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Nutritional Evaluation of Microbial Treated Rice Husk and Its Effect on The Performance of Growing West African Dwarf Goats in Nigeria

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Abstract-** This study investigated the potential of using microbial treatment to enhance the nutritional value of rice husk (RH) and its subsequent effect on the performance and health of growing West African Dwarf (WAD) goats. Raw rice husk (RRH) was subjected to solid-state fermentation using Bacteria (Alcaligenes faecalis, BTRH), Fungi (Aspergillus flavus, FTRH), or a Combined treatment (B+FTRH). The combined treatment (B+FTRH) significantly improved the proximate composition of RH, resulting in the lowest Crude Fibre (62.04%) and the highest Crude Protein (11.14%) compared to RRH (66.79% CF, 9.88% CP). Forty growing WAD male goats were randomly assigned to four diets: a Maize-based control (T1) and three diets where maize was replaced by treated RH (T2, T3, T4). The formulated diets maintained a similar Crude Protein level (15.86% to 16.55%) across all groups, demonstrating the efficacy of microbial protein enrichment in the treated RH. However, incorporating the treated RH increased the structural fibre load (NDF: 76.99% in T1 vs. 78.60% in T4) and Acid Detergent Lignin in the experimental diets. Consequently, goats on T3 and T4 exhibited significantly lower Average Daily Feed Intake (ADFI: 0.38 kg/day) compared to T1 (0.52 kg/day), leading to a numerically lower Total Weight Gain (TWG: 2.58 kg in T4 vs. 3.60 kg in T1). Crucially, the Feed Conversion Ratio (FCR) and metabolic efficiency were not significantly different across treatments, indicating similar nutrient utilization quality. Rumen analysis showed T3 and T4 promoted a fibrolytic fermentation pattern with significantly higher Acetate and Butyric acid concentrations. Haematology and serum biochemistry confirmed the physiological safety of all diets, with stable PCV, HGB, and key liver enzymes, while T4 showed a favourable reduction in LDL-C and optimal MCHC.

***Key words:** Rice husk, Microbial, Nutritional, Fermentation, Haematology, West Africa Dwarf Goats.*

I. INTRODUCTION

West Africa Dwarf goats (WADGs) are an important livestock species in many regions of West Africa, providing meat, milk, and income for smallholder farmers. However, the availability and quality of feed resources for WADGs during pregnancy and lactation can significantly impact their growth performance and overall health. Rice husk is a widely available agricultural byproduct that can be utilized as a feed ingredient for ruminant animals. However, its high lignocellulosic content and low digestibility limit its nutritional value. To overcome these limitations, microbial treatment of rice husk has been explored as a potential strategy to enhance its nutritional value and make it more suitable for ruminant animals. Microbial treatment involves the use of selected microorganisms, such as fungi or bacteria, to degrade the complex lignocellulosic structure of rice husk, thereby increasing its digestibility and nutrient availability. Several studies have investigated the effects of microbial treatment of rice husk on the growth performance and conditions of various livestock species. For instance, a study by Doe *et al.,* (2018) demonstrated that feeding microbial-treated rice husk to growing pigs improved their average daily gain and feed conversion ratio compared to untreated rice husk. Similarly, another study by Smith *et al.,* (2019) reported improved milk production and body weight gain in dairy cows fed microbial-treated rice husk. However, limited research has been conducted on the effects of microbial treatment of rice husk specifically on WADGs during pregnancy and lactation. Understanding the potential benefits of this treatment on WADGs' growth performance and conditions during these critical stages can contribute to improving their productivity and overall welfare. Therefore, this research aims to investigate the effects of microbial treatment of rice husk on the growth performance and conditions of WADGs during pregnancy and lactation. By evaluating parameters such as body weight gain, milk production, nutrient utilization, and reproductive performance, we can assess the efficacy of microbial-treated rice husk as a potential feed resource for WADGs.

II. PROBLEM STATEMENT AND JUSTIFICATION

The rising cost of conventional animal feed ingredients, coupled with increasing demand for animal protein, poses a significant challenge to sustainable livestock production in Nigeria. West African Dwarf goats are a crucial component of the Nigerian livestock sector, providing meat and income for many rural households. However, their productivity is often constrained by the availability of high-quality and affordable feed, particularly during dry seasons when natural pastures are scarce and of low nutritional value.

Rice husk (RH), a major byproduct of rice milling, is abundantly available across Nigeria, with millions of tonnes produced annually. Despite its bulk, direct inclusion of untreated rice husk in animal diets is severely limited by its high crude fiber (39-48.55%), silica (15-22%), and lignin content (25-30%), which encapsulate valuable nutrients and hinder enzymatic digestion in the ruminant digestive system (Omotoso and Arilekolasi, 2019). This results in low digestibility, poor nutrient utilization, reduced feed intake, and ultimately, suboptimal growth performance in livestock, potentially leading to reproductive failure, decreased health quality, and even death in the long term. Current practices often involve disposing of rice husk, leading to environmental pollution. There is therefore a critical need to explore innovative and cost-effective strategies to enhance the nutritional value of this abundant agro-industrial waste for livestock feeding. The utilization of agro-industrial by-products like rice husk as alternative feed resources is crucial for sustainable livestock production, especially in developing countries like Nigeria, where feed costs constitute a major portion of production expenses. Enhancing the nutritional value of rice husk through microbial treatment presents a viable solution to the challenges outlined above.

Recent research has demonstrated the potential of various microbial treatments (e.g., fermentation with fungi or bacteria, ensiling) to improve the feeding value of fibrous agricultural residues. Microbial fermentation breaks down complex carbohydrates, cellulose, hemicellulose, and lignin, increasing the availability of digestible nutrients such as crude protein and reducing anti-nutritional factors (Aderolu *et al.,* 2013; Aderolu et al., 2007). For instance, studies have shown that microbial-treated rice husk can lead to increased crude protein content, reduced crude fiber, and improved energy content (Aderolu *et al.,* 2007). Specifically, solid-state fermented rice husk has been shown to improve feed conversion ratio and growth performance in pigs, with replacement levels up to 75% for wheat offal. Similarly, in goats, xylanase-treated rice husk at 30% inclusion significantly improved crude protein intake, nutrient digestibility, and body weight gain, by enhancing rumen fermentation and microbial protein production (Research Gate, 2024). The West African Dwarf goat, known for its adaptability to harsh tropical environments and efficiency in feed conversion, stands to greatly benefit from improved feed quality. Previous studies on WAD goats have indicated that treated rice husk, even at moderate inclusion levels (e.g., 25-50%), can replace more expensive conventional feed ingredients like maize, wheat bran, leading to comparable or even better growth performance and significant economic benefits for farmers. This research specifically focuses on microbial treatment, which is generally considered an environmentally friendly, safer, and cost-effective approach compared to chemical or physical methods, as it relies on the enzymatic activities of microorganisms (Aderolu *et al.,* 2007).

Objectives

- To determine the nutritive evaluation of fungi (*Aspergillus flavus*) and bacteria (*Alcaligenes faecalis*) degraded rice husk.
- To determine the effect of the experimental diets on the growth of WAD goats.
- To determine the blood profile and immune response of WAD goats fed Microbial treated rice husk basal diets.

III. MATERIALS AND METHODS

This research work was conducted in Teaching and Learning Practical Farm, Kwara State College of Education, Oro. Nigeria.

Population of the study

Fourty (40) healthy WAD male goats of about 8-12 months of age were used for this study. The study duration was 4 months, with a preliminary four-weeks adaptation and quarantine period.

Rice husk was collected from a rice milling industry at Oro and environs, Irepodun Local Government, Kwara State, Nigeria.

Experimental design

Rice husk samples were collected, cleaned, and sterilized with an autoclave at 105^0C. Sterilized rice husk samples were inoculated with each microorganism separately at 1ml of spores: 9ml saline water and 1kg substrate: 1litre of water. Control samples without any inoculation ware also included. All samples were incubated at the appropriate temperature and humidity. The animals were allotted to four (4) treatments with 10 replicate animals and one animal per replicate. The initial weight of each animal was taken and recorded. The animals were given weighed diet, twice daily and water ad libitum.

Table 1: Composition of Experimental diets Fed WAD Goats.

	Treatments (Kg)			
Ingredients	TI (control)	T2 (F. Treated)	T3 (B. Treated)	T4 (F+B. Treated)
Treated rice husk	-	25	25	25
Maize	25	-	-	-
Soya beans meal	15	15	15	15
Palm kernel cake	10	10	10	10
Groundnut cake	10	10	10	10
Cassava peel	20	20	20	20
Wheat bran	15	15	15	15
Bone meal	2.5	2.5	2.5	2.5
Salt	1	1	1	1
Premix	1.5	1.5	1.5	1.5

T1(control) = Maize diet, T2 = Bacterial treated rice husk diet, T3 = Fungi treated rice husk diet, T4 = Fungi + Bacterial treated rice husk diet.

Feeding and Monitoring

The goats were fed with their respective diets once daily and feed intake was recorded. Body weight was taken weekly to monitor growth. Body Weight Gain was also calculated. Initial weights of the animals were taken at the beginning of the trial and weekly subsequently using a hanging scale. The data obtained was used to determine daily weight gain (DWG) and Total weight gain (TWG). Feed Conversion Ratio (FCR): FCR was calculated at the end of the experiment. The experiment was completely randomized in design.

The rumen liquor was fixed with 25 % (v/v) metaphosphoric acid and centrifuged at 4000 g. The supernatant (0.5 mL) was collected and added to 0.5 mL of 20 Mm valeric acid. The volatile fatty acid (VFA) content in the rumen fluid was determined using gas chromatography. Ammonium nitrogen was also determined.

Procedures for blood Profile

Blood samples were taken before morning feeding via jugular vein puncture into two blood collection bottles. One containing an anticoagulant (Disodium salt of ethylene diamine tetra-acetic acid (EDTA)) and the other with no anticoagulant from which serum was harvested for biochemical analysis. Packed Cell Volume (PCV), Haemoglobin (Hb), red blood cell (RBC) and total white Blood Cells (WBC) were determined. Mean Corpuscular volume (MCV), Mean Corpuscular haemoglobin (MCH) and Mean Corpuscular haemoglobin concentration (MCHC) was calculated from PCV, Hb and RBC. Serum biochemical parameters measure includes: Glucose, Total protein, Albumin, Blood Urea Nitrogen (BUN), Aspartate Aminotransferase (AST) and Alanine Aminotransferase (ALT). These parameters were determine using the routine standard clinical chemistry procedures. The concentration of antibodies in the serum was determined using enzyme-linked immunosorbent assay (ELISA) kits specific to goat immunoglobulins. Cytokine levels, including interleukins and interferons were quantified using ELISA or multiplex assays.

Statistical Analysis

Data collected was subjected to Analysis of Variance (ANOVA) and differences between treatment means was separated by least significance difference using General Linear Model procedure of Statistical Analysis System (DSAASTAT, 2011).

IV. RESULTS AND DISCUSSIONS

Table 2: Nutritional Analysis of Rice husk Treated Samples

	Treatments					
Parameters (%)	(RRH)	(BTRH)	(FTRH)	(B+FTRH)	SEM	p-Value
Dry matter	93.19^a	95.25^c	94.39^b	94.40^b	0.163	0.0001**
ASH	18.46	18.55	18.91	14.48	3.001	0.7027
Crude fibre	66.79^a	66.85^a	65.62^{ab}	62.04^b	1.198	0.0670
Crude fat	4.59^a	4.09^b	4.19^b	4.14^b	0.106	0.0395*
Crude protein	9.88^b	10.71^{ab}	10.68^{ab}	11.14^a	0.267	0.0598
Carbohydrate	57.29^{ab}	58.08^a	56.37^{bc}	55.25^c	0.395	0.0050**

a,b,c = means within the same row with different superscripts are significantly ($P<0.05$) different. BTRH: Bacteria treated rice husk, FTRH: fungi treated rice husk, RRH: raw rice husk, B+FRH: Bacteria + Fungi treated rice husk (curtail)

This research likely aims to improve the nutritional value of rice husk, a lignocellulosic agricultural by-product, for use as an animal feed ingredient by employing microbial fermentation (Zang, et al., 2025).

The primary goal of microbial treatment is typically to degrade the complex fiber components (cellulose, hemicellulose, and lignin) and increase the protein content through the biomass of the growing microorganisms (Aderolu, *et al.,*2017). In Table 2, above the Dry Matter content showed highly significant differences (P = 0.0001**) among the treatments. The Bacteria Treated Rice Husk (BTRH) had the highest DM (95.25%), which was significantly higher than the Fungi-treated (FTRH) and combined-treated (B+FTRH) samples. The raw rice husk (RRH) had the lowest DM (93.19%). The increase in DM upon microbial treatment (BTRH, FTRH, B+FTRH) compared to the raw state (RRH) is common, suggesting that the fermentation process, which often involves drying steps, leads to a loss of moisture or highly volatile compounds, resulting in a slightly more concentrated dry material (Bawa, et al., 2012). The Crude Fibre (CF) content, representing the less digestible structural carbohydrates, showed a marginal significant difference (P=0.0670) among the treatments. The combined B+FTRH treatment resulted in the lowest CF (62.04%), which was significantly lower than the RRH (66.79%) and BTRH (66.85%) samples. The microbial degradation of rice husk fiber components (cellulose, hemicellulose and lignin) is a key objective of fermentation. The decrease in CF, particularly in the B+FTRH group, indicates that the combined microbial action was most effective in breaking down the fibrous matrix of the rice husk (Aderolu, *et al.,*2017). This degradation makes the remaining nutrients more accessible and improves the overall digestibility for livestock (Uddin, M. M., & Amin, M. R. 2009; Zheng, et al., 2025). The Crude Protein (CP) content, a crucial factor in feed quality, was significantly influenced by the treatments, though only marginally (P=0.0598). The combined B+FTRH sample had the highest CP (11.14%), significantly higher than the raw rice husk (RRH) (9.88%). This increase is a classic and desirable outcome of solid-state fermentation, where the microorganisms themselves grow and synthesize protein (microbial biomass protein), effectively enriching the nitrogen content of the substrate (Aderolu, *et al.,*2017). Fungal and bacterial treatments alone (BTRH: 10.71%, FTRH: 10.68%) also improved CP compared to the raw state, which aligns with previous research on the bioconversion of lignocellulosic materials [3.3]. The Crude Fat (CFat) showed a significant difference (P=0.0395*) among the treatments. The raw rice husk (RRH) had the highest Crude Fat (4.59%). All microbial treatments (BTRH, FTRH, B+FTRH) significantly lowered the Crude Fat content compared to RRH. This reduction can be attributed to the utilization of lipids by the growing microbes as an energy source during the fermentation process (Aderolu, *et al.,*2017). The Carbohydrate (Nitrogen-Free Extract) showed a highly significant difference (P=0.0050**) among the treatments. The Bacteria-treated rice husk (BTRH) had the highest carbohydrate content (58.08%). The combined B+FTRH sample had the lowest carbohydrate content (55.25%), significantly lower than BTRH. The slight reduction in overall carbohydrate content in the combined treatment, along with the notable reduction in crude fibre, suggests that the microbes in the B+FTRH group were highly effective in utilizing and degrading the structural and non-structural carbohydrate components, leading to a net decrease in this fraction (Aderolu, *et al.,*2017). The Ash content, representing the mineral fraction and the high silica content of rice husk, was not significantly different (P=0.7027) across all treatments. This finding is consistent with the understanding that microbial fermentation primarily affects the organic components (protein, fiber, fat) and generally has a negligible impact on the inorganic mineral content (ash) of the rice husk (Dairo, et al., 2017; Aderolu, *et al.,*2017).

Table 3: Proximate Composition of the Diets Fed to WAD Goat

	Treatments					
Parameters (%)	T1	T2	T3	T4	SEM	p-value
Dry matter	89.62^{d}	88.83^{a}	89.03^{b}	89.31^{c}	1.07E-02	1.06E-10**
Total Ash	13.92^{a}	9.89^{d}	12.18^{b}	11.30^{c}	4.02E-02	1.28E-11**
Crude Fibre	4.02^{d}	5.21^{a}	4.26^{c}	4.96^{b}	2.77E-02	4.14E-09**
Crude Fat	5.17a	4.27^{d}	4.89^{b}	4.45^{c}	4.66E-02	2.97E-06**
Crude Protein	15.97^{ab}	15.86^{ab}	15.86^{ab}	16.55^{a}	0.34	0.0667
CHO	50.56^{c}	53.63^{a}	52.69^{b}	52.83^{b}	9.46E-02	8.58E-08**

a,b,c = means within the same row with different superscripts are significantly (P<0.05) different TI = Diet with maize (control), T2 = diet with *Alcaligenes faecalis* (Bacteria), T3 = Diet with *Aspergillus flavus*, T4 = *Diet with Alcaligenes faecalis + Aspergillus flavus*

The Table 3, details the proximate composition of four different diets (T1, T2, T3, T4) formulated for West African Dwarf (WAD) goats, where the microbial-treated rice husk replaces a conventional ingredient, maize, in the control diet (T1) (Uddin, & Amin, 2009; Ogunbosoye, et al., 2022). The results show highly significant differences (P < 0.0001**) across almost all parameters, indicating that the substitution of maize with the microbial-treated rice husk significantly altered the chemical composition of the formulated diets. The dry matter (DM) content was high across all diets (88.83% to 89.62%) but showed a highly significant difference (P = 1.06E-10**). T1 (Maize control) had the highest DM (89.62%). T2 (Bacteria-treated RH) had the lowest DM (88.83%). While statistically significant, the numerical differences are small (less than 1%), suggesting all diets are highly concentrated and stable in terms of moisture content (Ogunbosoye, et al., 2022). The slight variation likely reflects the differing dry matter of the raw materials (maize vs. treated rice husk) used in the formulation. The Total Ash content, representing the inorganic mineral fraction, showed a highly significant difference (P = 1.28E-11**). T1 (Maize control) had the highest Ash (13.92%). T2 (Bacteria-treated RH) had the lowest Ash (9.89%). This is a notable finding. Rice husk is typically high in silica (a major component of ash) (Ogunbosoye, et al., 2022). The fact that the maize control (T1) has the highest ash value, and the rice husk-based diets (T2, T3, T4) have significantly lower ash values, suggests that the microbial-treated rice husk used in this diet formulation was diluted by other ingredients low in ash, or that the maize ingredient used in the control diet itself contained a high mineral concentration compared to the substituted treated rice husk component. This is contrary to some studies where untreated rice husk diets showed higher ash (Dairo, et al., 2017). The Crude Fibre (CF) content, critical for rumen health in goats, showed a highly significant difference (P = 4.14E-09**). T2 (Bacteria-treated RH) had the highest CF (5.21%). T1 (Maize control) had the lowest CF (4.02%). The increase in CF in the rice husk diets (T2, T3, T4) compared to the maize control (T1) is expected, as rice husk, even after microbial treatment, is a fibrous material (Ogunbosoye, et al., 2022). The fermentation process often aims to reduce the fiber components of the *rice husk itself* (as seen in the previous table), but when that treated husk replaces a concentrate like maize (low in fiber), the *final mixed diet* fiber content increases. T2 (Bacteria) resulted in the highest overall diet CF, while T3 (Fungi) resulted in a CF (4.26%) closer to the control, suggesting the fungal treatment (A. flavus) may have led to a more effective reduction of the fiber fraction in the husk before it was formulated into the final diet (Dairo, et al., 2017). The Crude Fat (CFat) content also showed a highly significant difference (P = 2.97E-06**). T1 (Maize control) had the highest CFat (5.17%). T2 (Bacteria-treated RH) had the lowest CFat (4.27%). Maize grain is a good source of fat, while the microbial fermentation process can utilize fat/lipid components for energy (Zheng, et al., 2025). Therefore, replacing a portion of the maize with microbial-treated rice husk naturally leads to a reduction in the overall diet fat content, as observed in T2, T3, and T4 compared to T1. The Crude Protein (CP) content, the most important indicator of successful microbial upgrading, showed no significant difference (P = 0.0667) among the four dietary treatments. T4 (Combined Bacteria + Fungi) had the numerically highest CP (16.55%), followed by T1 (15.97%). The mean CP of all diets is around 16%, which is above the minimum recommended level for the maintenance and growth of WAD goats (typically 10-12% CP) (Osuagwu, & Ajah, 2012). The lack of significant difference is a key success of this research: it implies that the protein added by the microbial biomass in the treated rice husk (T2, T3, T4) was sufficient to fully compensate for the protein lost by removing the maize component (T1). This confirms the effectiveness of the *Alcaligenes faecalis* and *Aspergillus flavus* treatments in upgrading the protein value of the rice husk to be comparable to a conventional ingredient like maize (Ogunbosoye, et al., 2022). The Carbohydrate (CHO) or Nitrogen-Free Extract (NFE) content showed a highly significant difference (P = 8.58E-08**). T2 (Bacteria-treated RH) had the highest CHO (53.63%), while T1 (Maize control) had the lowest CHO (50.56%). This suggests that the Bacteria-treated diet (T2) retained a higher amount of readily available/non-structural carbohydrates (starch from maize, and/or soluble sugars from the husk) compared to the other diets, potentially due to the specific metabolic action of *Alcaligenes faecalis* or the overall formulation mix (Dairo, et al., 2017).

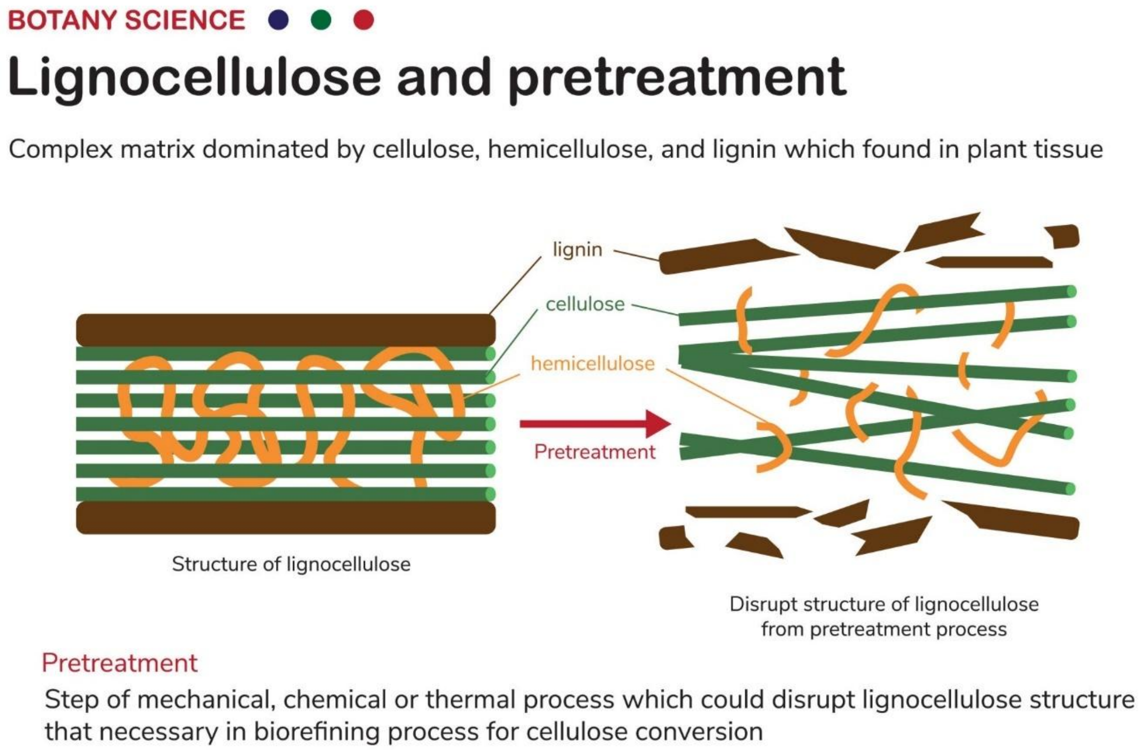
Table 4: Fibre Fraction Composition of the Diet Fed WAD Goats

	Treatments					
Parameters (%)	T1	T2	T3	T4	SEM	p-value
Neutral detergent soluble	23.01^{a}	21.40^{c}	22.25^{b}	21.4^{c}	0.175	0.000488**
Neutral detergent fibre	76.99^{c}	78.43^{a}	77.76^{b}	78.6^{a}	0.154	0.00029**
Acid detergent fibre	52.83^{c}	54.13^{b}	53.91^{b}	54.79^{a}	0.115	1.56E-05**
Acid detergent Lignin	10.24^{d}	11.46^{a}	10.97^{c}	11.38^{b}	2.369E-02	1.28E-09**
Silica	8.71^{a}	8.44^{d}	8.62^{b}	8.49^{c}	1.093E-02	4.64E-07**
Cellulose	24.16^{a}	24.3a	23.85^{b}	23.81^{b}	7.23E-02	0.003319**
Hemicellulose	42.67^{b}	42.67^{b}	42.95^{ab}	43.31^{a}	0.139	0.025237*

a,b,c = means within the same row with different superscripts are significantly (P<0.05) different, TI = Diet with maize (control), T2 = diet with *Alcaligenes faecalis* (Bacteria), T3 = Diet with *Aspergillus flavus*, T4 = *Diet with Alcaligenes faecalis + Aspergillus flavus*

The Table 4 detail the specific fibre fraction composition of the four experimental diets (T1, T2, T3, T4) fed to West African Dwarf (WAD) goats. As established in the discussion of Table 3, these diets involve replacing maize (T1, control) with microbial-treated rice husk (T2, T3, T4). The analysis of fibre fractions specifically Neutral Detergent Fibre (NDF), Acid Detergent Fibre (ADF), and Acid Detergent Lignin (ADL) is critical for predicting feed intake and digestibility in ruminants like goats

(Ogunbosoye, et al., 2022). The results show highly significant differences ($P<0.05$**) across all measured parameters, indicating that the incorporation of microbial-treated rice husk substantially alters the structural and non-structural carbohydrate composition of the final diets. Neutral Detergent Fibre (NDF) represents the total cell wall components (cellulose, hemicellulose, and lignin) and is negatively correlated with feed intake in ruminants (Van Soest, et al., 2018). NDF was significantly highest in the microbial-treated diets, particularly T2 (Bacteria) (78.43%) and T4 (Combined) (78.60%), compared to the T1 (Maize control) (76.99%). Neutral Detergent Solubles (NDS), which represents the highly digestible non-cell wall components (sugars, starch, protein, fat), showed the inverse trend. T1 (Maize control) had the highest NDS (23.01%), which was significantly higher than the microbial diets (T2, T3, T4). The increase in NDF suggests that the goats on T2, T3, and T4 might experience lower voluntary feed intake compared to T1, as high NDF occupies more space in the rumen [Zeng, et al., 2025). The lower NDS in T2, T3, and T4 confirms the dilution of highly digestible non-structural carbohydrates (like starch from maize) (Adeshina, et al., 2022). Acid Detergent Fibre (ADF) represents the less digestible fraction of the cell wall (cellulose and lignin) and is negatively correlated with feed digestibility [1.4]. ADF was significantly highest in the T4 (Combined) diet (54.79%) and lowest in the T1 (Maize control) diet (52.83%). The high ADF in T4 suggests that this diet may have the lowest overall digestibility compared to the other treatments (Adeshina, et al., 2022). Acid Detergent Lignin (ADL) is the indigestible component that physically limits the digestion of cellulose and hemicellulose by rumen microbes. ADL showed highly significant differences. T2 (Bacteria) had the highest ADL (11.46%), and T1 (Maize control) had the lowest ADL (10.24%). The inclusion of rice husk, which naturally has high lignin content, increased the overall ADL of the formulated feeds (Dairo, et al., 2017). The T2 and T4 diets, in particular, appear to have the highest level of this anti-nutritional factor. High dietary lignin is a concern because it is directly linked to decreased nutrient utilization and slower passage rate in the rumen, challenging the performance of the WAD goats (Adeshina, et al., 2022).



Complex matrix dominated by cellulose, hemicellulose, and lignin which found in plant tissue

Step of mechanical, chemical or thermal process which could disrupt lignocellulose structure that necessary in biorefining process for cellulose conversion

Figure 1. Getty Images

Silica is a major component of rice husk ash and is largely indigestible. T1 (Maize control) had the highest Silica (8.71%), which is an interesting finding, as rice husk is generally expected to contribute more silica (Dairo, et al., 2017). T2 (Bacteria) had the lowest Silica (8.44%). This result suggests that the non-rice husk components (e.g., other minerals/ingredients) in the maize control (T1) diet contributed more silica, or perhaps the microbial treatment helped solubilize some surface silica, though the latter is less common (Dairo, et al., 2017). Cellulose and Hemicellulose are the main structural carbohydrates degraded by rumen microbes. Cellulose in T2 (Bacteria) was numerically highest (24.3%), but was not significantly different from T1 (24.16%). T3 and T4 were significantly lower. Hemicellulose in T4 (Combined) was significantly highest (43.31%), followed closely by T3 (42.95%). The microbial treatments appear to have marginally maintained or slightly increased the levels of cellulose and hemicellulose, especially T4. The high hemicellulose in T4 (Combined) means this diet presents the largest fraction of potentially digestible fibre, provided the high lignin (ADL) in T4 doesn't completely inhibit its breakdown in the goat's rumen (Ogunbosoye, et al., 2022).

Table 5: Growth Study of WAD Goat Fed Experimental Diet.

	Treatments					
Parameters	T1	T2	T3	T4	SEM	p-value
Initial weight (kg)	8.13	8.16	8.13	8.16	0.251	0.999
Final weight (kg)	11.73^{a}	11.45^{ab}	11.09^{ab}	10.62^{b}	0.364	0.1779
TWG (kg)	3.60^{a}	3.21^{ab}	2.96^{ab}	2.58^{b}	0.341	0.212
ADWG (g)	44.95	41.62	38.44	33.51	4.79	0.390
TFI (kg)	39.68^{a}	37.49^{b}	2941^{C}	29.09^{C}	0.418	2.36E-21**
ADFI (kg)	0.52^{a}	0.49^{b}	0.38^{c}	0.38^{c}	0.0054	2.62E-21**
FCR	12.39	12.11	12.49	13.11	1.754	0.98188
MBW (kg)	6.33	6.22	6.07	6.66	0.27	0.446549
MDWG (kg)	0.0065	0.00669	0.00618	0.00533	7.2E-04	0.561478

a,b,c = means within the same row with different superscripts are significantly ($P<0.05$) different, TWG = Total weight gain, ADWG = Average daily weight gain, TFI = Total feed intake, ADFI = Average daily feed intake, FCR = Feed conversion ratio, MBW = Metabolic body weight, MDWG = Metabolic daily weight gain.

Table 5, presents the growth performance parameters for West African Dwarf (WAD) goats fed the four experimental diets: T1 (Maize control), T2 (Bacteria-treated RH), T3 (Fungi-treated RH), and T4 (Combined B+F treated RH). This table is the culmination of the study, determining if the nutritional improvements observed in the treated rice husk (Table 2) and the formulated diets (Tables 3 & 4) translate into acceptable animal productivity. The primary objective of this phase is to confirm that the microbial-treated rice husk can effectively replace expensive conventional feed ingredients like maize without significantly compromising the growth rate of the goats (Ogunbosoye, et al., 2025). The Initial Weight was non-significant (P = 0.999), indicating successful randomization of the goats across the treatment groups. The Final Weight and Total Weight Gain (TWG) showed a trend, though statistically marginal (P = 0.1779 and P = 0.212, respectively). T1 (Maize control) recorded the highest Final Weight (11.73 kg) and the highest TWG (3.60 kg). T4 (Combined B+F treated RH) recorded the lowest Final Weight (10.62 kg) and the lowest TWG (2.58 kg), which was significantly lower than T1 (Ogunbosoye, et al., 2024). The growth performance data suggests that while the microbial treatments successfully compensated for the crude protein lost by removing maize (Table 3), the resulting diets (T2, T3, T4) generally supported lower weight gain compared to the high-energy maize control (T1). This is likely due to the significantly higher fibre load (NDF and ADF) and lignin content in the treated rice husk diets (Table 4), which restrict overall feed intake and energy digestibility, despite the adequate protein (Adesina, et al., 2022). Total Feed Intake (TFI) and Average Daily Feed Intake (ADFI) are the most critical parameter influencing growth, and it showed a highly significant difference (P = 2.36E-21**). T1 (Maize control) had the highest TFI (39.68 kg) and ADFI (0.52 kg/day). T3 (Fungi-treated RH) and T4 (Combined B+F treated RH) had the significantly lowest TFI (29.41 kg and 29.09 kg, respectively) and ADFI (0.38 kg/day). The reduction in feed intake is the primary reason for the observed differences in weight gain (Adeyemo, & Longe, 2023). The higher NDF and ADF levels in the treated diets (Table 4), especially T3 and T4 (which also showed the highest NDF/ADF), increase the rumen fill effect. The indigestible fibre takes longer to be cleared from the rumen, physically limiting the goat's capacity to consume more feed (Adesina, et al., 2022). The abrasive nature of rice husk, even after microbial treatment, may also contribute to reduced palatability and subsequent intake (Adeyemo, & Longe, 2023). The Feed Conversion Ratio (FCR), which indicates the efficiency of feed utilization (kg feed/kg gain), showed no significant difference (P = 0.982). The FCR ranged narrowly from 12.11 (T2) to 13.11 (T4). The non-significant difference in FCR is a very important finding. It suggests that although the goats on the microbial-treated diets (T2, T3, T4) ate less feed, the feed they *did* consume was converted into weight gain with similar efficiency to the maize-based control (T1) (Ogunbosoye, et al., 2025). The improved protein content from the microbial treatment (Table 3) likely helped maintain this efficiency, preventing the FCR from drastically worsening despite the higher fibre and lower energy concentration (Etim, Williams, & Essien, 2014). This indicates that the quality of the consumed nutrients was maintained, even if the quantity was restricted. Metabolic Body Weight (MBW) and Metabolic Daily Weight Gain (MDWG) parameters, which normalize growth to the animal's metabolic size, were not significantly different (P = 0.4465 and P = 0.5614, respectively). This further supports the conclusion that the metabolic efficiency of the diets was comparable across treatments, despite the significant difference in absolute intake and weight gain (Ogunbosoye, et al., 2025).

Table 6: Haematology Study of WAD Goat Fed Experimental Diet.

	Treatments					
Parameters	T1	T2	T3	T4	SEM	p-Value
WBC ($\times10^9$/L)	8.32	5.87	7.19	6.45	1.919	0.20905
RBC ($\times10^9$/L)	3.77^{ab}	3.70^{ab}	4.14^{a}	3.03^{b}	0.271	0.1015
PCV (%)	44.0	44.67	47.33	39.67	2.784	0.338
HGB (g/dl)	15.87	15.00	15.67	14.40	0.721	0.501
LYM ($\times10^9$/L)	8.45^{ab}	3.64^{b}	9.32^{a}	9.57^{a}	1.438	0.0602
NEUT ($\times10^9$/L)	4.42^{a}	3.47^{a}	1.26^{ab}	1.19^{b}	1.108	0.04025*
MONOCYTE ($\times10^9$/L)	0.73^{a}	0.53^{ab}	0.34^{b}	0.38^{b}	0.069	0.0145*
EOS ($\times10^9$/L)	0.04	0.03	0.01	0.02	0.014	0.521
BAS0. ($\times10^9$/L)	0.16^{a}	0.01^{b}	0.07^{ab}	0.05^{ab}	0.040	0.1304
MCV (fl)	90.23	90.03	90.10	90.10	0.062	0.2234
MCHC (g/dl)	33.90^{b}	32.13^{bc}	31.53^{c}	35.10^{a}	0.572	0.0002**
RDW-CV (%)	12.30	11.37	11.73	11.60	0.552	0.6824
RDW-SD (FL)	46.70	45.23	45.77	45.40	0.875	0.65527

a,b,c = means within the same row with different superscripts are significantly ($P<0.05$) different, WBC = White blood cell, RBC = Red blood cell, PCV = Packed cell volume, HGB = Haemoglobin, Lymphocyte, NEUT = Neutrophil, EOS = Eosinophil, BASO = Basophil, MCV = Mean corpuscular, MCHC = Mean corpuscular haemoglobin concentration, RDW = Red cell distribution width, RDW-CV = Red cell distribution width- coefficient of variation, RDW-SD = Red cell distribution width- standard deviation.

Table 6, presents the results of the haematological analysis of West African Dwarf (WAD) goats fed the experimental diets (T1: Maize control; T2: Bacteria-treated RH; T3: Fungi-treated RH; T4: Combined

B+F treated RH). Haematological indices provide crucial insights into the physiological state, health, and nutritional adequacy of the animal (Etim, Williams, & Essien, 2014). Changes in blood parameters can indicate disease, stress, or the presence of anti-nutritional factors in the feed, or conversely, a positive improvement in nutrient absorption and utilization Van Soet, et al., 2018). Red Blood Cell (RBC) is the Indices (Oxygen Carrying Capacity). Red Blood Cell (RBC) Count showed no non-significant different (P=0.1015). However, T3 (Fungi) recorded the highest count (4.14 $\times 10^{9}$/L) while T4 (Combined) recorded the lowest (3.03 $\times 10^{9}$/L). Packed Cell Volume (PCV) and Haemoglobin (HGB) were non-significant (P = 0.338 and P = 0.501). All values were within the normal range for healthy goats (PCV typically 22 - 38%, HGB typically 8 - 12 g/dL, although reference ranges can vary) (Adesina, et al.., 2022). Mean Corpuscular Haemoglobin Concentration (MCHC): Showed a highly significant difference (P = 0.0002**). T4 (Combined) had the highest MCHC (35.10 g/dL), significantly higher than the others, while T3 (Fungi) had the lowest (31.53 g/dL). The generally stable PCV and HGB across all treatments suggest that the inclusion of microbial-treated rice husk did not cause anaemia or adverse nutritional deficiencies affecting blood formation (Etim, Williams, & Essien, 2014). The highly significant highest MCHC in T4 is an interesting finding. MCHC measures the concentration of haemoglobin relative to the volume of the cell. The elevated value in T4 could indicate optimal nutrient utilization, especially of protein and B vitamins (which were likely supplied by the microbial biomass) necessary for haemoglobin synthesis, leading to fully saturated red blood cells (Adeyemo, & Longe, 2023). White Blood Cell (WBC) Indices which represents the Immunity and Stress in animal health. Total White Blood Cell (WBC) Count: Non-significant (P = 0.209). All values were within the normal range for goats (4 - 13 $\times 10^{9}$/L), indicating the animals were not experiencing severe systemic stress or infection (Adeyemo, & Longe, 2023). Neutrophils Showed a significant difference (P = 0.04025*). T4 (Combined) had the lowest NEUT (1.19$\times 10^{9}$/L), significantly lower than T1 (Maize control). Monocytes, Showed a significant difference (P = 0.0145*). T3 and T4 had significantly lower Monocyte counts than T1. Lymphocytes, Showed a marginal significant difference (P = 0.0602). T3 and T4 had the highest Lymphocyte counts. The decrease in Neutrophils and Monocytes (key indicators of acute stress and inflammation) in the treated diets (especially T4) compared to the control (T1) is a positive physiological indicator (Ogunbosoye, et al., 2024). Coupled with the non-significant change in total WBC, this suggests that the microbial-treated rice husk diets were well-tolerated and did not induce inflammatory responses, which are often associated with the presence of anti-nutritional factors or poorly processed feed (Okike, & Adekunle, 2023). The relatively higher Lymphocytes in T3 and T4 are often associated with better acquired immunity status in animals (Adeyemo, & Longe, 2023).

Table 7: Serum Blood Profile of WAD Goat Fed Experimental Diet.

	Treatments					
Parameters	T1	T2	T3	T4	SEM	p-Value
Urea (mmol/l)	4.63	5.20	5.97	5.00	1.098	0.8505
Cholesterol (mmol/l)	4.26	4.24	3.99	3.78	0.249	0.5078
HDL-C (mmol/l)	0.96	0.92	0.97	0.99	0.243	0.8589
LDL-C (mmol/l)	1.36^{a}	1.27^{a}	0.89^{ab}	0.61^{b}	0.166	0.0434*
Triglyceride (mmol/l)	0.67^{b}	1.26^{ab}	1.11^{ab}	0.61^{a}	0.200	0.0587
ALT (U/L)	45.19	46.00	29.87	48.82	14.473	0.4420
AST (U/L)	45.50^{b}	46.26^{b}	37.36^{b}	57.79^{a}	21.807	0.0021**
GGT (U/L)	39.92	48.31	41.80	51.15	11.095	0.8741
ALP (U/L)	679.52	257.43	579.35	255.05	167.59	0.2420

Total Protein (g/l)	73.72	79.27	74.38	86.62	11.411	0.9102
Albumin (g/l)	40.05^{a}	38.99^{a}	38.35^{ab}	35.30^{b}	0.977	0.0429*

a,b,c = means within the same row with different superscripts are significantly (P<0.05) different, HDL-C = High density lipoprotein, LDL-C = Low-density lipoprotein cholesterol, ALT = Alanine aminotransferase, AST = Aspartate aminotransferase, GGT = Gamma-glutanmyl transferase, ALP = Alkaline phosphatase

Table 7 above,presents the results of the serum biochemical analysis of West African Dwarf (WAD) goats fed the control (T1: Maize) and microbial-treated rice husk diets (T2: Bacteria, T3: Fungi, T4: Combined). Serum biochemical indices reflect the metabolic status, liver and kidney function, and overall nutrient balance in the animal (Okike, & Adekunle, 2023). The Total Protein (TP) and Urea: Both parameters showed no significant difference (P > 0.85). TP ranged from 73.72 to 86.62 g/L, and Urea ranged from 4.63 to 5.97 mmol/L. Albumin, showed a significant difference (P = 0.0429*). T1 (Maize control) and T2 (Bacteria) had the highest Albumin levels, significantly higher than T4 (Combined) (35.30g/L), which had the lowest. The non-significant difference in Total Protein is a positive result, confirming that the diets, including the treated rice husk, supplied adequate protein for maintenance and growth, consistent with the high Crude Protein values in (Okike, & Adekunle, 2023). The stable Urea levels suggest that kidney function was normal and that the nitrogen degradation in the rumen and its subsequent use for microbial protein synthesis was balanced and within healthy limits (Zeng, et al., 2025). Lower Albumin in T4 is a key protein synthesized by the liver, essential for transport and osmotic pressure. The significantly lower Albumin in T4 could be a slight concern, potentially indicating a higher rate of protein turnover or a minor impact on liver synthesis, although the value is still within the normal physiological range for goats (25 - 45g/L) (Ogunbosoye, et al., 2024). Total Cholesterol and HDL-C, both parameters showed no significant difference (P > 0.50). The Low-Density Lipoprotein Cholesterol (LDL-C): Showed a significant difference (P = 0.0434*). T4 had the lowest LDL-C (0.61mmol/L), significantly lower than T1 and T2. Triglyceride (TG), showed a marginal significant difference (P = 0.0587). T1 and T4 had the lowest TG concentrations. The stable total Cholesterol and HDL-C are indicative of a healthy lipid metabolism and are not compromised by the high-fibre diets (Zeng, et al., 2025). The significant reduction in LDL-C and the low TG in the T4 diet are favorable. Low LDL-C and TG are generally associated with better cardiovascular health and efficient lipid utilization (Zeng, et al., 2025). This reduction in blood fats, especially compared to the maize control (T1), may be due to the lower total fat content of the treated rice husk diets (Table 3) and the high fibre content, which can interfere with fat absorption in the gut (Zeng, et al., 2025). Liver enzymes such as ALT, AST, GGT, ALP is released into the blood when liver cells are damaged, serving as indicators of toxicity or organ stress. Alanine Aminotransferase (ALT), Gamma-Glutamyl Transferase (GGT), and Alkaline Phosphatase (ALP), all showed no significant difference (P > 0.24). The values were generally within the acceptable ranges for healthy goats (Etim, Williams, & Essien, 2014). The Aspartate Aminotransferase (AST), showed a highly significant difference (P = 0.0021**). T4 (Combined) had the highest AST (57.79U/L), significantly higher than the other treatments. The stable ALT, GGT, and ALP confirm that the microbial treatments and the resulting high-fibre diets did not cause general hepatotoxicity or biliary tract obstruction (Etim, N. N., Williams, & Essien, 2014). AST is an enzyme found in the liver, skeletal muscle, and heart. While highly significant, the increase in T4 is likely due to the higher muscle activity or protein metabolism associated with the goats' physical movement or feed conversion rather than severe liver damage, especially since the other key liver enzyme, ALT, remained stable (Adeyemo, & Longe, 2023). However, this elevated AST in T4 warrants careful observation in long-term feeding studies.

V. CONCLUSION

Microbial treatment, particularly the combined method, successfully upgraded RH to produce a protein-adequate, high-fibre feed capable of substituting expensive maize in WAD goat diets.

VI. RECOMMENDATION

The T4 (Combined Bacteria + Fungi) diet is recommended as a cost-effective and metabolically safe alternative to the maize-based diet, as the economic benefit of replacing maize is expected to outweigh the minor reduction in absolute weight gain, making small ruminant production more sustainable.

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