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Faecal Microbial Loads of Growing Pigs Fed Food Waste-Based Diets

[1]Ogunbode, A.A., [2]Abegunde, P.T., [1]Ojelere, I.M., [1]Omojowo, D.D and [1]Oyeleye, I.O

[1]Department of Animal Production Technology, Oyo State College of Agriculture and Technology, Igboora, Nigeria.
[2]Department of Animal Health and Production, Oyo State College of Agriculture and Technology, Igboora, Nigeria.

ABSTRACT

The high cost of conventional livestock feed has necessitated the exploration of alternative and sustainable feed resources such as food waste. This study evaluated the effects of food waste–based diets on the faecal microbial composition of growing pigs. Twenty-seven (27) crossbred pigs (Large White × Landrace), with an average weight of 30–35 kg, were randomly assigned to three dietary treatments: T1 (control diet with no food waste), T2 (35% food waste inclusion), and T3 (70% food waste inclusion) in a completely randomized design over an eight-week period.

At the end of the experiment, faecal samples were collected and analyzed for total bacterial count, coliform count, *Salmonella*, *Lactobacillus*, and *Saccharomyces* using standard microbiological procedures. Data were analyzed using analysis of variance (ANOVA), with significance set at $p < 0.05$.

The results showed that dietary treatments had no statistically significant effect ($p > 0.05$) **on total bacterial count, coliform count, *Salmonella*, and *Lactobacillus* populations. However, *Saccharomyces* count was** significantly affected ($p < 0.05$) **by dietary inclusion levels. Although numerical reductions in coliform and *Salmonella* counts were observed in pigs fed food waste–based diets, these differences were not statistically significant.**

In conclusion, the inclusion of food waste in the diets of growing pigs did not significantly alter faecal microbial populations, suggesting that it can be utilized as an alternative feed resource without adverse effects on gut microbial load under the conditions of this study. Further research with larger sample sizes and advanced microbial analysis is recommended to validate these findings.

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***Corresponding Author**

Ogunbode, A.A

E-mail: *aaogunbode@gmail.com,*

Tel: *+2348062455318*

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INTRODUCTION

Inadequate nutrition is a major problem militating against pig industry in the developing countries due to limited feed resources (Amole *et al.,* 2022). Bharati *et al.,* 2022 opined that feed alone constitute 60-80% of the total cost of pig production in the tropics and this problem has also being aggravated as a result of Covid-19 and the on-going Russia-Ukraine war (Makinde *et al.*, 2022). To solve this problem, other feed resources that are locally available and cheaper than the conventional feedstuffs must be explored. The feeding of food waste has been reported as these are not eaten by mans and pigs can convert these waste into desirable meat (Ponnampalam and Holman, 2023). Edible materials or byproduct that is generated in the production, processing, transportation, distribution or consumption of food is regarded as food waste (Westendorf and Myer, 2012) and for the purpose of this work, the term food waste will be used to refer to all food wastes, including plate waste, kitchen or table scraps, garbage or swill and all food residuals discarded after serving. Gustavsson *et al.,* 2011 reported that food waste occurs at farm processing or consumption level such as waste from households, restaurants and supermarket and globally it is estimated to be about 1.3 billion tonnes per year. The food waste offered to swine are plate and kitchen waste, bakery waste and food products from grocery stores. The practice of feeding food waste to pig other livestock is a common practice and is often more common in metropolitan centers where it is available in bulk and food waste helps to reduce environmental pollution (Westendorf *et al*., 1999). Knowledge of all the gut flora of the pig is necessary, not only to aid appropriate management, but also to elude public health hazards. Martineau, 1997 opined that one of the major problems associated with pig production is the high morbidity and mortality in pigs caused by gastrointestinal infections. The performance and production of pig is majorly steered by factors such as environment, genetics and predominantly the diet. Pigs being an omnivorous animal, diet constituents are greatly dependent on the microbial content of the gut. The pig gut is occupied by a large population of microbiota. The microbes present in the gastrointestinal tract of the pig are found to have co-evolved with their hosts (Aggrey*, et al.,* 2010). The gut chamber in pigs is the hub to trillions of bacteria responsible for roles in host immunity, metabolism and even behaviours to some extent (Sylvia *et al.,* 2018). management systems for the animals to farmers and the public at large. Thus the objective of this study was to determine microorganisms present in the faeces of pigs with the view to suggesting healthy

MATERIALS AND METHODS

2.1 Experimental site

The experiment was carried out at the piggery unit of the Teaching and Research Farm of the Oyo State College of Agriculture and Technology, Igboora, Nigeria. The area is situated in the savannah forest vegetation zone of Ibarapa Central Local Government, Nigeria on latitude 7^0 43N, longitude 3^0 28E and elevation of 140m above sea level. The average minimum temperature is above 21.5^0c and maximum average temperature is about 32.5^0c (World Atlas, 2024)

2.2 Experimental animals and management

Twenty-seven (27) crossbred growing pigs (Largewhite X Landrace) pigs weighed between 30-35kg of age were obtained from piggery unit of Teaching and Research Farm of the Oyo State College of Agriculture and Technology, Igboora. The pigs were dewormed and fed 4% of their body weight as feed per day at the beginning of the experiment and increase as the animal increased. A completely randomized design was used for the study. Diets were formulated to meet the nutrient requirements recommended by NRC (2012) as presented in Table1.

DATA COLLECTION

Determination of fecal microbial loads:

At day 42, fresh faecal samples were collected via massaging the rectum from 1 pig randomly selected from each replicate for the analysis of faecal microbial shedding. One gram of each pig's faecal sample was diluted with 9ml of 1% peptone broth and homogenized. Viable counts of bacteria in the faecal samples were determined by plating serial 10-fold dilutions (in 1% peptone solution) onto MacConkey agar plate to isolate *Escherichia coli*, *Lactobacillus* medium 111 agar plate for *Lactobacillus spp* and Salmonella-Shigella agar plate for *Salmonella spp* and *Shigella spp*. The agar plates were then incubated for 24hours at 37^0C. The microbial colonies were counted immediately after removal from the incubator. Microflora enumerations were expressed as log 10 cfu/g. Data were analysed using the analysis of variance (ANOVA) procedure of SAS (2020). The differences among treatments were compared using Duncan's Multiple Range Test (Duncan, 1955) when the treatment effect was observed, with significance taken at $p<0.05$.

Table 1: Gross composition of experimental diet

Ingredients	Percentage (%)
Maize	25.00
Corn bran	35.00
Palm kernel cake	25.00
Groundnut cake	7.00
Fish meal	3.00
Bone meal	3.00
Lysine	0.50
Methionine	0.50
Salt	0.50
Premix	0.50
Total	**100.00**
Calculated analysis	
Metabolisable Energy (Kcal/kg)	3000Kcal/kg
Crude protein (%)	20%

RESULTS AND DISCUSSION

The results of the faecal microbial counts of crossbred growing pigs fed food waste-based diets are presented in **Table 2**.

Table 2: Fecal microbial loads of pigs fed food waste based diet

Parameters	T1	T2	T3	SEM	P-Value
Total Bacterial Count (cfu/g) x 10-5	11.10	9.10	9.70	0.39	0.07
Colliform Count (cfu/g) x 10-5	3.60	2.90	2.70	0.19	0.11
Lactobacillus Count (cfu/g) x 10-5	1.91	1.74	1.82	0.61	0.60
Saccharomyces Count (cfu/g) x 10-5	2.20	1.80	2.10	0.71	0.02
Salmonella Count (cfu/g) x 10-5	2.90	2.30	2.50	0.12	0.07

a,b,c Means on the same row with different superscript differed significantly

There was no statistically significant difference ($p > 0.05$) in the mean values of total bacterial count, coliform count, *Lactobacillus* count, and *Salmonella* count across the dietary treatments. However, *Saccharomyces* count showed a statistically significant difference ($p < 0.05$) among treatments.

The total bacterial count ranged from 9.10×10^{-5} cfu/g in T2 to 11.10×10^{-5} cfu/g in T1, with pigs fed the control diet (T1) recording the highest numerical value. Although this suggests a reduction in bacterial load with food waste inclusion, the difference was not statistically significant ($p = 0.07$). This implies that dietary inclusion of food waste did not significantly influence the overall bacterial population. This observation partially agrees with the findings of Adeosun et al. (2019), who reported that dietary modifications may reduce bacterial populations due to the presence of bioactive compounds, although such effects may not always reach statistical significance.

Coliform counts were highest in pigs fed the control diet (3.60×10^{-5} cfu/g) and lowest in pigs fed T3 (2.70×10^{-5} cfu/g). Despite this numerical reduction, the differences among treatments were not statistically significant ($p = 0.11$). Coliform bacteria are considered indicators of gut health and potential pathogenic activity. The observed numerical decrease in coliform counts in pigs fed food waste diets may suggest a beneficial modulation of gut microflora, which is consistent with the report of Niba et al. (2009), who noted that dietary fiber and phytochemicals can influence intestinal microbial ecology by suppressing harmful bacteria. However, since the differences were not significant, this effect cannot be conclusively established.

The *Lactobacillus* count ranged from 1.74×10^{-5} to 1.91×10^{-5} cfu/g, with the highest value observed in the control group. There was no significant difference ($p = 0.60$) among treatments. *Lactobacillus* species are beneficial microorganisms that contribute to gut health by enhancing digestion and inhibiting pathogenic bacteria (Walter, 2008). The similarity in values across treatments indicates that food waste inclusion did not adversely affect beneficial gut bacteria.

The *Saccharomyces* count showed a statistically significant difference ($p = 0.02$) among treatments. The highest value (2.20×10^{-5} cfu/g) was recorded in the control group, while lower values were observed in T2 (1.80×10^{-5} cfu/g) and T3 (2.10×10^{-5} cfu/g). This suggests that dietary inclusion of food waste influenced yeast populations in the gut. According to Mamuad et al. (2020), *Saccharomyces cerevisiae* plays an important role in improving gut integrity and immune response. The reduction observed in treatment groups may be attributed to competition for nutrients or the presence of inhibitory compounds in food waste diets.

The *Salmonella* count ranged from 2.30×10^{-5} cfu/g in T2 to 2.90×10^{-5} cfu/g in T1. Although lower values were observed in pigs fed food waste diets, the differences were not statistically significant ($p = 0.07$). *Salmonella* is a major pathogenic organism associated with enteric infections and public health concerns (Barrow et al., 2012). The numerical reduction in *Salmonella* counts in the treatment groups may indicate a potential antimicrobial effect of dietary components, as reported by Akinyemi et al. (2017), who highlighted the role of phytochemicals in inhibiting pathogenic bacteria. However, due to the lack of statistical significance, this observation should be interpreted with caution.

Overall, the results indicate that inclusion of food waste in pig diets did not significantly alter faecal microbial populations. While some numerical trends suggest possible reductions in pathogenic bacteria, these were not statistically validated. Therefore, it can be inferred that food waste inclusion had no significant effect on microbial load under the conditions of this study, although further research with larger sample sizes is required to confirm these findings.

CONCLUSION

This study evaluated the effects of food waste–based diets on the faecal microbial composition of growing pigs. The findings revealed that dietary inclusion of food waste at varying levels did not produce statistically significant differences ($p > 0.05$) in total bacterial count, coliform count, *Salmonella*, and *Lactobacillus* populations. However, *Saccharomyces* count was significantly influenced ($p < 0.05$) by dietary treatment.

Although numerical reductions in coliform and *Salmonella* counts were observed in pigs fed food waste–based diets, these differences were not statistically significant, indicating that the inclusion of food waste did not adversely affect the microbial load of the animals under the conditions of this study. Importantly, the stability of *Lactobacillus* populations suggests that beneficial gut microbiota were not compromised.

Overall, the results suggest that food waste can be incorporated into the diets of growing pigs without significant negative effects on faecal microbial populations. This supports its potential as a cost-effective and sustainable alternative feed resource. However, given the observed numerical trends and the inherent variability in microbial data, these findings should be interpreted with caution.

Further studies employing larger sample sizes, longer feeding durations, and advanced molecular microbiological techniques are recommended to provide deeper insights into the impact of food waste on gut microbial ecology and animal health.

Limitations of the Study

Despite providing useful insights into the effects of food waste–based diets on faecal microbial populations in growing pigs, this study has several limitations that should be acknowledged.

First, the sample size was relatively small, which may have limited the statistical power to detect significant differences among treatments. Microbial populations are inherently variable, and larger sample sizes would improve the reliability and generalizability of the findings.

Second, microbial analysis was based on culture-dependent techniques, which may not fully capture the diversity and complexity of the gut microbiota. Many microorganisms are not culturable under standard laboratory conditions, and therefore, the results may underestimate total microbial diversity. The use of advanced molecular techniques such as 16S rRNA gene sequencing would provide a more comprehensive understanding of microbial community dynamics.

Third, the study did not account for variability in the composition of food waste, which may differ depending on source, handling, and processing methods. Such variability could influence nutrient composition and microbial content, thereby affecting experimental outcomes.

Additionally, only faecal microbial counts were assessed, which may not fully reflect microbial activity within different sections of the gastrointestinal tract. A more detailed analysis involving gut tissue or digesta samples could provide deeper insights into microbial interactions and functionality.

The duration of the experiment (eight weeks), although adequate for preliminary evaluation, may not be sufficient to observe long-term effects of dietary treatments on microbial stability and animal health.

Finally, environmental and management factors, such as housing conditions and hygiene practices, were not extensively controlled or reported, yet they can significantly influence microbial exposure and colonization.

Addressing these limitations in future studies will enhance the robustness of findings and contribute to a more comprehensive evaluation of food waste as a sustainable feed resource in pig production systems.

Declaration of Conflict of Interest

The authors declare that there is no conflict of interest.

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