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Autolyzed *Saccharomyces cerevisae* reduce microbiological carcass contamination in feedlot steers

Suplementação com *Saccharomyces cerevisae* autolisada reduz contaminação microbiológica da carcaça de novilhos terminados em confinamento

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Highlights

Yeast decreased fecal excretion of E. coli and coliforms in cattle in feedlots.
The feedlot system increased skin contamination of cattle.
Reduced fecal excretion of pathogens minimized the contamination of bovine carcasses.
Yeast supplementation produced bovine carcasses with higher sanitary quality.

Abstract

The present work aims to verify whether the autolyzed *Saccharomyces cerevisiae* reduces total coliforms, *Escherichia coli* and *Salmonella* spp. from the hide, feces and carcass of feedlot-finished steers. Eighteen half-Angus steers were subjected to three treatments daily for 105 days: control (n=6), Lev 4 g (diet with 4 g yeast animal day^{-1}, n=6) or Lev 7 g (diet with 7 g yeast animal day^{-1}, n=6). On Days 29 and 90 after entrance into the feedlot, fecal samples, skin swabs, water and food were collected to identify and count *E. coli* and total coliforms and identify *Salmonella* spp. On the day of slaughter, carcasses were collected to identify and quantify *E. coli*, total coliforms, and mesophiles. There were reductions in *E. coli* and total coliforms in fecal samples (P=0.0001 and 0.001, respectively) and mesophilic aerobics in carcasses (P= 0.05) in the treated groups, and no *Salmonella* spp. was observed in any of the samples collected. It was concluded that supplementation reduced fecal excretion of and, consequently, carcass contamination by *E. coli*, mesophiles and total coliforms in confined animals and that this technique is a beneficial and residue-free sanitary measure to improve the microbiological quality of meat.

Key words: Carcass contamination. *Escherichia coli.* Foodborne pathogens. Yeast.

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Resumo

Este trabalho objetivou verificar se o prebiótico a base de parede celular de *Saccharomyces cerevisiae* reduz coliformes totais, *Escherichia coli* e *Salmonella* spp da pele, fezes e da carcaça de bovinos terminados em confinamento. Para tanto, 18 novilhos, ½ sangue Angus foram submetidos a três tratamentos diários durante 105 dias: controle (n=6), Lev 4g (dieta com 4 g de levedura por animal dia^{-1}, n=6) ou Lev 7g (dieta com 7 g de levedura por animal dia^{-1}, n=6). Nos dias 29 e 90 após a entrada no confinamento, coletou-se amostras de fezes, swab de pele, água e alimento para contagem de *Escherichia coli* e coliformes totais e isolamento de *Salmonella* spp. No dia do abate, realizou-se coleta nas carcaças para identificação de *Salmonella* spp e quantificação de *Escherichia coli*, coliformes totais, mesófilos. Notou-se redução de *Escherichia coli* e coliformes totais nas amostras de fezes (P=0,0001 e 0,001 respectivamente) e de *Escherichia coli*, coliformes totais e aeróbios mesófilos na carcaça (P=0,06; 0,10 e 0,05 respectivamente) nos grupos tratados. Houve ausência de *Salmonella* spp. em todas as coletas realizadas. Concluiu-se que a suplementação reduziu a excreção fecal e consequentemente, a contaminação da carcaça pela *Escherichia coli*, mesófilos e coliformes totais dos animais confinados, sendo uma medida sanitária benéfica e livre de resíduos para melhorar a qualidade microbiológica da carne.

Palavras-chave: Contaminação de carcaça. Doenças transmissíveis por alimentos (DTA). *Escherichia coli.*

Introduction

In 1980, finishing cattle in feedlots for meat production started to be used in Brazil due to the advantages of this system, such as early animal termination, higher carcass yield, better quality meat, a greater number of animals per area, and a faster return on the working capital invested in fattening (Associação Brasileira das Indústrias de Exportadoras de Carne, 2021).

Therefore, this system has attracted the interest of ranchers in technologies that maximize the efficiency of feed use by confined animals. In this sense, it is important to use feed additives that modulate the ruminal environment, such as live yeasts or fragments (Fereli et al., 2010). The most widely used yeast in cattle feed is *Saccharomyces cerevisiae.* When used in culture, it reduces the acidification of the ruminal environment by stimulating the growth of lactic acid-using bacteria, which are mainly responsible for rumen acidification when the feed is concentrated above 50%. This process may cause subacute ruminal acidosis syndrome, which is responsible for decreased performance and increased susceptibility to infectious diseases such as the bovine respiratory complex (Broadway et al., 2015; Virmond et al., 2020).

S. cerevisiae in fragmented form contains cell wall fragments that are rich in polysaccharides such as Beta glucan and mannan oligosaccharides that activate phagocytes, maximizing the animal's immune system (Broadway et al., 2015). In addition, these polysaccharides act mainly in the intestine, adsorbing intestinal pathogenic bacteria and increasing the absorption area of the intestinal villi, resulting in a lower incidence of diarrhea and greater absorption of nutrients (Broadway et al., 2015; Liu et al., 2008). Despite this effect on the intestinal tract, few studies have evaluated the effects of yeast on the fecal excretion of pathogenic

microorganisms in ruminants (Stella et al., 2007; Ghazanfer et al., 2015).

According to Jardim et al. (2006), animals from extensive rearing had greater amounts of dirt and microorganisms on the hide, which promoted greater contamination of the carcass after skinning when compared to feedlot animals. In contrast, Casagrande et al. (2012) reported that confined animals subjected to a more energetic diet may harbor more generic *E. coli* in the gastrointestinal microbiota, which may contribute to greater contamination of the carcass by *E. coli* at the time of slaughter.

Therefore, any measure that does not generate antibiotic residues in the carcass and that also reduces its contamination is important for producing a final product with sanitary quality, a longer shelf life and less possibility of transmitting diseases (Brandão et al., 2012; Elder et al., 2000).

In general, *S. cerevisiae*-based prebiotics contribute to increased immunity in animals (Martins et al., 2005) and favor the growth of beneficial colonies to the detriment of pathogenic colonies in the gastrointestinal environment (Ghazanfer et al., 2015). The objective of this study was to evaluate whether the use of an autolyzed *S. cerevisiae* rich in cell wall reduces the fecal excretion of *E. coli*, total coliforms and *Salmonella* spp. and consequently minimizes the contamination of bovine carcasses at slaughter after evisceration.

Materials and Methods

The study was conducted at the Nucleus of Animal Production (NUPRAN) of the Master's Degree Course in Veterinary Sciences of the Agricultural and Environmental Sciences Sector of the Universidade Estadual do Centro Oeste (UNICENTRO), located in Guarapuava-PR, and was approved by CEUA 048/2018.

The experimental design was completely randomized and consisted of three groups: control (n=6); Lev 4 g (diet with 4 g yeast per animal day^{-1}, n=6) and Lev 7 g (diet with 7 g yeast per animal day^{-1}, n=6). The product used was an autolyzed *Saccharomyces cerevisiae* rich in cell wall containing 2x10^{10} cell gram^{-1} commercial (RumenYeast®, ICC, São Paulo, Brazil).

The evaluated batch consisted of 18 half-Angus animals, weighing approximately 350 kg and 11 months old, arranged in 9 pens with 2 animals per pen in a feedlot system with an area of 15 m^2 each (2.5 m x 6.0 m). Each pen had a concrete feeder measuring 2.30 m long, 0.60 m wide and 0.35 m deep and a metal drinker regulated by a float. The animals were previously dewormed with oral albendazole and transported from a breeding farm to the experimental unit approximately 50 km away. After a period of adaptation to the experimental facilities for 15 days, daily supplementation of yeast according to the groups was initiated and continued for 104 days; the lyophilized product was added once a day on top of the total diet of the animal soon after filling the trough. At 105 days of the experiment, the animals were slaughtered in a commercial facility. The diet served in the feedlot was the same as that on the farm of origin, consisting of 5% predried ryegrass, 35% corn silage and 60% commercial concentrate, on a dry basis, *ad libitum.* The following feedstuffs were used to manufacture the concentrate: soybean meal, soybean hulls, barley rootstock, ground corn

kernels, limestone, dicalcium phosphate, common salt, livestock urea and vitamin-mineral premix. Feeds were administered at 6:00 am and 5:30 pm in the form of a total mixed ration (TMR). Voluntary food intake was recorded daily by weighing the amount offered and the leftovers from the previous day to adjust the daily intake, and 5% dry matter (DM) was maintained (Table 1).

Table 1
Chemical composition of the feedstuffs used in animal feeding and mean values of the experimental diet, based on total dry matter

Parameter	Predried ryegrass (5%)	Corn silage (35%)	Concentrate (60%)	Experimental diet[1]
Dry matter, % DM	57.35	40.63	90.40	71.33
Mineral matter, % DM	5.59	2.51	6.36	4.97
Crude protein, % DM	12.43	8.44	20.20	15.70
Ether extract, % DM	3.28	2.65	2.05	2.32
Neutral detergent fiber, % DM	48.89	46.14	31.47	37.48
Acid detergent fiber, % DM	37.89	25.98	13.08	18.84
Lignin, % DM	6.90	3.43	4.73	4.38
Total digestible nutrients, % DM	54.74	68.66	78.68	73.98
Ca, % DM	0.58	0.14	1.67	1.08
W, % DM	0.26	0.22	0.58	0.44

[1] Guaranteed level of the premix per kg of concentrate: vit. A: 16000 IU; vit. D3: 2000 IU; vit. E: 25 IU; S: 0.36 g; Mg: 0.74 g; Na: 3.6 g; Co: 0.52 mg; Cu: 22.01 mg; F: 18.00 mg; I: 1.07 mg; Mn: 72.80 mg; Se: 0.64 mg; and Zn: 95.20 mg.

Sample collection and preparation

On Days 29 (D29) and 90 (D90) after the start of yeast administration, samples of feces, water, food and hide were collected for counting of *E. coli* and total coliforms and isolation of *Salmonella* spp. At 105 days (at slaughter), microbiological analysis was performed on the carcasses for quantification of mesophiles, *E. coli*, and total coliforms and identification of *Salmonella* epifocal samples were collected individually from the rectal ampulla of the animals with sterile gloves. Microbiological samples of the hide were obtained using sterile swabs from a total area of 200 cm^2 $animal^{-1}$ from the scapular regions and flanks of the animals on each side. The swabs were pooled according to the experimental groups in transport solution (0.1% buffer peptone water-BPW). In addition, 100 mL of water and 100 g of food were collected from two pens at random.

The carcass samples on the day of slaughter were collected in the slaughter room shortly after evisceration and division of the carcasses and before washing. The samples were harvested using sterile swabs applied to an area of 100 cm^2 in the scapular region and flank areas on the outer surface of

each half carcass. Likewise, the swabs were transferred to a test tube containing 0.1% BPW solution.

The material was transported at a temperature of 4 °C or less to the Laboratory for Inspection of Products of Animal Origin of UNICENTRO and to the Center for Agroindustrial Diagnosis. For the quantification of total coliforms, *E. coli* and mesophilic aerobic bacteria, serial dilutions were performed according to IN n° 62 (Instrução normativa 60, 2018). The water samples underwent a chlorine neutralization process to prevent the continuation of the bactericidal effect. A total of 0.1 mL of 10% sodium thiosulfate solution ($Na_2S_2O_3$) was added for each 100 mL of collected sample (final concentration =100 mg l^{-1}) to neutralize 15 mg of residual chlorine per liter of sample.

Microbiological analyses

Total coliform and *E. coli* counts were performed in Petrifilm plates (6404, *E. coli* and coliform, 3M, São Paulo, Brazil). One milliliter aliquots of each serial dilution were inoculated into Petrifilm plates and incubated at 35 °C for 48 h. Reddish-blue and red colonies with gas production were considered total coliforms, and blue colonies with gas production were identified as *E. coli.* The water, feed and hide counts were expressed in colony-forming units (CFU) per g or cm^2 mL^{-1}, while for carcasses and feces, the results were expressed in log CFU per g or cm^2 mL^{-1}.

For the isolation of *Salmonella* spp. from feces, water, food and hide samples, the Petrifilm system was used (6536, SALX, Salmonella Express, 3M, São Paulo, Brazil). Initially, a 10^{-1} dilution was prepared, and Salmonella enrichment medium (3M, São Paulo, Brazil) was added, followed by incubation at 41.5 °C for 18 to 24 h. Because the stool samples were highly contaminated, after incubation, 0.1 mL was removed, added to 10 mL of Rappaport–Vassiliadis broth (RVS), homogenized and incubated at 41.5 °C for 18 at 24 h. After the incubation period, an aliquot was removed with a sterile platinum loop and streaked onto Petrifilm plates, which were placed in an oven at 41.5 °C for 18 to 24 h.

Subsequently, a *Salmonella* confirmation disk (3M, São Paulo, Brazil) was placed on the plates that showed presumptive colonies of *Salmonella* (red to brownish with a yellow zone, with associated gas or bubbles), and the disk was placed again in the oven at 41.5 °C for 4-5 h. Next, the reading was performed, in which bluish green, dark or blackish colonies were considered positive, according to the manufacturer's recommendation.

For identification of *Salmonella* spp. in carcass samples, the ISO 6579/2017 methodology was used. In the nonselective preenrichment process, the initial suspension (25 g of sample in 225 mL 1% BPW) was incubated at 36 °C (±2 °C) for 18 h ± 2 h. For enrichment, 0.1 mL of the diluted and incubated sample was transferred to a tube containing 10 mL of RVS, which was incubated in a water bath at 41.5 °C (± 1 °C) for 24 h ± 3 h. One milliliter of the diluted and incubated sample was also transferred to a 10 mL tube containing Muller-Kauffmann tetrathionate with novobiocin (MKTTn) with 0.2 mL of iodine–iodide solution and incubated at 37 °C (± 1 °C) for 24 h ± 3 h.

After incubation, 10 µl of the culture obtained in the RVS medium was streaked with a loop onto two plates of bismuth sulfite agar (BSA) and two plates of xylose lysine deoxycholate agar (XLD). Similarly, approximately 10 µL of the culture obtained was streaked in MKTTn medium on two plates of BSA and two of XLD. The plates were incubated at 37 ± 1 °C for 24 h ± 3 h. After incubation, the plates were read for the presence of typical and atypical *Salmonella* colonies. In the BSA medium, positive colonies were colorless, pink, translucent or opaque, and in the XLD medium, they had a translucent appearance and a black center with a pink or reddish background. If colonies with these characteristics were found, they were confirmed by biochemical tests.

The counting of mesophilic aerobic microorganisms was performed in Petrifilm (RAC, Rapid Aerobic Count, 3M, São Paulo, Brazil). One milliliter of the serial dilutions was inoculated onto the surface of Petrifilm plates and then incubated at 35 °C for 48 h. The reading was performed by counting plates containing between 30 and 300 colonies that were considered positive (red), according to the manufacturer's recommendation. The results were expressed in CFU per g, cm² and or mL.

The minimum detection limit of mesophilic aerobics was considered 2 CFU cm^{2-1}.

Statistical analysis

The counts of microorganisms in feces and surface samples of bovine carcasses were analyzed with the statistical program GraphPad Instat; the T test was applied for paired samples for the time interaction, analysis of variance (ANOVA) was used for unpaired samples, and Tukey's post hoc test was used for the treatment interaction, at a significance level of $p \leq 0.05$.

For the mesophilic aerobic counts, the value of 1.00 log10 CFU cm^{2-1} was adopted in the statistical analyses when the result was the absence of mesophilic aerobics. For the total coliform and *E. coli* counts, the value of 0.40 log10 CFU cm^{2-1} was adopted in the statistical analyses when the result was the absence of total coliforms or the absence of *E. coli.* These values were determined based on the detection limits of the microbiological analyses.

Results and Discussion

Supplementation with autolyzed *S. cerevisiae* rich in cell walls promoted a higher reduction in the fecal excretion of *E. coli* and total coliforms when a higher dosage was used. These results are similar to those found by Stella et al. (2007), who noted that supplementation with *S. cerevisiae* for 30 days reduced the presence of total coliforms and *E. coli* in the fecal microbiota of young goats.

The mean counts of *E. coli* and total coliforms in the fecal microbiota of cattle subjected to different types of treatment by supplementing the yeast *S. cerevisiae* are shown in Table 2.

Table 2
Effect of *S. cerevisiae* supplementation on *E. coli* and total coliform counts in the fecal microbiota (log CFU g^{-1} of feces) of feedlot cattle

Groups		D29	D90	SEM	P time	P treatment x time
E. coli	Control	3.29aA	3.31aA	0.08	0.17	0.0001
	Lev 4 g	3.23aA	3.21aAB	0.11	0.08	
	Lev 7 g	3.27aA	2.56bB	0.15	0.02	
	P treatment	0.89	0.0008			
Total coliforms	Control	5.76aA	5.51bA	0.05	0.006	0.001
	Lev 4 g	5.77aA	5.58bA	0.07	0.05	
	Lev 7 g	5.76aA	5.23bB	0.08	0.03	
	P treatment	0.91	0.008			

Different lowercase letters in the same row indicate significant differences in the time interaction. T test, different uppercase letters in the same column indicate significant differences in the treatment interaction, P<0.05%. D= day; SEM: standard error of the mean; Lev 4 g: 4 g yeast animal-1; Lev 7 g: 7 g yeast animal-1.

Regarding *E. coli,* the microbiota of the feces was the same between the groups on D29, and only the Lev 7 g group showed a reduction in counts compared to the control and Lev 4 g groups on D90 (P = 0.0008). Regarding the time interaction, there wasn´t a decrease in the number of microorganisms excreted in the feces in relation to D29 in the Lev 4g group (P=0.08). In the Lev 7 g group, there was a significant decrease in the fecal excretion of *E. coli* (P = 0.02) on D90 compared to that on D29.Regarding total coliforms, the fecal microbiota was the same between groups on D29; on D90, only the Lev 7 g group showed a reduction in counts compared to the control and Lev 4 g groups (P=0.008) in the interaction between treatments. Regarding time, all groups showed a significant reduction in microorganisms in fecal excreta on D90 compared to D29 (P=0.006, 0.05 and 0.003, for the control, Lev 4 g and Lev 7 g, respectively). No *Salmonella* spp. was isolated in the fecal microbiota of cattle subjected to different types of treatment by supplementation with the yeast *S. cerevisiae.*

While Ghazanfer et al. (2015) found a reduction in total coliforms in the feces of heifers supplemented with *S. cerevisiae* culture, Ran et al. (2018) found a reduction in the fecal excretion of *E. coli* in feedlot-finished cattle supplemented with freeze-dried yeast. Although no studies were found describing the effect of yeast cell walls on the intestinal microbiota of ruminants, it is believed that yeast fragments contain a higher concentration of polysaccharides responsible for the adsorption of pathogenic bacteria in the small intestine, which contributes to improve the animal health and safer animal food production (Broadway et al., 2015; Ran et al., 2018).

The results for the pooled hide samples are shown in Table 3. There was an increase in contamination in the animals of the control, Lev 4 g and Lev 7 g groups, for both coliforms and *E. coli.* No *Salmonella* spp. was identified in cattle hides.

Table 4 shows the results for the water and feed samples at D29 and D90.

The contamination levels of both *E. coli* and total coliforms in water increased over time. However, the feed contained no contamination of total coliforms or *E. coli* at either time. No *Salmonella* spp. was isolated in water or feed from the stall selected at D90.

Table 3
Effect of *S. cerevisiae* supplementation on the counts of *E. coli* and total coliforms in pooled hide samples of feedlot cattle (CFU cm^{2-1})

Groups		D29	D90
E. coli	Control	<1x10¹	1.5x10²
	Lev 4 g	2x10¹	1.2x10²
	Lev 7 g	3x10¹	9x10¹
Total coliforms	Control	<1x10¹	1.4x10²
	Lev 4 g	1.3x10²	1.9x10²
	Lev 7 g	5x10¹	2.4x10²

D=day; Lev 4 g: 4 g yeast $animal^{-1}$; Lev 7 g: 7 g yeast $animal^{-1}$.

Table 4
Total *E. coli* and coliform counts in feedlot water and feed

Sample	Microorganisms	D29	D90
Water	*E. coli*	<1.0x10¹	1.1 x 10²
	Total coliforms	<1.0x10¹	1.6x10²
Feed	*E. coli*	<1.0x10¹	<1.0x10¹
	Total coliforms	<1.0x10¹	<1.0x10¹

D=day.

The average counts of E. coli, total coliforms and mesophiles on the carcass surfaces of cattle subjected to the different yeast supplementation treatments on the day of slaughter are shown in Table 5. The control group presented higher carcass contamination of mesophiles than the other groups in relation (p-0.05).

Table 5
Effect of *S. cerevisiae* supplementation on *E. coli,* total and mesophilic coliform counts on the carcass surface (log10 cm$^{2-1}$) of feedlot cattle at slaughter

Groups		Slaughter	SEM	
E. coli	Control	0.55A	0.16	
	Lev 4 g	0.20A	0.08	0.06
	Lev 7 g	0.20A	0.06	
Total coliforms	Control	0.76A	0.2	
	Lev 4 g	0.31A	0.17	0.10
	Lev 7 g	0.25A	0.16	
Mesophiles	Control	1.60A	0.12	
	Lev 4 g	1.20B	0.13	0.05
	Lev 7 g	1.24B	0.11	

Different capital letters in the same column indicate significant differences between groups. Tukey's test, P<0.05%. SEM: standard error of the mean, Lev 4 g: 4 g yeast animal^{-1}; Lev 7 g: 7 g yeast animal^{-1}.

Similar to the fecal samples, no Salmonella spp. was isolated or identified on the bovine carcass surfaces.

The fact that contamination by *E. coli* and fecal coliforms increased in water and hides in the three groups over time suggests environmental contamination. Pereira and Dutra (2012) found that cattle feedlot promotes the concentration of animals in a too small space and that pen conditions such as bedding, drinkers and feeders, as well as poor sanitary management, favor a higher rate of environmental contamination and consequently greater dirtiness of the pen and hide. In contrast, Jardim et al. (2006) found that cattle kept in pastures had higher hide contamination than feedlot cattle. However, soon after the spray bath, no significant difference was found for carcass contaminants (*E. coli* and total coliforms), indicating that the spray bath efficiently eliminates contaminants, thus preventing a high load of microorganisms on the carcass.

According to Bacon et al. (2000), acceptable carcass counts are means of 4.1 to 7.1 log10 CFU cm$^{2-1}$ for total mesophilic aerobics, 1 to 4 log10 CFU cm$^{2-1}$ for total coliforms and 0.6 to 3.3 log10 CFU cm$^{2-1}$ for *E. coli.* Jardim et al. (2006) and Bell (1997) found lower values, such as 2, 0.40 and 0.40 log10 CFU cm$^{2-1}$, respectively, for the mentioned microorganisms, and these values are close to those found in the present study.

This difference in counts can be explained by the application of self-control programs in the different stages of slaughter, such as cleaning and sanitizing the environment and industrial equipment, quality of supply water, pest control, health and hygiene of workers, temperature control, and APPCC (Analysis of Hazards and Critical Control Points) (Ministério de Agricultura, Pecuária e Abastecimento [MAPA], 2005).

It is noteworthy that other factors also favor the contamination of carcasses, such as transport and the stress of the animals experienced in the *ante-mortem inspection,* which may reduce skin immunity and favor the colonization of environmental pathogens on the skin (Brandão et al., 2012; Fontoura et al., 2020). Therefore, the most critical steps regarding contamination of bovine carcasses are skinning and evisceration, during which the skin and viscera can come into contact with the meat, carrying various pathogenic microorganisms (Brandão et al., 2012). Thus, the cattle husbandry system used, as well as the feeding approach, can minimize such contamination (Casagrande et al., 2012; Jardim et al., 2006).

Regarding the evaluation of *Salmonella* spp., Matos et al. (2013) studied 100 bovine carcasses and found *Salmonella* spp. in only nine. In the present study, *Salmonella* spp. was not isolated, probably due to greater environmental control of the bacterium.

As the levels of contamination of the environment and hide increased and the microbiological counts in the feces decreased with the use of yeast, it is believed that low counts in the carcass are linked to a reduction in fecal contamination. This result is consistent with that reported by Elder et al. (2000), who found the same correlation when evaluating the presence of *E. coli* O157 in the feces, hide and carcasses of beef cattle. The same authors also mentioned that sanitary management practices during slaughter, such as team hygiene and respect for critical control points, favor a reduction in carcass contamination.

Thus, it is beneficial to implement management protocols that respect the welfare of animals, preserve their physical integrity and seek to minimize the impact of fecal microbiota in slaughtering processing and consequently reduce the bacterial load in carcasses without promoting antibiotic residues in products of animal origin (Bacon et al., 2000; Bell, 1997; Elder et al., 2000). In addition, the quantification of the microorganisms in carcasses is an important factor in determining the efficiency of sanitary management within the slaughterhouse, as well as the quality and shelf life of meat, to reduce the incidence of foodborne diseases in humans (Fontoura et al., 2020)

Conclusions

Supplementation with autolyzed *S. cerevisiae* rich in cell walls promotes a reduction in the fecal excretion of total coliforms and *Escherichia coli,* which favors less contamination of these agents in the carcass after evisceration; a dose of 7 g day^{-1} is the most effective.

Thus, supplementation of feedlot cattle diets with autolyzed S. cerevisiae rich in cell walls favors better sanitary control and a reduction in contamination rates in the beef production line, resulting in lower risks of transmitted diseases.

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