International Journal of Engineering Research & Technology (IJERT)
ISSN: 2278-0181
Vol. 15 Issue 10 , October - 2026

Utilization of Canteen Food Waste through Anaerobic Digestion and Preliminary Characterization of Acid-Producing Bacterial Isolates from Biogas Digester Sludge

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Abstract - Canteen food waste represents a biodegradable feedstock for anaerobic digestion, while biogas digester sludge provides a potential source of microorganisms involved in organic-acid production. This study evaluated five recorded food-waste treatment observations, examined nutrient-response data, and assessed the acid-producing potential of bacterial isolates obtained from digester sludge. Food waste was mechanically shredded, mixed with water to form a slurry, and introduced into an anaerobic digester. Recorded carbohydrate content ranged from 35% to 72%, protein content ranged from 12% to 32%, and daily fuel-use duration ranged from 4 to 10 h. Treatment T2 recorded the longest daily fuel-use duration of 10 h. Bacterial isolates were screened using Carr medium and glucose–yeast extract–calcium carbonate medium, followed by incubation in ethanol-containing medium (5%) at 30°C and 150 rpm for seven days. Based on the recorded titration inputs of 0.3 mL of 0.5 M sodium hydroxide for a 1.5 mL culture aliquot, the calculated titratable acidity was 6.01 g/L, expressed as acetic-acid equivalents, corresponding to 0.60% (w/v). Assuming an initial concentration of zero, the apparent average productivity over seven days was 0.86 g/L/day. Statistical analysis of the five treatment observations showed positive associations between carbohydrate content and fuel-use duration (\(r = 0.452\)) and between protein content and fuel-use duration (\(r = 0.314\)). In the nutrient-response dataset, the highest recorded response was 1.70 for treatment N5. These findings provide preliminary quantitative information for further investigation of food-waste digestion, nutrient optimization, and microbial acid production.

Keywords: Canteen food waste; anaerobic digestion; biogas; acid-producing bacteria; acetic-acid equivalents; titratable acidity; nutrient optimization; resource recovery.

1. INTRODUCTION

Food waste generated from institutional canteens represents an important biodegradable resource that can be converted into useful products through biological treatment. Anaerobic digestion is a well-established biological process for treating organic waste while recovering energy in the form of biogas, primarily comprising methane and carbon dioxide. The process involves several interconnected microbial stages, including hydrolysis, acidogenesis, acetogenesis and methanogenesis. The efficiency of anaerobic digestion is influenced by feedstock composition, organic loading rate, pH, temperature, hydraulic retention time and microbial community structure (Wang et al., 2022; Harirchi et al., 2022; Sharma et al., 2023).

During anaerobic digestion, complex organic compounds are converted into soluble intermediates and volatile fatty acids (VFAs). These organic acids can subsequently be converted into methane or recovered as valuable biochemical products through controlled acidogenic fermentation. Food waste has been recognized as a suitable substrate for VFA production, with substrate characteristics, fermentation conditions and microbial community composition influencing acid accumulation and process performance (Ramos-Suárez et al., 2021; Zhang et al., 2020; Feng et al., 2022). Recent investigations have also explored process intensification, seasonal variation and operational optimization to improve VFA production from organic waste streams (Sun et al., 2024; Castro-Fernandez et al., 2024).

The production of volatile fatty acids from food waste depends on several interacting biological and operational factors. Microbial community composition, substrate concentration, fermentation pH and organic loading rate influence the distribution and

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accumulation of individual organic acids (Wang et al., 2023; Xiao et al., 2024; Zheng et al., 2025). Furthermore, controlled acidogenic fermentation can be used to direct organic matter conversion towards short-chain organic acids rather than complete methane production (Beschkov & Angelov, 2025).

Acetic acid is an important organic acid with applications in food processing, chemical manufacturing and biotechnology. Acetic acid bacteria are capable of oxidizing ethanol into acetic acid under suitable oxygenated conditions. Their identification and characterization are important for understanding microbial acid production and developing efficient fermentation systems (Ribič & Trček, 2024; Román-Camacho et al., 2024). However, acetate formation under anaerobic conditions can involve different microbial pathways and organisms. Therefore, microbial screening, molecular identification and analytical confirmation are essential when investigating acid production by bacterial isolates obtained from anaerobic digestion systems.

The present study investigated recorded observations from five canteen food-waste treatments, examined the relationship between feedstock composition and daily fuel-use duration, evaluated a preliminary nutrient-response dataset and estimated titratable acidity expressed as acetic-acid equivalents using available titration measurements. Furthermore, bacterial isolates obtained from biogas digester sludge were screened for their acid-producing potential and subjected to preliminary molecular characterization using 16S rRNA gene sequencing.

2. MATERIALS AND METHODS

2.1. Collection and preparation of food waste

Food waste generated from a college canteen was collected and mechanically shredded to reduce particle size. The shredded material was mixed with water to prepare a slurry and introduced into an anaerobic digester for biological treatment.

Five treatment observations were available for analysis. The recorded variables included carbohydrate content, protein content, and daily fuel-use duration. Fuel-use duration was considered an operational observation associated with the digestion system.

2.2. Food-waste treatment dataset

The recorded values for the five treatments are presented in Table 1.

Table 1. Recorded composition and daily fuel-use duration of food-waste treatments

Treatment	Carbohydrate (%)	Protein (%)	Fuel-use duration (h/day)
T1	72	12	7.0
T2	52	24	10.0
T3	35	32	6.0
T4	37	12	4.0
T5	38	23	6.5

The carbohydrate and protein contents of the five food-waste treatments can help explain differences in their potential for biogas generation. However, the recorded fuel-use duration is an indirect operational indicator, not a direct measurement of the fuel-generation rate. To calculate an actual rate, the volume of biogas produced per unit time and its methane content would be required.

Treatment T2 recorded the longest daily fuel-use duration (10 h/day), despite having a lower carbohydrate content than T1. T1 contained the highest carbohydrate proportion (72%) but supported a recorded fuel-use duration of 7 h/day. This suggests that carbohydrate content alone may not explain the observed operational performance.

T2, containing 52% carbohydrate and 24% protein, showed the highest recorded duration. Its composition may have provided a more balanced substrate profile, but this explanation requires experimental verification. T3 had the highest protein content (32%) and a fuel-use duration of 6 h/day, while T4, with 37% carbohydrate and 12% protein, recorded the shortest duration (4 h/day). T5 showed an intermediate duration of 6.5 h/day.

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The exploratory Pearson analysis found a positive association between carbohydrate content and fuel-use duration (\(r=0.452,\ p=0.445\)) and a weaker positive association between protein content and fuel-use duration (\(r=0.314,\ p=0.607\)). Neither association was statistically significant at the 5% level. Because the dataset contains only five observations, these relationships should be treated as preliminary.

duration of 10 h/day. Although T1 had the highest carbohydrate content, its recorded duration was only 7 h/day, indicating that carbohydrate concentration alone may not determine system performance. The observed data suggest that feedstock composition and other digestion parameters may jointly influence fuel availability. However, the small dataset and absence of direct biogas-volume and methane-content measurements prevent definitive conclusions about generation rate or conversion efficiency. Further replicated experiments measuring daily biogas yield, methane composition and substrate degradation are required to identify the optimum food-waste composition for biogas production.

2.3. Isolation and preliminary screening of bacterial isolates

Sludge collected from the outlet of the biogas digester was used as the microbial source. Bacterial isolates were screened using Carr medium and glucose–yeast extract–calcium carbonate (GYC) medium. Selected colonies were examined by Gram staining as part of the preliminary characterization.

For secondary screening, cultures were grown in medium containing 5% ethanol and incubated at 30°C with agitation at 150 rpm for seven days. The cultures were subsequently evaluated for acidity using the available titration procedure.

Growth on screening media and the development of titratable acidity were considered preliminary indicators of acid-producing potential.

2.4. Estimation of acetic-acid-equivalent concentration

The recorded titration observation specified 0.3 mL of 0.5 M sodium hydroxide (NaOH) consumed by a 1.5 mL aliquot of the original culture.

The concentration of titratable acidity, expressed as acetic-acid equivalents, was calculated using the following equation:

$$C_{\mathrm{acid}} = \frac{C_{\mathrm{NaOH}} \times V_{\mathrm{NaOH}}}{V_{\mathrm{sample}}} \times 60.052$$

where:

- \(C_{\mathrm{NaOH}}\) is the molarity of NaOH in mol/L.
- \(V_{\mathrm{NaOH}}\) is the volume of NaOH consumed.
- \(V_{\mathrm{sample}}\) is the original culture aliquot volume.
- \(60.052\) g/mol is the molar mass of acetic acid.

Substitution of the recorded values gives:

$$C_{\mathrm{acid}} = \frac{0.5 \times 0.3}{1.5} \times 60.052$$

$$C_{\mathrm{acid}} = 6.0052\ \mathrm{g/L}$$

The calculated value was rounded to 6.01 g/L, equivalent to 0.60% (w/v).

Apparent average volumetric productivity was calculated using:

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$$P=\frac{C_f-C_i}{t}$$

where C_f and C_i represent final and initial concentrations, respectively, and t is the incubation period in days.

Assuming an initial concentration of zero and a final concentration of 6.01 g/L after seven days:

$$P=\frac{6.01-0}{7} =0.86\ \mathrm{g/L/day}$$

These calculations represent titratable acidity expressed as acetic-acid equivalents. They do not independently establish the concentration of acetic acid specifically.

2.5. Nutrient-response analysis

Five recorded nutrient combinations containing glucose, yeast extract, and calcium carbonate ($CaCO_3$) were evaluated against the corresponding recorded response.

Table 2. Nutrient combinations and recorded response

Observation	Glucose	Yeast extract	$CaCO_3$	Recorded response
N1	0.5	0.4	0.5	1.40
N2	1.0	0.6	1.0	0.70
N3	1.5	0.8	1.5	0.80
N4	2.0	1.0	2.0	1.25
N5	2.5	1.2	2.5	1.70

The nutrient-response analysis revealed variation among the five tested formulations, with recorded responses ranging from 0.70 to 1.70. Formulation N5, containing glucose at 2.5, yeast extract at 1.2, and calcium carbonate at 2.5 in the recorded units, produced the highest response (1.70). In contrast, N2 showed the lowest response (0.70), despite containing greater nutrient quantities than N1, which recorded a response of 1.40. This non-linear pattern indicates that the recorded response did not increase proportionally with nutrient addition. Glucose availability, nutrient supplementation, and buffering capacity may influence microbial growth and acid production; however, their individual effects cannot be established because all three components were increased simultaneously. The observed Pearson correlations were positive but not statistically significant ($r=0.435,\ p=0.464$). Consequently, N5 can be considered the best-performing formulation among the five recorded observations, but it cannot yet be designated the statistically validated optimum. Further replicated experiments using independent nutrient variation and a clearly defined response measurement are required to establish the optimum conditions.

2.6. Preliminary molecular identification

The available laboratory notes reported an approximately 1,452 bp 16S rRNA sequence and sequence matches of approximately 91–94% identity to listed Acetobacter entries. The isolate was therefore described as a candidate acid-producing bacterial isolate pending further sequence analysis.

2.7. Statistical analysis

Descriptive statistics included mean, sample standard deviation, median, minimum, and maximum. Pearson correlation coefficients were calculated to examine the associations between carbohydrate content and fuel-use duration, protein content and fuel-use duration, and nutrient quantities and recorded response.

The analysis was based on five observations per dataset. Statistical results were interpreted as exploratory descriptions of the recorded data.

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3. RESULTS

3.1. Food-waste composition and fuel-use duration

The carbohydrate content of the five treatments ranged from 35% to 72%, while protein content ranged from 12% to 32%. Daily fuel-use duration varied from 4 to 10 h.

Treatment T2 recorded the highest daily fuel-use duration at 10 h, followed by T1 at 7 h, T5 at 6.5 h, T3 at 6 h, and T4 at 4 h.

The recorded values indicate variation in fuel-use duration among the five treatments and provide a basis for further investigation of the relationship between substrate composition and digestion-system performance.

3.2. Molecular Identification of the Acid-Producing Bacterial Isolate by 16S rRNA Gene Sequencing

The bacterial isolate designated ND was subjected to 16S rRNA gene sequencing, yielding a reported sequence length of 1,452 bp. The sequence was compared with reference sequences in the NCBI nucleotide database using BLAST analysis. The highest reported sequence identity was 94% with *Acetobacter pasteurianus* strain AUC25 (accession number FM179768.1) and an *Acetobacter* sp. clone ace4 (accession number OQ519651.1). Additional matches included *A. pasteurianus* strains AUC29, BAC24, AUC17, AUC13, CCM 3614 and YVB24, with reported identities of 93%. An *Acetobacter* sp. strain S12909 (accession number KF956626.1) showed 91% identity.

Table 3. Reported BLAST matches for bacterial isolate ND

Sl. No.	Reported organism	Accession number	Reported identity
1	*Acetobacter pasteurianus* strain AUC25	FM179768.1	94%
2	*Acetobacter* sp. clone ace4	OQ519651.1	94%
3	*Acetobacter pasteurianus* strain AUC29	FM179769.1	93%
4	*Acetobacter pasteurianus* strain BAC24	FM179770.1	93%
5	*Acetobacter pasteurianus* strain AUC17	FM179767.1	93%
6	*Acetobacter pasteurianus* strain AUC13	FM179766.1	93%
7	*Acetobacter pasteurianus* strain CCM 3614	FM178868.1	93%
8	*Acetobacter pasteurianus* strain YVB24	KX831391.1	93%
9	*Acetobacter* sp. strain S12909	KF956626.1	91%

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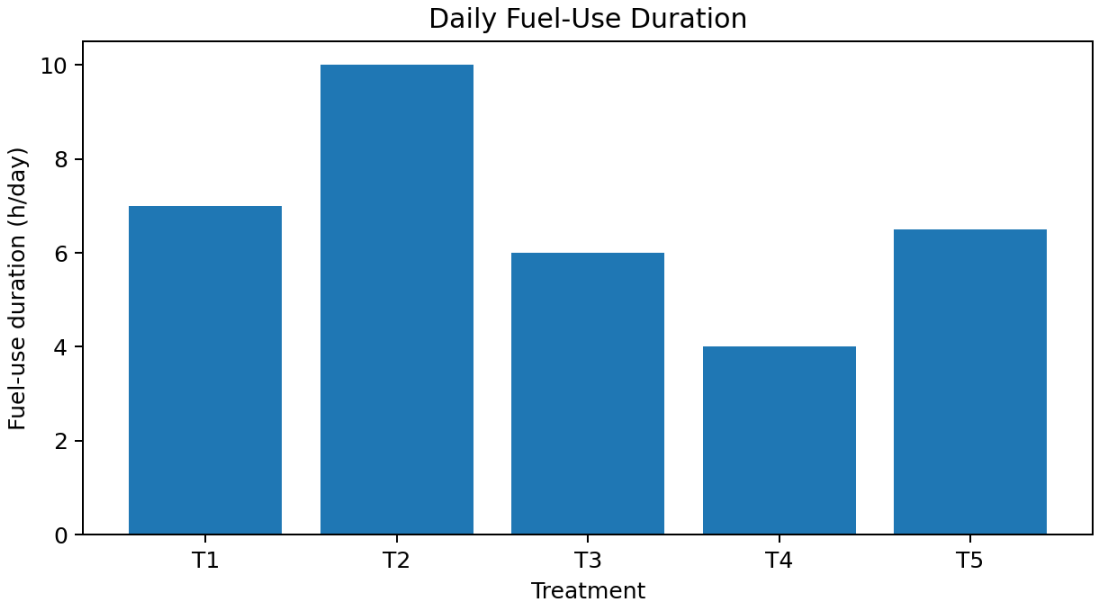


Figure 1. Daily fuel-use duration across the five food-waste treatments.

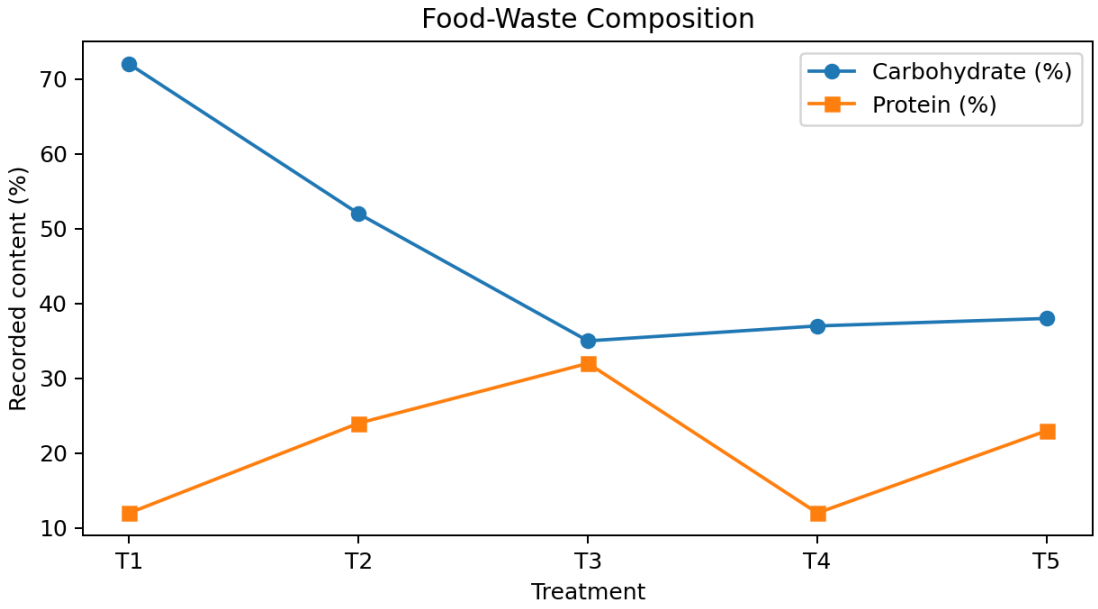


Figure 2. Recorded carbohydrate and protein content across treatments.

Recorded operational duration for the five food-waste treatments.

3.2. Descriptive statistical analysis

The descriptive statistics calculated from the five treatment observations are presented in Table 3.

Table 3. Descriptive statistics for food-waste composition and fuel-use duration

Variable	Mean	Sample SD	Median	Minimum	Maximum
Carbohydrate (%)	46.80	15.61	38.00	35.00	72.00

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International Journal of Engineering Research & Technology (IJERT)
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Protein (%)	20.60	8.59	23.00	12.00	32.00
Fuel-use duration (h/day)	6.70	2.17	6.50	4.00	10.00

The mean recorded fuel-use duration was 6.70 h/day, with a sample standard deviation of 2.17 h/day. Mean carbohydrate and protein contents were 46.80% and 20.60%, respectively.

These statistics summarize the variability among the five available treatment observations.

3.3. Relationship between composition and fuel-use duration

Pearson correlation analysis was used to examine the relationship between food-waste composition and daily fuel-use duration.

Table 4. Pearson correlation analysis of composition and fuel-use duration

Variables	Pearson correlation (\(r\))	p-value
Carbohydrate vs. fuel-use duration	0.452	0.445
Protein vs. fuel-use duration	0.314	0.607

Carbohydrate content showed a positive correlation with fuel-use duration (\(r=0.452\)). Protein content also showed a positive correlation, with a coefficient of \(r=0.314\).

Within the available dataset, the carbohydrate association was numerically stronger than the protein association. These findings describe the observed relationships and provide a basis for further testing using replicated treatment experiments.

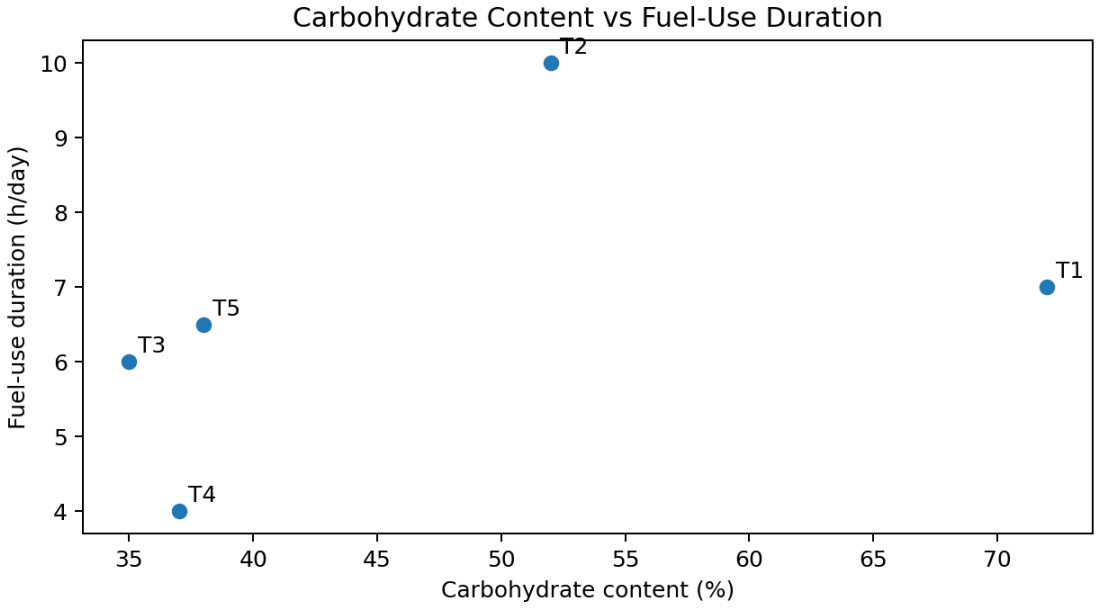


Figure 3: Relationship between carbohydrate content and fuel-use duration

Carbohydrate content showed a moderate positive correlation with fuel-use duration (\(r = 0.452\)); however, this relationship was not statistically significant (\(p = 0.445\)). Protein content also exhibited a positive correlation with fuel-use duration, although the

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association was weaker (\(r = 0.314\), \(p = 0.607\)). Thus, within the five recorded treatments, higher carbohydrate and protein contents tended to be associated with longer fuel-use durations, with carbohydrate showing the stronger numerical association.

3.4. Nutrient-response observations

The recorded nutrient-response values ranged from 0.70 to 1.70. The calculated mean was 1.17, the sample standard deviation was 0.42, and the median was 1.25.

Table 5. Descriptive summary of nutrient-response observations

Statistic	Recorded response
Mean	1.17
Sample standard deviation	0.42
Median	1.25
Minimum	0.70
Maximum	1.70

Treatment N5 produced the highest recorded response of 1.70, followed by N1 (1.40), N4 (1.25), N3 (0.80), and N2 (0.70).

The recorded nutrient-response values ranged from 0.70 to 1.70, with a mean of 1.17, a sample standard deviation of 0.42, and a median of 1.25. These statistics indicate variation in the measured response among the five nutrient combinations.

Treatment N5 produced the highest recorded response (1.70), followed by N1 (1.40), N4 (1.25), N3 (0.80), and N2 (0.70). The response did not increase consistently with increasing nutrient concentrations, as demonstrated by the decrease from N1 to N2 despite the higher nutrient levels in N2. The response subsequently increased from N2 through N5.

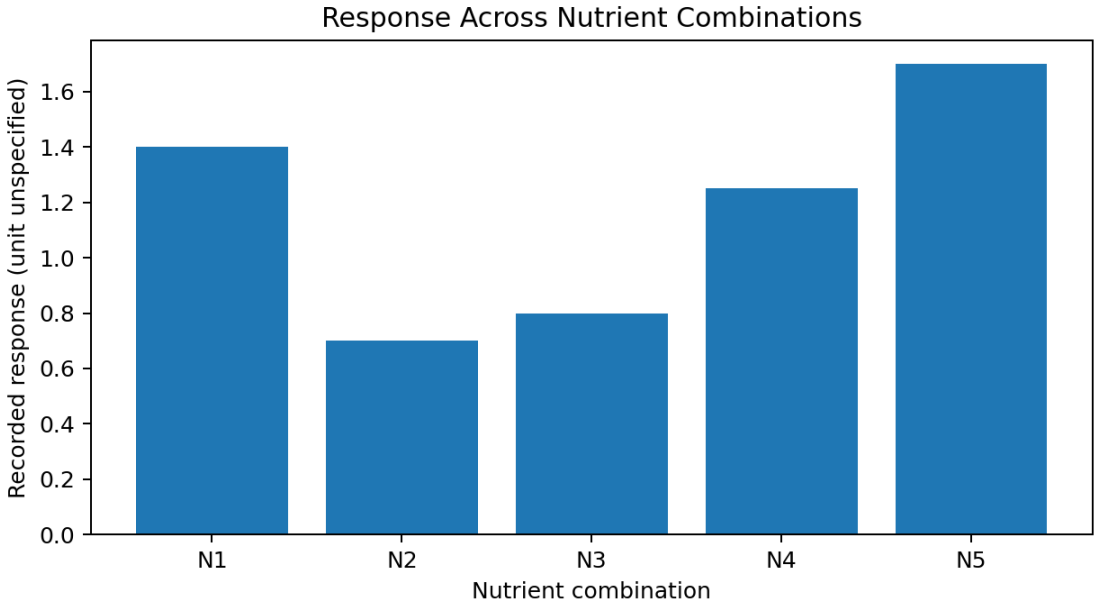


Figure 4. Recorded response across nutrient combinations.

Response units were not specified in the original dataset.

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Pearson correlations between the individual nutrient variables and the recorded response are summarized in Table 6.

Table 6. Correlation between nutrient quantities and recorded response

Nutrient variable	Pearson correlation (\(r\))	p-value
Glucose	0.435	0.464
Yeast extract	0.435	0.464
$CaCO_3$	0.435	0.464

The three nutrients had identical correlation coefficients because their recorded quantities followed aligned increasing patterns across the five observations. The recorded response was highest in N5, providing a useful starting point for subsequent controlled nutrient optimization.

3.5. Acetic-acid-equivalent concentration and productivity

Based on the recorded titration inputs, the calculated titratable acidity was 6.01 g/L expressed as acetic-acid equivalents. This corresponds to approximately 0.60% (w/v).

Assuming that the initial concentration was zero and the final concentration was reached after seven days, the calculated apparent average volumetric productivity was 0.86 g/L/day.

Table 7. Calculated acidity and apparent productivity

Parameter	Calculated value
NaOH concentration	0.5 M
NaOH volume consumed	0.3 mL
Original culture aliquot	1.5 mL
Acetic-acid-equivalent concentration	6.01 g/L
Equivalent percentage (w/v)	0.60%
Incubation period	7 days
Apparent average productivity, assuming zero initial acidity	0.86 g/L/day

The calculated concentration represents total titratable acidity expressed as acetic-acid equivalents. Chromatographic analysis would be required to quantify acetic acid specifically and establish the acid profile of the culture.

4. DISCUSSION

4.1. Food-waste utilization and digestion performance

The recorded treatment data demonstrate the potential of canteen food waste as a feedstock for biological resource recovery. Treatment T2 showed the longest daily fuel-use duration, at 10 h/day. This observation provides an operational reference point for subsequent experiments designed to measure digestion performance directly.

The mean daily fuel-use duration across the five treatments was 6.70 h/day. Variation in carbohydrate and protein contents suggests that substrate composition may be an important factor to investigate alongside operational parameters. Previous studies have emphasized the importance of feedstock characteristics, organic loading, pH, retention time and microbial community structure in anaerobic digestion (Wang et al., 2022; Harirchi et al., 2022; Gyadi et al., 2024). Microbial community dynamics also contribute to the different stages of organic matter degradation during anaerobic digestion (Sharma et al., 2023; Tang et al., 2023).

Food waste and other organic residues have been investigated as substrates for biogas production and acidogenic fermentation, highlighting their potential for resource recovery and sustainable waste management (Yaser et al., 2022; Ramos-Suárez et al.,

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2021). Future evaluation of the present system would benefit from recording gas volume, methane fraction, substrate loading, pH, temperature and digestion time. These measurements would enable fuel-use observations to be interpreted alongside quantitative indicators of biogas production.

4.2. Composition and fuel-use relationships

The Pearson correlation between carbohydrate content and fuel-use duration was positive (r = 0.452), while the corresponding relationship for protein content was also positive (r = 0.314). The observed carbohydrate association was numerically stronger.

Previous studies have demonstrated that substrate characteristics and operating conditions influence the efficiency of anaerobic digestion and the conversion of organic matter into biogas and volatile fatty acids (Feng et al., 2022; Wang et al., 2022; Gyadi et al., 2024). However, the present correlation analysis involved only five observations, and neither relationship was statistically significant.

Therefore, these coefficients should be interpreted as descriptive associations rather than predictive relationships. A larger dataset with replicate measurements and controlled feedstock composition would help establish whether these patterns are reproducible.

4.3. Nutrient optimization and response patterns

The nutrient-response dataset recorded the highest response in N5, which contained glucose at 2.5, yeast extract at 1.2 and $CaCO_3$ at 2.5 in the recorded units. The corresponding response was 1.70.

Nutrient availability and fermentation conditions play important roles in microbial growth and organic-acid production. Previous investigations have highlighted the influence of substrate characteristics, fermentation conditions and microbial metabolic activities on VFA production from organic waste (Ramos-Suárez et al., 2021; Feng et al., 2022). Recent studies have also explored optimization strategies to improve acid production and fermentation efficiency (Sun et al., 2025; Zheng et al., 2025).

The present observation identifies N5 as the highest-response combination among the five recorded formulations. However, since glucose, yeast extract and calcium carbonate were increased simultaneously, their individual effects cannot be established. A factorial experimental design or response-surface methodology would help evaluate the individual and interactive effects of these nutrients.

For reproducibility, the nutrient quantities, response units, culture volume and analytical method should be specified in subsequent experiments.

4.4. Interpretation of acetic-acid-equivalent concentration

The titration calculation yielded 6.01 g/L of titratable acidity expressed as acetic-acid equivalents. Under the assumption of zero initial acidity and a seven-day incubation period, the apparent average volumetric productivity was 0.86 g/L/day.

Acidogenic fermentation of organic waste can produce a mixture of volatile fatty acids, including acetic, propionic and butyric acids, depending on substrate composition, microbial activity and operating conditions (Ramos-Suárez et al., 2021; Feng et al., 2022). Therefore, titration-based acidity measurements should be interpreted as total titratable acidity rather than a specific measurement of acetic acid.

The calculated concentration represents the total acidity neutralized by sodium hydroxide and does not independently distinguish acetic acid from other organic acids. Previous investigations of VFA production and recovery have emphasized the importance of suitable analytical and separation approaches for determining individual organic acid concentrations (Sun et al., 2024).

High-performance liquid chromatography (HPLC) or gas chromatography (GC) would be required to determine the actual acetic acid concentration and identify other organic acids. Initial and final acidity measurements, blank correction and replicate cultures would also improve the accuracy of productivity estimates.

4.5. Preliminary characterization of acid-producing bacteria

The sludge-derived bacterial isolates were screened on Carr and glucose–yeast extract–calcium carbonate media and subsequently incubated in ethanol-containing medium. The titration observations provided preliminary quantitative information regarding their acid-producing potential.

Acetic acid bacteria are commonly associated with ethanol oxidation under oxygenated conditions. Their metabolic characteristics, diversity and molecular identification have been investigated in relation to industrial vinegar production and other fermentation applications (Ribič & Trček, 2024; Román-Camacho et al., 2024).

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Accordingly, the incubation conditions, aeration and oxygen-transfer characteristics should be documented when evaluating the metabolic pathway of the isolate. The presence of titratable acidity alone does not establish that acetic acid was the predominant product.

The available 16S rRNA sequence information provides a starting point for molecular investigation. However, the reported sequence similarities of approximately 91–94% to the listed *Acetobacter* entries are insufficient to establish reliable genus- or species-level identification. Further sequence-quality assessment, comparison against curated reference databases and phylogenetic analysis are necessary to support more precise taxonomic characterization.

Recent investigations have highlighted the importance of appropriate molecular markers and advanced sequencing strategies for distinguishing closely related acetic acid bacteria (Ribič & Trček, 2024; Román-Camacho et al., 2024). Therefore, additional molecular characterization and chromatographic analysis are essential to establish the identity of isolate ND and confirm its acid-producing profile.

5. CONCLUSION

The present study evaluated canteen food-waste treatment observations, nutrient-response patterns and the preliminary acid-producing potential of bacterial isolates obtained from biogas digester sludge. Among the five treatment observations, T2 recorded the longest daily fuel-use duration of 10 h. The mean fuel-use duration was 6.70 ± 2.17 h/day, while mean carbohydrate and protein contents were 46.80 ± 15.61% and 20.60 ± 8.59%, respectively.

The correlation analysis indicated positive associations between carbohydrate content and fuel-use duration ($r = 0.452$) and between protein content and fuel-use duration ($r = 0.314$). However, neither association was statistically significant, indicating the need for further replicated investigations.

The nutrient-response dataset recorded its highest value of 1.70 in N5, identifying this formulation as a candidate for further controlled optimization. Based on the recorded titration inputs, the calculated titratable acidity was 6.01 g/L as acetic-acid equivalents, corresponding to 0.60% (w/v). Assuming zero initial acidity over seven days, the apparent average volumetric productivity was 0.86 g/L/day.

Preliminary 16S rRNA sequencing of isolate ND revealed reported sequence similarities of 91–94% with selected *Acetobacter* reference entries. These similarities were insufficient to establish its taxonomic identity, and further molecular characterization is required.

Overall, the findings provide a preliminary quantitative foundation for developing food-waste resource-recovery processes and investigating candidate acid-producing bacteria. Further work involving replicated experiments, direct biogas and methane measurements, controlled nutrient optimization, chromatographic confirmation of individual organic acids and validated molecular identification will strengthen the characterization of the system and its potential applications.

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International Journal of Engineering Research & Technology (IJERT)
ISSN: 2278-0181
Vol. 15 Issue 10 , October - 2026

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