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Probiotics role of *Saccharomyces cerevisiae* and *Bacillus subtilis* in improving the health status of rabbits' gastrointestinal tract

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Abstract

Background: Probiotics are direct-fed microbial feed supplements which can modulate the gut microflora by competing intestinal pathogens through a competitive process. The present study was conducted to investigate the effect of feeding *Saccharomyces cerevisiae*, *Bacillus subtilis* or their mixture on blood biochemical constituents, intestinal pathogenic load and intestinal histological changes of growing New Zealand White (NZW) rabbits.

Results: Serum total protein, albumin, and globulin were ($P \le 0.05$) increased for rabbits fed supplemented diets. Microbial pathogenic load of small intestinal and caecal contents (*E. coli* and *C. perfringens*) showed reduction ($P \le 0.05$) for rabbits fed supplemented diets, while, *lactobacillus spp.* recorded higher counts ($P \le 0.05$) in intestinal and caecal contents of rabbits fed probiotics supplemented diets than control group. Small intestine length, villus height and crypt depth were higher ($P \le 0.05$) with probiotic diets than control. Musculosa depth was depressed ($P \le 0.05$) with probiotic diets.

Conclusions: It could be concluded that the addition of *Bacillus subtilis* or *Saccharomyces cerevisiae* to diets of growing NZW rabbits by 0.1% is recommended to minimize the pathogenic intestinal load and increasing of beneficial lactobacillus strains as well as improving the intestinal barriers integrity.

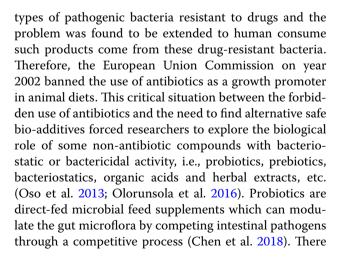
Keywords: Blood constituents, Intestinal and caecal pathogens, Probiotics, Rabbits, Small intestine histomorphology

Background

Rabbits have a unique digestive system; they are both mono-gastric and herbivore animals with special digestive and physiological characterization. It was stated that any imbalance of microflora in the digestive tract of rabbits can result in alteration of pH, dysbiosis and proliferation of pathogens with serious effects on the animal's health and productivity. Antibiotics have been widely used to resist exogenous pathogens and protect the health of gut (Becattini et al. 2016). But the long term and extensive use of antibiotics has led to the appearance of some

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are numerous feed bio-additives which are live beneficial microorganisms i.e. Lactobacillus spp., Streptococcus spp., Bacillus spp. and Saccharomyces spp. These bio-active cultures were found to have specific dynamic effects on competing harmful gut flora and stimulating, immune system resistance against infectious agents, promote feed digestion and absorption and promote the development of intestinal tract (Chen et al. 2018). Furthermore, probiotics can be used as feed or water supplements either in the form of mono or mixed cultures of live microorganisms (Todorov et al. 2007). The ability of probiotics to resist the enteric diseases caused by enteric pathogens such as Escherichia coli, Clostridium perfringens or other enteric pathogens in animals has been discussed in several studies (Alvarez et al. 2001; Kritas and Morrison 2005; Timmerman et al. 2005).

Many strains of bacteria including Bacillus subtilis and yeast as Saccharomyces cerevisiae were noted to have noticeable promising effects on host animals by improving body weight gain, feed conversion efficiency and nutrients digestibility, as well as, preventing proliferation of harmful microorganisms, maintaining intestinal comfort and stimulating the immune system (Kalima et al. 2016; Wang et al. 2017). The effect of bacterial or yeast on intestinal morphology and cell proliferation were histologically examined as length of villi, depth of crypts and glands and villi/crypt ratio. The villus height and the crypt depth are considered as indicators of good intestinal functions. On the contrary, the shorter villi and deeper crypts have been associated with the presence of toxins (Yason et al. 1987), and in such condition it has been resulted in decrease in the surface area for adequate nutrients absorption. Additionally, many researchers found a correlation between the crypt depth and the proliferation rate of epithelial cells, whereas Simon (1989) reported that the number of proliferations and the epithelial cell turnover has great impact on protein and energy requirements of the small intestine mucosa. Fan et al. (1997) reported that the increase in villus height-tocrypt depth ratio are directly correlated with the increase in epithelial turnover and they concluded that, probiotics are affecting the development of intestinal epithelia.

The aim of this study was to evaluate the effect of supplementing rabbit's diet with two types of probiotics (*Bacillus subtilis* and *live Saccharomyces cerevisiae*) or their mixture on blood constituents, intestine and caecum microbial load and intestinal morphological changes of growing NZW rabbits.

Methods

The experimental design and all the research protocols were approved by the Medical Research Ethics Committee (MREC) of the National Research Center with ethical approval code 20/173.

Animals and feeding system

In a feeding experiment lasted 10 weeks, sixty males growing New Zealand White rabbits (NZW) aged eight weeks with an average body weight of 837.0 ± 20.0 g were randomly distributed by weight into four equal groups (15 animals/group), each of five replicates. Growing NZW rabbits were obtained from a commercial farm (Agri-Feed farm, Buhaira governorate, Egypt). Experimental rabbits were housed in galvanized metal wire cages with separate feeding and water trough. The first group (control, R1) was fed on a basal diet consisted of: 32% alfalfa hay, 21% soybean meal (44%), 16% ground yellow corn, 16% barley, 9.2% wheat bran, 3% cane-molasses, 1% lime stone, 0.6% Di-calcium phosphate, 0.5% sodium chloride, 0.5% vitamin & mineral premix and 0.2% DL-Methionine. The second, third and fourth groups (R2, R3 and R4) were fed on the basal diet supplemented with 0.1% live Saccharomyces cerevisiae (dry yeast of 10⁸ cfu/g Rumi Yeast-Saccharomyces cerevisiae Sc47, Neovia, France), 0.1% Bacillus subtilis (bacterial dry media of 3*10⁷ cfu/g Enviva Pro-Bacillus subtilis-Dupont, USA), and a mixture of 0.05% Saccharomyces cerevisiae and 0.05% Bacillus subtilis, respectively. Experimental rations were fed in pellets of 0.3 cm diameter. The chemical composition of the basal diet shown in Table 1 indicates that the total crude protein was 17% and the crude fiber was 13.4% and the calculated digestible energy was around 2650 kcal/ kg which seemed sufficient to provide growing rabbits with their nutritional requirements of energy and protein (De Blas and Mateos 2010).

Experimental diets were offered *ad libitum* once daily at 8.30 a.m. Clean drinking water was freely available at

Table 1 Chemical composition of the basal experimental diet

Item	Nutrients content	
Moisture, %	10.00	
Dry matter composition (DM), %		
Organic matter (OM)	93.15	
Crude protein (CP)	17.00	
Crude fiber (CF)	13.44	
Ether extract (EE)	4.56	
Nitrogen-free extract (NFE)	58.15	
Ash	6.85	

all times. During the whole experimental period, rabbits were kept in a good ventilation brick made ben with daily cleaning by water and anti-septic reagents. At the end of the feeding experiment, five representative rabbits from each group were fasted for 12 h, and then slaughtered to detect the impact of feeding bacterial or yeast probiotics on blood constituents, intestinal microbial load and intestinal morphological changes.

Blood sampling

Blood samples were individually collected at slaughter time in plain centrifuge tubes, left to clot then centrifuged at 4000 rpm for 10 min for serum separation. Serum samples were stored at -20 °C until used for the biochemical parameters. Serum total protein, creatinine and urea were determined according to the method described by Henry (1974). Determination of serum albumin was carried out according to Dumas et al. (1997). Globulin concentration was calculated as the difference between total plasma protein and albumin. Total cholesterol was determined according to Trinder (1969). Triglycerides content was determined according to Fossati and Prencipe (1982). Liver enzymes alanine aminotransferase (ALT) and aspartate aminotransferase (AST) levels were measured by using the method of Reitman and Frankel (1957).

Microbial load of small intestine and caecum

Samples of small intestine and caecum contents from the slaughtered rabbits were individually collected for the microbiological examination. The samples were strained through fourfold of gauze. The microbial counts were studied using their selective media as described by Zimbro and Power (2009) for *E. coli* and *Clostridium perfringens*, while the method described by Kim and Goepfert (1971) was used for *Lactobacillus spp*.

Method of isolating bacteria from the small intestine and caecum in rabbits

Collected samples of small intestine and caecum were strained through four folds of gauze and directly dropped in sterilized tubes and kept in an ice bath for bacterial counts. The samples were then transferred into peptone water at ratio of 1:9 (w/v) and serial dilutions (tenfold) were prepared from each sample. One hundred microliter (100 μ l) aliquot of these dilutions were plated on MacConkey agar medium for *E. coli* and incubated overnight at 37 °C; MRS agar for *Lactobacillus spp.* under anaerobic conditions overnight at 48 °C or Shahidi Ferguson Perfringens (SFP) agar contains 5% egg yolk emulsion and a selective supplement for *Clostridium perfringens* and incubated under anaerobic conditions overnight at 37 °C, depending on the growth characteristics of the

bacterial species and the colonies were counted on culture dishes expressed as cfu/g.

Length measurement of small intestine

Small intestine length of slaughtered rabbits was measured by a scaled ribbon, where the intestine was separated from the whole GIT at the posterior pyloric region as a beginning point and the junction of the ileum with caecum and colon as an end point. Each of the two ends was tied with a surgical thread before separation. The small intestinal length was then measured and recorded in cm.

Intestinal histomorphometry

The small intestine of one randomly chosen animal per replicate from the four groups was taken for histo-morphometric examination. The ilium samples approximately 4-5 cm from the pylorus were carefully dissected (2 cm of tissue samples) during the slaughter time and were first rinsed with saline (0.85% Nacl) and preserved in 10% formalin solution. The routine histological methods were applied to the specimen and were trimmed and transverse sections of 4-5 micron were stained with hematoxylin and eosin. The slides were examined under ×10 magnification and micrographs were taken with trinocular light microscope (Labomed, LX 400. Labo America, Inc. USA) supplied with a computerized digital camera (IVU 3000). Images were analyzed to measure the crypt depth and villi height using stereological image software (Wayne Rasband, National Institute of Health, USA), which its scale was calibrated to the micrometer unit (μm) using a micrometric ruler (PZO-WARS ZAWA-Made in Poland). The villus height was measured (3-5 villi per sample) from the villus tip to villus-crypt junction. Measurements for crypt depth were taken from the base of the villus to the submucosa. The villus: crypt ratio was also calculated for each segment. The muscular layer thickness (Musculosa depth) was the shortest vertical distance from the point between the epimysium to the submucosa layer.

After collecting all needed samples, all slaughtered rabbits terminated hygienically according to the Safety and Health Committee at National Research Centre, Egypt.

Statistical analysis

Data were subjected to one-way analysis of variance according to the following mathematical model:

$$Y_{ij} = \mu + T_j + E_{ij}$$

ltem	Experimental groups				
	R1	R2	R3	R4	
Total proteins, g/dl	$6.04^{b} \pm 0.05$	$7.01^{a} \pm 0.09$	$6.97^{a} \pm 0.02$	$6.93^{a} \pm 0.03$	
Albumin, g/dl	$3.05^{b} \pm 0.08$	$3.38^{a} \pm 0.03$	$3.41^{a} \pm 0.03$	$3.43^{a} \pm 0.02$	
Globulin, g/dl	$2.99^{b} \pm 0.03$	$3.63^{a} \pm 0.03$	$3.56^{a} \pm 0.04$	$3.50^{a} \pm 0.06$	
Creatinine, mg/dl	0.78 ± 0.02	0.77 ± 0.03	0.78 ± 0.01	0.76 ± 0.03	
Urea, mg/dl	$41.49^{a} \pm 0.56$	$39.96^{b} \pm 0.32$	$39.27^{b} \pm 0.50$	$39.47^{b} \pm 0.49$	
Triglycerides, mg/dl	$182.67^{a} \pm 6.17$	$157.67^{b} \pm 5.24$	$154.00^{b} \pm 5.57$	139.67 ^b ±6.36	
Cholesterol, mg/dl	$132.67^{a} \pm 5.81$	$111.67^{b} \pm 4.06$	$105.00^{b} \pm 6.66$	$96.67^{b} \pm 3.48$	
AST, IU/L	29.29 ± 0.66	29.11 ± 0.50	28.86 ± 0.31	28.74 ± 0.17	
ALT, IU/L	19.41 ± 0.49	19.01 ± 0.36	19.03 ± 0.26	18.73 ± 0.49	

R1: control; R2: 0.1% S. cerevisiae; R3: 0.1% B. subtilis; R4: 0.05% S. cerevisiae + 0.05% B. subtilis

a, b and c: means in the same row with different superscripts are significantly different at ($P \le 0.05$)

where $\mu = \text{general}$ mean, $T_j = \text{effect}$ of probiotics source, $E_{ii} = \text{experimental error}$.

The General Linear Model of SAS (1994) for PC was applied, and significant differences among treatment means were separated by using Duncan's multiple range test (Duncan 1955) at 5% level of probability.

Results

Blood biochemical constituents

Data presented in Table 2 showed that, dietary supplementation of probiotics alone or in a mixture significantly ($P \le 0.05$) showed noticeable increases in serum total protein and albumin concentrations compared with un-supplemented control, while creatinine values showed no significant differences among experimental groups. The results of urea and triglyceride levels showed that, rabbits of the control diet (R1) recorded the highest values ($P \le 0.05$) compared with all supplemented groups

(R2, R3 and R4). Similar trend was almost observed for serum concentration of cholesterol.

Intestinal and caecal microbial load

The current results regarding the presence of *E. coli and C. perfringens in* small intestine and caecum of male rabbits are presented in Table 3. The addition of probiotics in the feed had significant ($P \le 0.05$) effects on reducing *E. coli* and *C. perfringens* counts compared to control group (R1). In contrast, numbers of *lactobacillus spp.* as beneficial bacteria in small intestine and caecum of rabbits fed supplemented diets with *Bacillus s.*, live yeast or their mixture (R2, R3, R4) were greater ($P \le 0.05$) when compared to rabbits fed free probiotics diet (R1). In addition, the greatest number of *lactobacillus spp.* was recorded for rabbits received the probiotics mixed culture (R4) group, both in small intestine and caecum.

Table 3 Effect of probiotics dietary supplementation on microbial counts of small intestine and caecum contents of NZW
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ltem	Experimental groups			
	R1	R2	R3	R4
Microbial count in small intestine conter	nts			
Escherichia coli (cfu/g)	$19.10 \times 10^{5 a}$	3.98 × 10 ^{4 b}	$4.45 \times 10^{4 \text{ b}}$	1.16×10^{4} c
Clostridium perfringens (cfu/g)	8.71 × 10 ^{5 a}	1.12 × 10 ^{5 b}	1.41 × 10 ^{5 b}	2.14×10^{4} c
Lactobacillus spp. (cfu/g)	2.92 × 10 ^{7 c}	5.58 × 10 ^{7 a}	$6.25 \times 10^{7 a}$	4.57 × 10 ^{7 b}
Microbial count in caecum contents				
Escherichia coli (cfu/g)	21.30 × 10 ^{6 a}	4.17 × 10 ^{5 b}	6.61 × 10 ^{5 b}	2.57 × 10 ^{5 c}
Clostridium perfringens (cfu/g)	$24.50 \times 10^{5 a}$	5.25 × 10 ^{5 c}	8.91 × 10 ^{5 b}	3.18 × 10 ^{5 c}
Lactobacillus spp. (cfu/g)	2.14 × 10 ^{8 c}	9.55 × 10 ^{8 a}	6.61 × 10 ^{8 b}	15.10×10^{8} ^a

R1: control; R2: 0.1% S. cerevisiae; R3: 0.1% B. subtilis; R4: 0.05% S. cerevisiae + 0.05% B. subtilis

a, b and c: means in the same row with different superscripts are significantly different at ($P \le 0.05$).

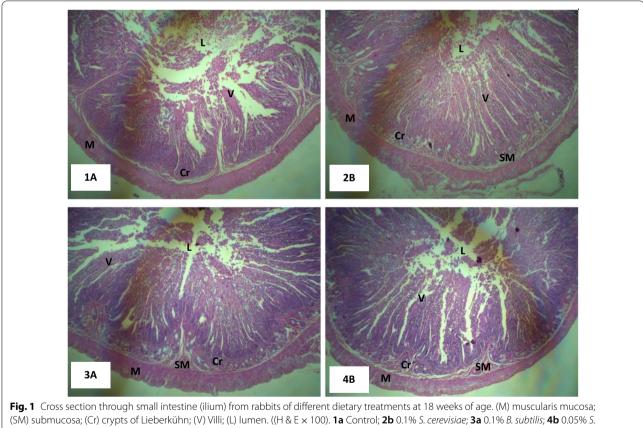
ltem	Experimental groups				
	R1	R2	R3	R4	
Small intestine length, (cm)*	$138.5^{\circ} \pm 0.87$	152.1 ^b ±1.40	$159.0^{a} \pm 1.70$	$152.5^{b} \pm 2.00$	
Villus height, (µm)	$359.7^{b} \pm 18.04$	$446.1^{a} \pm 13.40$	$423.5^{ab} \pm 16.13$	$473.7^{a} \pm 12.36$	
Crypt depth, (μm)	$68.7^{b} \pm 0.33$	$81.2^{a} \pm 2.29$	$80.2^{a} \pm 4.12$	$88.1^{a} \pm 3.02$	
Villus height: crypt depth	5.24 ± 0.34	5.59 ± 0.28	5.28 ± 0.22	5.60 ± 0.28	
Musculosa depth, (µm)	$112.8^{a} \pm 11.86$	$86.9^{b} \pm 3.44$	$94.1^{b} \pm 5.61$	$79.0^{b} \pm 2.90$	

 Table 4
 Effect of probiotics dietary supplementation on small intestine length and histo-morphological parameters (mean ± SE) of NZW rabbits

* Each value is a mean of five replicates.

R1: control; R2: 0.1% S. cerevisiae; R3: 0.1% B. subtilis; R4: 0.05% S. cerevisiae + 0.05% B. subtilis

a, b and c: Means in the same row with different superscripts are significantly different at ($P \le 0.05$).



cerevisiae + 0.05% B. subtilis

Small intestinal length and its histo-morphological changes

The supplementation of probiotics to the experimental diets significantly increased the length of small intestine compared to un-supplemented group, Table 4. The bacterial probiotic has a superior significant effect on intestinal length where it was increased by 15%, while yeast

or mixed probiotic groups increased the length by 10% than that of the control group. The microarchitecture of ilium of the rabbits fed different probiotic diets is given in Fig. 1. Muscularis mucosa layer, submucosa, mucosa, crypts of Lieberkühn, and villi are clearly identified and measured.

In the present study, the histo-morphological analysis of the ilium showed that the supplementation of growing rabbit diets with S. cerevisiae (R2), B. subtilis (R3) or their mixture (R4) has significant positive effects ($P \le 0.05$) on the length of villi (µm) as compared with the control group. It was noticeable that, rabbits of R2 and R4 groups had higher villi length compared to that of rabbits of R3 group, and numerically but not statistically significant the R4 had the highest villus. On the other side, crypt depth (µm) increased ($P \le 0.05$) in all experimental groups compared with the control and the superiority was for R4 group. However, villus height: crypt depth ratio was not significantly affected among experimental groups. Musculosa depth showed significant decreases ($P \le 0.05$) in muscular layer thickness of the ilium in all experimental groups compared with the control one.

Discussion

Blood biochemical constituents

These findings are in agreement with many studies (Abdo 2004; Ooi and Liong 2010; El-Shafei et al. 2019), who reported that blood cholesterol decreased significantly by dietary probiotics. They hypothesized the effect of probiotics on lipid metabolism as: posing bile salt hydro-lase activity and precipitation of cholesterol by some microorganisms such as *Lactobacillus* and *Bifidobacterium*, incorporation of cholesterol or binding to bacteria and making of short-chain fatty acids by probiotic bacteria. Fukushima and Nakano (1995) had been stated another explanation. The authors stated that, probiotics hold hydroxymethyl-glutaryl-coenzyme A; an enzyme involved in the cholesterol synthesis pathway, and therefore decrease the cholesterol synthesis.

It is clearly that the insignificant differences found among all experimental groups for both ALT and AST activity and creatinine concentration might point out to that rabbits could tolerate the addition of probiotics up to 0.1% without any deleterious effects on kidney or liver functions. The significantly increases in serum total proteins, and subsequently albumin and globulins is another indicator of healthy liver as most of blood proteins synthesized in liver. Moreover, previous study (Rishi et al. 2009) found that probiotics supplementation decreased bacterial translocation in the liver of mice challenged with *Salmonella typhimurium* and decreased levels of serum aminotransferases.

Intestinal and caecal microbial load

Probiotics might promote changes on enteric microbiota, so some pathogens cannot adhere effectively (Mattar et al. 2001). These results agreed with (Lee et al. 2000) who found that *E. coli* count was reduced by 25% in the small intestine of rabbits received probiotics. Also, some

probiotics caused reduction of Clostridium associated disease in humans (McFarland 2006; Yamano et al. 2006; Sivamaruthi et al. 2019). The sole addition of probiotic type in particular *B. subtilis* was ($P \le 0.05$) effective than live yeast or the mixed probiotics additives in reducing *E. coli and C. perfringens* counts in small intestine and caecum.

The positive effect of the sole addition of bacteria or yeast (R2 or R3), regarding intestinal *Lactobacillus spp.*, was clearly greater than the mixture supplementation (R4). It could be explained as EL-Badawi et al. (2017) mentioned in our previous study that, there is an antagonistic effect between bacteria and live yeast probiotics when fed in mixed culture.

These results are in agreement with Hamrany et al. (2000) who found a positive effect of a probiotic on E. coli occurrence in the caecum and small intestine of young rabbits. These may be regarded to that Bacillus spp. could stimulate biosynthetic capacities of *Lactobacillus* strains. As the result of increasing beneficial bacteria, mainly lactobacillus, and decreasing of Clostridium and E. coli populations in the small intestine and caecum the normal intestinal microflora can competitively inhibit the survival and proliferation of harmful flora by competing for nutrients in the intestinal habitat, in turn better feed utilization is expected. Furthermore, probiotics improve intestinal balance of host animal and creating gut microorganism conditions that inhibit pathogenic bacteria like E. coli and Clostridium and support beneficial bacteria like Lactobacillus which was reflected on better feed digestion and absorption (Chen et al. 2013; Alhasan et al. 2015; Markowiak and Śliżewska 2018).

Small intestinal length and its histo-morphological changes

It seems logic to state that, bacterial or live yeast probiotics could promote the development of intestinal tract. In this concern, Slezak et al. (2014) found that the length of small intestine in sterilized mice was significantly smaller than that in normal ones. This description was also stated by William and Linda (2000). Villus height and the ratio of villus height to crypt depth are indicators of gastrointestinal tract morphology (Shamoto and Yamauchi 2000) and intestinal histomorphology are one of the important indications of gut health in different animal species.

It is well-known that, intestine transfer nutrients required for maintenance and production of animals. The surface area of the intestinal villi plays an important role in the absorption of nutrients by small intestine. In addition, animal immunity affects by intestinal epithelium status, because of its action as a natural barrier against to pathogenic bacteria and toxic substances present in the intestinal lumen (Paul et al. 2007). Therefore, the improvement of intestinal morphology prompts more available nutrients which leads to improvement of absorption process and intestinal health development (Fan et al. 1997; Choct 2009; Celi et al. 2017).

It was noticed that the increase in villus height and villus height to crypt depth ratio are directly correlated with an increase in intestinal epithelium turnover (Fan et al. 1997), and longer villus is also associated with activated cell proliferation (Parker et al. 2017), whereas shortening of villus and deeper crypts lead to poor nutrients absorption and increased gastrointestinal secretion, and consequently cause reduction of animal performance (Xu et al. 2003). In addition, intestinal villi elongation could enhance enzyme production and digestion by increasing the effective absorptive area and improving the nutrients transport system in intestinal tract (Awad et al. 2009).

Recently, many of researchers achieved beneficial effects of probiotic on gastrointestinal health in many animal species. Increasing the villi length and width led to increase in mucosal surface area by 36.2 and 62.48% in duodenum and jejunum of goats fed selenium yeast compared to control (Ahmed et al. 2016). Moreover, the improvement of available nutrients in intestine would, result in increasing weights of visceral organs and improving growth performance of animal. Also, Peker et al. (2014) reported that the addition of 3 g S. cerevisiae/kg diet of rabbits affected the duodenum morphology by increasing the total mucosa, villus height, and the gland depth. In another study, Seyidoglu and Peker (2015) reported that the villus height, crypt depth, gland depth and total mucosa were increased significantly by yeast (S. cerevisiae) addition (2 g/kg and 4 g/kg) in rabbits' diet, although the villus crypt ratio was not changed. This enhancement in duodenum morphology was dosedependently of S. cerevisiae. So, administration of S. cerevisiae in either low or high doses had positive effect on digestive and absorptive functions of the intestinal mucosa. In a recent research by Guo et al. (2017), rabbits fed with *B. subtilis* showed good probiotic potential in rabbits, resulted in improving growth performance, serum immunoglobulin, immune organ index, intestinal homeostasis, and immune response of rabbits, as well as its antibacterial benefits.

Finally, although there are many improvements in blood metabolites, intestinal and caecum microbial load as a result to the mixture of *B. subtilis* and *S. cerevisiae*, however it was not extended to productive performance in comparison with the single addition of *B. subtilis* or *S. cerevisiae*. The taller small intestine, for rabbits fed on the sole addition of *B. subtilis* or *S. cerevisiae*, and not for their mixture, may be having the key to explain why rabbits of groups R2 and R3 showed high final body weight with low feed conversion. So, wide surface area

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for nutrients absorption, therefore high feed utilization, is closer related to good productive performance of rabbits than improvements in blood metabolites, intestinal and caecum microbial load.

Conclusions

This study demonstrated that the addition of *Bacillus subtilis* or *Saccharomyces cerevisiae* to diets of growing NZW rabbits by 0.1% is recommended to minimize the pathogenic intestinal load and increasing the beneficial lactobacillus strains as well as improving the intestinal barriers integrity.

Abbreviations

g: Gram; P: Probability; cfu: Colony-forming unit; ALT: Alanine aminotransferase; AST: Aspartate aminotransferase; DM: Dry matter; OM: Organic matter; CP: Crude protein; CF: Crude fiber; EE: Ether extract; NFE: Nitrogen-free extract; GIT: Gastrointestinal tract; SAS: Statistical Analysis System.

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Authors' contributions

Conceptualization was carried out by F.H. and A.E.; data curation was performed by A.E. and O.A.; investigation was done by S.E., M.S., and S.A.; S.A., M.S., O.A., and S.A. contributed to methodology; supervision was done by F.H. and A.E.; validation was carried out by F.H. and A.E.; visualization and writing—original draft were performed by F.H., A.E. and M.S.; writing—review and editing were done by A.E. and O.A. All authors read and approved the final manuscript.

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on request.

Declarations

Ethics approval and consent to participate

The experimental design and all the research protocols were approved by the Medical Research Ethics Committee (MREC) of the National Research Center with ethical approval code 20/173.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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