DETERMINATION OF MICROBIAL LOAD ON SOME INTERNAL ORGANS OF CHICKENS SOLD IN JOS METROPOLIS

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ABSTRACT
This study investigated the microbial load in some internal organisms (liver, lungs and heart) of chicken (local and broiler) in Jos Metropolis. Organ meat samples (n = 90) were collected aseptically from three different markets namely, Faringada (n = 30), Terminus (n = 30) and Bukuru (n = 30). All samples were subjected to aerobic plate count, coliform plate count, shigella and salmonella detection. In terms of breed type, the lung, liver and heart of local chicken had the highest total Aerobic Plate Count (APC) of 187.80, 73.47 and 14.40 $(x104CFU/g)$ *respectively and a total coliform count of 71.00, 23.13, and 8.33 (x10^{4}CFU/g) respectively as compared to broilers lung, liver and heart whose (APC) are 92.07, 32.73 and 8.23 (x10^{4}CFU/g) respectively and Total Coliform Count (TCC) of 55.00, 19.20 and 4.40 (x10^{4}CFU/g) respectively. With respect to location, the lung and liver in Bukuru had the highest Aerobic Plate Count (APC) of 154.00 and 58.70 (x10^{4}CFU/g) respectively while the Total Coliform Count (TCC) were 100.60 and 28.20 (x10^{4}CFU/g) respectively as compared to Terminus which the APC for the above organs were 114.90, 45.70 (x10^{4}CFU/g) respectively and the (TCC) were 55.60, 23.10 (x10^{4}CFU/g) in that order. At Faringada, Aerobic Plate Count (APC) for the lung, liver and heart were: 150.90, 52.40 and 14.10 (x10^{4}CFU/g) respectively and the Total Coliform Count (TCC) for the same organs were 33.80, 12.20 & 4.20 (x10^{4}CFU/g) respectively. In terms of organs, the lung has the highest APC of 154.00 (x10^{4}CFU/g) and (TCC) of 100.60 (x10^{4}CFU/g), followed by liver having APC of 58.70 (x10^{4}CFU/g) and TCC of 28.20 (x10^{4}CFU/g), then the heart has APC of 14.10 (x10^{4}CFU/g) and (TCC) of 8.80 (x10^{4}CFU/g). Pathogenic organisms, Salmonella and Shigella were not detected in the samples experimented across all locations. However, the samples collected at Bukuru Market had the highest value of APC and TCC, which could, imply a low level of hygiene and also insinuates a possible role in spoilage and foods-borne illness. This study highlights the need for improved sanitation in poultry processing and stricter monitoring to ensure food safety, particularly in locations like Bukuru with higher contamination levels. Implementing better rearing practices for local chickens could further reduce microbial contamination.*
Keywords: Chicken organs, Micro-organisms, Total coliform count, Aerobic Plate Count, Food Safety

INTRODUCTION

Nigeria poultry industry comprises about 180 million birds, out of which 80 million are raised in extensive system, 60 million in semi extensive and the remaining 40 million intensive systems (FAO, 2019). Poultry meat products are widely consumed all over the world due to their high nutritional value, cost of production which is considerably low and short cooking process
(Huang *et al*., 2018). Among poultry meat products, chicken carcasses, cuts and processed products are most consumed, followed by turkey and to a lesser extend duck (Rouger *et al*., 2017). Chicken meat is filled with high quality protein and does not contain much fat. Beyond its rich protein content, chicken also contain vitamin B_{12}, tryptophan, and minerals such as zinc, iron and copper. Poultry raised within the family has been increasingly recognized as one of the entry points to address the problems of malnutrition, food insecurity, low income and poverty as a whole (Gawandele *et al.,* 2007) and (Dei *et al*., 2009). Poultry is a profitable venture and eventually a tool for livelihood improvement (Dilbert 2007, Fasina *et al*., 2007). Poultry contributes subsidiary rural family income and this has empowered women financially and improves the educational and nutritional status of children (Potter *et al*., 2003). Domesticated poultry also contributes to environmental protection and conservation as people no longer have a need to hunt (FAO, 2019). Meat is a good source of animal protein along with sensory qualities which is appealing to the consumer easily, and as it contains sufficient nutrients needed to support the growth of microorganisms, it is seen as the most perishable food (Magnus, 1981). Ensuring the microbial safety of poultry meat products is a key issue in production as well as

consumption (Rouger *et al.,* 2017). It has been reported that poultry meat has high biological value which contains all the essential amino acids and unsaturated fatty acids required for human diet (Takma *et al.,* 2019).

Fresh chicken meat is highly perishable due to it physical and chemical properties. Its high-water holding capacity allows the creation of suitable condition for microbial growth and proliferation (Odeyemi *et al*., 2020). Microbial proliferation is one of the major causes of quality deterioration in meat and meat products either in fresh, cold or frozen condition (Mario and Cova, 2014; Akarpat *et al*., 2018). A great diversity of microbe inhibits fresh meat generally, different type may become dominant depending on pH, composition, texture, storage temperature and transportation means of raw meat (Ercolini *et al*., 2006; Adu-Gyamfi, *et al*., 2012). During slaughter, processing, storage and market display, the quality attributes of meat also deteriorate faster as a result of microbial proliferation (Kazancinski *et al*., 2006; Alvarez-Astroga, *et al*., 2012). Contamination by pathogenic microorganisms can cause a major consumer health risk and economic loss to the meat retailers in term of food poisoning and meat spoilage. Their growth and metabolic activity during shelf life leading to alteration in colour, odour, taste or texture are responsible for waste and losses of food products and therefore have and an important impact on the meat production sector, as a result, meat products are spoiled every year (Rouger, *et al*., 2017).

Poultry farming serves as a critical component of the food supply chain, contributing significantly to the availability of animal protein. However, concerns arise regarding the potential microbial contamination of poultry products, particularly in the internal organs of broilers and local chickens. The extent of microbial contamination within the internal organs of poultry, including the liver, spleen, and intestines, remains inadequately understood in the context of both broiler and local chicken. The pathogenic microbes in the chicken organs can significantly affect the health and welfare of the animals themselves. Meat is one of the major sources of foodborne diseases in humans (Xavier, *et al.,* 2014; Adley, *et al.,* 2011). The principal pathogens which can be transmitted through meat include: *Bacillus cereus*, *Campylobacter spp*., *Clostridium perfringens*, *Clostridium botulinum*, *Escherichia coli*, *Lysteriamonocytogenes*, *Salmonella spp*., *Staphylococcus aureus*, *Yersinia enterocolitica*, *Aeromonas*, *Brucella*, *Clostridium difficile*, *Enterobacter* and *Shigella* (Sofos, *et al.,* 2011; Xavier, *et al.,* 2014; Sofos, *et al.,* 2010). *B. cereus* can pose a serious hazard to the meat industry, since a mild heat treatment cannot guarantee its complete inactivation (Antolinos, *et al.,* 2011). This microorganism causes intoxication or toxi-infection after spores' germination and multiplication in meat foods (Granum, *et al.,* 2014). Most cases of infection with *Campylobacter jejuni* and *Campylobacter coli* are attributed to handling and consumption of raw poultry products, with cross-contamination being very important (Sofos, 2014; Mataragas, *et al.,* 2008).

C. botulinum and *C. perfringens* may become problematic when the meat product is temperature abused and allows growth of this pathogen. Spores of *Clostridium perfringens* become activated by heat treatment and upon time– temperature abuse they germinate, multiply and produce enterotoxin, which is released during sporulation in the intestine, leading to illness. Spores of *Clostridium botulinum*, after activation and germination, grow in anaerobic or micro-aerobic conditions and produce deadly neurotoxins in the meat food (Sofos, 2014). Potential sources of Clostridium include beef, pork and poultry products (Akhtar, *et al.,* 2009). *Escherichia coli* are harmless inhabitants of the humans' gastrointestinal tract and other warm-blooded animals. From the gastrointestinal tract, it contaminates the animals, the soil and water, and consequently the meat products. Escherichia species are of the most concern in undercooked poultry meat products, especially non-intact meat products, such as beef (;Sofos, *et al.,* 2010]. The infection with *L. monocytogenes* is usually associated with ready-to-eat pork or poultry-meat products, or reheated meat products, partially cooked pork products and poultry foods contaminated after processing. The *Listeria's* growth occurs during prolonged storage even at refrigeration temperatures. This pathogen is sensitive to normal cooking but it may contaminate the meat products after heating, when exposed to the environment during cutting, slicing and repackaging. *Listeria* is ubiquitous in the environment and may be found in many animals, in floors, walls, drains, condensed and standing water, and food residues on equipment in meat processing environments. Meat and poultry products are considered major sources of Salmonella. The infection with Salmonella is associated with the consumption of processed pork or poultry-meat products (ready-to-eat or to be reheated) and partially cooked pork products (Sofos, *et al.,* 2010; Mataragas, *et al.,* 2008). Meat may be contaminated with Salmonella throughout the slaughtering, dressing and boning process, starting with the carcass during knife incision for

hide removal. *S. aureus* has a huge impact on animals' health and welfare and causes major economic losses in livestock's production (Peton and Le Loir, 2014). It may become a problem in processed meat products, especially ready-to-eat pork products, where it is introduced usually by humans (Sofos, *et al.,*2010).
However, understanding the microbial loads in the chicken, can help identify potential source of infection to human, improve veterinary practices and develop strategies to prevent food-borne diseases. Addressing these issues is critical for safeguarding public health, ensuring the safety of poultry products, and enhancing the overall sustainability and resilience of the poultry industry. This study focused on assessing the bacterial load present in the internal organs of poultry, specifically broilers and local chickens, within the Jos metropolis for effective management practices aimed at reducing microbial contamination in poultry.

MATERIALS AND METHODS

Study Location

Jos metropolis is located between latitudes $9^0$54' N and $10^0$10' N and longitudes 8^0 48' E and 9^0 3^0' E. The study area comprises Jos South and Jos North local government areas with their headquarters in Bukuru and Jos respectively. The area is situated within the Northern Senatorial Zone of Plateau State, and is bounded by Barkin-Ladi and Jos East to the East, Riyom to the South and BassaLocal Government Areas to the West (in Figure 1). The area extent of Jos Metropolis, from North to South is 104km while from East to West is about 80km on an elevation of 1,250m Above Sea Level, with Shere Hills having the highest peak of 1,777m Above Sea Level, and an area of 1002.19 Km^2(Mohammed, *et al.*, 2010). This research covered three market places within
the Jos metropolis namely: FarinGada, Terminus and Bukuru markets.

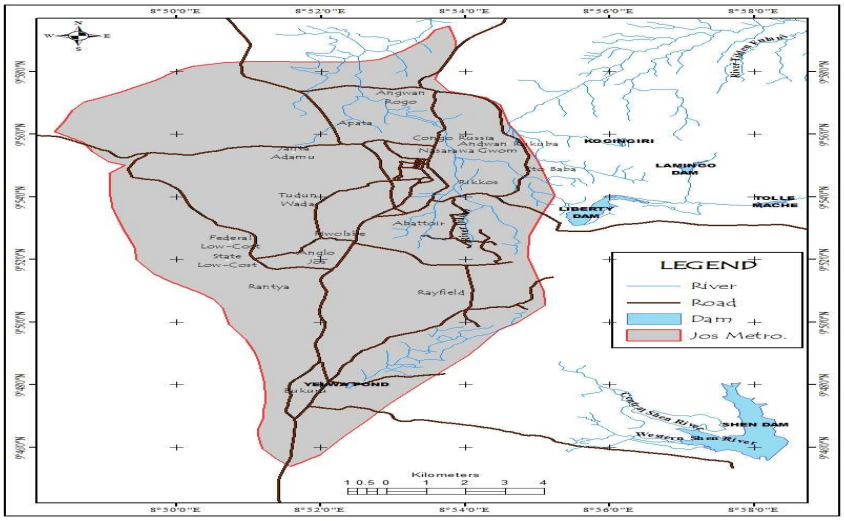

Figure 1: Jos Metropolis, Plateau State, Nigeria.
(Source: GIS Lab, Department of Geography and Planning, University of Jos, 2018)

A random sampling method was used, in which 30 samples were randomly selected at the point of slaughter in each market. All samples were collected aseptically immediately after slaughter between 8.00am and 10.00am within the month of April from 12th, 19th and 25th for Faringada, Terminus and Bukuru respectively. Samples were packaged and labeled appropriately before placing them into Ice- cooler and transported to the microbiological laboratory of the Veterinary Teaching Hospital, Polo, Jos.

Meat samples presented to the laboratory were washed using sterile distilled water so as to reduce the possibility of contamination during collection and transportation. Using a digital weighing scale, 1g of each organ was weighed, cut into tiny pieces and enriched by culturing in a 10ml Brain-Heart Infusion Broth (BHI) and incubated for 24hours at 37^0C

The BHI enriched cultures were cultured to agar plates of McConkey and Blood by striking. 1ml of each of the samples was serially diluted (10-fold) to a dilution factor of 10^{-5}. 1ml of 10^{-4} dilution was pipette into a

clean sterile petri dish before adding a molten medium of nutrient agar. The mixture was swelled gently for even distribution before allowing to solidify. The cultures were incubated at 37^0C for 24hours aerobically.

Bacterial Identification and Characterization

The cultures on McConkey agar and Blood agar were macroscopically characterized considering the colour of colonies, the size, the elevation, the consistency, the margin as well as the haemolytic properties. Isolates were further sub-cultured to obtain a pure culture which were then Gram stained considering shape (circular or rod), cells arrangement (chains or clusters), grams reaction (gram-positive or gram-negative) and subjected to biochemical characterization (catalase, oxidase, citrate, Tsi, glucose. Numeric data obtained in the work were analysed using SPSS. Two-way and p-value <0.05 was considered statistically significant at 95% confidence interval.

RESULTS

Microbial Load of Heart, Lungs and Liver of Chicken Based on the Study Locations

Table 1 below, shows the main effect of location on microbial count. The total aerobic plate count in the heart of the chicken samples showed significant ($p<0.05$) difference amidst the locations covered in this study, with Faringada, Terminus and Bukuru having 14.10, 10.30 and 9.60 x10^4CFU/g respectively. The total coliform count, however, differs significantly, with Farin Gada having the lowest count at 4.20, Terminus at 6.10, and Bukuru the highest at 8.80x10^4CFU/g. The total aerobic plate count in the lung samples showed a significant difference with the least level observed in Terminus (114.90 x10^4CFU/g) and the highest microbial load in Bukuru (154 x10^4CFU/g). Moreover, the total coliform count in the lungs also showed a significant difference, with Farin Gada at 33.80 x10^4CFU/g, Terminus at 55.60 x10^4CFU/g, and Bukuru at 100.60 x10^4CFU/g, indicating that Bukuru has a much higher contamination level. However, Salmonella Shigella plate count is zero across all locations, suggesting effective control over these pathogens in lung samples.

The total aerobic plate count in liver samples shows a significant difference among locations, with Farin Gada at 52.40 x10^4CFU/g, Terminus at 45.70 x10^4CFU/g, and Bukuru at 58.70 x10^4CFU/g. Bukuru again has the highest microbial load. The total coliform count in the liver also differs significantly, with Farin Gada at 12.20 x10^4CFU/g, Terminus at 23.10 x10^4CFU/g, and Bukuru at 28.20 x10^4CFU/g, indicating higher contamination in Bukuru.

Table 1: Main effect of location on microbial count

Organs	Parameters	Farin gada	Terminus	Bukuru	SEM	P-value
Heart	Total Aerobic Plate count (x10^4CFU/g)	14.10^a	10.30^{ab}	9.60^b	3.83	0.512
	Total Coliform count (x10^4CFU/g)	4.20^b	6.10^{ab}	8.80^a	3.56	0.012
	Salmonella shigella plate count (x10^4CFU/g)	0	0	0	0	0
Lungs	Total Aerobic Plate count (x10^4CFU/g)	150.90^{ab}	114.90^b	154.00^a	39.05	0.005
	Total Coliform count (x10^4CFU/g)	33.80^b	55.60^b	100.60^a	23.44	0.003
	Salmonella shigella plate count (x10^4CFU/g)	0	0	0	0	0
Liver	Total Aerobic Plate count (x10^4CFU/g)	52.40^{ab}	45.70^b	58.70^a	10.9	0.005
	Total Coliform count (x10^4CFU/g)	12.20^b	23.10^{ab}	28.20^a	2.24	0.014
	Salmonella shigella plate count (x10^4CFU/g)	0	0	0	0	0

$^{a, b, c, d}$ means with different superscripts on the same column differ significantly ($P<0.05$)
SEM means standard error of mean.

Microbial Load of Heart, Lungs and Liver of Chicken Based on Breed Type

Table 2 shows the main effect of breed types on microbial count. Broiler chicken heart has a Total Aerobic Plate count (TAPC) of 8.23x10^4CFU/g, while local chicken heart has a higher Total Aerobic Plate count of 14.40 x10^4CFU/g. Broiler chicken heart shows a Total Coliform count (TCC) of 4.40 x10^4CFU/g, compared to 8.33 x10^4CFU/g in local chicken heart, with a P-value of 0.012, indicating a significant difference. Local chickens have higher coliform counts. Both broiler and local chicken hearts have a count of 0, indicating no presence of these pathogens.

Broiler chicken lungs have a Total Aerobic Plate count of 92.07 x10^4CFU/g, while local chicken lungs have a significantly higher Total Aerobic Plate count of 187.81 x10^4CFU/g, with a P-value of 0.005. Local chickens

show higher microbial load. The Total Coliform count are 55.00 x10^4CFU/g for broilers and 71.00 x10^4CFU/g for local chickens. The P-value of 0.003 indicates a significant difference, with local chickens having higher coliform counts. Both broiler and local chicken lungs have a count of 0, showing no presence of these pathogens.

Broiler chicken liver has a Total Aerobic Plate count of 32.73 x10^4CFU/g, while local chicken liver has a significantly higher Total Aerobic Plate count of 73.47 x10^4CFU/g, with a P-value of 0.005. The Total Coliform counts are 19.20 x10^4CFU/g for broilers and 23.13 x10^4CFU/g for local chickens. The P-value of 0.014 indicates a significant difference, with local chickens having higher coliform counts. Both broiler and local chicken livers have a count of 0, indicating no presence of these pathogens.

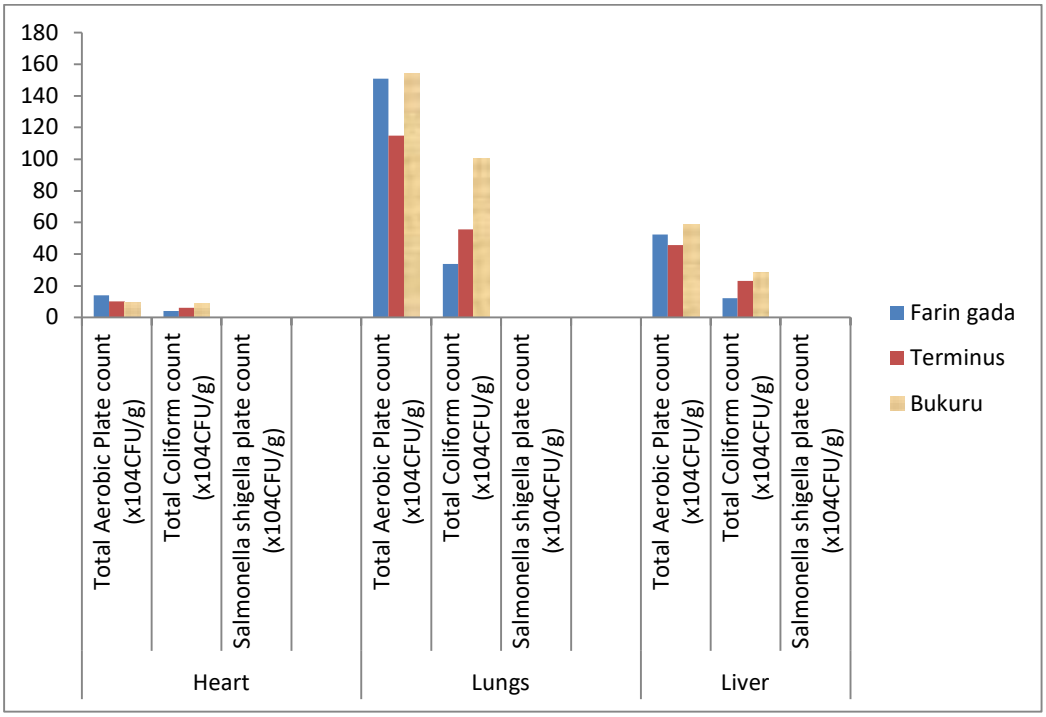

Fig. 2: Effects of location on the microbial load

Table 2: Main effect of breed types on microbial count

Organs	Parameters	Broiler chicken	Local chicken	SEM	P-value
Heart	Total Aerobic Plate count (x10^4CFU/g)	8.23^b	14.40^a	2.59	0.512
	Total Coliform count (x10^4CFU/g)	4.40^b	8.33^a	2.40	0.012
	Salmonella shigella plate count (x10^4CFU/g)	0	0	0	0
Lung	Total Aerobic Plate count (x10^4CFU/g)	92.07^b	187.80^a	26.38	0.005
	Total Coliform count (x10^4CFU/g)	55.00	71.00	29.18	0.003
	Salmonella shigella plate count (x10^4CFU/g)	0	0	0	0
Liver	Total Aerobic Plate count (x10^4CFU/g)	32.73^b	73.47^a	7.36	0.005
	Total Coliform count (x10^4CFU/g)	19.20	23.13	8.27	0.014
	Salmonella shigella plate count (x10^4CFU/g)	0	0	0.00	0

$^{a, b, c, d}$ means with different superscripts on the same column differ significantly (P<0.05)
SEM means standard error of mean.

DISCUSSION

These findings varied with the previous study by Baruah *et al*. (2023), who reported a lower average viable count of the liver 6.45 ±1.27 (log_{10} cfu/g ±SE) and heart 6.36 ±1.19 (log_{10} cfu/g ±SE) of raw chicken meat. Bukuru location generally has the highest TAPC for lungs 154 ± 39.05 and liver 58 ± 10.9 (log_{10} cfu/g ±SE) samples, suggesting higher contamination levels which could be as a result of poor hygiene practices which agreed with the findings of Ahmad *et al.,* (2013) that reported that microbial load of raw meat from abattoirs

and retail shops in Lahore is high which insinuates its possible role in spoilage and food-borne illness. In the same vein, the high coliform count observed is an indicative of fecal contamination (Franco and Landgraf, 2008). The significantly higher microbial counts, especially coliform counts in Bukuru samples, indicate a need for improved sanitation practices and more stringent monitoring of the processing environment.

Farin Gada typically has lower microbial counts for all samples as compared with other location, indicating better hygienic conditions or handling practices, but has the highest TAPC for heart 14.10 x10^4CFU/g samples as compared with other location. Terminus shows intermediate values with some significant differences in certain parameters. Local/indigenous chickens exhibited higher microbial counts in hearts, lungs, and livers as compared to broiler chickens, with significant differences in all organs. This could be as a result of differences in feed type and free-range rearing practices which exposed them to more environmental bacteria. The liver had 23.13 x10^4CFU/g which is higher than that reported by Fahim (2020), who recorded 6.1 x10^4CFU/g in the liver of chicken carcasses while Yammine and Karam, (2020) also reported 5.1 log CFU/g in the chicken liver samples.

From this study, local chicken samples were analyzed to have higher microbial loads; however, targeted interventions such as improved rearing practices, vaccination programs, and biosecurity measures can help reduce the contamination. Moreover, encouraging controlled environments for local chickens, similar to those used for broilers, can minimize exposure to environmental contaminants. Broiler and local chicken lungs, liver and heart show no presence of Salmonella or Shigella across all locations, indicating effective control of these pathogens. However, continue vigilance is necessary to maintain and improve these standards in Jos metropolis. This is highly imperative because these bacteria are significant foodborne pathogens, often associated with poultry (WHO, 2020). The findings from this study were in contrast with the one initially reported by Fahim (2020), who detected *Salmonella spp* in the chicken liver of the samples examined. However, the presence of *Salmonella* spp. in chicken depends on the prevalence as well as number of these pathogens in the animal itself on the skin, hair, feathers, and in the intestinal tract.

CONCLUSION

The interactive effects of location and breed type on microbial counts reveal significant insights into the factors influencing microbial contamination in chicken meat. Indigenous chickens generally exhibit higher microbial loads, while location-specific factors also play a crucial role in contamination levels. Implementing improved hygiene practices, standardized handling procedures, and targeted interventions can significantly reduce microbial contamination.

By addressing these factors extensively, the overall safety and quality of chicken meat can be improved, thereby reducing the risk of foodborne illnesses and ensuring better and safer chicken products for consumers in Jos Metropolis.

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