



Effect of Dietary Supplementation of Probiotics on Faecal Coliforms in Weaned PIGS

KEYWORDS

Probiotic, Pig, Weaning, Faecal microflora

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ABSTRACT The study was conducted to investigate the effect of dietary supplementation of *Lactobacillus acidophilus* and *Saccharomyces cerevisiae* on faecal coliforms in weaned piglets. Thirty weaned Large White Yorkshire piglets (56 days) were grouped in to three groups of ten each. The control (T1) group was fed with basal diet and treatment (T2) and (T3) were fed diet supplemented with 0.1 per cent *Saccharomyces cerevisiae* 10.0 billion CFU/g and 0.1 per cent *Lactobacillus acidophilus* 10.0 billion CFU/g, respectively. During the twelve weeks faecal samples were collected at every four weeks interval to assess coliform count. The average counts of coliform bacteria (CFU at 10-4 dilution) at the start of the study were 11.17 ± 0.72 (T1), 11.98 ± 0.43 (T2) and 12.07 ± 0.62 (T3), and at the end of the 12th week were 9.80 ± 0.62 (T1), 9.93 ± 0.28 (T2) and 9.53 ± 0.17 (T3) groups, respectively. The statistical analysis revealed that, there were no significant differences ($P > 0.05$) between control and treatment groups. It can be concluded from the above study that probiotics at 0.1 per cent of the diet does not have significant effect on faecal coliforms of weaned piglets.

INTRODUCTION

Weaning is a crucial factor involved in pig farming and it is a stressful event for a piglet. When piglets are weaned, the intestinal flora of piglet is altered (Jensen, 1998). Weaned piglets are exposed to environmental and nutritional stress, causing proliferation of pathogenic intestinal bacteria, diarrheal syndrome and growth retardation, as well as increase in both morbidity and mortality. Normal gut structure and function is a result of complex interactions between host animal and micro-organisms colonizing the gut, which may have profound effects on the animal health (Massi *et al.*, 2006). Antibiotics have been supplemented in piglet diets to address digestive and excretory tract issues by increasing growth performance and reducing the incidence of diarrhoea (Wang *et al.*, 2011). However, in recent years, there has been an increased interest to eliminate or minimize the use of antibiotics in livestock as growth promoters, because of the risk of developing cross-resistances against pathogenic bacteria in both human and livestock, linked to the therapeutic and sub-therapeutic use of antibiotics in livestock (Flickinger and Fahey, 2002). The application of probiotics can be a potential alternative strategy to the antibiotic to ameliorate the weaning stress by maintaining gastrointestinal microflora and improve the performance (Rai *et al.*, 2013).

Probiotics are live microorganisms which have been found to confer a health benefit on the host when administered in adequate amounts (Weichselbaum, 2009). Lactic acid bacteria (LAB) acts by production of lactic acid and antimicrobial substances, lowering the pH, and consequently reducing *E. coli* and *Enterobacteria* counts (Nousiainen

and Setälä, 1998). The probiotic yeast *Saccharomyces*, has been found effective in stimulating intestinal immunity and protecting the host from diarrhoea (Buts *et al.*, 1990). The current study was carried out to evaluate the effect of *Lactobacillus acidophilus* and *Saccharomyces cerevisiae*, supplemented to a basal diet on faecal bacteria counts in weaned pigs.

MATERIALS AND METHODS

Twenty weaned Large White Yorkshire piglets of similar body weight and age (eight weeks) were distributed randomly into two groups of ten animals each, maintaining equal sex ratio. The animals were fed to meet the nutrient requirements as specified by ICAR, 2013. The animals in group 1 (T1) served control were fed with basal diet and group 2 (T2) and group 3 (T3) was fed with basal diet supplemented with *Saccharomyces cerevisiae* (10 billion CFU/g) and *Lactobacillus acidophilus* (10 billion CFU/g), respectively at the rate of 1g/kg of basal diet. The ingredient composition and chemical composition of the basal diet are presented in Table 1 and Table 2, respectively. The feeding trial was conducted for 12 weeks. The animals were maintained under standard managerial practices. The animals were fed twice daily and the leftover was recorded to calculate the feed intake. Clean drinking water was provided ad libitum. Feed samples were analysed for proximate principles (AOAC, 2005).

Faecal samples were collected from six animals in each group, once in four weeks (day '0', at end of Week-4, Week-8 and Week-12 of the experiment), by using a sampling spoon, rectal faeces were collected from piglets,

placed in sterile plastic zip lock bags and kept at -20°C and the same were used for fecal coliform count. The procedure followed was as per Giang *et al.* (2010). HiCrome ECC Selective HiVeg[®] Agar (Composition given in Table 3) was used for determining CFU from faecal samples. Data obtained from the study were statistically analysed using one way ANOVA using Graphpad Prism 5.01, computerised software.

RESULTS AND DISCUSSION

The average counts of coliform bacteria recorded during the study for the three treatments is given in Table 4. The graphical representation of the same is depicted in Figure 1.

The average counts of coliform bacteria (CFU/g at 10^4 dilution) at the start of the study were 11.17 ± 0.72 (T_1), 11.98 ± 0.43 (T_2) and 12.07 ± 0.62 (T_3), and at the end of the 12th week were 9.80 ± 0.62 (T_1), 9.93 ± 0.28 (T_2) and 9.53 ± 0.17 (T_3) groups, respectively. The statistical analysis revealed that, there were no significant differences ($P>0.05$) between control and treatment groups. This is in agreement with Mohana Devi and Kim (2014) where they observed no significant difference in faecal microflora in weanling pigs supplemented with probiotic *Enterococcus faecium*. In contrary Giang *et al.* (2011) and Dong *et al.* (2013) observed significantly lower *E. coli* counts and increased *Lactobacillus* counts in the probiotic supplemented groups. Probiotics containing different strains of microorganisms have different efficacy, and some strains may provide certain benefits for the host whereas others do not (Weichselbaum, 2009).

CONCLUSION

The findings from the present study suggests that the two probiotics studied *Lactobacillus* and *Saccharomyces* do not have any effect on faecal coliforms count in the faecal sample. Further studies need to be conducted with combinations of probiotics and also at different levels.

Table 1. Ingredient composition of the basal diet

Ingredients	% level of inclusion
Maize	64.2
Soybean meal	21.9
Wheat bran	12.4
Mineral mixture	1.0
Salt	0.5
Total	100

Table 2: Chemical composition of the diet

Chemical composition (per cent)	Basal Diet
Dry matter	89.90
Crude protein	18.2
Crude fat	3.00
Crude fiber	3.40
Total ash	5.16

Table 3: Composition of the Culture media used

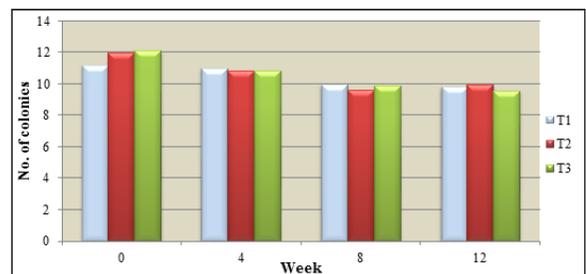
Composition	g/L
HiVeg special peptone	6.000
HiVeg hydrolysate	3.300
Sodium dihydrogen phosphate	0.600
Disodium hydrogen phosphate	1.000
Sodium chloride	2.000
Sodium pyruvate	1.000
L-Tryptophan	1.000
Sorbitol	1.000
Tergitol 7 0	0.150
Chromogenic mixture	0.430
Agar	10.000
Final pH at 28°C	6.8 ± 0.2

Table 4: Average weekly counts of coliform bacteria (CFU/g) (at 10^4 dilution)

Week	Treatments		
	T_1	T_2	T_3
0	11.17 ± 0.72	11.98 ± 0.43	12.07 ± 0.62
4	10.95 ± 0.70	10.82 ± 0.29	10.83 ± 0.18
8	9.93 ± 0.55	9.60 ± 0.17	9.83 ± 0.17
12	9.80 ± 0.62	9.93 ± 0.28	9.53 ± 0.17
Mean \pm SE	10.46 ± 0.35	10.58 ± 0.53	10.57 ± 0.58

Note : Non-significant at level $P>0.05$

Fig. 1: Average counts of coliform bacteria (CFU/g)



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