L	99.89	98.356	98.438	98.711	98.433	98.988	99.003	99.548	99.877	99.11	99.055	99.014	98.487

Figure 2

Resue batch cycles according to phenol degradation comparing phenol concentrations of 500, 750 and 1000 mg/L.

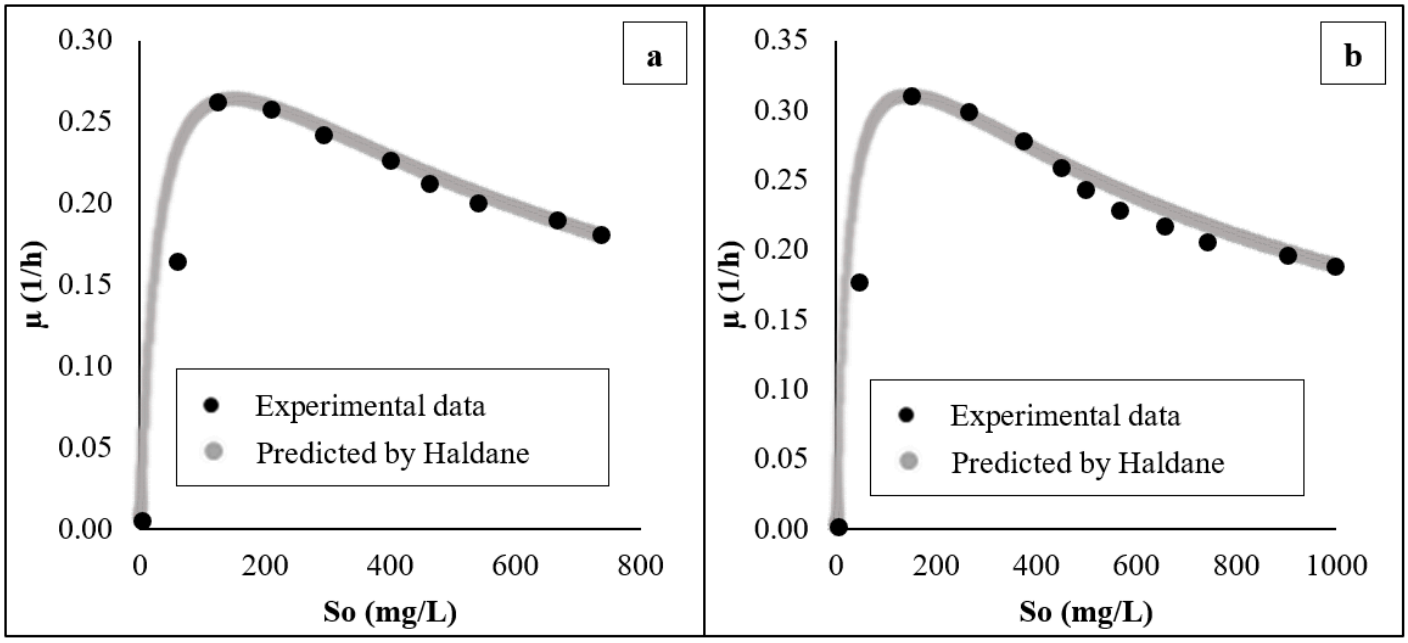


Figure 3

Haldane-Andrees Model adjustment to experimental data of phenol degradation