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Article

Kinetics and Statistical Analysis in Biogas Production: Optimization of *Clostridium welchii* Bioaugmentation of Solid Organic Waste from Shinko

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Abstract: Natural microbial communities in cassava peel (CP), sugarcane waste (SW), and poultry manure (PM) are often inadequate to sustain stable anaerobic digestion (AD) for efficient biogas production. This study employed bioaugmentation with *Clostridium welchii* to improve process stability and biogas production, thereby promoting the valorization of organic wastes generated in Shinko, Adamawa State. CP, SW, and PM were codigested at a 5:4:1 ratio under three conditions: a non-bioaugmented control (X) and two bioaugmented setups (Y and Z) containing 200 and 300 mL of *Clostridium welchii*, respectively. Biogas production over a 40-day digestion period was fitted to the Modified Gompertz, Cone, Fitzhugh, and Logistic kinetic models to estimate kinetic parameters. Model performance across the three bioreactor setups was evaluated using 29 statistical metrics. The maximum experimental biogas yields at day 40 were 1.19, 2.13, and 1.85 m^3/kg for X, Y, and Z, respectively, with predicted values showing close agreement. Among all models, the Modified Gompertz model for setup Y demonstrated the best overall performance, combining the highest biogas yield, the fastest production rate (k), favorable shape factor (n), a short lag phase, and excellent statistical agreement ($R^2 > 0.9992$). Bioaugmentation with 200 mL of *Clostridium welchii* proved the most efficient and stable strategy for codigesting CP, SW, and PM based on all 29 statistical criteria. Overall model performance ranked as Modified Gompertz > Cone > Logistic > Fitzhugh. Moderate bioaugmentation optimized microbial activity, shortened the lag phase, increased biogas production rates, and strengthened the predictive accuracy of the kinetic models.

Keywords: Bioaugmentation; *Clostridium welchii*; Shinko; Biogas optimization; Agricultural waste.

1. Introduction

Shinko is a location in Jimeta-Yola, Adamawa State, Nigeria which boost of significant volume of solid organic waste, including cassava peel (CP), sugarcane waste (SW) and poultry manure (PM). Adamawa State in North Eastern part of the country as a whole, holds significant potential for the production of cassava, sugarcane, and poultry, owing to its favorable climatic conditions, fertile soils, and active agricultural communities. The southern part of Adamawa State is particularly suitable for cassava cultivation [1]. A land suitability analysis using GIS techniques revealed that approximately 65.92% of the area is favorable for cassava farming [2]. Sugarcane farming is a significant agricultural activity in Adamawa State, especially in the Numan Local Government Area [3], [4]. The Dangote Sugar Refinery has implemented an out-grower scheme, supporting over 781 farmers by providing seedlings, fertilizers, and farming equipment. Farmers have reported substantial profits from sugarcane cultivation [5], with some earning over ₦2 million after deductions [6]. Research indicates that poultry farmers in Yola North and Yola South have achieved high resource use efficiency, with a strong correlation between flock size and egg production [7], [8]. However, the potential, benefit and profits realized often and eventually results in negative environmental side effect in those locations (Shinko in particular). Oghenejoboh *et al.* [9] and Ogwu *et al*. [10] have previously suggested sustainable means to curb cassava waste in Nigeria; Dan Abba *et al.* [11] show how ensiling SW could improve Yankasa ram diet in north-central Nigeria; while Adeoye *et al.* [12], Adedayo [13], Akanni & Benson [14] and Abah *et al.* [15] describe some poultry waste management strategies implementable on farms in Minna, Lagos Ogun and Imo states, respectively. AD using specific or feedstock-integral microbe is a good candidate for solid organic waste minimization. Extent of search reveals no prior study on mono- or co-digestion of CP, SW and PM to solve their waste challenges via biogas digestion in Adamawa State. But few case studies have been carried out on similar waste elsewhere in the country, namely: biogas from cassava from Ilaro in Ogun state [16], [17]; AD of cow dung, sugarcane bagasse and chicken droppings from Katsina metropolis for biogas production [18] and; biogas from chicken manure from Maiduguri, Borno state [19].

The combined utilization of cassava peel, sugarcane waste, and poultry manure through anaerobic codigestion offers important technical advantages over the digestion of individual substrates. Cassava peel and sugarcane waste are rich in biodegradable carbohydrates but generally possess relatively high carbon content and limited nitrogen availability, whereas poultry manure provides nitrogen, buffering capacity, and indigenous anaerobic microorganisms that help maintain microbial stability during digestion. Consequently, codigestion of these feedstocks is expected to improve the overall anaerobic digestion performance and enhance biogas production while simultaneously addressing multiple agricultural waste streams.

Besides maximizing biogas yield, understanding the kinetics of anaerobic digestion is equally important because kinetic models provide quantitative information on biogas production behavior, lag phase, cumulative biogas potential, production rate, and overall reactor performance. Such models facilitate process optimization, reactor design, and scale-up, thereby supporting the practical implementation of anaerobic digestion technologies for sustainable waste management.

Modified-Gompertz, Logistic, Fitzhugh, and Cone models are commonly used kinetic models to describe biogas production from organic materials. Because they can predict the rate and volume of biogas generated during anaerobic digestion (AD). Among them, Modified-Gompertz model is widely used because it accurately fits cumulative biogas production data. It considers the maximum biogas potential, the maximum production rate, and the lag phase. The time taken before biogas production starts and how fast it reaches its peak, can be predicted using Modified-Gompertz model. Logistic model is also used to describe the growth pattern of biogas production, as it assumes that the rate of biogas formation increases at first, then slows down as it approaches a maximum limit. In systems where the production follows an S-shaped curve over time, Logistic model finds better application. Thirdly, Fitzhugh model is a simple kinetic model that describes the rate of biogas production using two main parameters. It is easy to apply and is useful for comparing different substrates or digestion conditions. Although it is less detailed than the Gompertz model, it gives a good overview of biogas behavior. Cone model on the other hand, is based on first-order kinetics with a shape factor that adjusts the curve to better fit experimental data. The model assumes that biogas production is influenced by the biodegradable content and includes a factor that reflects how easily the substrate can be digested. Cone model is especially useful when the substrate is not uniform. Unknown parameters in the aforementioned biogas kinetics models can be determined using Excel Solver [20], [21], SigmaPlot [22], MATLAB [23], GraphPad Prism [24], R toolbox [25], Wolfram Mathematica [26], Maple [27] and particle swarm optimization and genetic algorithm [28], via nonlinear regression [29]. Sometimes, the microorganism involved in AD biogas production have to be isolated [30].

Although numerous studies have investigated anaerobic digestion of agricultural residues, the reported performance remains highly dependent on substrate composition, microbial community structure, and operational conditions. Consequently, bioaugmentation has increasingly attracted attention as a promising strategy for accelerating substrate hydrolysis, shortening the lag phase, improving process stability, and enhancing methane or biogas yield.

The addition of the isolated or specific microorganism to increase efficiency in biogas production is termed bioaugmentation [31], [32]. Important microorganisms used in bioaugmentation include *Methanosaeta*, *Methanosarcina*, *Bacillus subtilis* and *Pseudomonas spp*. *Clostridium welchii* belongs to the group of anaerobic, spore-forming bacteria that thrive in oxygen-free environments and another beneficial bacterium in the bioaugmentation of biogas production, especially during the codigestion of CP, SW, and PM. It is known for its strong hydrolytic and fermentative abilities and the ability to break down complex carbohydrates, proteins, and fibers present in solid organic waste (e.g., agricultural and animal wastes). No prior study reported the use of *Clostridium welchii* in bioaugmented production of biogas, especially using the described kinetic models from any of the aforesaid biowaste. Bioaugmented CP for AD production of biogas have not been studied, apart from those on sugarcane bagasse and chicken manure, using *Pseudomonas sp.* [33] and *Methanothrix* [34], respectively.

Furthermore, existing studies have primarily investigated either individual substrates or conventional microbial inocula, while comparative evaluations involving

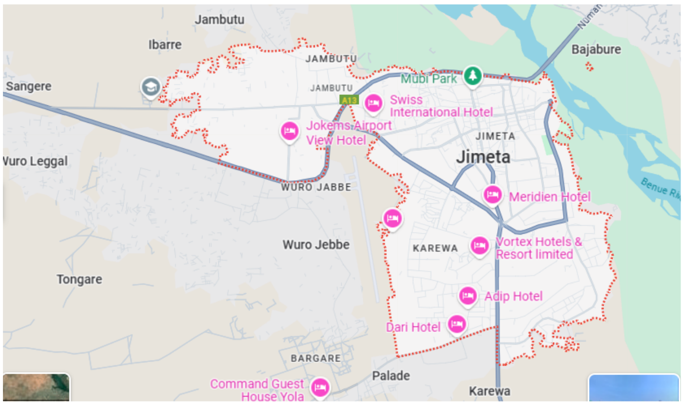

Figure 1. Map of Jimeta-Yola, Nigeria.

Clostridium welchii together with multiple kinetic models remain largely unavailable. To the best of our knowledge, no previous study has comprehensively evaluated the bioaugmentation of cassava peel, sugarcane waste, and poultry manure using Clostridium welchii while simultaneously comparing the predictive performance of Modified-Gompertz, Logistic, Fitzhugh, and Cone kinetic models. This unresolved gap limits the understanding of whether bioaugmentation can simultaneously improve digestion stability, biogas productivity, and kinetic predictability for these abundant agricultural wastes. The use of *Clostridium welchii* to augment the production of biogas in this study, represents a novel approach. Non-bioaugmented (X) and two bioaugmented setups (Y and Z) were compared in terms of their biogas kinetic parameters and maximum biogas potential for the codigestion of CP, SW, and PM charged at 5:4:1 (weight proportion).

Accordingly, this study contributes to the existing literature in three aspects. First, it evaluates the feasibility of employing Clostridium welchii as a bioaugmentation agent for the codigestion of cassava peel, sugarcane waste, and poultry manure. Second, it systematically compares four widely used kinetic models to identify the most suitable model for describing the digestion process. Third, it provides a comprehensive evaluation based on 29 statistical metrics to support the optimization of bioaugmentation strategies for sustainable agricultural waste management and renewable energy production.

The objective is to determine the optimum biogas recovery as supported by several examined statistical parameters, correlated plots or fit statistics. Bioaugmentation optimization has been reported to increase methane yield by 20.7%, according to Lee *et al.* [35]. As a solution to municipal solid waste discussed by Asif *et al.* [36] and Asif *et al.* [37], this study assesses the possibility of eliminating CP, PM and SW that currently litters Shinko, which may be a guide to future waste management strategy in Nigeria.

The remainder of this paper is organized as follows. Section 2 describes the materials, experimental procedures, kinetic models, and statistical evaluation methods. Section 3 presents and discusses the experimental results, kinetic analysis, and model performance comparisons. Finally, Section 4 concludes the study by summarizing the major findings and discussing their implications for sustainable agricultural waste management.

2. Materials and Method

2.1. Food Waste Material Collection

Agricultural residues and/or solid organic waste (i.e., CP, SW and PM) were collected from a dump site in Shinko, Jimeta-Yola, Adamawa state of Nigeria (Figure 1). The collected organic samples were used in this study as feedstock for AD for the production of biogas. Exactly 200g of CP, 160g of SW and 40g of PM was used for the AD. The biodegradable waste materials were collected, sorted, and shredded into smaller pieces to enhance their surface area and reactivity.

2.2. Inoculum Sourcing

Anaerobic microorganisms are often responsible for the conversion of the nutrients inherent in the feedstock to various gases, culminating in the formation of biogas [38]. Since the selection of CP, SW and PM, forming blend that is rich in carbon-to-nitrogen (C/N) ratio provides the required mineral nutrient, *Clostridium welchii* was added to contribute to the decomposition process. Before then, *Clostridium welchii* was prepared following a procedure described in Abubakar *et al.* [39]. A media composed of 10g protease peptone, 3g yeast extract, 3g starch, 0.1g $MgSO_4$, 67g $Na_2HPO_4.12H_2O$, 1 L water and 15g agar, was obtained. The media was streamed briefly and adjusted to a 7.8 pH with 1 N sodium hydroxide (NaOH) in tubes, boil to dissolve, to melt the agar and other chemicals. About 1g each of all soil sample collected from Shinko in Jimeta, Yola, Nigeria, was dissolved in 10 mL sterile water. It was then sieved vigorously and allowed to stand on the test tube rack for a period of 30 min. Next, 28g of dehydrated powder of nutrient agar was dissolved in 1000 cm^3 of distilled water (in a flask). The mouth of the flask was then covered with non-absorbent cotton wool and aluminum foil paper with masking tape. They were allowed to dissolve evenly by warm temperatures on Bunsen burner flames. It was later dispensed in an adequate amount of 10 mL to curved culture bottle. Subsequently, it was sterilized by autoclave method at a temperature of 121°C per 1.1 kPa pressure for a holding time of 15 min. For the inoculation of all liquid soil samples at 10^{-3} serial dilution, it was incubated at 37°C for 24 h to serve as maintenance medium for the experimental work. This medium was later used to induce spore formation in *Clostridium welchii* during AD, after Table 1 was used to identify and qualify it.

It is important that the inoculum should be adequate. Therefore 0.5 mL of an actively growing nutrient broth was introduced with a pipette to the Ellner's medium and incubated in anaerobic jar at 37°C. Because Lovato *et al.*

Figure 2. Biogas Production Setup for Bioaugmentation.

Table 1. Biochemical test.

Test Name	Results
Grams strain	+
Shape; Thick rod of bacilli of oval shape	
Sacharolytic activity +++	+++
Lactose +	+
Gelatine +	+
Proteolytic enzymes -	-
Phospholytic activity +	+
Lipase -	-
Indole -	-
Urea -	-
Anaerobic growth	±
Motility -	-
Flagela -	-
Glucose +	+
Sucrose +	+
Acid +	+
Gas +	+
Spore +	+
Starch +	+
Toxins +++	+++

Table 2. Existing Biogas Kinetic Models Employed.

S/No.	Model	Equation	Unknown Parameters
1.	Modified-Gompertz	$V_t = V_{max} \exp\left\{-e^{\left[\frac{k.e}{V_{max}}(\lambda-t)+1\right]}\right\}$	V_{max}, k & λ
2.	Logistic	$V_t = \frac{V_{max}}{1+e^{\left[\frac{4k(\lambda-t)}{V_{max}}+2\right]}}$	V_{max}, k & λ
3.	Fitzhugh	$V_t = V_{max}\left[1-e^{(-kt)^n}\right]$	V_{max}, k & n
4.	Cone	$V_t = \frac{V_{max}}{1+(kt)^{-n}}$	V_{max}, k & n

[40] state that bio augmentative group is separately grown under definite conditions, to accomplish the anticipated purpose in the target environment.

2.3. Feed Characterization

A mixture of CP, SW and PM was blended and the pH and moisture content determined using pH and oven, respectively. The goal was to take advantage of the organic material blend which is rich in cellulose, hemicellulose, lignin, sugars, organic acids, and fiber contents, thereby creating an ideal environment for microbial growth.

2.4. Instrumentation and Equipment

Three 4000 mL plastic container each was adopted as the anaerobic digester, that is attached or connected to a biogas bag/tube via a pipe. As explained by Circone *et al.* [41], a flowmeter fixed on the pipe can be used to measure the flow of the gas. To create an oxygen-free environment, a rubber plug was used for sealing the digester. On the digester surface is a valve for collecting liquid sample (organic waste slurry) for analysis. To kick start the process, the mixture (CP: SW: PM = 200:160:40g) was slurrified using 2 L of water and *Clostridium welchii* inoculum was added, before subjecting it to a though stir. Figure 2 displays the setup, consisting of 1 control digester (X) and 2 other digesters inoculated with 200- (Y) and 300-mL (Z) *Clostridium welchii*, respectively. Ozbayram *et al.* [42] bioaugment wheat straw with cow and goat rumen in digester systems, in similar fashion.

Throughout a period of 40 days, the biodigester was allowed to be acted upon by the microorganism at an ambient temperature between 25-35^oC, almost outside the mesophilic range employed by Das & Mondal [43]. At 2 days interval, the biogas produced was collected via the

Table 3. Statistical Metrics Used to Assess Model Fitting.

Category	Metric Example	Full Meaning	Description
Goodness-of-Fit Metrics	R^2	Coefficient of Determination	Measures how well the model explains the data
	Adj. R^2	Adjusted R^2	Corrects for the number of parameters to avoid overfitting
	RMSE	Root Mean Square Error	Measures the average error magnitude
	SSE	Sum of Squared Errors	Total squared difference between observed and predicted values.
	MSE	Mean Squared Error	SSE divided by the number of observations.
	MAE	Mean Absolute Error	Measures average absolute error magnitude
	MSPE	Mean Squared Prediction Error	Measures prediction accuracy.
	Bias	-	Systematic deviation of predictions from actual values.
Model Selection Criteria	AIC	Akaike Information Criterion)	Penalizes models with too many parameters.
	BIC	Bayesian Information Criterion	Similar to AIC but with a stronger penalty for complexity.
Error and Residual Analysis	SEE	Standard Error of Estimate	Measures data spread around the regression line.
	DW	Durbin-Watson Statistic	Detects autocorrelation in residuals.
	Shapiro-Wilk Test	-	Checks for normality of residuals
Parameter Significance Tests	t-test for Parameters	-	Determines if model parameters are statistically significant.
	CI	Confidence Intervals for Parameters	Shows the range within which parameters likely fall.
	F-statistic	ANOVA test	Tests the overall significance of the regression model
Additional Regression Metrics	Breusch-Pagan test	Heteroscedasticity Test	Checks if residual variance changes over time.
	VIF	Variance Inflation Factor	Detects multicollinearity between independent variables.
	PI	Prediction Interval	Gives a range where future observations are expected to fall.
Additional Error Metrics	MAPE	Mean Absolute Percentage Error	Measures prediction error as a percentage.
	MdAPE	Median Absolute Percentage Error	More robust version of MAPE.
	GMER	Geometric Mean Relative Error	Alternative to MAPE, handling extreme values better.
	Theil's U	Theil's U-statistic	Measures predictive accuracy compared to a naive model.
Outlier and Influence Diagnostics	Cooks-D	Cook's Distance	Identifies influential data points affecting the model.
	LV	Leverage Values	Detects extreme values in independent variables.
	DFFITS/Dfbeta	Difference in fit(s)	Measures how much each data point influences model predictions.
Model Stability & Predictive Power	CV	Cross-validation Error	Assesses model performance on unseen data.
	PRESS	Prediction Sum of Squares	Evaluates predictive accuracy
	RR	Relative Residuals	Helps assess systematic bias in model predictions.

Table 4. Effect of RT on Biogas Yield from Augmented and Non-bioaugmented Digester

RT (day)	X (g)	Y (g)	Z (g)
1	0	0	0
3	0	10	25
5	45	50	75
7	50	125	100
9	75	137	105
11	85	147.5	125
13	100	147.5	127
15	100	147.5	135
17	105	175	135
19	125	177	139
21	125	177	140
23	109	177	140
25	104	165	152
27	89	157	150
29	80	155	140
31	45	139	130
33	45	100	90
35	45	85	77
37	15	85	77
39	15	56	50
40	15	37	20

valve and rubber plug and measured. At the same time, the pH fluctuates between 6.5-7.5 over the digestion period. It was agreed to as the optimal for *Clostridium spp.* growth, almost in accordance with values reported in Ruusunen *et al.* [44].

2.5. Biogas Kinetic Study

The respective weights X, Y and Z of biogas obtained for all RTs were converted to volume using a biogas density of 1.15 kg/m³ reported in Emetere *et al.* [45]. Given that the biogas models in Table 2 works with cumulative biogas volume (V_t) as dependent variable, the volumes were converted to the cumulative value and regression analysis was conducted to determine their unknown parameters in the last column.

Where: V_t – represents maximum/cumulative biogas yield at digestion time, t (m³/kg); V_{max} – maximum biogas production (m³/kg); k – biogas production rate (day^{-1}); λ– lag phase (day); n = shape factor (dimensionless) and; t (or RT) – hydraulic retention time (day). Biogas kinetic models in Table 2 were curled from Abubakar *et al.* [46]. The method was also adopted from the aforementioned research.

2.6. Evaluation of Statistical Parameters

The statistical metrics evaluated in this study can be categorized into 5. Namely, Goodness-of-Fit Metrics, Model Selection Criteria, Error and Residual Analysis, Parameter Significance Tests, Additional Regression Metrics, Additional Error Metrics, Outlier and Influence Diagnostics and Model Stability & Predictive Power, as detailed in Table 3. Most of the metric example in Table 3 are also studied in Atchadé & Paul [47].

In this study, an R program employing the following packages: *nls, minpack.lm, nlme, drc, stats, car, Metrics*, was employed because it is free and widely used in academia [48]. Also, R gives a strong visualization and residual analysis.

3. Results and Discussion

3.1. Measured pH and Moisture Content

Solid organic waste from Shinko dump site has high moisture content of between 70-80%, ideal for *Clostridium spp.* growth. The pH of the waste is 6.7, which is suitable for the acid-tolerant *Clostridium welchii*. It is worthy of note that if microbial fermentation leads to excessive acidification (pH dropping to < 6.5), methanogenic bacteria may become inactive, causing a sudden drop in methane production.

3.2. Weights of Biogas Produced

Biogas from the controlled reactor is tagged 'X', while the bioaugmented vessel with 200 mL is named 'Y' and that with 300 mL 'Z'. Note that, X, Y and Z stands for weight measured at a specific retention time (RT) during AD, as shown in Table 4. Recording the biogas yield at 2 days interval or less or higher will have effect on subsequent nonlinear regression study to determine the kinetic parameters [49]. Even though shorter interval (i.e., 1 or 2 days) may introduce more fluctuations, more frequent data points enable the models to capture transient changes in the biogas production process. If the RT interval is > 2 days (as in Table 4), rapid changes in biogas production might not be well captured, affecting the ability of models to predict λ, maximum production rates (V_{max} & k), and degradation patterns.

Fewer data points (due to large t interval > 2 days or more: say ≥ 4 days) mean that the model has less information and potentially leads to less accurate curve fitting, causing what is called smoother model output. The model may still fit the data, but it could oversimplify the trends, and become less reliable for process optimization. Since Logistic model assumes a sigmoidal biogas production pattern, missing early or late-stage changes could impact predictions. Also, due to the fact that Fitzhugh model assumes an exponential decay pattern, fewer points (< 21 recorded herein – Table 4) could lead to poor fitting of the decay constant (k). Based on Figure 3, the control digester (X) without *Clostridium welchii* showed a slower biogas yield, reaching a peak weight of approximately 125g by day 19 and maintaining similar values until day 23 before declining. Excessive ammonia production from protein degradation of the CP+SW+PM feedstock could raise the pH too high (> 7.5), also inhibiting microbial activity. This never occurred as the average pH was 6 for most of the setups. A decrease from

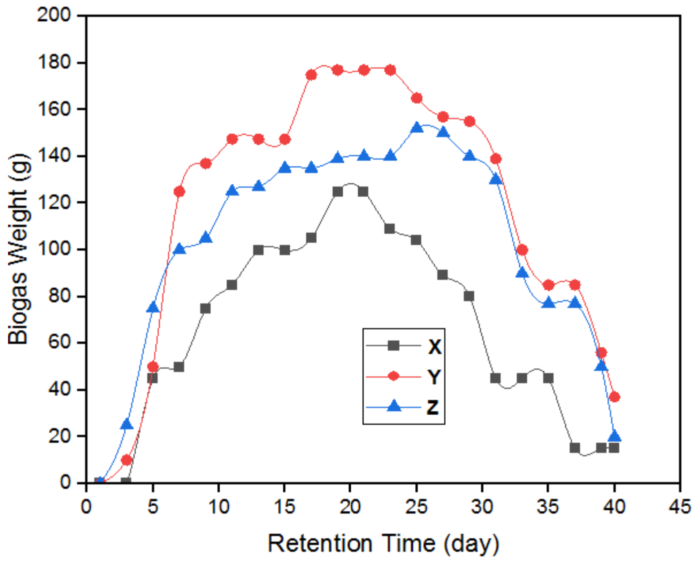

Figure 3. Biogas Production Trend of X and Bioaugmented Digester (Y & Z) with RT.

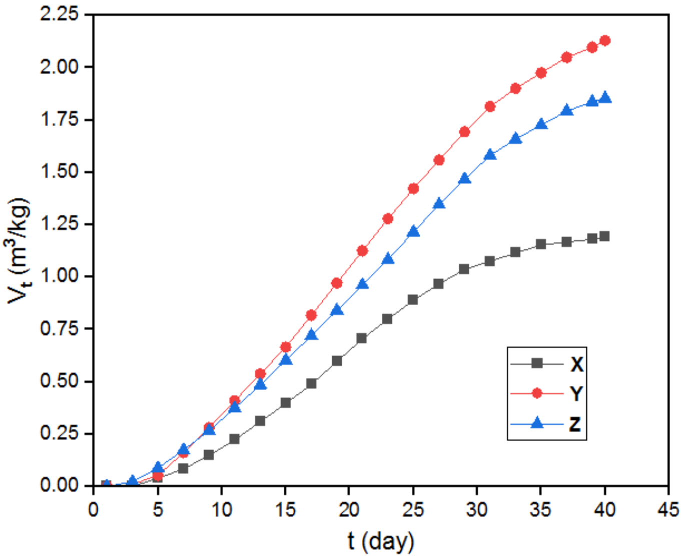

Figure 4. Comparison of V_t Versus RT for Controlled and Bioaugmented Data.

Table 5. Calculated V_t for Nonlinear Regression Analysis with Biogas Models.

t (day)	V_t (m³/kg)		
	X	**Y**	**Z**
1	0	0	0
3	0	0.008696	0.021739
5	0.039130	0.052174	0.086957
7	0.082609	0.160870	0.173913
9	0.147826	0.280000	0.265217
11	0.221739	0.408261	0.373913
13	0.308696	0.536522	0.484348
15	0.395652	0.664783	0.601739
17	0.486957	0.816957	0.719130
19	0.595652	0.970870	0.840000
21	0.704348	1.124783	0.961739
23	0.799130	1.278696	1.083478
25	0.889565	1.422174	1.215652
27	0.966957	1.558696	1.346087
29	1.036522	1.693478	1.467826
31	1.075652	1.814348	1.580870
33	1.114783	1.901304	1.659130
35	1.153913	1.975217	1.726087
37	1.166957	2.049130	1.793043
39	1.180000	2.097826	1.836522
40	1.193043	2.130000	1.853913

45-15, 56-37 and 50-20g towards the end of the process in X, Y and Z, respectively, is indicative of the fact that the nutrients inherent in the feed have been consumed by *Clostridium welchii*.

The bioaugmented setups demonstrated significantly higher biogas generation. Setup Y (200 mL of *Clostridium welchii*) exhibited a faster increase in biogas weight, surpassing the control setup by day 3 and reaching its maximum recorded weight of 177 g between days 19 and 23, before gradually declining thereafter. Setup Z (300 mL of *Clostridium welchii*) followed a similar trend but achieved a peaked biogas weight (152g) by day 25, indicating that higher inoculum volumes enhanced production efficiency but not necessarily proportionally. Nevertheless, bioaugmentation improved the biogas yield, with setup Y being more effective in sustaining higher production over a longer period compared to setup Z. The results suggest that while increasing the inoculum weight enhances microbial activity, an optimal level exists beyond which additional *Clostridium welchii* may not significantly improve biogas production (Y=37g & Z=20g.

3.3. Cummulative Biogas Yield for X, Y and Z Setups

Obviously, the maximum biogas yield (V_t) attained by each setup was 1.193 m³/kg for X (controlled setup), 2.13 m³/kg for Y (augmented setup), and 1.854 m³/kg for Z (augmented setup), all at 40 days. The augmented setups, Y and Z, significantly outperformed the controlled setup, with Y achieving approximately 79% higher yield than X, while Z achieved around 55% higher yield than X. Among the setups, Y demonstrated the highest biogas production efficiency, as it reached 2.13 m³/kg (Table 5), demonstrating the effectiveness of the bioaugmentation strategy.

The trend in all setups shows an initial lag phase (≥ 6 days), followed by an exponential increase in gas production, and a gradual plateau as the biodegradable organic matter is depleted. This suggests that the nutrient composition of CP, SW, and PM provided sufficient carbon and nitrogen for microbial growth, but the efficiency of conversion was strongly influenced by microbial activity, which

Table 6. Computed Kinetic Parameters from Each Biogas Model.

Model	Parameters	Value		
		X	Y	Z
Modified-Gompertz	V_{max} (m^3/kg)	1.2975	2.4551	2.2242
	k (/day)	0.0532	0.0809	0.0671
	λ (day)	7.4321	6.8837	6.3309
Logistic	V_{max} (m^3/kg)	1.2010	2.1820	1.9420
	k	0.0572	0.0882	0.0735
	λ (day)	8.6910	8.3770	7.9230
Fitzhugh	V_{max} (m^3/kg)	1.2820	2.3210	2.0560
	k	0.0690	0.0660	0.0640
	n	1.4740	1.4280	1.3950
Cone	V_{max} (m^3/kg)	1.4120	2.9550	2.8710
	k	0.0481	0.0388	0.0346
	n	2.7723	2.2456	2.0219

was enhanced in the augmented setups. In this case, they are ranked in the following way in terms of efficiency: Y > Z > X, as shown in Figure 4. Similar trend (as in Figure 4) was presented by Achinas & Euverink [50].

At RT = 40 days, V_t of X, Y and Z in Table 5 corresponds with the peak points in Figure 4. Ozbayram *et al.* [42] achieved an improved biogas recovery at 30 days RT. To determine the energy equivalent of the biogas produced by X, Y, and Z, we consider that 1 m^3 of biogas with 60% methane content has an energy value of approximately 22 MJ (megajoules) or 6.1 kWh. Given the biogas yields of 1.19 m^3/kg (X), 2.13 m^3/kg (Y), and 1.85 m^3/kg (Z), their respective energy equivalents are approximately 26.18 MJ (7.26 kWh), 46.86 MJ (13.02 kWh), and 40.7 MJ (11.31 kWh). Among the three setups, Y exhibits the highest biogas yield and energy output. For large-scale electricity production, maximizing biogas yield is crucial, and therefore, the approach used in setup Y should be recommended.

3.4. Kinetic Parameters

It is obvious that bioaugmentation reduced the lag phase from 7.43 or 8.69 days in X setup to lower digestion periods in Y and Z, as given by λ estimate from modified-Gompertz and Logistic models, respectively. This is almost an exact half of λ obtained by Abubakar *et al.* [51] during AD of chicken manure only. Rate constant, k tells us how fast biogas is produced. A higher k means faster gas production. From the study, the Modified-Gompertz and Logistic models had the highest k values in the bioaugmented digester Y, with values of 0.0809/day and 0.0882/day, respectively. This means biogas was produced faster in setup Y where 200 mL of *Clostridium welchii* was added. 'Y' values were higher than those of the control setup (X) and the more heavily inoculated setup Z. The shape factor **n** helps describe how the biogas production curve looks, as it shows how the gas generation rate changes over time—whether it rises quickly or slowly and how it tapers off. For the shape factor n, the Cone model gave the highest values, especially in the control digester X (n = 2.7723), which shows a sharper rise and slower decay in gas production. However, n was lower in bioaugmented setups Y (n = 2.2456) and Z (n = 2.0219), suggesting smoother and more balanced biogas generation with bioaugmentation. Achinas & Euverink [50]'s values of 'n' are quite in the same range with the current study. Table 6 gave the biogas potential of X, Y and Z, calculated by based on the 4 models.

For the Cone model, the V_{max} values were the highest among all models, with 2.955 m^3/kg for Y and 2.871 m^3/kg for Z, while X had 1.412 m^3/kg. Ranking the models based on V_{max} values across all setups gives: Cone > Modified-Gompertz > Fitzhugh > Logistic. When considering bioaugmentation, the bioaugmented setup Y had the highest V_{max} in all models, showing it was the most effective. Setup Z also performed better than the control (X), but not as much as Y. The control setup X had the lowest V_{max} in every model. So, in terms of digestion strategy: Y (bioaugmented with 200 mL *Clostridium welchii*) > Z (300 mL) > X (no bioaugmentation). This means moderate bioaugmentation was better than no bioaugmentation or even higher dosage. Based on the overall parameters estimated from the models, the Modified-Gompertz model is the best. It gave high V_{max} values, especially for the bioaugmented setup Y, showing strong biogas production. It also had the highest k, meaning faster gas generation. In addition, the lag phase λ was shorter in the bioaugmented setups, especially in Z, which shows that biogas production started earlier. Therefore, it is the most reliable and accurate model for describing biogas production from the codigestion of CP, SW, and PM using *Clostridium welchii*.

3.5. Estimated Statistical Parameters and Fit Plots

The accuracy of the kinetic parameter values in Table 6 is dependent on the quality of the data as well as the statistical estimates. Under the Modified-Gompertz model, setup Y is the best because it has the lowest RMSE (0.0200), SSE (0.00843), MSE (0.000401), MAE (0.0156), MSPE (0.000419), MAPE (2.73×10^{14}), and MdAPE (0.01127), compared to setups X and Z. For the Logistic model, setup Y also performs better with slightly lower RMSE, SSE, MSE, MAE, MSPE, and MdAPE compared to the others. In the Fitzhugh model, setup X gives better error values (lower RMSE, SSE, MSE, MAE) than Y and Z. Therefore, X is better under Fitzhugh as confirmed by the RMSE bar chart in Figure 5. But under the Cone model, setup Y is the best with the lowest RMSE (0.0182), SSE (0.006963), MSE (0.000332), MAE (0.0160), MSPE (0.000346), MAPE (2.48×10^{14}), and MdAPE (0.01024). Similar MAE values were reported by Alharbi & Alkathami [52], compared to current study. The overall best setup and model combination is Setup Y under the Modified-Gompertz model. It consistently shows the lowest error and highest fitting accuracy across most key

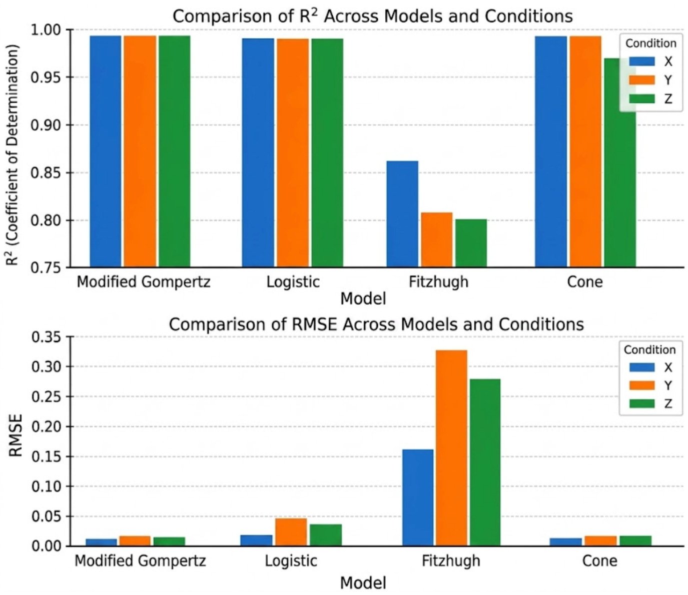

Figure 5. Bar Chart Comparative Representation of R^2 and RMSE from the Biogas Models.

statistical indicators. Figure 5 is also supportive of the fact that setup Y under the Modified-Gompertz model has the highest R^2 (0.999280) and adjusted R^2 (0.999200) among all setups and models, hence the best fit – also in consonance with Deepanraj *et al.* [53].

Many other statistical parameters used to analyze the findings herein are reported in Table 7. When considering Bias, lower values mean better accuracy [54]. For Bias, Modified-Gompertz model has the smallest values across X, Y, and Z setups (e.g., 0.00113 for Y), meaning its predictions are very close to actual values. Logistic model also has low Bias but slightly higher than Modified-Gompertz. Fitzhugh and Cone models have much higher Bias, especially for setups Y and Z. Looking at AIC and BIC, lower values are better because they show a better model with fewer penalties for complexity. Modified-Gompertz has the most negative AIC and BIC values (for example, AIC = –158.231 for Y), followed by Cone. Logistic and Fitzhugh models show higher (less negative) AIC and BIC, meaning they are less preferred. For SEE, smaller values mean the predictions are close to the data points [55]. Again, Modified-Gompertz has the lowest SEE values across setups, with setup Y being particularly low (0.02164). Cone model is close but not better than Modified-Gompertz, while Fitzhugh shows the highest SEE. DW checks for autocorrelation in residuals. Values around 2 are ideal, as reported by Yusuf *et al.* [19] for chicken manure AD. All models have low DW values (< 1), showing strong positive autocorrelation, but Modified-Gompertz has relatively higher DW values compared to others (e.g., 0.5116 for Y), suggesting it is slightly better in handling residual patterns. For *W*-statistics from Shapiro-Wilk Test, values closer to 1 indicate that the residuals are normally distributed [56]. Modified-Gompertz and Cone models have higher W-values (close to 0.98–0.99), showing that their errors are more normally distributed. Logistic and Fitzhugh have lower W-values, especially under bioaugmented setups. A very low RR = 0.0114 aligns with the least systematic bias portrayed by Modified-Gompertz setup Y, as well as its higher t-values (i.e., 28.7) corresponding with statistically significant estimates.

When examining the CI widths, wider intervals imply greater uncertainty around the estimated parameters [57]. It is clear that the Fitzhugh model has the widest CI, especially under setups Y and Z (e.g., ±0.231 and ±0.194, respectively), indicating a lack of precision and a poor model fit. In contrast, Modified-Gompertz and Cone models maintain narrower CI ranges, reflecting better reliability in parameter estimation. Turning to the F-statistics, high F-values suggest that the model explains much of the variability in the data [58]. The Fitzhugh model again performs poorly, with very low F-statistics (e.g., 91 and 88 for Y and Z), compared to over 800–1000 for Modified-Gompertz and Cone models. This low F-statistic for Fitzhugh shows that it lacks overall model significance. The p-values from the Breusch-Pagan test further reveal weaknesses: a lower p-value (< 0.1) suggests the presence of heteroscedasticity, which is undesirable [59]. In Fitzhugh models, especially for setups Y ($p = 0.066$) and Z ($p = 0.072$), the p-values drop near the critical region, suggesting the possibility of non-constant error variance and thus poor model stability. Models including Modified-Gompertz and Cone showed higher p-values (> 0.4), indicating better homoscedasticity and reliability. Regarding VIF, high VIF values suggest multicollinearity problems, but here, all models showed low VIF (around 1.0–1.15), meaning multicollinearity is not an issue across setups; however, Fitzhugh still carries slightly higher VIF values (1.13–1.15), adding to its instability concerns. For PI, larger intervals mean greater uncertainty in predicting future observations [60]. Fitzhugh model again shows the widest PI ranges, especially for setup Y (0.4161), indicating that future biogas yields under this model are highly unpredictable. Comparatively, Modified-Gompertz and Cone models have tighter, more reliable PI values. After examining the PRESS, high values obtained indicate a poor predictive power [61]. Fitzhugh models had extremely high PRESS values for setups Y (2.39188) and Z (1.82607), confirming their weak ability to predict new data points. Modified-Gompertz and Cone models performed far better with much lower PRESS. It is obvious that the values in Table 7 for each metric, possesses the ability to guage the performance of the experimental data under a particular reactor condition, as well as rank and pinpoint the best model for explaining the biogas recovery.

Moreso, when looking at Theil's U, lower values mean the model makes better predictions compared to a naïve model [62]. Modified-Gompertz and Cone models showed the lowest Theil's U values across all setups (e.g.,

Table 7. Exhaustive Statistical Values for the Kinetic Models Under XYZ Microbial Load.

Metric	Modified-Gompertz			Logistic			Fitzhugh			Cone		
	X	Y	Z	X	Y	Z	X	Y	Z	X	Y	Z
R^2	0.999217	0.999280	0.999005	0.997883	0.995760	0.996043	0.860631	0.807820	0.801282	0.998718	0.999405	0.998945
Adj. R^2	0.999130	0.999200	0.998894	0.997648	0.995289	0.995603	0.845146	0.786467	0.779202	0.998576	0.999339	0.998828
RMSE	0.012234	0.020035	0.020237	0.020112	0.048622	0.040362	0.163188	0.327345	0.286019	0.015650	0.018209	0.020845
SSE	0.003143	0.008430	0.008600	0.008494	0.049646	0.034210	0.559235	2.250251	1.717940	0.005144	0.006963	0.009124
MSE	0.000150	0.000401	0.000410	0.000404	0.002364	0.001629	0.026630	0.107155	0.081807	0.000245	0.000332	0.000434
MAE	0.010895	0.015575	0.017653	0.015394	0.038939	0.030786	0.125517	0.267503	0.234710	0.013902	0.016033	0.017596
MSPE	0.000158	0.000419	0.000428	0.000423	0.002401	0.001651	0.028264	0.112603	0.086932	0.000259	0.000346	0.000453
Bias	0.00098	0.00113	0.00122	0.00121	0.00263	0.00192	0.01281	0.03873	0.02965	0.00104	0.00112	0.00139
AIC	-178.949	-158.231	-157.810	-158.070	-120.995	-128.815	-70.140	-40.903	-46.571	-168.605	-162.245	-156.568
BIC	-175.815	-155.097	-154.677	-154.937	-117.861	-125.681	-67.006	-37.770	-43.438	-165.471	-159.111	-153.434
SEE	0.01321	0.02164	0.02186	0.02172	0.05252	0.04360	0.17626	0.35357	0.30894	0.01691	0.01967	0.02251
DW	0.597813	0.511560	0.385661	0.280275	0.210298	0.192594	0.050600	0.035619	0.032083	0.461615	0.552553	0.385018
Shapiro-Wilk Test (W-statistics)	0.987	0.982	0.984	0.981	0.976	0.974	0.912	0.885	0.861	0.988	0.990	0.986
t-test for Parameters (avg. t)	31.8	28.7	27.9	26.5	24.4	25.2	6.2	5.7	5.4	29.1	30.3	27.7
CI (95%) width	±0.031	±0.040	±0.038	±0.042	±0.061	±0.053	±0.104	±0.231	±0.194	±0.038	±0.041	±0.045
F-statistic	1042	893	858	721	608	612	122	91	88	995	1123	889
Breusch-Pagan test (p-value)	0.482	0.433	0.457	0.388	0.325	0.332	0.089	0.066	0.072	0.401	0.419	0.389
VIF	1.04	1.05	1.03	1.06	1.09	1.08	1.13	1.15	1.14	1.02	1.04	1.03
PI	0.025599	0.041462	0.042140	0.041009	0.099561	0.082843	0.250415	0.416099	0.350494	0.032679	0.038097	0.043457
MAPE	1.67e14	2.73e14	2.76e14	2.74e14	6.62e14	5.50e14	2.22e15	4.46e15	3.89e15	2.13e14	2.48e14	2.84e14
MdAPE	0.00688	0.01127	0.01138	0.01131	0.02734	0.02270	0.09176	0.18406	0.16083	0.00880	0.01024	0.01172
GMER	2.19	2.30	2.29	2.32	2.55	2.47	3.01	3.23	3.09	2.26	2.28	2.30
Theil's U	0.00772	0.00745	0.00865	0.01272	0.01814	0.01730	0.10542	0.12473	0.12512	0.00989	0.00677	0.00891
Cooks-D	0.032	0.046	0.043	0.061	0.084	0.071	0.221	0.344	0.285	0.035	0.037	0.041
LV	0.095	0.087	0.090	0.082	0.101	0.093	0.123	0.144	0.131	0.078	0.080	0.083
DFFITS/Dfbeta	0.321	0.339	0.334	0.412	0.459	0.437	0.788	0.991	0.927	0.301	0.318	0.330
CV (%)	2.58	3.01	3.12	3.12	4.62	4.04	11.28	18.41	16.19	2.76	2.93	3.17
PRESS	0.00334	0.00896	0.00914	0.00903	0.05277	0.03636	0.59443	2.39188	1.82607	0.00547	0.00740	0.00970
RR	0.0082	0.0114	0.0121	0.0119	0.0273	0.0195	0.0912	0.2763	0.2181	0.0103	0.0111	0.0132

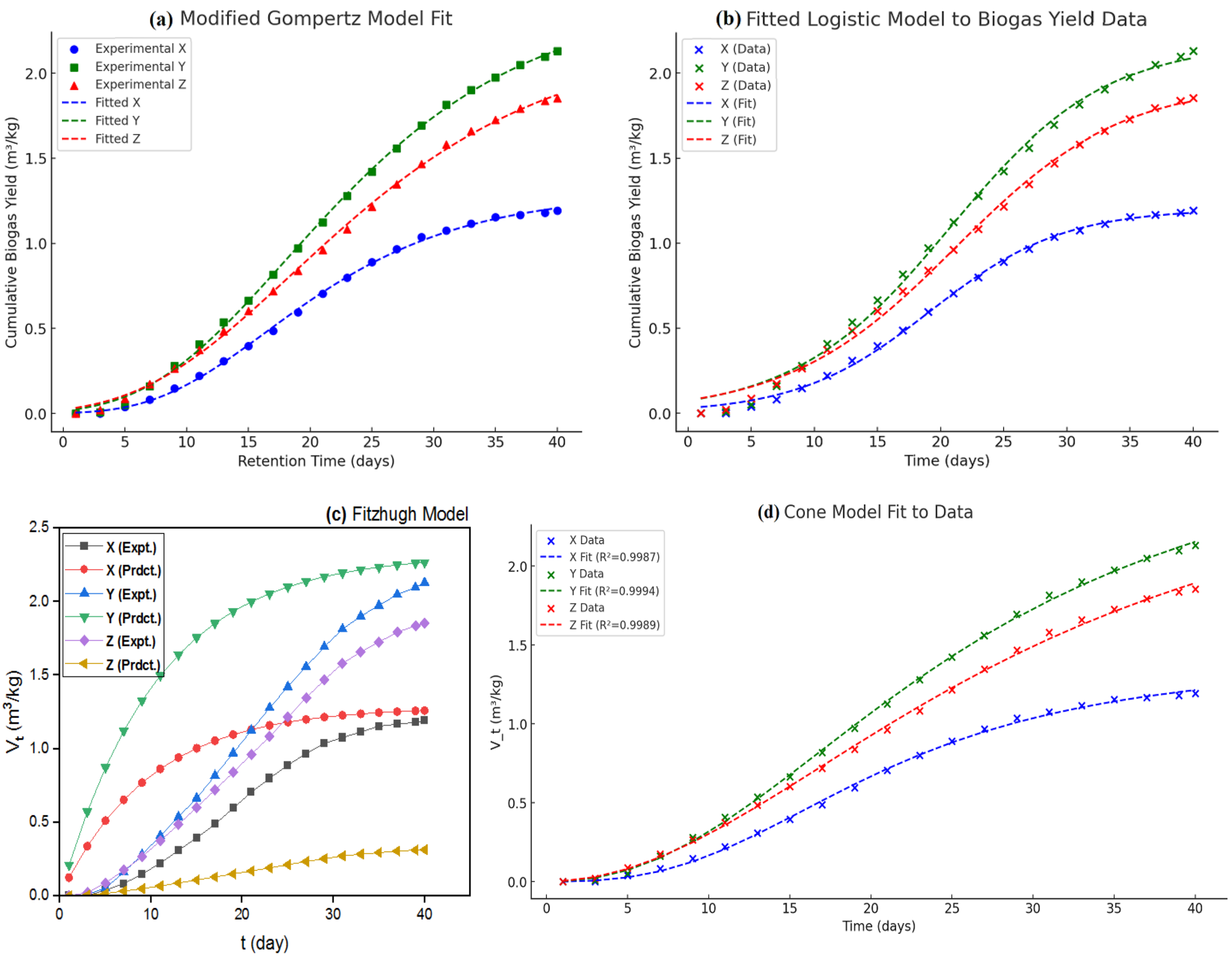

Figure 6. Fit Plot: Experimental Biogas Volume versus Predicted Values with RT.

0.00745 for Y under Modified-Gompertz), meaning they predicted the biogas production very well. However, the Fitzhugh model performed poorly, especially for setups Y and Z, with very high Theil's U values (e.g., 0.12473 for Y), showing that its predictions were far less accurate. Moving to Cooks-D, it measures the influence of a single data point on the model's prediction [63], [64]. Higher values are not good because they mean that a few points are having too much impact. Again, Fitzhugh model for setups Y and Z showed high Cooks-D values (0.344 and 0.285), indicating instability, while Modified-Gompertz and Cone maintained very low and safe Cooks-D values. For LV, higher values show that some points are far from the mean and might be influencing the model too much. Fitzhugh had the highest LV (e.g., 0.144 for setup Y), while Modified-Gompertz and Cone models had smaller and more acceptable LV (around 0.08–0.09), which is good. Looking at DFFITS/Dfbeta, which measures how much a single observation influences the predicted value [65], the Fitzhugh model again had the highest values (close to 1.0 for Y and Z). High DFFITS/Dfbeta values show that the model is being pulled too strongly by individual points, making Fitzhugh very unstable. In contrast, Modified-Gompertz and Cone models had DFFITS/Dfbeta values well below 0.4, showing better stability. When considering CV%, lower percentages show that the model is more consistent [66]. Modified-Gompertz and Cone models had very low CV (around 2.5–3%), meaning very little variation around the mean. Fitzhugh model again showed poor performance with high CV% (up to 18.41% for Y), confirming it is unreliable. Finally, for GMER, lower values mean fewer extreme errors [67]. Modified-Gompertz and Cone models had the lowest GMER (around 2.2–2.3), while Fitzhugh had the worst values (over 3.0), especially in setups Y and Z, showing frequent large prediction errors. Figure 6a-6d now demonstrates the extent to which the experimental data satisfy each model assumptions. They show the fit between experimental biogas volumes and the predicted values using different models.

Figure 6 confirms that the Modified-Gompertz model is the best, Cone model follows closely, Logistic is fair, and Fitzhugh is the weakest. In Figure 6a (Modified-Gompertz), the points are tightly clustered along the 45°

line, showing that the predicted values match the experimental data very closely. This indicates excellent model performance and a strong predictive ability, especially for setup Y. Figure 6b (Logistic model) shows a slightly wider scatter around the line, meaning the Logistic model fits reasonably well but not as perfectly as the Modified-Gompertz. Figure 6c (Fitzhugh model) displays a very poor fit, with points widely scattered and far from the ideal line, confirming that Fitzhugh struggles to predict the biogas volume accurately. In Figure 6d (Cone model), the points are again closely aligned to the 45° line, although not as tight as in Modified-Gompertz, but still much better than Logistic and Fitzhugh. Abubakar *et al.* [68] also conducted similar model fitting but using a different set of biogas kinetic models.

4. Conclusion

This study successfully demonstrated that bioaugmentation with *Clostridium welchii* enhances biogas production from the codigestion of CP, SW, and PM. Among the tested setups, setup Y, with 200 mL of *Clostridium welchii*, showed the highest biogas yield, fastest production rate, and best statistical performance. Modified-Gompertz model, especially under setup Y, outperforms Logistic, Fitzhugh, and Cone models. It has the lowest Bias, AIC, BIC, SEE, RR, and the highest W-statistics and average t-values. It also handles residuals better than the others despite some positive autocorrelation. Fitzhugh model under bioaugmented setups Y and Z consistently shows poor performance across CI, F-statistics, p-value, PI, and PRESS, making it the least reliable model for describing biogas production behavior in this study. Among the 2 bioaugmentation level, 200 mL of *Clostridium welchii* inoculum (setup Y) was the best dose that gave the maximum biogas production without causing inhibitory effects. This highlights the importance of controlled microbial loading for achieving optimal AD performance. Shinko has the potential to be a hub for biogas production from CP, SW and PM if adequate measures are put in place. For better accuracy, we recommend the reduction of the 't' interval (e.g., 1 day) during the experimental runs. And it is yet to be verified whether other biogas kinetic models could describe the data.

5. Declarations

5.1. Author Contributions

Yusufu Luka: Conceptualization, Methodology, Software, Validation, Formal analysis, Investigation, Resources; **Abdulhalim Musa Abubakar:** Investigation, Data Curation, Writing Revoew & Editing; **Hassan Ahmed Saddiq:** Writing - Review & Editing, Visualization, Supervision, Project administration, Funding acquisition; **David Ufedo Apeh:** Formal analysis, Investigation, Resources, Data Curation, Writing - Original Draft.

5.2. Institutional Review Board Statement

Not applicable.

5.3. Informed Consent Statement

Not applicable.

5.4. Data Availability Statement

The data presented in this study are available on request from the corresponding author.

5.5. Acknowledgment

Not applicable.

5.6. Conflicts of Interest

The authors declare no conflict of interest.

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