



## Microbial Loads of Pigs Fed Sundried Soybean Milk Residue

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### Abstract

Screening of raw pig manure collected from crossbred growing pigs fed sundried soybean milk residue were carried out at the piggery unit of the Oyo State College of Agriculture and Technology, Igboora, Nigeria. Eighteen (18) crossbred (Largewhite X Landrace) obtained from piggery unit of Oyo State College of Agriculture and Technology, Igboora, Nigeria weaned pigs were used for the study and the experimental animals were allotted into three treatments with six animals per treatment and two animals per replicate. The experimental design used was completely randomized design, data collected were analyzed using one way analysis of variance of statistical system software. The microbiological assays of fresh faecal, total microbial count, lactobacillus, coliform, salmonella and saccharomyces were isolated from pig manure. The experiment lasted eight weeks. At the end of the experiment, bacteria and protozoa counts were not significantly ( $p > 0.05$ ) different. The highest count ( $3.61 \times 10^9$  cfu/ml) was obtained at T1 (control) and the lowest value ( $3.65 \times 10^9$  cfu/ml) were obtained in pigs fed 10% (T3) sundried soybean milk residue for total microbial count. Lactobacillus value ranged from ( $2.82 \times 10^3$  cfu/ml) to ( $2.85 \times 10^3$  cfu/ml). The highest value of coliform, salmonella and saccharomyces were recorded in pigs kept in the control diet ( $1.66 \times 10^{-1}$ ,  $1.38 \times 10^{-1}$  and  $2.14 \times 10^{-2}$ ) respectively. It can be concluded that sundried soybean milk residue had no influence on the microbial load of pigs.

**Keywords:** Growing Pigs; Microbial Load; Sundried; Soybean Milk Residue

### Introduction

There are a large number and a wide species of symbiotic bacteria living in the intestines of animals. The population of microbes in the intestines of animals is up to  $10^{14}$  early 10 times the number of animal body cells, and the mass can be as high as 1.2 kg which is close to the mass of the human liver. The examples of these microorganisms are bacteria, virus and fungi among which bacteria are the most numerous [1]. Kim and Isaacson, [2] opined that the intestinal flora can provide nutrients and energy for the body, regulate immunity, antagonize pathogenic microorganisms, participate in metabolism and even affect host behavior [3]. Pig gut microbes are mainly distributed in the caecum and the number of microorganisms in the intestinal contents (per gram) is  $10^{12}$

-  $10^{13}$  colony-forming units (CFU), composed of 400-500 kinds of microbes, mainly Bacteroides species (8.5-27.7%) and the thick-walled *Clostridium* XIV group (10.8-29.0%) with the *Clostridium* IV group (25.2%) constituting the advantageous bacterium group [4]. Studies have shown that gut microbes are also involved in regulating animal growth. [5] reported that *Lactobacillus johnsonii* BS15 could significantly improve the daily weight gain and diarrhea index of piglets and improve the growth and development ability and disease resistance of piglets. Animal production has continued to play vital roles in sustaining global agricultural systems, producing products such as meat, milk and egg needed in mitigating protein global malnutrition challenges [6]. However, according to [7] while animals may be seen mainly as sources of these food

products, in practice they produce more dung than anything else. Animal dung is a major source of soil nutrients, especially nitrogen, phosphorus other minerals and organic matter needed by plants for optimal growth and yield [8]. Animal dung has also been used to improve the physical and biological properties of soils and forms a good substrate for bioremediation of toxic pollutants in farming environments [9]. Utilization of animal dung as bioenergy resource, gasification, liquefaction and direct combustion is also widely practiced [6]. Recent increases in animal production have essentially led to increased animal dung generation with consequent disposal challenges that now constituting major environmental hazards in livestock production environments [10]. This study lays a foundation for improving the scientific knowledge of the regulation of economically important characteristics of pigs by the intestinal flora.

**Materials and Methods**

- **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 study areas lies within 7° 15 North and 3° 30 East of equator with an average rainfall of 1278 mm and average annual temperature of 27°C [11].
- **Experimental diet:** The test ingredient (soybean milk residue) in its wet form was collected from women produces soy-milk within Igboora metropolis and sundried for three weeks depending on environmental temperature and intensity of sun and afterwards packed in a polythene bags for further laboratory analysis.
- **Experimental animals and their management:** Eighteen (18) crossbred (Largewhite X Landrace) grower pigs were obtained from the piggery unit of the Oyo State College of Agriculture and Technology, Igboora. The pigs were fed 4% of their body weight as feed per day at the beginning of the experiment and increased as the pigs were advance in age while water was supplied ad libitum. The pigs were allowed three (3) days acclimatization and the animals were fed twice daily morning 7.00am and evening by 4.00pm. The experiment lasted eight (8) weeks.
- **Determination of fecal microbial load:** A fresh fecal sample was collected and analyze, a 9ml of sterilized distill water is left to cool and a gram of sample is measured and poured in

the 9ml making the source, 1ml of the sample is collected. Six seral dilution of 9ml of distill water in each bottle is sterilized and collected from source which is dispensed into one of the labelled bottle (10<sup>-1</sup>, 10<sup>-2</sup>, 10<sup>-3</sup>), 1 ml is collected from one bottle to the other, different agar are used to determine the amount of each type of the bacteria and fungi in each fecal sample. Agar is include MaConkey Agar (used to determine coli from the bacteria), Nutrient agar (to determine total microbes in the fecal), Elu 3 agar (used to determine the amount of Samonella and Enterobacteria in the fecal) MRs agar (used to determine the amount of lactic acid bacteria in fecal was incubated in 300c for 48 hours as described by [12]. PDA agar used to determine amount of Saccharomyces cereviceae (yeast fungi) in feaces.

Ingredients	T1 (0%)	T2 (5%)	T3 (10%)
Maize	46.30	44.62	42.94
Corn bran	15.00	15.00	15.00
Soybean Meal	10.00	9.00	8.00
Sundried Soybean Residue	0.00	2.68	5.36
Palm Kernel Cake	23.00	23.00	23.00
Fish Meal	3.00	3.00	3.00
Bone Meal	2.00	2.00	2.00
Salt	0.50	0.50	0.50
Grower Premix	0.20	0.20	0.20
Total	100.00	100.00	100.00
Determined Analysis			
Dry matter (%)	91.90	90.41	91.71
Moisture (%)	8.94	9.60	8.29
Crude protein (%)	11.20	8.35	18.29
Crude fibre (%)	6.10	5.50	7.10
Ash (%)	5.00	4.61	8.10
Ether extract (%)	3.10	2.80	3.90
Nitrogen free extract (%)	77.60	84.75	62.90
Digestible energy ( kcal/kg)	3410.00	3951.60	3322.09

**Table 1:** Gross composition of experimental diet.

Parameters	T <sub>1</sub>	T <sub>2</sub>	T <sub>3</sub>	SEM
Total microbial count	3.61 X 10 <sup>-9</sup>	3.57 X 10 <sup>-9</sup>	3.56 X 10 <sup>-9</sup>	0.11
Lactobacillus count	2.85 X 10 <sup>-3</sup>	2.83 X 10 <sup>-3</sup>	2.82 X 10 <sup>-3</sup>	0.04
Coliform count	1.66 X 10 <sup>-1</sup>	1.63 X 10 <sup>-1</sup>	1.64 X 10 <sup>-1</sup>	0.14
Salmonella count	1.38 X 10 <sup>-1</sup>	1.36 X 10 <sup>-1</sup>	1.34 X 10 <sup>-1</sup>	0.05
Saccharomyces count	2.14 X 10 <sup>-2</sup>	2.21 X 10 <sup>-2</sup>	2.20 X 10 <sup>-2</sup>	0.05

**Table 2:** Faecal sample of crossbred growing pigs fed sundried soybean milk residue.

## Results and Discussion

The results of microbial loads count of crossbred growing pigs fed sundried soybean milk residue are presented in Table 3. The dietary treatments had no significant ( $p > 0.05$ ) effect on the microbial loads of crossbred growing pigs. Total microbial loads range from  $3.56 \times 10^{-9}$  to  $3.61 \times 10^{-9}$ . The highest lactobacillus count ( $2.85 \times 10^{-3}$ ) was obtained in pigs fed the control diet. [13] reported that Lactobacillus plays a key role in the enzymatic digestion and absorption of starch in the small intestine while the large intestine primarily ferments non starch polysaccharides via bacteria and produces SCFAS which serve as important nutrients for the epithelium and body tissue. In this study, it was found that Lactobacillus had the highest proportion in the intestinal tract. Lactobacillus contributed to the increasing intestinal digestive capacity leading to the high accumulation of Lactobacillus in the intestines of pigs. Colliform was highest ( $1.66 \times 10^{-1}$ ) in pigs fed the 0% inclusion of sundried soybean milk residue while pigs on diet 2 (5% inclusion of sundried soybean milk residue) recorded the least value ( $1.63 \times 10^{-1}$ ). Salmonella values ranged from  $1.34 \times 10^{-1}$  in diet 3 to  $1.38 \times 10^{-1}$  in pigs fed the control diet. Pigs fed 5% inclusion of sundried soybean milk residue recorded the highest value ( $2.21 \times 10^{-2}$ ) for Saccharomyces count while the lowest value ( $2.20 \times 10^{-2}$ ) was obtained in pigs fed 10% inclusion of sundried soybean milk residue. There are a large number of microorganisms present in the intestine and a large number of studies have shown that the intestinal flora has a significant regulatory effect on the growth performance of animals. Total microbial count, lactobacillus, coliform and salmonella were high in control diets in microbial loads this could be as a result of no yeast that enhances the gut integrity and health of the pigs thus reducing the faecal microbial count. A reduction in the amount of microbes may be due to events that occur during fermentation process such as competition for receptor sites of lactobacilli ingested from fermented feed [14], lactic acids and volatile fatty acid created by LAB and fermented feed [15], antimicrobial compounds pro-

duced by LAB [16], low pH [17] and a combination of these factors. Colliform is an important pathogen that inhibits the gastrointestinal tracts of animals, it is regarded as an important resistance and improves digestibility of protein and hemicelluloses [18]. Salmonella is a pathogen of considerable importance in worldwide animal production and the emergence of antibiotic-resistant strains, because of the therapeutic use of antimicrobial agents in animals [19] the findings shows that salmonella values were low in the microbial counts of pigs fed sundried soybean milk residue and this was in contrary to the findings of [20] who reported higher microbial loads in the dung of pigs and other livestock confirming their value in transformation of the wastes components dung into beneficial products. Bacteria and protozoa count of pigs offered sundried soybean milk residue at varying levels reduced at the end of the experiment compared with the control diet, this reductions can be attributed to the presence of some secondary compounds like phytate, saponin, glycoside in sundried soybean milk residue. According to [21] these chemical substance possess antimicrobial, antioxidative, anti-inflammatory and immune-modulatory properties. The activity of bacteriocin in sundried soybean milk residue could be another factor that reduces pathogenic bacteria [22]. Therefore, sundried soybean milk residue may have therefore be responsible for the changes in the ceecal bacteria profile of the pigs. The reduction in Lactobacillus, coliform and numbers caused by feeding sundried soybean milk residue suggests that sundried soybean milk residue feeding is safe to swine and produces a lower contamination level of enteropathogenic bacteria in the gastrointestinal tract.

## Conclusion

The result of this study shows that sundried soybean milk residue is a good feed resource and should be included in the feed of growing pig without any deleterious effect on the microbial load of pigs.

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