

# **INTERNATIONAL JOURNAL OF AGRICULTURE, MANAGEMENT AND TECHNOLOGY**



**Vol 7(1) 2023**

**Published by**  
Federal College of Agriculture,  
Ishiagu Ebonyi State

## POTENTIAL OF MIXED FORAGES (*CALOPOGONIUM MUCUNIODES* AND *PANNICUM MAXIMUM*) AS FEED RESOURCES IN GUT MICROBIAL POPULATION USING PIG

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### ABSTRACT

The gut of pig is a fundamental organ which plays an important role in digestion and host defence. In this a trial was conducted to determine the potential of fresh forages (*Calopogonium mucunoides* and *Panicum maximum*) combination using pigs. A total of 30 grower pigs at average weight of 18kg were used in the 63-day feeding. Five diets were formulated which contained 0, 10, 15, 20 and 25% levels of fresh forage respectively. Each diet formed a treatment which was fed to the pigs. Pigs were fed 4% of their body weight, and water given ad-libitum. Treatments were replicated thrice, and each contained two pigs in a completely randomised design. The parameters taken were the gut contents from the stomach, caecum and colon which were collected by dissecting the segments. The digesta from the segments were collected into a plane sterile tube and taken to the laboratory for microbial gut population count. Result from the treatments show that the numerical values of these beneficial microbes significantly ( $p < 0.05$ ) increased in the forage treated diets when compared with the control except for the stomach which had little fluctuation in the trend of increase. The study, therefore, concludes the dietary inclusion of forage in pigs can improve the gut status thereby benefiting the animal through the production of digestive enzymes.

**Keywords;** Forage, Gut, microbes, Diet and Pig.

### INTRODUCTION

The gut of pig is the fundamental organ which plays important role in digestion of fibre and host defence (Agboola, *et al.*,2015). The microbial population in the gastro-intestinal tract of monogastric animals play key roles in the normal digestion process and maintaining animal health (Falaki, *et al.*,2011).

It has been reported that the population of beneficial bacteria the gut of monogastric increase the pH of gastro-intestinal tract (GIT) due to increase production volatile fatty acid (VFA) Zigger, (2000), but the use probiotics has addressed this problem using digestive enzymes, synthesis of vitamin B and immune stimulation (Buba *et al.*,2018).

The use of forage in growing pigs has significantly improved the caecum and colon beneficial gut microbial population count (Jorgensen *et al.*,1996). Introducing high forage diet in pigs, initially reduced microbial gut population on the colon, but later in few days several cellulotic bacteria increased (Varel,1987). Other findings have shown that the

introduction of forage in the of pigs caused much increase volume caecal digesta (;

This trial, therefore, is aimed at investigating the gut microbial population as affected by dietary combination forages in growing pigs.

### MATERIALS AND METHODS

Site of study

The experiment was conducted at the Department of Animal Nutrition and Forage Science, College of Animal Science and Animal Production, Michael Okpara University of Agriculture, Umudike

### Procuring and processing of experimental material

The forages used for the study were obtained from the university environment. The fresh forages cut at their bloom stage were chopped into small sizes and incorporated into the concentrate feed at 0, 10, 15, 20 and 25% supplementary levels respectively shown in table 1

**Table 1. Composition of experimental diets**

Ingredients	T <sub>1</sub>	T <sub>2</sub>	T <sub>3</sub>	T <sub>4</sub>	T <sub>5</sub>
Concentrates (%)	100.00	90.00	85.00	80.00	75.00
Grass + Legume (%)	0.00	10.00	15.00	20.00	25.00
<b>Total</b>	<b>100.00</b>	<b>100.00</b>	<b>100.00</b>	<b>100.00</b>	<b>100.00</b>
<b>Analysed Composition</b>					
Dry Matter (%)	85.44	86.53	85.94	87.23	85.58

Crude Protein (%)	20.18	19.49	19.15	18.81	17.96
Ether Extract (%)	3.76	3.93	4.02	4.04	4.19
Crude Fibre (%)	11.13	12.81	13.66	14.49	15.34
Ash (%)	9.50	9.81	9.79	10.12	10.28
Nitrogen Free Extract (%)	45.74	43.99	43.09	42.29	41.84
Gross Energy ((kcal/kg)	4.00	3.94	3.92	3.90	3.88

### Experimental design and management of pigs.

Completely randomised design was used. 30 grower pigs of Large white and Landrace strain cross were used. They were divided into five dietary treatments (T<sub>1</sub> -T<sub>5</sub>). Each treatment was replicated three times and each replicate had two pigs. Five different diets were formulated as shown in table 1. The pigs were stabilised with the concentrate diet for two weeks before the commencement of the trial. Within this period, broad spectrum antibiotic, multivitamin and de-wormer were administered to keep the animals fit for the trial, after this, they were randomly allocated to five different treatment groups after taking initial weights. Feeding was daily at 8.00hours and 16.00 hours at 4% of their body weight. Water was also provided *ad- libitum* both in the wallow and drinking trough respectively.

### Data collection and analysis

Two pigs were randomly selected from each of the treatment groups for gut microbial population count. The pigs were slaughtered, and the intestine was removed, then using a surgical blade the gut content from the stomach, caecum and colon were collected by dissecting the segments. The gut content was then placed in a plane sterile tube and taken to the laboratory for microbial population count. The data collected were subjected to analysis of variance (ANOVA) using (SAS, 2004) and significant means were separated using Duncan Multiple Range Test (DMRT) obtained in the same statistical package.

### RESULTS AND DISCUSSION

Table 2 shows the effect of grass + legume forage combination on microbial gut population of pigs. Observation showed that the numerical values of beneficial microbes significantly.

( $p < 0.05$ ) increased in the forage treated diets when compared to the control, except for stomach which had little fluctuation in the trend of increase. This could explain the reason for microbial increase from the stomach to distal small intestine and further to colon as reported by Aro *et al.* (2009). This could have beneficial barrier against pathogen as reported by Linge (2005). Ziggers (2000) in another work reported that the population of useful bacteria like lactobacillus in the ileum of chicken increased the p<sup>H</sup> of the GIT due to increasing production of volatile fatty acids, as a result, the environment of the GIT becomes unsuitable for the activity and multiplication of pathogens. It could also be that the increase in the population of the micro flora in the gut of pigs inhibit colonization of pathogens as reported by Nurmi and Rantala (1973), this could be responsible for increased fermentation which was observed in the pigs fed with forage containing diets. The low population of the microbes in the stomach and trend of significance could be traced to the acidity of stomach as well as the bile secretion from the duodenum which hinder the proliferation of gut microbes as has been similarly reported by Hara and Shanaha (2006).

**Table 2: Effects of Grass + Legume Forage Combination on the Microbial Gut population of Pig**

Parameters	T <sub>1</sub>	T <sub>2</sub>	T <sub>3</sub>	T <sub>4</sub>	T <sub>5</sub>	SEM
Caecum (x10 <sup>4</sup> cfu/ml)	5.50 <sup>c</sup>	7.80 <sup>b</sup>	7.70 <sup>b</sup>	9.50 <sup>a</sup>	10.25 <sup>a</sup>	
Colon (x10 <sup>4</sup> cfu/ml)	6.60 <sup>b</sup>	10.40 <sup>a</sup>	10.60 <sup>a</sup>	10.70 <sup>a</sup>	10.80 <sup>a</sup>	
Stomach (x10 <sup>3</sup> cfu/ml)	4.30 <sup>ab</sup>	3.80 <sup>b</sup>	3.90 <sup>ab</sup>	4.20 <sup>ab</sup>	4.40 <sup>a</sup>	

a-b means along the same row with different superscripts are significantly ( $P < 0.05$ ) different. SEM = Standard Error of Mean

### CONCLUSION

The study shows that dietary inclusion of fresh combined forages affected the gut microbial population of benefit in the stomach, caecum and colon of pigs with the forage containing diets having

higher population of microbes in different segments of the GIT.

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