

## Microorganisms Associated with Poultry Feeds in South West, Nigeria

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### Article History

Received: 27 Feb 2023

Accepted: 14 May 2023

First Online: 25 May 2023

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### Keywords

Poultry

Animal

Feeds

Pathogenic

Microorganisms

### Abstract

The rate of mortality of poultry as a result of contaminated feeds is of the increase in the recent times. This study was carried out to determine the level of contamination, microbial loads and spoilage of selected poultry feeds in south west Nigeria. Rabiun Feeds, Caps Feeds, Ayo Best Feeds and Top feeds were selected and sampled. Standard pour plate methods were used for the analyses. Results obtained revealed average range of total viable count, coliform counts, *Staphylococcus* counts and fungal counts of  $2.35 - 7.10 \times 10^4$  Cfug,  $0.55-2.65 \times 10^4$ ,  $0.50-2.90$  Cfug and  $1.30-3.30 \times 10^4$  Cfug respectively. Microorganisms obtained include fifteen bacteria, eight yeast and five mould isolates. The genera are *Bacillus*, *Pseudomonas*, *Klebsiella*, *Enterobacter*, *Escherichia*, *Staphylococcus*, *Micrococcus*, *Alcaligenes*, *Acinetobacter*, *Salmonella*, *Serratia*, *Corynebacterium*, *Clostridium*, *Erwinia*, *Flavobacterium*, *Saccharomyces*, *Candida*, *Geotrichum*, *Rhodotorula*, *Kluyveromyces*, *Torulopsis*, *Hansenula*, *Pichia*, *Aspergillus*, *Rhizopus*, *Fusarium*, *Mucor* and *Talaromyces*. Fifty percent of the isolates were known pathogenic microorganisms. This study therefore, concludes and recommends that stringent hygienic measures during production and storage of poultry feeds should be followed and enforced to the later. Constants inspection by the Standard Regulatory Bodies to the production sites should be encouraged.

### Introduction

Poultry are birds of economic value contributing significantly to human food as a primary supplier of meat, egg, raw materials to industries (feathers, waste products), source of income and employment to people compared to other domestic animals (Demeke, 2004; Onajobi et al., 2020). Food for farm fowl, such as chickens, ducks, geese, and other domestic birds, is known as poultry feed (Bonnie, 2013).

Prior to the 20<sup>th</sup> century, grain, kitchen scraps, calcium supplements like oyster shell, and garden waste were frequently added to chicken diet as supplements. To maintain healthy birds, the feeds are

kept fresh as much as possible at all times. However, in Southwest of Nigeria, it is quite difficult at times to maintain the freshness of the feed, where high temperature and oxidation destroy certain vitamins.

Feed spoilage is caused by the growth of undesirable molds and bacteria. Poultry feed spoilage reduces the feed value and palatability. Poultry feed is known to contain *Salmonella*, and other microorganisms which are detrimental to the health of poultry animals (Eugene, 2012). As a result, this study aim is to evaluate the microbial quality of poultry feeds in south west region of Nigeria.

## Materials and Methods

### Study area

The study area is three reputable commercial poultry feed Companies within the southwest Nigeria. These includes; Rabiun Feeds – Ijebu-Ode, Ogun State, F.A. Feeds–Ijebu–Ode, Ogun States, Hybrid Feeds–Osogbo, Osun State and Top Feeds–Ibadan, Oyo State.

### Sample collection

A total of 12 samples were used. Samples consisted of Chicks Mash, Grower Mash, and Layers Mash from each commercial poultry feed companies respectively. The samples were collected in a clean polythene bag and transported to Federal Institute of Industrial Research, Oshodi, Lagos State (FIRO) for further analysis. Each selected commercial feed depot was visited two times for sample collections during the study period.

### Preparation of media diluents

23 g of Nutrient agar, 67g of MarConkey agar and 38g of Potato dextrose agar is weighed using a digital chemical balance and suspended into 1 liter amount of distilled water homogenized on hot plate magnet stirrer to form a uniform solution. Diluents (dilution blanks 0.1%) made up of 90ml and 9ml amount of distilled water were made sterilized at 121°C. 15 pounds per pressure (PSI) for 15 minutes in the autoclave. At the end of the sterilization period, media were cooled to 45°C in water bath preset at 45°C order to inhibit bacterial growth, streptomycin (0.14w/v) was aseptically weighed and added to potato dextrose agar only.

### Isolation of microorganisms from sample

Ten grams (10g) of sample were weighed with sterile spatula using chemical balance. The samples were put into a sterile pestle and mortar, crushed with 90 milliliters of sterile distilled water. The sample was aseptically poured into the bottle of 90ml of sterile distilled water above burner. This was properly mixed together-1ml portion from the above dilution was aseptically taken with a sterile pipette and introduced into 9ml-amount of sterile water  $10^{-1}$  dilution and from this dilution the samples were serially diluted up to the required dilution  $10^{-5}$  dilutions according to Onajobi et al. (2015).

Disposable petri dishes were set out and labeled accordingly while inoculation was carried out using pour plate method. From the  $10^{-4}$  and  $10^{-5}$  dilutions, avqurt (1.0ml) of inoculums was aseptically pipette and inoculated into sterile petri dishes, cool molten of Nutrient agar, MacConkey agar and potato dextrose

agar poured onto the inoculums respectively and mixed clockwise and anticlockwise for evenly distribution of the inoculums. The plates were allowed to set properly and incubated in an incubator at 35+2°C for 24 hours for bacteria and 28 +2°C for 3 – 5 days for fungi.

At the end of incubation period, the colony observed on the culture plates is counted using coulter colony counter. The colony or viable count per ml was calculated by multiplying the average number of colonies per countable plate by the reciprocal of the dilution. Report as Colony forming units/ml (Cfu) or (Cful/g) was according to Onajobi et al. (2017).

### Casein hydrogen

Nutrient agar (250ml) was prepared only 1%w/v (2.5g % casein) casein powder was added to Nutrient agar homogenized on hot plate magnetic stirrer. The medium was sterilized in an autoclave at 115°C for 10 mins allowed to cool to about 45–50°C and poured aseptically in petri dishes. The plates were allowed to set and dry at 45°C. Fresh culture or isolation of 18 -24 hours were inoculated into plates of casein agar. Incubated at 35+/-2°C for 5 days. Plates were examined for clearing of the medium around the bacteria growth using 20% and mercuric chloride (HCl and HgCl<sub>2</sub>) solution (Onajobi et al., 2020).

### Identification of moulds

The observed moulds growth was subcultured on fresh potato dextrose agar (PDA) plates and incubated at 28+2°C 5 days and therefore an accurate description of the fungus as grown on the medium was observed and examined at frequent intervals for colonial or cultural characteristics.

The colonial morphology of the mold isolates was performed based on the size, colour and aerial mycelia growth. Microscopy morphology is determined using blue stain. The fungal growth was stained using wet mount techniques. With a sterile inoculating needle, mycelia growth is picked from the culture plates and placed onto cleaned grease free glass slide on which a drop of saline water had been dropped. The fungal mycelia were teased out properly. One drops of lactophenol cotton blue stain was added and the preparation was covered with clean cover slips. The preparation was subsequently viewed under the X40 microscope objective (Cheesbrough, 2010).

### Screening of poultry samples for toxins

Chromatographic method was used to screen for poultry samples for the presence of toxins. 50 ml of 80% methanol was added to 10g of inoculated poultry feed each and were grinded into fine particles using a high-speed blender for 3 minutes. They were transferred back into conical flask and was shaken for 30 minutes on a shaker. The mixture was then filtered.

through Whitman paper and the extract collected in a 250ml flask, 20ml distilled water was added to ease separation. 15ml dichloromethane was added and shaken for proper mixture.

After separation, dichloromethane layer was filtered out through 20g of anhydrous sodium Sulphate to remove residual H<sub>2</sub>O. The extraction was collected in polypropylene cup and evaporated to dryness in a fume cupboard. The residue was redissolved in 1ml of dichloromethane. Aflatoxin standards and extracts were separated on thin layer chromatography plate. Aflatoxin plate was observed under long wavelength U.V light pitted in a black cabinet (Cheesbrough, 2010).

#### Characterization and identification of bacterial isolates

Pure cultures of bacterial isolates from feeds are identified based on their colonial morphology, cellular morphology and biochemical characteristics whereby the following analysis were carried out gram and spore staining, catalase production (Ramachandran et al., 2014), gelatin hydrolysis, starch hydrolysis, carbohydrate utilization oxidase test, indole production, nitrate reduction, coagulase test, urease test and methyl-red voges proskauer test (Cheesbrough, 2010).

#### Results and Discussion

Average range of count of 2.35-7.1×10<sup>4</sup>cfu/g for total viable bacteria 0.55-2.65 x 10<sup>4</sup> for coliforms counts, 0.5-2.9 Cfu/g for *Staphylococcus* and 1.3-3.3×10<sup>4</sup>Cfu/g for fungi (yeast counts were recorded respectively in all the samples analyzed from all poultry feeds investigated in table 1, 2 and 3 below. Slight variations were observed amongst the group of microorganisms within each poultry feeds. The average rate of occurrence and distribution of ten (10) members of the fungi group (Yeasts) were significantly different from the bacteria group.

Table 4, 5, 6 and 7 revealed vast array of microorganisms were detected and isolated among the various groups of microorganisms isolated were *Bacillus* species, *Corynebacterium* species, *Clostridium* species, *Flavobacterium* species, *Pseudomonas* species, *Micrococcus* species, *Alcaligenes* species, *Acinetobacter* species, *Proteus* species, *Staphylococcus* species, *Erwinia* species, *Enterobacter* species, *Klebsiella* species, *Serratia* species, *Citrobacter* species, *Salmonella* species, *Escherichia* species, *Sporosarcina* species and *Xanthomonas* species were among the bacteria group while the fungi group included: *Saccharomyces cererisiae*, *Saccharomyces exigins*, *Saccharomyces rouxii*, *Candida* species, *Pichia* species, *Geotrichum* species, *Rhodotorula glutinis*, *Hansenula anomala*, *Torulopsis stellate* and *Kluyveromyces maxians*.

**Table 1.** Physicochemical characteristics of poultry feed samples

Sample Location	Types of Feed	Sample No	Dtae of Collection	Moisture Content	PH	Colour	Texture	Odour
Rabiu Feeds (Ijebu Ode) Ogun State	i.Layers Mash	1	1 – 8 – 16	1. 16.5%	6.6	Light	Coarse	Faint
	ii.Grower Mash	2	"	2. 17.0%	6.5	Brown	Coarse	Faint
	iii.Chick Mash	3	"	3. 15.5%	6.7	Light Brown Light Brown	Coarse	Very Faint
F. A Feeds (Ijebu Ode) Ogun State	i.Layers Mash	4	"	1. 16.3%	6.6	Brown	Coarse	Faint
	ii.Grower Mash	5	"	2. 16.7%	6.5	Brown	Coarse	Faint
	iii.Chick Mash	6	"	3. 16.0%	6.6	Brown	Coarse	Faint
Hybrid Feeds Osogbo Osun State	i.Layers Mash	7	"	1. 16.6%	6.7	Light	Coarse	Faint
	ii.Grower Mash	8	"	2. 17.0%	6.4	Brown	Coarse	Faint
	iii.Chick Mash	9	"	3. 15.8%	6.7	Light Brown Light Brown	Coarse	Faint
Top Feeds (Ibadan) Oyo State	i.Layers Mash	10	"	1. 16.8%	6.4	Brown	Coarse	Faint
	ii.Grower Mash	11	"	2. 16.4%	6.5	Brown	Coarse	Faint
	iii.Chick Mash	12	"	3. 16.0%	6.6	Brown	Coarse	Faint

**Table 2.** Total mesophile aerobic microbial population of poultry fee

Sample Location	Types of Feed	Total Viable Count	Coliform Count	<i>Stapylococcus</i> Count	Fungi Count
Rabiu Feeds (Ijebu Ode) Ogun State	i. Chick Mash	$71 \times 10^3$	$11 \times 10^3$	$29 \times 10^3$	$33 \times 10^3$
	ii. Layer Mash	$31 \times 10^3$	$09 \times 10^3$	$07 \times 10^3$	$17 \times 10^3$
	iii. Grower Mash	$24 \times 10^3$	$06 \times 10^3$	$05 \times 10^3$	$14 \times 10^3$
F. A Feeds (Ijebu Ode) Ogun State	i. Chick Mash	$33 \times 10^3$	$06 \times 10^3$	$10 \times 10^3$	$16 \times 10^3$
	ii. Layer Mash	$47 \times 10^3$	$17 \times 10^3$	$13 \times 10^3$	$22 \times 10^3$
	iii. Grower Mash	$64 \times 10^3$	$23 \times 10^3$	$21 \times 10^3$	$25 \times 10^3$
Hybrid Feeds Osogbo Osun State	i. Chick Mash	$30 \times 10^3$	$09 \times 10^3$	$07 \times 10^3$	$13 \times 10^3$
	ii. Layer Mash	$31 \times 10^3$	$13 \times 10^3$	$19 \times 10^3$	$21 \times 10^3$
	iii. Grower Mash	$46 \times 10^3$	$10 \times 10^3$	$14 \times 10^3$	$25 \times 10^3$
Top Feeds (Ibadan) Oyo State	i. Chick Mash	$41 \times 10^3$	$11 \times 10^3$	$10 \times 10^3$	$20 \times 10^3$
	ii. Layers Mash	$47 \times 10^3$	$20 \times 10^3$	$12 \times 10^3$	$20 \times 10^3$
	iii. Grower Mash	$57 \times 10^3$	$27 \times 10^3$	$14 \times 10^3$	$27 \times 10^3$

**Table 3.** Mean of total mesophile aerobic microbial population of poultry feeds

Sample Location	Types of Feed	Total Viable Count	Coliform Count	<i>Stapylococcus</i> Count	Fungi Count
Rabiu Feeds (Ijebu Ode) Ogun State	1. Chick Mash	$39 \times 10^3$	$10 \times 10^3$	$09 \times 10^3$	$19 \times 10^3$
		$42 \times 10^3$	$12 \times 10^3$	$10 \times 10^3$	$21 \times 10^3$
	2. Layer Mash	$48 \times 10^3$	$19 \times 10^3$	$11 \times 10^3$	$18 \times 10^3$
		$45 \times 10^3$	$20 \times 10^3$	$12 \times 10^3$	$22 \times 10^3$
		$55 \times 10^3$	$25 \times 10^3$	$13 \times 10^3$	$25 \times 10^3$
F. A Feeds (Ijebu Ode) Ogun State	1. Chick Mash	$28 \times 10^3$	$09 \times 10^3$	$06 \times 10^3$	$12 \times 10^3$
		$32 \times 10^3$	$08 \times 10^3$	$07 \times 10^3$	$14 \times 10^3$
	2. Layer Mash	$53 \times 10^3$	$14 \times 10^3$	$20 \times 10^3$	$20 \times 10^3$
		$48 \times 10^3$	$11 \times 10^3$	$18 \times 10^3$	$22 \times 10^3$
		$49 \times 10^3$	$12 \times 10^3$	$12 \times 10^3$	$24 \times 10^3$
Hybrid Feeds Osogbo Osun State	1. Chick Mash	$42 \times 10^3$	$08 \times 10^3$	$14 \times 10^3$	$26 \times 10^3$
		$68 \times 10^3$	$13 \times 10^3$	$26 \times 10^3$	$30 \times 10^3$
	2. Layer Mash	$74 \times 10^3$	$09 \times 10^3$	$32 \times 10^3$	$36 \times 10^3$
		$33 \times 10^3$	$10 \times 10^3$	$05 \times 10^3$	$18 \times 10^3$
		$28 \times 10^3$	$08 \times 10^3$	$08 \times 10^3$	$16 \times 10^3$
Top Feeds (Ibadan) Oyo State	3. Grower Mash	$25 \times 10^3$	$07 \times 10^3$	$04 \times 10^3$	$13 \times 10^3$
		$22 \times 10^3$	$04 \times 10^3$	$06 \times 10^3$	$15 \times 10^3$
	1. Chick Mash	$31 \times 10^3$	$05 \times 10^3$	$10 \times 10^3$	$15 \times 10^3$
		$34 \times 10^3$	$07 \times 10^3$	$09 \times 10^3$	$17 \times 10^3$
		$46 \times 10^3$	$15 \times 10^3$	$12 \times 10^3$	$20 \times 10^3$
2. Layers Mash	$48 \times 10^3$	$18 \times 10^3$	$13 \times 10^3$	$24 \times 10^3$	
	$66 \times 10^3$	$24 \times 10^3$	$18 \times 10^3$	$26 \times 10^3$	
	$62 \times 10^3$	$22 \times 10^3$	$24 \times 10^3$	$23 \times 10^3$	

Amongst the bacterial group *Bacillus subtilis*, *Bacillus megaterium*, *Bacillus brevis*, *Bacillus cereus*, *Bacillus polymyxa*, *Staphylococcus aureus*, *Staphylococcus albus*, *Staphylococcus hominis*, *Micrococcus luteus*, *Micrococcus roseus*, *Enterobacter cloacea*, *Escherichia coli*, *Klebsiella oxytoca*, *Euterobacter intermedius*, *Alcaligenes faecalis*, *Acinetobacter mallei*, *Klebsiella aurogenes*, *Klebsiella liquefascieus*, *Pseudomonas aeruginosa* and *Flavobacterium rigense* were most prevalent while *Saccharomyces cerevisiae*, *Saccharomyces rouxii*, *Candida utilis*, *Hansenula anomala* and *Candida parapsilosis* were most prevalent among the fungi group.

Thirteen species of *Bacillus* were encountered and they were identified. They were all Gram-positive rods, catalase positive, motile, oxidase positive, most are citrate, starch, gelatin, casein and Proskaeur positive. Most species fermented glucose, sucrose, lactose, mannitol, fructose, Arabinose and Xylose (Table 4). They were mostly present in all poultry feeds samples.

Two species of *Clostridium* were isolated and identified as *Clostridium tertium* and *Clostridium septicum*. They were all gram-positive rods, catalase, oxidase, indole, methyl red, voges proskaeur, citrate, urease negative. They were both motile, casein, positive spore formers. *Clostridium tertium* reduced nitrate to nitrite, fermented glucose, sucrose, lactose mannitol, maltose and fructose, while *Clostridium septicum* liquefied gelatin, NO<sub>3</sub> reduction negative, fermented glucose, sucrose, lactose, xylose and fructose. The organism identified as *Flavobacterium* species, was yellow/orange, short rods, gram negative rods, catalase, oxidase positive *Flavobacterium rigense* is motile, urease positive and liquefied nutrient gelatin, fermented glucose, sucrose/mannitol.

Five species of *Pseudomonas* were encountered and they were identified as *Pseudomonas aeruginosa*, *P. mendocina*, *P. cepaciae*, *P. mallie* and *P. fluorescens*. They were all Gram-negative rods, catalase and oxidase positive, motile, urease negative. Most species liquefied nutrient gelatin. The species did not hydrolyse starch. Most species reduced nitrate to nitrite. *P. mendocina* fermented only glucose, other species fermented glucose, sucrose, mannitol, Arabinose / raffinose. *P. aeruginosa* did not ferment xylose, lactose and salicin whereas *P. fluorescens* fermented xylose, mannitol and salicin.

The next genus was identified as *Alcaligenes*, it was isolated from the five samples. The colonies were white, entire and raised. Cellular observation showed that they were coccibacilli in shape and Gram negative. The cells were motile, catalase, oxidase, citrate utilization and voges proskaeur positive, urease, indole, methyl red, starch and gelatin tests were all negative. The organisms did not ferment lactose, xylose, salicin, sorbitol, mannitol, maltose, arabinose, raffinose and fructose. It was subsequently identified as a strain of *Alcaligenes faecalis*.

The organism identified as *Acinetobacter iumiwoffi* was short rod, gram negative and non-motile. It was catalase, urease and citrate test positive and did not produce acid from most carbohydrate sugars tested, except glucose and mannitol sugars.

The next species were *Eriwinia*, they were identified as *Eriwinia carotovora* and *E. uredovor*. They were gram negative rods, motile, catalase positive, and voges proskaeur positive, liquefied nutrient gelatin, nitrate reduced. They both fermented carbohydrate sugars such as glucose, xylose, salicin, mannitol and arabinose, *E. uredovor* did not ferment sucrose, lactose sorbitol, maltose, raffinose and fructose. The organic identified as *Xanthomonas campestris* was yellow in colour, gram-negative rods in shape, motile, catalase positive, starch hydrolyzed and liquefied nutrient gelatin, they fermented glucose, sucrose, maltose, arabinose and fructose. They did not ferment lactose, xylose, sorbitol, Salicin, mannitol, and raffinose.

Two species of *Staphylococcus* were isolated and identified as *Staphylococcus albus*, and *S. ariettae*. Both were Gram-positive cocci, catalase positive, non-motile, oxidase negative except *S. albus*, indole, methyl red, citrate utilization tests negative, they did not hydrolysed and liquefied nutrient gelatin as shown in table 6. Both were voges proskaeur test positive and Urease positive. *Staphylococcus albus* did not ferment xylose, ribose, galactose, raffinose, arabinose, but *Staphylococcus ariettae* fermented almost all the sugars except galactose in which acid was not produced. *Micrococcus* species (*Intense*, *Candidus* and *Roseus*). They were all gram-positive cocci, catalase positive, oxidase positive except *Micrococcus roseurs* which was oxidase negative. *Micrococcus candidus* was urease, Voges proskaeur positive and liquefied nutrient gelatin. They all fermented glucose, sucrose, xylose and maltose sugars. Out of 12 poultry feed samples investigated, a total of 24 isolates were obtained. Gram negative isolates were about 12 isolates. Table 7 shows the identified fungi isolates (yeast isolates) *Saccharomyces* species (*cerevisiae*, *rouxii*, and *exigus*) *Candida* species (*parapsilosis*, *utilis*, *castelli*, *sphaenical*, and *glabaruta*) *Geotrichum* species (*Klebahnii* and *capitatum*) *Torulopsis stellate*, *Kluyveromyces maxicans*, *Hansenula anomola*, *Pichiaohmeri*, and *Rhodotorula glutinis*. They were all catalase positive, motile. Nitrate was not reduced except *Hansenula anomalla* in which nitrate was reduced to nitrite. *Saccharomyces* species, *Kluyveromyces* species, *Pichiaohmeri*, *Hansenula* species produced/formed ascospores from their asci. Carbohydrate sugars were fermented by the most yeast species. The fungi (molds) groups were significantly differently from the bacteria group and were in the order *Aspergillus niger*, *Rhizopus stolonifer*, *Mucorplumbeus*, *Fusarium oxysporium*, *Aspergillus chevalieri*, *Rhizopus arrhizus*, *Nigrospora oryzae*, *Absidiiaspinosa*, *Aspergillus flavus*, *Aspergillus amstelodami*. Among the fungi (moulds) the most prevalent species were *A. niger*, *A. flavus*, *Fusarium oxysporum*, *Rhizopus arrhizus*, *Rhizopus stolonifer*, and *Absidiiaspinosa* as shown in Figure 1.

**Table 4.** Biochemical test on isolated bacteria

Isolate code	Colour/pigment	Gram reaction	Cellular morphology	Catalase test	Oxidase test	Indole test	Motility test	Mr-methyl/red	Vp-voges prophase	Urease	Citrate utilization	Gelatin hydrolysis	Stenrch hydrolysis	No <sub>3</sub> reduction	Probable identification
<b>Top Feed</b>															
1	Cream	+ve	Rods	-	-	-	+	-	-	-	-	-	-	+	<i>Clostridium tertium</i>
1	Cream	+ve	Rods	-	-	-	+	-	-	-	-	+	-	-	<i>Clostridium septicum</i>
2	Yellow Orange	-ve	Rods	+	+	-	+	-	-	+	+	+	-	-	<i>Flavobacterium rigense</i>
2	Yellow Orange	-ve	Rods	+	+	-	-	-	-	-	-	-	-	+	<i>Pseudomonas mendocina</i>
3	Cream White	+ve	Cocci	+	+	-	-	-	+	-	-	-	-	-	<i>Staphylococcus albus</i>
3	Cream White	-ve	Rods	+	+	-	-	-	-	-	-	+	-	+	<i>Pseudomonas cepaciae</i>
<b>Hybrid Feed</b>															
1	Yellow	+ve	Cocci	+	+	-	-	-	-	+	-	+	-	-	<i>Micrococcus intense</i>
1	Cream	-ve	Rods	+	-	-	+	-	+	-	-	+	-	+	<i>Ervinia carotovora</i>
2	Pinkish	-ve	Rods	+	-	-	-	-	-	+	+	-	-	+	<i>Acinetobacter iwoffi</i>
2	Orange Yellow	+ve	Cocci	+	-	-	-	-	+	-	-	-	-	-	<i>Staphylococcus ariettae</i>
3	Red	+ve	Cocci	+	-	-	+	-	+	-	-	-	-	+	<i>Micrococcus roseus</i>
3	Yellow	-ve	Rods	+	-	-	+	-	-	-	-	+	+	-	<i>Xanthomonas campestris</i>
<b>Rabiu Feed</b>															
1	Green	-ve	Rods	+	+	-	+	-	-	+	-	+	-	-	<i>Pseudomonas mallei</i>
1	Green	-ve	Rods	+	+	-	+	-	-	-	+	+	-	+	<i>Pseudomonas aeruginosa</i>
2	Bluish Green	-ve	Rods	+	+	-	+	-	-	-	-	+	-	+	<i>Pseudomonas fluorescens</i>
2	Yellow	+ve	Cocci	+	+	-	-	-	+	+	-	+	-	-	<i>Micrococcus candidus</i>
3	Yellow	+ve	Cocci	+	+	-	-	-	+	+	-	+	-	-	<i>Micrococcus candidus</i>
3	Pink	+ve	Cocci	+	-	-	+	-	+	-	-	-	-	+	<i>Micrococcus roseus</i>
<b>F.A. Feed</b>															
1	Yellow	+ve	Cocci	+	+	-	-	-	+	+	-	+	-	-	<i>Micrococcus candidus</i>
1	Yellow	-ve	Rods	+	-	+	+	-	+	-	-	+	-	+	<i>Ervinia uredovora</i>
2	Cream	-ve	Rods	+	-	-	+	-	+	-	-	+	-	+	<i>Ervinia carotovora</i>
2	Pinkish	-ve	Rods	+	+	-	+	-	+	-	-	-	-	-	<i>Alcaligenes faecalis</i>
3	Cream Butter	+ve	Rods	+	+	-	+	-	+	-	+	+	+	+	<i>Bacillus cereus</i>
3	Cream Butter	+ve	Rods	+	+	-	+	-	+	-	+	+	+	+	<i>Bacillus cereus</i>

CODE: 1 = Chick Mash 2 = Layers Mash 3 = Growers Mash

**Table 5.** Biochemical test on isolated coliforms

Sample location	Isolate code	Colour/pigment	Gram reaction	Cellular morphology	Catalase test	Oxidase test	Indole test	Motility test	Mr-methyl/red	Vp-voges prophase	Urea se utilization	Citrate	Starch	No <sub>3</sub> reduction	Probable identification
<b>Top Feed</b>															
	1	Pink	-ve	Rods	+	-	+	-	-	+	+	+	+	+	<i>Klebseiella oxytoga</i>
	1	Pink	-ve	Rods	+	-	-	+	-	+	+	-	+	-	<i>Enterobacter aerogeres</i>
	2	Pink	-ve	Rods	+	-	-	-	+	-	+	+	-	-	<i>Klebseiella liquefezium</i>
	2	Black	-ve	Rods	+	-	-	+	-	-	-	+	-	-	<i>Salmonella arizonic</i>
	3	Black	-ve	Rods	+	-	+	+	+	-	-	-	-	+	<i>Escherichia coli</i>
	3	Red	-ve	Rods	+	-	-	+	+	+	-	+	-	-	<i>Serratia liquefaciens</i>
<b>Hybrid Feed</b>															
	1	Pink	-ve	Rods	+	-	-	+	+	+	-	+	-	+	<i>Enterobacter intermedines</i>
	1	Cream	-ve	Cocci	+	-	+	+	+	-	-	+	-	+	<i>Citrobacter diversus</i>
	2	Cream	-ve	Rods	+	-	+	-	-	-	-	+	-	-	<i>Citrobacter koseri</i>
	2	Pinkish	-ve	Rods	+	-	-	+	-	+	+	+	+	-	<i>Enterobacter cloacae</i>
	3	Pinkish	-ve	Rods	+	+	-	+	-	-	-	+	-	-	<i>Alkaligenes faecalis</i>
	3	Pink	-ve	Rods	+	-	-	-	+	+	+	+	+	+	<i>Klebseiella planticola</i>
<b>Rabiu Feed</b>															
	1	Cream	-ve	Rods	+	-	-	+	+	-	+	+	-	-	<i>Citrobacter freundii</i>
	1	Pinkish Cream	-ve	Rods	+	-	-	-	-	-	-	+	-	-	<i>Acinetobacter mallei</i>
	2	Pink	-ve	Rods	+	-	-	+	-	+	-	-	-	+	<i>Enterobacter amigenus</i>
	2	Black	-ve	Rods	+	-	-	+	+	-	-	+	-	+	<i>Salmonella bougori</i>
	3	Pink	-ve	Rods	+	-	-	+	+	+	-	+	-	+	<i>Enterobacter agglomerans</i>
	3	Black	-ve	Rods	+	-	+	+	+	-	-	-	-	+	<i>Escherichia coli</i>
<b>F.A. Feed</b>															
	1	Cream	-ve	Rods	+	-	-	+	+	+	-	+	+	-	<i>Proteus mirabilis</i>
	1	Black	-ve	Rods	+	-	+	-	+	-	-	-	-	+	<i>Escherichia coli</i>
	2	Pink	-ve	Rods	+	-	+	+	-	+	+	+	+	+	<i>Klebseiella oxytoga</i>
	2	Pink	-ve	Rods	+	-	-	+	+	+	-	+	-	+	<i>Enterobacter intermedium</i>
	3	Cream	-ve	Rods	+	+	-	+	-	-	-	+	-	-	<i>Alcaligenes faecalis</i>
	3	Pink	-ve	Rods	+	-	-	+	-	+	+	+	+	-	<i>Enterobacter cloacae</i>

CODE: 1 = Chick Mash 2 = Layers Mash 3 = Growers Mash

**Table 6.** Biochemical characterization of isolated *Staphylococcus* species

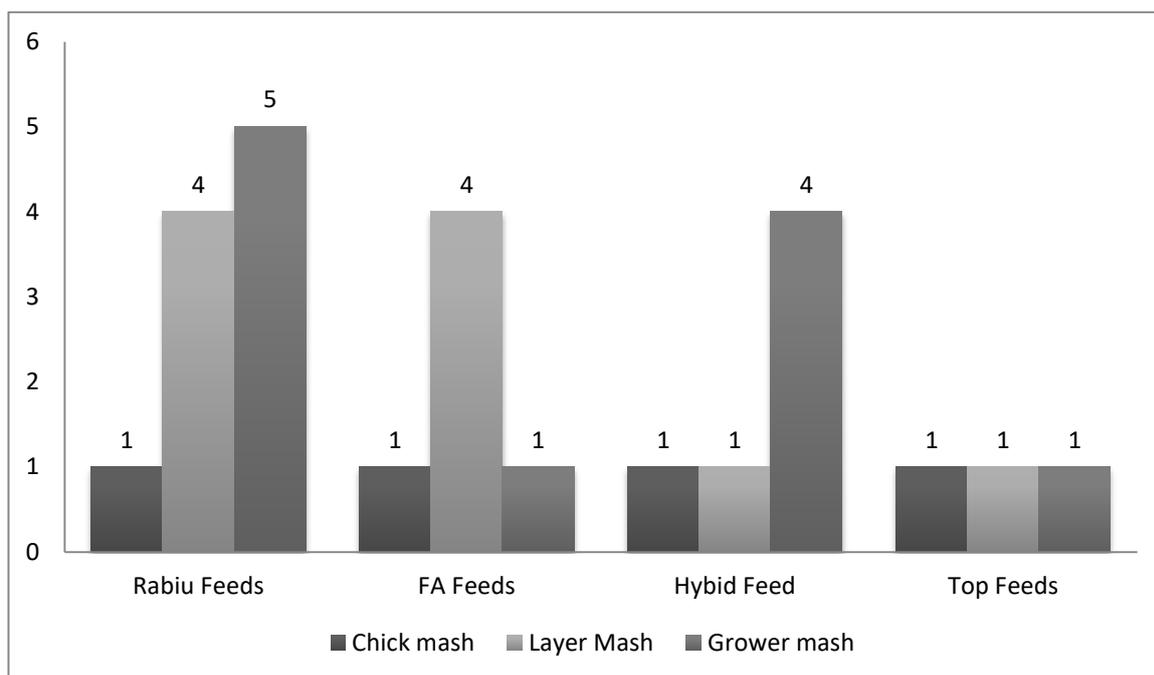
Staphylococcus	Colour	Gram reaction	Cellular morphology	Catalase test	Oxidase test	Indole test	Motility test	Mr-methyl/red	Vp-voges prosphase	Urease	Citrate utilization	No3 reduction	Probable identity
Isolate Code													
Top Feed													
1	White	ve	Cocci	+	+	-	-	-	+	-	-	-	<i>Staphylococcus albus</i>
1	Orange	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus aureus</i>
2	White	ve	Cocci	+	+	-	-	-	+	-	-	+	<i>Staphylococcus albus</i>
2	Orange	ve	Cocci	+	-	-	-	-	+	-	-	+	<i>Staphylococcus arietiae</i>
3	Cream	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus carnosus</i>
3	White	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus simulans</i>
Hybrid Feed													
1	Yellow	ve	Cocci	+	+	-	-	-	-	-	+	+	<i>Micrococcus varians</i>
1	Orange	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus aureus</i>
2	Yellowish	ve	Cocci	+	+	-	-	-	+	+	-	+	<i>Micrococcus kristinae</i>
2	White	ve	Cocci	+	+	-	-	-	+	-	-	+	<i>Staphylococcus albus</i>
3	Yellow	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus epidermid</i>
3	Orange	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus aureus</i>
Rabiu Feed													
1	Cream	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus hominis</i>
1	Yellow	ve	Cocci	+	+	-	-	-	+	+	-	+	<i>Micrococcus candidus</i>
2	Cream	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus hominis</i>
2	Red	ve	Cocci	+	-	-	+	-	+	-	-	+	<i>Micrococcus roseus</i>
3	Yellow	ve	Cocci	+	+	-	-	-	-	+	-	+	<i>Micrococcus luteus</i>
3	Cream	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus hominis</i>
F.A. Feed													
1	Red	ve	Cocci	+	-	-	+	-	+	-	-	+	<i>Micrococcus roseus</i>
1	Cream	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus hominis</i>
2	Orange	ve	Cocci	+	-	-	-	-	+	+	-	+	<i>Staphylococcus aureus</i>
2	Yellow	ve	Cocci	+	+	-	-	-	-	+	-	+	<i>Micrococcus luteus</i>

CODE: 1 = Chick Mash 2 = Layers Mash 3 = Growers Mash

**Table 7.** Biochemical characterization of isolated yeasts

Yeast	Colour	Cellular morphology	Catalase test	No3 reduction	Ascospaze formation	Motility test	Urease test	Pseudomycellium production	Glucose	Maltose	Meubrose	Probable Organism
ISOLATE CODE												
Top Feed												
1	Cream white	Oval budding	+	-	+	+	-	-	+	+	-	<i>Saccharomyces cerevisiae</i>
1	Cream dull	Oval	+	-	-	+	-	-	+	+	-	<i>Candida parapsilopsis</i>
2	Cream rough	Cylindrical	+	-	-	+	-	-	+	-	-	<i>Geotrichum klebahnii</i>
2	Cream	Oval budding	+	-	+	+	-	-	+	+	-	<i>Saccharomyces cerevisiae</i>
3	Cream	Ellipsoidal	+	-	-	+	-	-	+	-	-	<i>Saccharomyces rouxi</i>
3	Cream white	Oval budding	+	-	+	+	-	-	+	+	-	<i>Saccharomyces cerevisiae</i>
Hybrid Feed												
1	Cream dull	Oval budding (small)	+	-	+	+	-	-	+	+	-	<i>Candida utilis</i>
1	Cream	Round budding	+	-	+	+	-	-	+	-	-	<i>Saccharomyces exigus</i>
2	Cream	Round	+	-	-	+	-	-	+	-	-	<i>Torulopsis stellata</i>
2	Cream	Round	+	-	+	+	-	-	+	-	-	<i>Kluyveromyces maxians</i>
3	Cream	Oval budding	+	-	+	+	-	-	+	+	-	<i>Saccharomyces cerevisiae</i>
3	Cream	Oval budding	+	-	+	+	-	-	+	+	-	<i>Saccharomyces cerevisiae</i>
Rabiu Feed												
1	Cream	Round budding	+	+	+	+	-	-	+	-	-	<i>Hansenula anomola</i>
1	Cream	Round budding	+	-	+	+	-	-	+	-	-	<i>Pichiaohmeri</i>
2	Cream	Oval small	+	-	+	+	-	+	+	-	-	<i>Candida castelli</i>
2	Cream	Ellipsoidal	+	-	+	+	-	-	+	-	-	<i>Saccharomyces cerevis</i>
3	Cream white	Oval budding	+	-	+	+	-	-	+	+	-	<i>Saccharomyces cerevisiae</i>
3	Cream	Oval budding	+	-	+	+	-	-	+	+	-	<i>Saccharomyces cerevisiae</i>
F.A. Feed												
1	Red/Pink	Elongated	+	-	-	+	-	-	+	-	-	<i>Rhodoforula glutinis</i>
1	Cream	Cylindrical	+	-	-	+	-	-	+	+	-	<i>Geotrichum capitatum</i>
2	Cream	Oval small	+	-	-	+	-	-	+	+	-	<i>Candida sphaxrica</i>
2	Cream	Cylindrical	+	-	-	+	-	-	+	-	-	<i>Candida glabrata</i>

CODE: 1 = Chick Mash 2 = Layers Mash 3 = Growers Mash



**Figure 1.** Histogram showing level of aflatoxins in (3) different poultry feed

**Keys:** 1 – No Aflatoxin detected, 4 – Aflatoxin (B1) detected, 5 – Aflatoxin (G1) detected

**NOTE:** X- Axis – Sample Names (Rabiui feeds, FA feeds, Hybrid feeds and lastly Top feeds)

Y- Axis- Toxins Status (1- Not detected, 4- AF(B1), 5- AF (G1))

This study revealed the microorganisms associated with poultry feeds that are commonly used within the south western region of Nigeria. The presence and isolation of these microorganisms depict that they are the causal agents responsible for the spoilage of poultry feeds. The slightly high viable staphylococcus counts bacteria, fungi (yeast/moulds), recorded may be associated with inadequate post-processing handling practices as spreading on the floor, mat and sometimes on high density polythene spread on the floor during and after pre-mixed bagging and packaging and during haulage and storage. These may also be responsible for the vast array of microorganisms detected and isolated. These finding corroborate with the report of Lund et al. (2000).

Low counts of coliforms and *Salmonella* were detected. However, there presence appeared transient since no growth was detected on agar plate following analysis after 24 hours. This may be due to their inability to with stand the micro environmental condition. The high rate of occurrence and distribution of moulds such as a *Aspergillus*, *Fusarium*, *Rhizopus*, *Taloromyces*, *Absidia* and others may be traced to the inadequate post-processing handling practices, storage in high environmental conditions, the ubiquitous nature of their moulds and their ability to withstand and tolerate harsh environmental conditions such as low pH and low moisture content of the poultry feeds (Beatriz and Eliana, 2000).

It is a mandate of the World Health Organization (WHO) that chicken products be safe for human consumption. Important potential route for infections to enter the supply of food for humans is through microbial contamination of chicken feed (Kashiwazwki, 1999). To ascertain the load and the microorganisms connected with chicken diets in southwest Nigeria, this study was planned and executed. These are the primary industries that deal with poultry feeding. Despite the apparent similarity in contamination, market and factory-sourced feeds were analyzed independently due to the effects of storage, time, and environmental factors. A total of 132 isolates were discovered and acquired from the twelve (12) feeding samples that were analyzed. There were somewhat fewer Gram-negative isolates than Gram-positive ones. Gram-negative bacteria, particularly *Salmonella*, are more dangerous than Gram-positive bacteria, hence only a very small fraction of them were discovered here (Olajuyigbe et al., 2006 and Onajobi et al., 2017).

*Salmonella arizonae* and *Salmonella bongori* were both isolated from samples from Top feeds layer mash and Rabin feeds layer mash. This finding is consistent with previous work (Kidd et al., 2002). Feeds have been noticed to be the source of human infection due to eating chicken fed salmonella-contaminated feeds. Other feeds sources or samples were found free of salmonella but can be contaminated if stored in environment with about 20–25% moisture content.

The result showed that grower mash and chick mash were most contaminated due to period of feed storage and storage conditions are suspected to be behind the higher level of contamination. It was found that chick mash feed samples are the most contaminated followed by grower mash feed samples, followed by layer mash which was the least contaminated feed samples. This is mainly attributed to the high nutritive value of the feed samples (Sakazaki, 2000 and Onajobi et al., 2017).

Amongst Gram-negative bacteria *Escherichia coli*, followed by *Klebsiella* species *Enterobacter* species, *Citrobacter* species, *Pseudomonas* species, *Alcaligenes* species, *Acinetobacter* species, *Serratia* species, and *Proteus mirabilis* isolated from poultry feed was reported by Wadu (2002), additionally discovered in a poultry shop (Quinn et al., 1999).

The majority of feed sample isolates contained *Bacillus* species. According to, *Bacillus* spp. may be pollutants in poultry feed (Bryan and Doyl, 1995). In this experiment, the results were consistent with those established by Wadu (2002), who discovered that *Bacillus* species are the most prevalent isolate in chicken feed. Nada (2005) successfully isolated *Bacillus* species from chicken feed. The samples also included isolated *Staphylococcus* species, including *Staphylococcus aureus*, *Staphylococcus albus*, *Staphylococcus simulans*, and *Micrococcus* species. The public's health may be impacted by these organisms. The microflora in poultry feeds may be different and come from a variety of environmental factors, such as soil, temperature, dust, and insects. Pathogens may infect poultry feed ingredients at any moment when they are being grown, harvested, processed, or stored (Watkins et al., 2003).

Seventeen fungal isolates were recovered from the twelve feed samples. The yeasts found to spoil the feed samples were identified as *Saccharomyces roxii*, *Saccharomyces exigus*, *Geotrichum klebahaii*, *Candida utilis*, *Torulopsis stellata*, *Kluyveromyces maxians*, *Hansenula anomala*, *Candida castelli*, *Candida glabrata*, *Candida sphaerica*. *Geotrichum capitatum* and *Rhodotorula glutinis*, *Saccharomyces*, *Candida*, and *Geotrichum* species are dominant organisms in cereal-based foundation species of the genus *Saccharomyces* and *Candida* are widespread in nature and can be found on plants or material of plant origin in fermenting or spoiling food (Belgin and Kathryn, 2006).

Fungal colonies (moulds) selected from each plate were based on colony appearance. Colonies having characteristic features such powdery appearance, fluffy, velvety texture, low mycelia with colour ranging from white, gray to pinkish, pink, greenish yellow, black yellow, green, gray green and others were selected; fifteen fungal (moulds) isolated were selected, examined microscopically and identified by their cellular morphology and culture characteristics.

The moulds isolates encountered and identified are *Aspergillus niger*, *Talaromyces thermophilus*, *Fusarium oxysporium*, *Absidia spinosa*, *Mucor plumbeus*, *Aspergillus amstelodami*, *Nigrospora oryzae*, *Aspergillus chevalieri*, *Rhizopus arrhizus* and others. These groups of moulds have been variously linked with the production of various types of mycotoxins under various condition (Tournas, 1994). Exposure of mycotoxins through ingestion of contaminated foods of poultry feeds by birds or chicken and inhalation to toxins produced have been linked to acute and chronic toxicity in animals. Since poultry feeds require little or no further processing or treatment prior to consumption by the chicken, there is the possibility of ingesting large dosage over a period of time with possible health hazards. Hence the need to develop adequate processing, handling and storage techniques for this relish poultry feeds (Kayode and Oworunubi, 1988 and Onajobi et al., 2020).

## Conclusion

The present investigation or work revealed slightly high bioload and vast array of microorganism associated with poultry feeds and high rate of occurrence and prevalence of fungal producing mycotoxins. This is alarming and suggests early warning signals indicating the level of safety of available poultry feeds. It also warrants renewed vigilance on the efficacies of food processing conditions, feed handling and handlers' technical knowhow, hygiene practices and safety storage conditions.

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PROOF

RESEARCH PAPER

# Molecular Prevalence of Three Chicken Gastrointestinal Tract Pathogens and Phylogenetic Characterization of *Tetratrichomonas gallinarum* in Türkiye

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## Article History

Received: 14 Apr 2023

Accepted: 11 May 2023

First Online: 23 May 2023

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## Keywords

*Histomonas meleagridis*

*Heterakis gallinarum*

*Tetratrichomonas gallinarum*

Molecular prevalence

18S rRNA

## Abstract

Several species of parasites infect chickens and can cause economic losses. *Histomonas meleagridis*, its intermediate host *Heterakis gallinarum*, and *Tetratrichomonas gallinarum* are the most common parasites of poultry. The current study aimed to determine the molecular prevalence and phylogenetic relationships of *H. meleagridis*, *He. gallinarum*, and *T. gallinarum* in chickens in Central Anatolia Region of Türkiye. For this, a total of 100 fecal specimens from chickens were analyzed by using a PCR assay targeting the 18S rRNA gene region of *H. meleagridis* and *T. gallinarum* and the mtDNA COI gene region of *He. gallinarum*. PCR analysis identified *T. gallinarum* in 11 (1.1%) specimens, whereas other species were not found in all the examined specimens. Positive specimens were detected only in backyard chickens. Sequence analyses identified two novel genotypes named TRTgal1 and TRTgal3, and one known genotype (TRTgal2) of *T. gallinarum*. The TRTgal2 genotype was found to be identical to the human genotype (AY247746) and the four avian genotypes. Phylogenetic analyses of the obtained genotypes clustered in separate monophyletic clades. Our study provides the first data on *T. gallinarum* in chickens in Türkiye and contributes to public health with the identified zoonotic genotype and knowledge of the epidemiology of this parasite.

## Introduction

Poultry plays an important role in meeting animal protein needs, with short production cycles and low ecological requirements (Marangon and Busani, 2007). The poultry breeding is faced with diseases such as necrotic enteritis, coccidiosis and avian influenza that cause adverse economic effects. (Galarneau et al., 2020). Histomoniasis, mostly known as blackhead disease, caused by *Histomonas meleagridis*, represented by losses in turkeys with pathological lesions in the caeca and liver (Grabensteiner and Hess, 2006). In chickens, histomoniasis lesions are often confined to the caeca and associated with less severe production losses and some mortality (Esquenet et al., 2003). Hu et al. (2006) reported that the transmission dynamics of histomoniasis in chickens differ from

turkeys. In general, infections are transmitted by intermediate hosts such as mainly *Heterakis gallinarum*, an enteric nematode parasite that primarily affects turkeys and chickens. However, some reports suggest that transmission also occurs without vectors (Hu and McDougald, 2003). *Heterakis* worms are small, white, and thin, and found mostly in the ceca of birds, and several species infect poultry (McDougald, 2020). *Heterakis gallinarum* infections may cause weight loss in heavy infections, like enteric nematodosis. Moreover, the damage of *He. gallinarum* infection may increase depending on co-infection with histomoniasis (Cupo and Beckstead, 2019). *Tetratrichomonas gallinarum* is a widespread enteric flagellate that can colonize the digestive tract of galliform and anseriform

birds (Cepicka et al. 2005). The pathogenicity of this species is controversial (Amin et al., 2011). *T. gallinarum* is considered nonpathogenic but diarrhea and inflammation of the caecum have been reported in chukar partridges (Wichmann and Bankowski, 1956), mockingbird (Patton and Patton S, 1996), white pelican (Burns et al., 2013), and chickens (Landman et al., 2016). The first infection with *T. gallinarum* was described in chickens in 1911 (Martin and Robertson, 1911). Therewithal, *T. gallinarum*-like organisms were isolated from human patients in 2005 (Cepicka et al., 2005).

Molecular methods such as polymerase chain reaction and DNA sequencing have been successfully used for species identification and phylogenetic relationships (Cepicka et al., 2010). Different gene regions such as ITS1/5.8S/ITS2, 18S rRNA, and protein-coding genes are commonly used to describe the phylogenetic relationships of the species (Grabensteiner et al., 2010). Analysis of 18S rRNA gene is a good marker for species identification and characterization of trichomonads (Delgado-Viscogliosi, et al., 2000; Dimasuay and Rivera, 2013).

Studies on the current epidemiological status and molecular characterization of these three species in Türkiye are limited. Therefore, we aimed to determine the molecular prevalence, phylogenetic characterization of *H. meleagridis*, *He. gallinarum*, and *T. gallinarum* in backyard chickens and laying hens in Kirsehir province, Türkiye.

## Materials and Methods

### Collection of fecal samples

A total of 100 fresh fecal droppings from chickens, including 80 backyard and 20 laying hens, were collected, and placed in plastic individual containers, and labeled. Ethics approval was not required. All samples were stored at -20 °C until DNA extraction.

### DNA extraction and PCR amplification

Genomic DNA (gDNA) extraction was carried out from each fecal sample by using the QIAamp DNA Stool Mini Kit (Qiagen, Hilden, Germany), according to the manufacturer's instructions. The final nucleic acids were precipitated in a 50 µL elution buffer and stored at -20 °C. The DNA quality of each isolate was assessed by Qubit Fluorometric Quantitation (Thermo Fisher Scientific, Waltham, USA). All gDNA samples were examined with PCR analyses to determine the *H. meleagridis* and *T. gallinarum* by amplifying the partial sequence of the 18S rRNA gene region and *He. gallinarum* mtDNA COI gene region. Primer pairs used in PCR analyses are shown in Table 1. A total of ~25 ng of gDNA of each sample was included in the ready to use PCR Master Mix (Dream Taq Hot Start Green PCR Master Mix, Thermo Scientific, USA) in a final reaction

volume of 25 µL. The same cycling conditions for the PCR analyses were used as the references given in Table 1. The PCR amplifications were performed in a Sensoquest Labcycler (SensoQuest, Germany). Positive controls of each species and nuclease-free water as a negative control were used in all analyses. PCR products were electrophoresed on 1.5% agarose gel and visualized using the gel documentation system (Fig. 1).

### Sequencing and phylogenetic analysis

All PCR positive amplicons were purified by using GeneJET Gel Extraction Kit (Thermo Fisher Scientific, Waltham, MA, USA) and sequenced in both directions via Sanger sequencing (BMLabosis, Ankara, Türkiye). The raw sequence reads (~500 bp) were checked, aligned and assembled using Geneious Prime 2020.0.3 (<https://www.geneious.com>) software to create consensus sequences. Final sequences (469-490 bp) were compared with reference sequences in the GenBank database by BLAST analyses (Fig. 2). The phylogenetic analyses of the identified genotypes were performed by the Maximum Likelihood (ML) method with the HKY genetic distances model in MEGA X (Kumar et al., 2018). The best DNA model was determined according to the Akaike Information Criterion (AIC) algorithm by using jModeltest v.0.1.1. (Posada, 2008). Branch support was assessed with 1000 bootstrap replicates. For phylogenetic analyzes, the twenty-four *T. gallinarum* isolates from China, Philippines, France, Austria, Czechia, and Germany that had been found from a variety of hosts, including chickens, humans, and lemur, and had been registered in the Genbank database were employed. *Tetratrichomonas gallinarum* 18S rRNA gene region partial sequences obtained in the study were deposited in the GenBank database under accession numbers OP379566-68.

## Results

### Molecular prevalence of *H. meleagridis*, *He. gallinarum* and *T. gallinarum* in chickens

In the present study, 100 specimens were examined. *Tetratrichomonas gallinarum*-positive samples were found in 11 (1.1%), whereas *H. meleagridis* and *He. gallinarum* were not detected. All positive specimens were collected from backyard chickens.

### Nucleotide Sequence and phylogenetic analyses of *T. gallinarum*

Owing to sequence analysis of the partial 18S rRNA region of 11 *T. gallinarum* isolates, two novel genotypes (TRTgal1 and TRTgal3) and one (named as TRTgal2 by us) known genotypes were characterized.

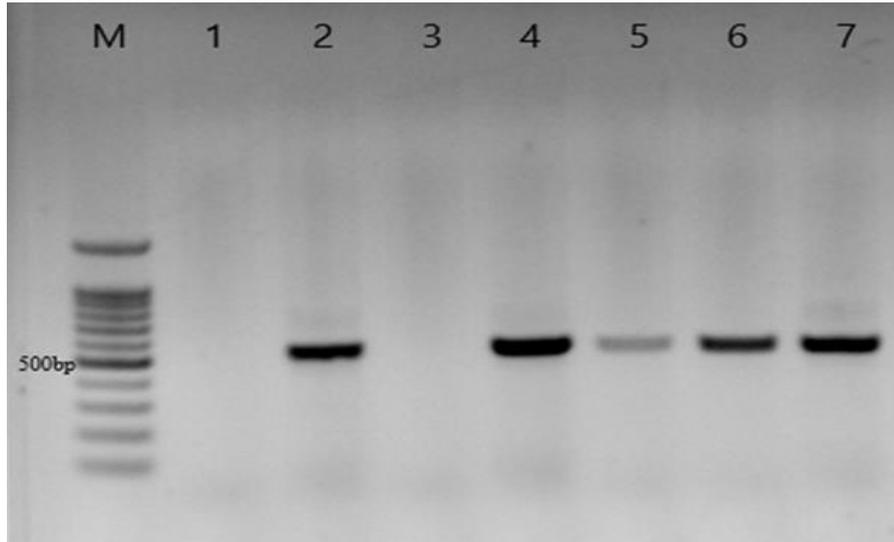


Figure 1. Some *T. gallinarum* positive samples on agarose gel. M: Marker (100bp), 4-7: Positive samples, 3: Negative samples, 2: Positive control, 1: Negative control

Table 1. Primer pairs were used in this study.

Species	Primers	Sequences	Amplicon size (bp)	References
<i>H. meleagridis</i>	Hmf	5'-GAAAGCATCTATCAAGTGGAA-3'	574	Grabensteiner and Hess, 2006
	Hmr	5'-GATCTTTTCAAATTAGCTTTAAA-3'		
<i>He. gallinarum</i>	P1	5'- ATATCCTCTAGGTGGTAAGCTCTTG-3'	696	Gu et al. 2018
	P2	5'-AGCCCCAAATAAAAACCTTCAAACACAC-3'		
<i>T. gallinarum</i>	Tgf	5'-GCAATTGTTTCTCCAGAAGTG-3'	526	Grabensteiner and Hess, 2006
	Tgr	5'-GATGGCTCTCTTTGAGCTTG-3'		

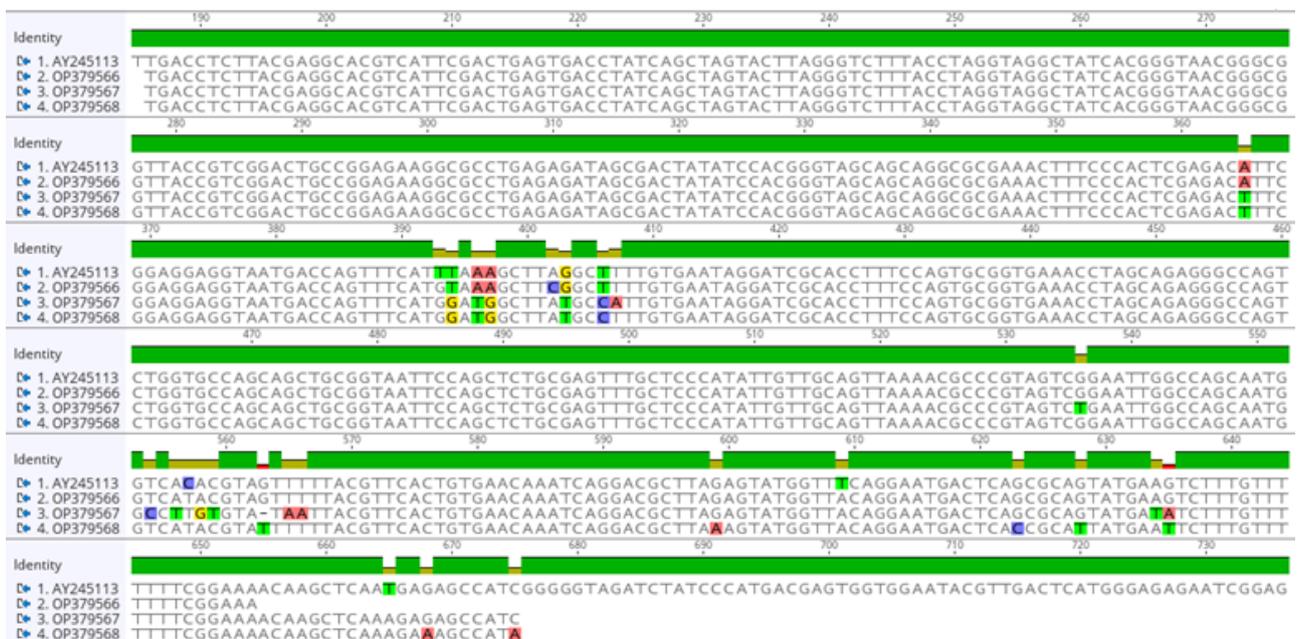


Figure 2. Sequence variation in the 18S rRNA region of *T. gallinarum* isolates. Polymorphic sites are represented by color

The identified genotypes contain 12-17 variable sites among them. The TRTgal2 (OP379567) isolate was found to be identical to isolates identified from duck (JX565083, JX565081), human (AY247746), turkey (AJ920324) and swan (AY245111). The molecular prevalence and identified genotypes with GenBank accession number are presented in Table 2.

Phylogenetic analyses of *T. gallinarum* 18S rRNA gene region clearly separated all the isolates in two monophyletic clades (53%). The first clade comprised of the genotypes from different hosts and countries while the second clade comprised of mainly chicken genotypes is shown in Fig. 3.

**Table 2.** Molecular prevalence, identified genotypes and GenBank accession number of *T. gallinarum*

<i>Tetratrichomonas gallinarum</i>					
Location	No. of samples	No. of positive	Prevalence (%)	Identified genotypes	GenBank Acc. No.
Kirsehir	100	11	11	TRTgal1 (n=4)	OP379566
				TRTgal2 (n=3)	OP379567
				TRTgal3 (n=4)	OP379568



**Figure 3.** Phylogenetic relationships between *T. gallinarum* genotypes obtained in this study (in red) and known genotypes previously reported from different countries and hosts. The tree was constructed using Maximum Likelihood analyses of 18S rRNA gene partial sequences. Numbers at the branches indicate bootstrap values (1000 replicates). The *Blastocystis* sp. genotype identified from chicken (MW093219) is used as an out group

In phylogenetic analysis, the TRTgal1 and TRTgal3 genotypes differed from the subgroup E (AY245113) in 4 and 17 nucleotides, respectively, and TRTgal2 genotype is identical to subgroup B1 (AY245111) of *T. gallinarum* reported by Cepicka et al. (2005).

## Discussion

Backyard chickens are often found in outdoors where biosecurity is poor, and they have close contact with each other, wild birds, other animals (especially turkeys), and humans. This makes them susceptible to sources of infection. In this study, the molecular prevalence of *H. meleagridis*, *He. gallinarum*, and *T. gallinarum* was investigated in backyard chickens and laying hens. We were unable to detect *H. meleagridis* and its intermediate host *He. gallinarum* in any of the specimens. In contrast, some reports of histomoniasis in chickens have been published in different countries. (Patra et al., 2013; van der Heijden and Landman 2011; Grafl et al., 2011; Nguyen et al., 2015). Das et al. (2021) reported in an experimental study that an average of one hundred histomonads were excreted from 1 g of feces and three to four thousand histomonads were excreted within 24 hours from chickens infected with *H. meleagridis*. In the same study, the average daily egg excretion varied from five hundred to two thousand from a bird infected with *He. gallinarum*. Grabensteiner and Hess (2006) investigated PCR specificity for identification of *H. meleagridis* and *T. gallinarum* in tissue samples from infected birds and reported that PCR assays (using the same primers as in our study) demonstrated to be a useful and sensitive diagnostic tool for identification of *H. meleagridis* and *T. gallinarum*. In this context, it can be presumed that the studied chickens were not infected with *H. meleagridis* and *He. gallinarum*.

Cepicka et al. (2005) analyzed 29 isolates of *T. gallinarum* sequences and divided them into five groups (A-E) with eleven subgroups and suggested that groups A and B predominate in domestic fowls. In addition, human tetratrachomonads were assigned to groups A and B, hypothesizing that infections in humans are transmitted by avian genotypes or host-specific genotypes. In this study, the TRTgal2 genotype (OP379567) was found to be identical to the human genotype (AY247746) and the avian genotypes including the group B. In this perspective, it can be suggested that human tetratrachomoniasis was originate from avian genotypes. However, this assumption needs to be supported by the detection of more common genotypes. The TRTgal1 and TRTgal3 genotypes were exhibited highest identities of 96.9% to 99.1% to the genotypes reported in chicken in Czechia, China, Iran, and Philippines. This similarity is probably due to high gene flow with migratory hosts or

neglected submission of sequences to genetic databases and low sampling. Novel genotypes are likely to be identified with studies that include new and large numbers of samples.

In conclusion, our results contribute to the molecular characterization and transmission dynamics of *T. gallinarum*. Moreover, to our knowledge, this is the first report on molecular characterization of *T. gallinarum* genotypes in chickens in Türkiye. Considering the zoonotic potential of *T. gallinarum*, chickens could pose a risk for public health. To better understand the molecular epidemiology, zoonotic potential, and transmission dynamics of *T. gallinarum*, further studies in a larger number of species with large-scale sampling are required.

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PROOF

RESEARCH PAPER

# Effects of Different Viol Types on Egg Qualities in Table Eggs at Different Storage Temperatures

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## Article History

Received: 14 Apr 2023  
Accepted: 11 May 2023  
First Online: 23 May 2023

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## Keywords

Cardboard viol  
Plastic box viol  
Cardboard box viol  
Shell strength  
Haugh unit

## Abstract

The purpose of this research was to examine the impact of storing table hen eggs in egg cardboard viol, plastic box viol, and cardboard box viols at various temperatures on the egg qualities. A total of 300 table chicken eggs were used in the study. The eggs were randomly distributed into three groups: standard cardboard viol, plastic box viol, and cardboard box viol. The eggs were stored at room temperature and in the refrigerator for 28 days. On the 0, 7, 14, 21, and 28 days of the experiment, ten eggs from each group were analyzed for egg weight loss, egg shell strength, Haugh unit, yolk index, and albumen pH. Viol type x storage temperature interaction effect was significant ( $P < 0.05$ ) only on egg weight loss, but its effect on other properties was insignificant. After 28 days of storage, egg weight loss was statistically insignificant between eggs stored in plastic box viols at 25°C and eggs stored in cardboard viols at 4°C. The effect of viol types on egg shell strength, yolk index, Haugh unit, and albumen pH was insignificant. Egg weight loss was found to be better in plastic box viols than in other groups ( $P < 0.05$ ). Eggs stored in refrigerator conditions are better than egg stored room conditions in terms of egg quality criteria except eggshell strength ( $P < 0.05$ ). As a result, it would be more appropriate to store eggs in plastic box viols in order to preserve egg quality for a longer period of time.

## Introduction

Although eggs are an animal protein source, their importance in human nutrition is high due to containing unsaturated fatty acids, vitamins, and minerals (Şenköylü 2001; Sarıca and Erensayın 2014; Puglisi and Fernandez 2022; Tian *et al.*, 2022). An egg obtained from a healthy animal has the highest quality value at the moment it is laid, but its quality may decrease depending on storage conditions, leading to marketing problems (Aygün 2017; Brasil *et al.*, 2019; Yenilmez and Bulancak 2020; Sariyel *et al.*, 2022).

Depending on the storage conditions, it is possible to observe a decrease in egg weight (Akyurek and Okur 2009; Sariyel *et al.*, 2022), a decrease in albumen

height and Haugh unit (Aktan and Kampus 2011; Baylan *et al.*, 2011), an increase in egg yolk index (Copur *et al.*, 2008), and an increase in albumen pH (Silversides and Budgell 2004). When eggs are collected from egg production companies, they need to be stored appropriately.

In the market, cardboard viols with a capacity of 30 eggs are used for storing or transporting eggs. However, in recent years, cardboard box viol and plastic box viol with a capacity of 6, 10, and 15 eggs have also started to be used. The use of cardboard box viol with a capacity of 6, 10, and 15 eggs during the sale of eggs makes it difficult for consumers to choose eggs

based on their outer appearance, as the dirt on the surface of the eggshell cannot be seen. On the other hand, plastic viols provide convenience for consumers in terms of choice. However, foreign materials on the surface of eggs in plastic box viol can be seen more easily, making it easier to evaluate the eggs based on their appearance. Additionally, during storage or sales, there is a possibility of condensation on the egg surface or inside the viols, which can lead to the eggs becoming wet and causing the preference for viols more important.

In our literature review, it was observed that there are a limited number of studies on the effect of storing table chicken eggs in cardboard box viols or plastic box viols (with a capacity of 6, 10, and 15 eggs) on egg quality. Therefore, the main question of the research is which tray type can preserve egg quality for a longer period of time during storage under different storage conditions. Therefore, the aim of this study is to investigate the changes in egg quality by storing table chicken eggs in carton, cardboard box viol, and plastic box viols under room and refrigerator conditions.

## Materials and Methods

Table eggs that were purchased daily from the Konya commercial egg producer were used in the study. A total of 300 table eggs were used. The research was carried out in the Egg Quality Laboratory of the Department of Animal Science, Faculty of Agriculture, Selcuk University. Eggs were randomly distributed into 3 groups: cardboard viol, plastic box viol, and cardboard box viol. For 28 days, eggs were stored at ambient temperature (25 °C) and in the refrigerator (4 °C) in viols. On days 0, 7, 14, 21, and 28 of the experiment, egg weight loss, eggshell strength, yolk index, Haugh unit, and albumen pH analyses were conducted on 10 eggs from each group. All eggs were weighed before the experiment and written on the egg. Egg weights were weighed with a precision digital balance (0.01 g). In the specified analysis periods, eggs (10 eggs from each group) were weighed again before the analysis, and egg weight loss was determined with the formula below.

Egg weight loss (%) = [initial egg weight (g) – end of storage egg weight (g)] / initial egg weight (g) x 100

Shell breaking strength was measured with the Egg Force Reader device (Orka Food Tech.i China) and its unit was expressed as kg (Sariyel *et al.*, 2022). After the albumen height was determined with the Egg Analyzer (Orka Food Tech.i China ) device, the Haugh unit was determined according to Haugh (1937).

The egg yolk was separated on a flat surface and the height of the egg yolk was determined with a digital height gauge. Egg yolk diameter was determined with a digital micrometer and calculated according to Funk (1948). After separating the egg

albumen from the yolk, it was measured with a pH meter (Mettler Toledo, Switzerland).

The experiment was carried out in 2x3 randomized plots according to a factorial design in order to compare the qualities of eggs packed in plastic, cardboard, and standard viols to be stored at room temperature and in the refrigerator (Düzgüneş *et al.*, 1987). The MINITAB 16 statistic software was used in the analysis, and the Tukey multiple range test was used to determine the different groups. The significance level of 0.05 was used for statistical evaluation.

## Results and Discussion

Table 1 summarizes the effects of storage temperature, viol types, and the storage temperature x viol type interaction on egg weight loss (%). During storage, storage temperature, viol types, and storage temperature x viol types interaction had a significant effect on egg weight loss. At the end of storage, the lowest weight loss was found in the C group (6.94%) stored at 25 °C, and the lowest egg weight loss was found in the CB group (2.20%) at 4 °C. After 28 days of storage, egg weight loss was statistically insignificant between eggs stored in plastic box viols at 25°C and eggs stored in cardboard viols at 4°C. When the effect of the viol type on the egg weight loss was examined, the lowest egg weight loss was detected in the PL group during the storage period.

When the effect of storage temperature on egg weight loss was examined, the weight loss of eggs stored at 4 °C during storage was found to be lower than that of those stored at 25 °C. Egg weight loss during storage occurs as a result of the evaporation of water from the egg (Drabik *et al.*, 2021; Eroglu *et al.*, 2021). Egg weight loss is desired to be minimal during storage. The most important criterion around the classification of eggs is egg weight. In general, the market shelf life of eggs around the world is 28 days. Egg weight loss gains even more importance as eggs are sold in markets in room conditions in Turkey. According to the result obtained from our study, it would be more appropriate to store eggs in plastic viols when it is necessary to store eggs in room conditions in terms of egg weight loss. Table 2 summarizes the effects of storage temperature, viol types, and the storage temperature x viol type interaction on egg shell strength (kg).

Viol type, storage temperature, and the storage temperature x viol type interaction effect were not significant in any period of storage. It is consistent with the research indicating that the eggshell strength during storage is not significantly impacted by the storage temperature (Jo *et al.*, 2011; Sert *et al.*, 2011; Sariyel *et al.*, 2022). For egg producers, the strength of a table egg's shell is a crucial economic factor. The greater the breaking strength, the less breakage will occur during egg collection, transport, and storage, resulting in reduced economic losses.

**Table 1.** The effect of storage temperature, viol types and storage x viol type interaction on egg weight loss (%)

Treatment	Initial Egg Weight	Egg Weight Loss (%)				
		7 days	14 days	21 days	28 days	
Storage Temperature (°C)	25	63.46	1.44	2.66	3.97	5.86
	4	61.75	0.64	1.28	1.84	2.62
	SEM	0.93	0.33	0.07	0.12	0.14
	P value	> 0.05	< 0.05	< 0.05	< 0.05	< 0.05
Viol type <sup>1</sup>	C	61.98	1.31 <sup>a</sup>	2.39 <sup>a</sup>	3.66 <sup>a</sup>	4.99 <sup>a</sup>
	CB	62.84	1.16 <sup>b</sup>	2.08 <sup>b</sup>	3.01 <sup>b</sup>	4.51 <sup>a</sup>
	PL	63.01	0.65 <sup>c</sup>	1.45 <sup>c</sup>	2.04 <sup>c</sup>	3.23 <sup>b</sup>
	SEM	1.14	0.04	0.08	0.14	0.17
	P value	> 0.05	< 0.05	< 0.05	< 0.05	< 0.05
Storage Temperature (°C) x Viol Type	25 x C	62.11	1.66 <sup>a</sup>	3.02 <sup>a</sup>	4.92 <sup>a</sup>	6.94 <sup>a</sup>
	25 x CB	63.05	1.74 <sup>a</sup>	3.15 <sup>a</sup>	4.28 <sup>a</sup>	6.83 <sup>a</sup>
	25 x PL	65.24	0.93 <sup>b</sup>	1.80 <sup>b</sup>	2.70 <sup>b</sup>	3.81 <sup>b</sup>
	4 x C	61.83	0.95 <sup>b</sup>	1.75 <sup>b</sup>	2.39 <sup>bc</sup>	3.03 <sup>bc</sup>
	4 x CB	62.61	0.58 <sup>c</sup>	1.00 <sup>c</sup>	1.74 <sup>cd</sup>	2.20 <sup>c</sup>
	4 x PL	60.77	0.37 <sup>c</sup>	1.09 <sup>c</sup>	1.37 <sup>d</sup>	2.65 <sup>c</sup>
	SEM	1.61	0.05	0.12	0.21	0.24
	P value	> 0.05	< 0.05	< 0.05	< 0.05	< 0.05

**Table 2.** The effect of storage temperature, viol types and storage x viol type interaction on egg shell strength (kg)

	Initial Egg Shell Strength (kg)	Egg Shell Strength (kg)				
		7 days	14 days	21 days	28 days	
Storage Temperature (°C)	25	4.45	4.39	4.27	4.48	4.61
	4	4.42	4.60	4.46	4.56	4.58
	SEM	0.106	0.09	0.09	0.11	0.08
	P value	0.866	> 0.05	> 0.05	> 0.05	> 0.05
Viol type <sup>1</sup>	C	4.45	4.41	4.48	4.32	4.69
	CB	4.37	4.47	4.37	4.67	4.62
	PL	4.48	4.61	4.25	4.56	4.48
	SEM	0.130	0.11	0.11	0.13	0.11
	P value	0.822	> 0.05	> 0.05	> 0.05	> 0.05
Storage Temperature (°C) x Viol Type	25 x C	4.56	4.45	4.48	4.26	4.67
	25 x CB	4.41	4.38	4.18	4.38	4.63
	25 x PL	4.37	4.34	4.16	4.79	4.53
	4 x C	4.35	4.38	4.47	4.38	4.72
	4 x CB	4.33	4.56	4.54	4.95	4.61
	4 x PL	4.59	4.88	4.34	4.32	4.42
	SEM	0.18	0.16	0.16	0.19	0.15
	P value	0.481	> 0.05	> 0.05	> 0.05	> 0.05

<sup>1</sup>C: Cardboard viol; CB: Cardboard box viol; PL: Plastic box viol; SEM: Mean of standard errors

Table 3 summarizes the effects of storage temperature, viol types, and the storage temperature x viol type interaction on the Haugh unit. The storage temperature x viol type interaction effect did not have a significant effect on the Haugh unit during storage. The effect of viol type on the Haugh unit was only significant on day 21 of storage ( $P < 0.05$ ). On the 21st day of storage, the Haugh unit of the eggs in the PL group (74.12) was higher than the Haugh unit of the eggs in the C group (67.24) ( $P < 0.05$ ), but the difference between the Haugh unit of the eggs in the PL group (74.12) and the Haugh unit of the eggs in the CB group (70.96) was statistically insignificant.

The effect of storage temperature on the Haugh unit in all periods was found to be statistically significant. The effect of storage temperature on the Haugh unit in all periods was found to be statistically significant.

It was determined that the Haugh unit value of eggs stored at 4 °C during storage was higher than that of those stored at 25 °C. In the egg industry, the Haugh unit is the main criterion for quality, and the greater the Haugh unit, the higher the albumen quality of the egg. During storage, the Haugh unit decreases due to the increase in clusterin and ovoinhibitory concentrations in albumen and the disordering of ovalbumin structure (Sheng *et al.*, 2018).

Table 4 summarizes the effects of storage temperature, viol types, and the storage temperature x viol type interaction on the yolk index. The effect of storage temperature x viol type interaction on the yolk index of eggs was significant only on day 28 of the storage period ( $P < 0.05$ ). On the 28<sup>th</sup> day of storage, the lowest yolk index value was found in group C eggs stored at 25°C, and the highest yolk index value in group C eggs stored at 4°C ( $P < 0.05$ ).

Viol type did not have a significant effect on the yolk index value in all periods of storage. The effect of storage temperature on the yolk index in all periods was found to be statistically significant. It was determined that the yolk index value of eggs stored at 4 °C during storage was higher than those stored at 25 °C. This finding appears to be consistent with research that demonstrates that as storage temperatures increase, the yolk index dramatically declines (Samli *et al.*, 2005; Akarca *et al.*, 2021; Güler *et al.*, 2022; Sariyel *et al.*, 2022). The egg yolk index, which assesses the resistance to stretching of the vitelline membrane in the yolk, can be used to determine how fresh an egg is. The quality of the egg yolks improves as the egg yolk index increases (Stadelman 1995). The egg yolk index drops as a result of the water in the egg white diffusing into the egg yolk as the vitelline membrane of the egg yolk deteriorates

(Didar 2019). Table 5 summarizes the effects of storage temperature, viol types, and the storage temperature x viol type interaction on albumen pH. Storage temperature x viol type interaction and viol type did not have a significant effect on the albumen pH in all periods of storage. The effect of storage temperature on the albumen pH in all periods was found to be statistically significant. It was determined that the albumen pH of eggs stored at 4 °C during storage was lower than that of those stored at 25 °C. This result is consistent with the studies stating that the pH value of egg whites also increased due to the increase in storage temperature (Sariyel *et al.*, 2022; Tan *et al.*, 2022). Albumen's pH increases as a result of a shift in the carbonic acid-bicarbonate buffer system caused by the release of carbon dioxide from the eggshell's pores during storage (Shin *et al.*, 2012; Mathew *et al.*, 2016).

**Table 3.** The effect of storage temperature, viol types and the storage temperature x viol type interaction on Haugh unit

Treatment	Initial Haugh Unit	Haugh Unit				
		7 days	14 days	21 days	28 days	
Storage Temperature (°C)	25	83.06	71.29	63.84	62.02	55.94
	4	83.35	81.87	84.24	79.53	77.00
	SEM	1.07	1.005	0.991	1.263	1.067
	P value	0.849	< 0.05	< 0.05	< 0.05	< 0.05
Viol type <sup>1</sup>	C	81.80	76.07	71.9	67.24 <sup>b</sup>	65.27
	CB	83.20	76.55	75.37	70.96 <sup>ab</sup>	67.28
	PL	84.60	77.10	74.78	74.11 <sup>a</sup>	66.84
	SEM	1.31	1.22	1.21	1.54	1.31
	P value	0.334	> 0.05	> 0.05	< 0.05	> 0.05
Storage Temperature (°C) x Viol Type	25 x C	82.49	72.39	61.03	58.30	53.91
	25 x CB	81.91	69.82	64.77	63.84	57.92
	25 x PL	84.79	71.66	65.72	63.91	56.00
	4 x C	81.13	79.77	82.91	76.19	76.63
	4 x CB	84.51	83.31	85.96	78.06	76.68
	4 x PL	84.43	82.54	83.84	84.31	77.72
	SEM	1.85	1.74	1.72	2.19	1.85
	P value	0.543	> 0.05	> 0.05	> 0.05	> 0.05

**Table 4.** The effect of storage temperature, viol types and storage x viol type interaction on yolk index

Treatment	Initial Yolk Index	Yolk Index				
		7 days	14 days	21 days	28 days	
Storage Temperature (°C)	25	0.44	0.38	0.33	0.27	0.20
	4	0.42	0.45	0.45	0.43	0.41
	SEM	0.01	0.010	0.010	0.010	0.010
	P value	0.068	< 0.05	< 0.05	< 0.05	< 0.05
Viol type <sup>1</sup>	C	0.42	0.41	0.40	0.34	0.32
	CB	0.44	0.41	0.39	0.35	0.30
	PL	0.43	0.42	0.39	0.36	0.29
	SEM	0.01	0.01	0.01	0.01	0.01
	P value	0.365	> 0.05	> 0.05	> 0.05	> 0.05
Storage Temperature (°C) x Viol Type	25 x C	0.43	0.37	0.34	0.26	0.19 <sup>c</sup>
	25 x CB	0.44	0.37	0.32	0.26	0.20 <sup>c</sup>
	25 x PL	0.45	0.39	0.33	0.27	0.21 <sup>c</sup>
	4 x C	0.41	0.46	0.46	0.41	0.46 <sup>a</sup>
	4 x CB	0.44	0.46	0.46	0.43	0.40 <sup>ab</sup>
	4 x PL	0.41	0.45	0.44	0.44	0.37 <sup>b</sup>
	SEM	0.01	0.02	0.01	0.01	0.02
	P value	0.442	> 0.05	> 0.05	> 0.05	< 0.05

<sup>a-c</sup> Significant differences exist between the means of a column using different superscripts (P<0.05); <sup>1</sup>C: Cardboard viol; CB: Cardboard box viol; PL: Plastic box viol; SEM: Mean of standard errors

**Table 5.** The effect of storage temperature, viol types and storage x viol type interaction on albumen pH

Treatment	Initial Albumen pH	Albumen pH				
		7 days	14 days	21 days	28 days	
Storage Temperature (°C)	25	9.08	9.59	9.75	9.63	9.77
	4	9.10	9.16	9.21	9.12	9.35
	SEM	0.04	0.01	0.01	0.02	0.01
	P value	0.731	< 0.05	< 0.05	< 0.05	< 0.05
Viol type <sup>1</sup>	C	9.07	9.37	9.47	9.40	9.57
	CB	9.14	9.41	9.47	9.36	9.57
	PL	9.06	9.34	9.48	9.36	9.55
	SEM	0.05	0.02	0.01	0.02	0.01
	P value	0.538	> 0.05	> 0.05	> 0.05	> 0.05
Storage Temperature (°C) x Viol Type	25 x C	9.09	9.56 <sup>a</sup>	9.74	9.64	9.77
	25 x CB	9.07	9.63 <sup>a</sup>	9.75	9.64	9.78
	25 x PL	9.08	9.59 <sup>a</sup>	9.76	9.60	9.74
	4 x C	9.04	9.19 <sup>b</sup>	9.21	9.16	9.36
	4 x CB	9.20	9.18 <sup>b</sup>	9.19	9.09	9.35
	4 x PL	9.06	9.10 <sup>b</sup>	9.23	9.10	9.33
	SEM	0.07	0.03	0.02	0.03	0.02
	P value	0.399	< 0.05	> 0.05	> 0.05	> 0.05

<sup>1</sup>C: Cardboard viol; CB: Cardboard box viol; PL: Plastic box viol; SEM: Mean of standard errors

## Conclusions

According to the results obtained from our study, it was determined that the type of viol affects only egg weight loss. In terms of egg weight, it was observed that storage in plastic box viol preserves egg weight better than other viol types. It is seen that storing eggs in plastic box viol will preserve their shelf life longer.

## Acknowledgments

This research is a summary of Zeynel Abdin Parmak's master's thesis, which was funded by Selcuk University (project number: 18201140).

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# Relationships Between Morphological Characteristics of Roosters in Broiler Breeders at Different Age Periods

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## Article History

Received: 09 Jun 2023  
Accepted: 12 Jun 2023  
First Online: 14 Jun 2023

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## Keywords

Morphological characteristics  
Fertility  
Age  
Broiler breeder

## Abstract

The aim of study was to determine the relationships between morphological characteristics of roosters and fertility in broiler breeders at different age periods. A total of 48 roosters and 480 hens Ross 308 broiler breeder were used. The body weight, comb width and length, wattle width and length, and tarsus length of roosters were measured for morphological characteristics at 42, and 53 weeks of age. A total of 1500 eggs were incubated at 37.7 °C and 50-55% relative humidity for 18 d, then eggs were incubated at 36.6 °C and 60% relative humidity for 3 d. The effect of age on comb length, comb index ( $P=0.002$ ), wattle width ( $P=0.008$ ), wattle area ( $P=0.015$ ) and tarsus length were found significant ( $P=0.000$ ). There were correlations between body weight and fertility at 53 weeks of age ( $r = 0.663$ ;  $P<0.05$ ). There was no correlation between fertility and comb length, comb width, comb area, comb index, wattle width, wattle area, wattle index, and tarsus length at 42 and 53 weeks of age ( $P>0.05$ ). In conclusion; some characteristics based on external appearance are used for male selection in broiler breeders, but no relationship was found between investigated morphological characteristics and fertility, except for body weight.

## Introduction

The fertility outcomes of broiler breeders are influenced by a variety of factors. Although both male and female breeders play important roles in fertility, genetic and non-genetic factors that occur in both males and females and are thought to be the most important factors influencing egg fertilization and embryo development. Especially, sperm motility, concentration, amount, and rate of abnormal and dead sperm are the main sperm characteristics that affect male fertility performance (Bansal and Cheema, 2014). In broiler breeders, roosters must be physically and behaviorally mature in order to be able to mate and successfully evoke the sexual response in females.

Fertility issues, particularly in lines descended from Cornish breeds can be brought on by an inability to mate successfully due to poor physical health and inappropriate sexual behavior (Wilson et al., 1979). Furthermore, the behavioral characteristics that allow roosters to successfully mate with chickens are dependent on the rooster's weight and leg health (Brillard, 2003). When it comes to mating behavior and optimum fertility, breeding males must be at the target body weight, should have the right leg lengths, and also should have a smooth leg structure without curled toes or abrasion problems on the sole (Anonymous, 2018). The length of the tarsus has a major influence on

fertility (Abad, 2020). Thus, tall males with a higher tarsus length may be more likely to win male-male competition, so they may have extra mating opportunities (Lei et al., 2019).

Secondary sexual characteristics in roosters are thought to play a role in increasing the frequency of mating with females. As a matter of fact, it was observed that females preferred males with large combs in case of Red Jungle Chicken (Zuk et al., 1995). If the secondary sexual characteristics of the roosters are fully developed, it indicates that they are healthier (Hamilton and Zuk, 1982), have better reproductive characteristics (Møller, 1994), and the relationship between fertility and testis weight is positive (McGary et al., 2002). Secondary sexual traits in poultry are regarded to be crucial in the selection of female mates. Comb size has been claimed to be an indicator of the amount of androgens in male's body (Verhulst et al., 1999). The exhibition of roosters has a phenotypic relationship with fertility (McGary et al., 2002), particularly during the early mating season females are attracted towards the roosters having the largest comb thus large combs may be associated to reproductive behavior in birds (Bilcik et al., 2005). It has been observed, for example, that roosters with larger combs exhibit more aggressive behavior and are more dominant against roosters with smaller combs (Bilcik et al., 2005; Mukhtar and Khan, 2012). However, in some studies; no significant link between the dimension of secondary sexual features, mating frequency, and sperm quality in predicting broiler breeder reproductive performance was reported (Wolanski et al., 2004; Bilcik et al., 2005). Roosters are often selected in breeding flocks based on characteristics such as posture, body structure, maturity, body size, leg and foot condition, head appearance, overall health and vigour. Although these traits aid in male selection, they do not guarantee a high fertility rate (Wilson et al., 1979).

In general, low-level fertility is an important problem in old aged broiler breeder flocks. Thus, this study was carried to investigate the relationships between morphological characteristics of roosters and fertility in broiler breeders at 42 and 53 weeks of age. Also, the correlations among the morphological characteristics were investigated.

## Materials and Methods

This study was conducted in a private broiler breeder company. A total of 48 roosters and 480 hens Ross 308 broiler breeders were placed in a separate compartment in breeder house. The flock age was followed to obtain morphological characteristics and incubation parameters. In the house a chain type feeder, nipple drinker system and pine sawdust litter were used. The broiler breeders were

fed with a standard broiler breeder feed containing (14.5% CP and 2750 ME) and water provided was ad libitum. The 13L: 11D light duration and 60 lux light intensity were applied according to broiler breeder standards.

All roosters' morphological characteristics such as; body weight, comb width and length, wattle width and length, and tarsus length were measured at 42 WOA (weeks of age), and then again measured at 53 WOA. The body weight of the roosters recorded by weighing 0.1 g with a precision balance then comb, wattle and tarsus measurements were taken from the same roosters. The comb area and wattle area were calculated according to Chung (2010); for this, the length and width of the comb, the length and width of the wattle were measured with a digital caliper from the left side of the roosters. The comb and wattle index were calculated according to Francesh et al. (2011). The length of the left tarsus bone was determined by measuring the distance between the knee joint and the sole of the foot with a digital caliper (Souza et al., 2017). The formulas used in the calculation of morphological characteristics are given below.

Comb area = comb width × comb height

Wattle area = wattle width × wattle height

Comb index = (comb length) / (comb width)

Wattle index = (wattle length) / (wattle width)

Eggs were obtained from separated experimental compartment at 42 WOA, then again obtained at 53 WOA. A total of 1500 eggs were incubated at each age period for fertility results. Eggs were stored at 18 °C temperature and 70-75% relative humidity (RH) for 5-7 d. Each tray in the incubator held 150 eggs, with 10 trays being used for each age. Eggs pre-warmed before incubation at 24 °C and 70-75% RH during 8 hours. Eggs were incubated in the setter at 37.7 °C and 50-55% RH for 18 d. Eggs were incubated in the hatcher at 36.6 °C and 60% RH for 3 d. At hatch chicks were counted and all unhatched eggs were examined for fertility and embryonic mortality. Then fertility was calculated.

The data were analyzed by using two sample T-test using the Minitab software (Minitab, 2013). After arcsine transformation, the percentage data analyses were carried out. The correlations between morphological characteristics and fertility were analyzed with Pearson correlation analysis (Minitab, 2013). Differences were considered significant at  $P \leq 0.05$  and the statistical difference at  $P < 0.10$  was described as a tendency.

## Results and Discussion

The morphological characteristic of roosters and fertility in broiler breeders at 42 and 53 WOA are given in Table 1. In the study, the effect of age on

**Table 1.** The morphological characteristics of roosters and fertility in broiler breeders at different age (mean  $\pm$  StDev)

Characteristics	42 WOA	53 WOA	P
Body weight, g	4693.9 $\pm$ 314	4737.5 $\pm$ 236	0.454
Comb length, mm	128.8 $\pm$ 9.74 <sup>b</sup>	135.5 $\pm$ 7.35 <sup>a</sup>	0.000
Comb width, mm	73.6 $\pm$ 7.42	73.1 $\pm$ 7.17	0.737
Comb area, mm <sup>2</sup>	9535 $\pm$ 1618	9913 $\pm$ 1226	0.212
Comb index	1.76 $\pm$ 0.12 <sup>b</sup>	1.87 $\pm$ 0.19 <sup>a</sup>	0.002
Wattle length, mm	54.5 $\pm$ 5.91	52.3 $\pm$ 5.03	0.056
Wattle width, mm	54.9 $\pm$ 5.73 <sup>a</sup>	52.1 $\pm$ 4.29 <sup>b</sup>	0.008
Wattle area, mm <sup>2</sup>	3030.9 $\pm$ 639 <sup>a</sup>	2742.3 $\pm$ 462 <sup>b</sup>	0.015
Wattle index	0.99 $\pm$ 0.03	1.00 $\pm$ 0.06	0.239
Tarsus length, mm	122.4 $\pm$ 6.57 <sup>a</sup>	116.9 $\pm$ 3.89 <sup>b</sup>	0.000
Fertility, %	96.07 $\pm$ 2.30	94.27 $\pm$ 2.27	0.096

<sup>a,b</sup>; Differences between means with different letters in the same column are significant (P<0.05). WOA: Weeks of age

comb length (P=0.000), comb index (P=0.002), wattle width (P=0.008), wattle area (P=0.015) and tarsus length were significant (P=0.000). But, effect of age on wattle length and fertility tend to be significant (P=0.056 and P=0.096; respectively). The effect of age on body weight, comb width, comb area, wattle index was not found significant (P>0.05).

The body weight is highly heritable and simple to determine (Groeneveld et al., 2010). Bird growth rates vary depending on age and species. In the study, body weight was not affected by age, but body weight at 53 WOA was numerically higher than 42 WOA. It was to be expected thus body weight is a trait affected by age (Hocking and Bernard, 1997). The results are in accordance with the Leão et al. (2017) who showed that body weight increased with age (25 to 45 weeks of age) in male broiler breeders. Meanwhile, Özdemir (2019) reported that an increase in bodyweight with age in both İspenç genotype roosters and chickens.

Along with the increase in age, comb length and comb index were increased. But the other comb characteristics such as, comb width and comb area were found similar in investigated age periods. However, Leão et al. (2017) revealed that there was no difference for histological comb score between the 25 and 45 WOA groups.

Along with the increase in age wattle width and wattle area decreased and, also wattle length tended to be lower at 53 WOA than in 42 WOA. But wattle index was found similar in investigated age periods. However, Nääs et al. (2008) reported that there was an increase in wattle width with increasing age in male broilers of Cobb 500. They also reported that there was no significant morphological difference found at 28 day of age, but at 35 and 48 day of age a difference in wattle width was found when compared to the other morphological characteristics. Also, Özdemir (2019) reported that a significant increase in wattle length, width and comb length, width, with the increased age in İspenç genotype roosters.

The tarsus length was found lower at 53 WOA than 42 WOA, and tarsus length was decreased with the increased age. A slight decrease in tarsus length was found at 53 WOA, it might be result of body weight getting heavier and deformation in the bones with age. But, Özdemir (2019) reported that there was no difference between tarsus lengths of İspenç roosters (small genotype) at different age periods.

In the study, fertility tend to be decreased with increased age. This finding in accordance with Yılmaz Dikmen and Şahan (2009) who reported that fertility rate decreased with increased age in broiler breeder. The decrease in fertility with increased age was also reported by some authors (Gumułka and Kapkowska, 2005; Abudabos, 2010; Mahammad et al., 2018).

The correlations between morphological characteristics of roosters and fertility in broiler breeders at different age are shown in Table 2. In the study, correlation between body weight and comb width ( $r = 0.265$ ;  $P = 0.068$ ) was found tend to be significant at 42 WOA, but there was no correlation between body weight and investigated comb characteristics at 53 WOA (P>0.05). According to these findings, there might be a slight relationship between body weight and comb characteristics at 42 WOA. Also negative correlations between body weight and comb index ( $r = -0.281$ ;  $P = 0.053$ ) was found tend to be significant at 42 WOA. Kumar et al. (2022) in a study carried on Aseel and Kadaknath chickens at 24 week of age reported a correlation between body weight and comb length. Almost similar study was carried by Leão et al. (2017) that showed positive significant correlation between histological comb score and live weight. Also, Rizzi and Verdiglione (2015) reported that there was a correlation between comb and wattles weight and body weight in Italian purebreds of Robusta lionata. There were no significant correlations found between body weight and all investigated wattle characteristics, also tarsus length in investigated age periods (P>0.05). In a study, Dahloun et al. (2016) showed males having stronger

**Table 2.** Correlations between morphological traits of roosters and fertility in broiler breeders at different age

	WOA	CL	CW	CA	CI	WL	WW	WA	WI	TL	F
BW	42	0.131 <sup>NS</sup>	0.265 <sup>0.068</sup>	0.212 <sup>NS</sup>	-0.281 <sup>0.053</sup>	-0.049 <sup>NS</sup>	-0.099 <sup>NS</sup>	-0.062 <sup>NS</sup>	0.195 <sup>NS</sup>	-0.009 <sup>NS</sup>	0.097 <sup>NS</sup>
	53	0.242 <sup>NS</sup>	0.038 <sup>NS</sup>	0.136 <sup>NS</sup>	0.111 <sup>NS</sup>	0.125 <sup>NS</sup>	0.087 <sup>NS</sup>	0.107 <sup>NS</sup>	0.091 <sup>NS</sup>	0.018 <sup>NS</sup>	0.663*
CL	42		0.769****	0.926****	-0.040 <sup>NS</sup>	0.091 <sup>NS</sup>	0.077 <sup>NS</sup>	0.092 <sup>NS</sup>	0.076 <sup>NS</sup>	-0.211 <sup>NS</sup>	0.226 <sup>NS</sup>
	53		0.176 <sup>NS</sup>	0.603****	0.365*	0.542****	0.513***	0.571****	0.156 <sup>NS</sup>	0.102 <sup>NS</sup>	0.234 <sup>NS</sup>
CW	42			0.951****	-0.667****	0.091 <sup>NS</sup>	0.063 <sup>NS</sup>	0.081 <sup>NS</sup>	0.123 <sup>NS</sup>	-0.145 <sup>NS</sup>	0.038 <sup>NS</sup>
	53			0.890****	-0.848****	0.362*	0.213 <sup>NS</sup>	0.323*	0.288 <sup>0.065</sup>	-0.003 <sup>NS</sup>	-0.015 <sup>NS</sup>
CA	42				-0.409**	0.103 <sup>NS</sup>	0.078 <sup>NS</sup>	0.097 <sup>NS</sup>	0.116 <sup>NS</sup>	-0.174 <sup>NS</sup>	0.149 <sup>NS</sup>
	53				-0.518****	0.556****	0.405**	0.531****	0.329*	0.043 <sup>NS</sup>	0.103 <sup>NS</sup>
CI	42					-0.031 <sup>NS</sup>	-0.007 <sup>NS</sup>	-0.015 <sup>NS</sup>	-0.094 <sup>NS</sup>	-0.008 <sup>NS</sup>	0.194 <sup>NS</sup>
	53					-0.070 <sup>NS</sup>	0.042 <sup>NS</sup>	-0.027 <sup>NS</sup>	-0.173 <sup>NS</sup>	0.047 <sup>NS</sup>	0.288 <sup>NS</sup>
WL	42						0.972****	0.992****	0.268 <sup>0.065</sup>	0.339**	0.131 <sup>NS</sup>
	53						0.760****	0.943****	0.542****	0.049 <sup>NS</sup>	0.178 <sup>NS</sup>
WW	42							0.989****	0.034 <sup>NS</sup>	0.308*	0.160 <sup>NS</sup>
	53							0.928****	-0.133 <sup>NS</sup>	-0.008 <sup>NS</sup>	0.254 <sup>NS</sup>
WA	42								0.162 <sup>NS</sup>	0.310*	0.158 <sup>NS</sup>
	53								0.238 <sup>NS</sup>	0.043 <sup>NS</sup>	0.217 <sup>NS</sup>
WI	42									0.179 <sup>NS</sup>	-0.215 <sup>NS</sup>
	53									0.080 <sup>NS</sup>	-0.406 <sup>NS</sup>
TL	42										0.192 <sup>NS</sup>
	53										0.103 <sup>NS</sup>

Correlation coefficient values (r). \*: P<0.05; \*\*: P<0.01; \*\*\*: P<0.001; \*\*\*\*: P< 0.0001, NS: Not significant  
 WOA: Weeks of age; BW: Body weight, CL: Comb length, CW: Comb width, CA: Comb area, CI: Comb index,  
 WL: Wattle length, WW: Wattle width, WA: Wattle area, WI: Wattle index, TL: Tarsus length, F: Fertility

correlations between body length and either body weight, tarsus length, or comb height than females' indigenous chicken genotype. In both the Hubbard and Arboracrae strains, a study by Yahaya et al. (2012) revealed a strong linear relationship between body weight and tarsus length. Another study conducted by Abdel-Latif (2019) found that in White leghorn chickens, there was a highly significant correlation between body weight and shank length and also correlation with shank diameter. Also positive correlation between body weight and tarsus length was reported by Adeogun and Adeoye (2004). In the study, there was moderate positive correlation between body weight and fertility at 53 WOA ( $r = 0.663$ ;  $P < 0.05$ ).

In the study correlations between comb length and comb width, comb area at 42 WOA ( $r = 0.769$ ,  $P < 0.0001$ ;  $r = 0.926$ ,  $P < 0.0001$ ); and comb area, comb index, wattle length, wattle width, wattle area at 53 WOA ( $r = 0.603$ ,  $P < 0.0001$ ;  $r = 0.365$ ,  $P < 0.05$ ;  $r = 0.542$ ,  $P < 0.0001$ ;  $r = 0.513$ ,  $P < 0.001$ ;  $r = 0.571$ ,  $P < 0.0001$ ) found significant. Females preferred larger-combed roosters, especially during the initial mating season. Thus, males who attempted mating more frequently had larger combs (Bilcik et al., 2005). There were positive correlations between comb length and comb width, comb area at 42 WOA ( $P < 0.0001$ ). Thus, Joseph et al. (2003) reported that a significant correlation between comb height, length, area; and also significant correlation between investigated comb traits and age in female broiler breeders. There were positive correlations between comb length and comb area; comb index at 53 WOA ( $P < 0.0001$  and  $P < 0.05$ ). However, there were negative correlations between comb width and comb index ( $P < 0.0001$ ), comb area and comb index ( $P < 0.01$  and  $P < 0.0001$ ) at all investigated age periods.

The comb and wattle size are related to gonadal development and sex hormone secretion (Nesheim et al., 1979). According to Tabbaa and Hassanin (2018) a numerical difference in comb size frequencies among different breeds was observed however no significant difference was noticed. In the study, there were positive correlations between comb length and wattle length, width, area ( $P < 0.0001$ ;  $P < 0.001$ ;  $P < 0.0001$ ); also, there were positive correlations between comb width and wattle length, wattle area at 53 WOA ( $P < 0.05$ ). According to these findings, it could be said that comb characteristics and wattle characteristics were positively related to each other in broiler breeder roosters. However, there were no correlations between investigated comb characteristics and tarsus length in all investigated age periods ( $P > 0.05$ ). Rizzi and Verdiglione (2015) measured comb and wattle weights of male chickens from three different Italian purebreds (*Robusta maculate*, *Ermellinata di Rovigo* and *Robusta lionata*),

the comb and wattle weight were significantly correlated in all purebreds.

It has been observed, that roosters with larger combs exhibit more aggressive behavior and more dominant against roosters with smaller combs (Bilcik et al., 2005; Mukhtar and Khan, 2012). In the study, there were no significant correlation between investigated comb characteristics and fertility in investigated all age periods ( $P > 0.05$ ). Thus, Pizzari et al. (2004) reported that there was no relation between comb size and sperm quality in cross breeds of domestic fowl and red jungle fowl.

In the study there were positive correlations found between wattle length and wattle width, area; also, there were positive correlations between wattle width and wattle area in investigated all age periods ( $P < 0.0001$ ). It might be a result of investigated wattle characteristics were positively related to each other. There was no correlation between wattle width and wattle index; no correlation between wattle area and wattle index in investigated all age periods ( $P > 0.05$ ). The correlation between wattle length and wattle index was tend to be significant at 42 WOA ( $P = 0.065$ ). The significant positive correlations were found between wattle width and wattle area at all investigated age periods ( $P < 0.0001$ ).

There were positive correlations between wattle length, width, area and tarsus length at 42 WOA ( $P < 0.01$ ,  $P < 0.05$ ,  $P < 0.05$ ; respectively). According to these findings, it could be said that some wattle characteristics such as; length, width, and tarsus length were positively related to each other in broiler breeder roosters. In the study, there were no correlation between investigated wattle characteristics and fertility in all investigated age periods ( $P > 0.05$ ). Similar to our findings Bilcik and Estevez (2005) reported that there was no correlation between wattle width and fertility in broiler breeders. However, McGary et al. (2003) reported that comb width, wattle length was positively related with sperm penetration and also fertility in male broiler breeder. Also, in the study, there were no correlation between tarsus length and fertility in all investigated age periods ( $P > 0.05$ ). These findings accordance with McGary et al. (2003) who measured that the leg and pelvic fluctuating asymmetry of male broiler breeder, and reported that there were no correlations between these traits and fertility or sperm penetration. Also, Yılmaz Dikmen and İpek (2006) reported that shank length had no discernible impact on fertility or hatchability in Japanese quails.

## Conclusion

In conclusion morphological characteristics such as; comb length, index, wattle length, width, area and tarsus length were affected by breeder age. Although

some characteristics based on external appearance are used for male selection in broiler breeders, but no relationship was found between investigated morphological characteristics and fertility, except for body weight.

## Highlights

The body weight, comb width and length, wattle width and length, and tarsus length of roosters were measured for morphological characteristics at 42, and then 53 weeks of age.

A total of 1500 eggs were incubated for fertility results at 42, and then 53 weeks of age.

Although some characteristics based on external appearance are used for male selection in broiler breeders, but no relationship was found between investigated morphological characteristics and fertility, except for body weight.

## Ethical Statement

This study was approved by the Bursa Uludağ University Animal Experiments Local Ethics Committee (Approval no: 2019-12/06).

## Acknowledgements

The authors would like to express their gratitude to the directors of the commercial breeder farm Hastavuk (Bursa, Türkiye), who provided the facilities for this study.

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# Ileal Villi Morphological Characteristics of Cobb 500 Broilers Fed Phytase and Tannase Treated Sorghum Based Diets

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## Article History

Received: 06 Jun 2023

Accepted: 20 Jun 2023

First Online: 22 Jun 2023

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## Keywords

Phytase

Sorghum diet

Tannase

Villus

## Abstract

The effects of phytase and tannase enzyme treatment of sorghum-based broiler diets on ileal villi characteristics were evaluated in Cobb 500 broilers. A total of three sorghum levels, 0, 50, and 100%, with 4 enzyme levels; 0, 5% phytase, 5% tannase and 5% phytase+tannase combination were used to develop 12 different dietary treatments. Three hundred and sixty broilers were randomly allocated to the 12 dietary treatments in a completely randomized design experiment. On day 42, two birds from each replicate were randomly selected and slaughtered for ileal villi morphometry analyses. A 2cm tissue sample of the ileum was cut and prepared for histological analyses. Villus height and width, muscularis externa thickness, and crypt depth were measured on a light microscope using a calibrated eyepiece graticule. The total villi surface area was calculated, which indicates the digestive and absorptive capacity of the ileum. The General Linear Models (GLM) procedure of the Statistical Analysis System ver 9.4 (SAS Institute Inc., 2011) was used to analyse the data. All tests were performed at  $p < 0.05$  significance. Villus height, width, and muscularis externa thickness significantly increased with increasing levels of sorghum in the diet ( $p < 0.001$ ). Birds fed complete sorghum diets supplemented with phytase enzyme had the longest villi ( $p < 0.001$ ). The 0% and 100% sorghum levels exhibited comparable crypt depth. Treatment significantly affected the apparent villi surface area ( $p < 0.0001$ ). The apparent villi surface area increased with increasing sorghum inclusion. Birds fed a complete sorghum diet supplemented with phytase had the highest villi surface area ( $15.48 \pm 0.241$  mm). It can be concluded that phytase and tannase can be added to complete sorghum broiler diets without compromising ileal villi integrity. Hence, we recommend the addition of phytase and tannase in sorghum-based broiler diets to counteract the effects of sorghum antinutrients.

## Introduction

Chicken meat has become the world's most consumed meat type (OECD, 2021). This is attributed to the fact that there are no negative cultural or religious perceptions associated with chicken consumption (Barbut and Leishman, 2022) and it has remarkable nutritional benefits (Farrell, 2022). However, the high cost of feed because of the unavailability of traditional feed ingredients limits poultry production (Ntuli and Oladele, 2013; Amponsah et al., 2015). Of major concern is the unavailability of maize, a key energy source used in poultry diets. Overall, 61% of global maize is used as livestock feed; however, its production is reduced by increasing trends of heat stress, severe

droughts, and changing agroecological conditions (Challinor et al., 2014). Maize deficit because of climate change elicited the need to evaluate other potential energy sources.

Sorghum is drought tolerant and has a low risk of failure under drought conditions compared with maize (Amelework et al., 2017; Widiyono et al., 2021; Ali et al., 2023) and can thus potentially substitute maize in poultry diets to rump up broiler feed production. The use of sorghum in broiler feeds remains low due to the presence of tannins and phytates, which reduce nutrient digestibility, absorption, and bioavailability (Rahman and Osman, 2011).

The secondary negative effects associated with phytic acid involve altering the digestion process and this may negatively affect the intestinal health and intestinal microbiota of broilers (Ptak et al., 2015; Moita et al., 2021), resulting in poor performance.

The benefits of phytase supplementation in reducing the effects of phytate are well documented (Amerah et al., 2014; Moita et al., 2021; Selle et al., 2023). Exogenous phytases liberate phytate-bound phosphorus and reduce the direct antinutritive properties of phytate or myo-inositol hexaphosphate (IP6) (Selle et al., 2023). The improved bioavailability of phosphorus and calcium may express different effects on intestinal health, morphology, and microbiota diversity of broiler chickens (Moita et al., 2021). The use of tannase to curb the effects of tannins in sorghum-based broiler feeds remains unexplored. Additionally, the effects of phytase and tannase enzyme combination on gastrointestinal tract organs and ileal villi morphology are poorly understood.

Morphology of the small intestine mucosa is an important indicator of intestinal health and integrity (Paiva et al., 2014) and hence has a significant effect on feed digestion, nutrients absorption, immune status (animal health), and animal performance at large (Kogut and Arsenault, 2016). The aim of the current study was to evaluate the effects of phytase and tannase supplementation alone or in combination on the morphology of the ileal villi of Cobb 500 broilers fed sorghum-based diets.

## Materials and Methods

### Animal ethics

All procedures followed in this study comply with national guidelines for the good care and management of research animals. The Zimbabwe's National Animal Research Ethics Committee approved the procedures outlined in this study and granted the animal ethics (Reference Number: 013/22).

### Study site

The study was conducted at Henderson Research Station, Poultry Section in Mazowe district, Zimbabwe. It is located in the agroecological region IIb characterized by an annual rainfall range of 750-1000 mm (Mavhura et al., 2021). The latitude and longitude for the area are 17.35°E and 300.58°S, respectively, while the altitude is 1300m. The temperature range for this area is between 15 and 29°C. The area is suitable for all farming systems, including dairy, piggery, horticulture, poultry, beef, and crop production (Mavhura et al., 2021).

### Experimental design and diets

All the ingredients were milled and analysed for dry matter, gross energy, crude protein, ash, fat,

calcium, and phosphorus composition according to the Association of Official Analytical Chemists standards (AOAC, 1995). Condensed tannins in sorghum were quantified using the method of Folin-Denis (Pratik et al., 2016). Formulation was done using the IDT Feed Formulation software® through substitution by weight of maize with sorghum at three levels (0, 50 and 100%). There were four enzyme inclusion levels (none, 5% Phytase, 5% Tannase as well as a combination of 5% phytase and 5% tannase) at each sorghum inclusion level. A total of 12 diets were developed comprising a starter, grower, and finishing diets.

Diets were developed to meet the recommended nutrient levels for broilers (NRC, 1994). The diets were analysed for dry matter, crude protein, gross energy, fat, calcium, and phosphorus using the AOAC procedures (AOAC, 1995) and the analysed nutrients composition are shown in Tables 1-3. Diets 1 to 4 are complete maize-based diets with different enzyme treatments (1 has no enzyme, 2 has 5% phytase, 3 has 5% tannase and 4 has 5% of both phase and tannase). Additionally, diets 5 to 8 are described by 50% substitution of maize with sorghum on weight bases and have different enzyme levels (5 has no enzyme, 6 has 5% phytase, 7 has 5% tannase and 8 has 5% of both phase and tannase). Diets 9 to 12 are complete sorghum-based diets with variations in enzyme levels; thus, 9 has no enzyme, 10 has 5% phytase, 11 has 5% tannase, and 12 has 5% of both phase and tannase.

A total of 360 unsexed Cobb 500-day-old chicks were randomly allocated to thirty-six 1 m × 2 m pens. The experiment followed a completely randomized design experiment with 12 dietary treatments replicated three times. A total of ten birds were placed in each pen. A 10 cm thick layer of dry grass was placed on the floor as bedding in the pens. Heat and lighting were provided using 75 W infra-red lamps. The starter, grower, and finisher diets were fed from day 1 to 14, day 15 to 28, and day 29 to 42, respectively. Feed and water were offered *ad libitum* throughout the feeding trial. Chicks were offered vitamins C and E as well as biotin (Stress pac®, Irvine's Zimbabwe) in drinking water on arrival to combat the stress experienced during transportation. A foot bath drenched with disinfectant (Virukill®, Veterinary distributors, Pvt Ltd, Zimbabwe) was placed at the entrance to the brooding house. Mortality was recorded during the entire experimental period.

### Data collection

On day 42, seventy-two birds from each dietary treatment comprise 2 birds/replicate were randomly selected for ileal villi morphology analyses. Birds were fasted overnight to limit intestinal throughput. The birds were humanely slaughtered using the neck dislocation method, carcasses were scalded in hot water at about 60°C for approximately 63 s, and the feathers were plucked manually.



**Table 3.** Ingredients and chemical composition of finisher diets

Diet	The percentage inclusion level of sorghum											
	0%			50%						100%		
	1	2	3	4	5	6	7	8	9	10	11	12
Maize meal	700	700	700	697	361	358	358	356	0	0	0	0
Sorghum meal	0	0	0	0	360	358	358	357	721	716	716	711
Soya meal	264	259	259	257	243	243	243	241	243	243	243	243
Limestone flour	12	12	12	12	12	12	12	12	12	12	12	12
Broiler maxipack	24	24	24	24	24	24	24	24	24	24	24	24
Phytase	0	5	0	5	0	5	0	5	0	5	0	5
Tannase	0	0	5	5	0	0	5	5	0	0	5	5
Total	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000
Proximate composition %												
DM	93.0	93.0	93.0	93.0	95.4	95.4	95.4	95.4	94.3	94.3	94.3	94.3
CP	17.17	17.17	17.17	17.17	17.0	17.0	17.0	17.0	17.8	17.8	17.8	17.8
Fat (EE)	2.32	2.32	2.32	2.32	2.42	2.42	2.42	2.42	2.13	2.13	2.13	2.13
CF	3.56	3.56	3.56	3.56	3.50	3.50	3.50	3.50	4.05	4.05	4.05	4.05
Ca	0.77	0.77	0.77	0.77	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.76
P	0.37	0.37	0.37	0.37	0.38	0.38	0.38	0.38	0.37	0.37	0.37	0.37
CT	0.02	0.02	0.02	0.02	0.73	0.73	0.73	0.73	1.38	1.38	1.38	1.38
GE(MJ/Kg)	17.77	17.77	17.77	17.77	17.8	17.8	17.8	17.8	17.6	17.6	17.6	17.6

Diet	The percentage inclusion level of sorghum											
	0%			50%						100%		
	1	2	3	4	5	6	7	8	9	10	11	12
maize meal	700	700	700	697	361	358	358	356	0	0	0	0
Sorghum meal	0	0	0	0	360	358	358	357	721	716	716	711
Soya meal	264	259	259	257	243	243	243	241	243	243	243	243
Limestone flour	12	12	12	12	12	12	12	12	12	12	12	12
Broiler maxipack	24	24	24	24	24	24	24	24	24	24	24	24
Phytase	0	5	0	5	0	5	0	5	0	5	0	5
Tannase	0	0	5	5	0	0	5	5	0	0	5	5
Total	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000	1000
Proximate composition %												
DM	93.0	93.0	93.0	93.0	95.4	95.4	95.4	95.4	94.3	94.3	94.3	94.3
CP	17.17	17.17	17.17	17.17	17.0	17.0	17.0	17.0	17.8	17.8	17.8	17.8
Fat (EE)	2.32	2.32	2.32	2.32	2.42	2.42	2.42	2.42	2.13	2.13	2.13	2.13
CF	3.56	3.56	3.56	3.56	3.50	3.50	3.50	3.50	4.05	4.05	4.05	4.05
Ca	0.77	0.77	0.77	0.77	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.76
P	0.37	0.37	0.37	0.37	0.38	0.38	0.38	0.38	0.37	0.37	0.37	0.37
CT	0.02	0.02	0.02	0.02	0.73	0.73	0.73	0.73	1.38	1.38	1.38	1.38
GE(MJ/Kg)	17.77	17.77	17.77	17.77	17.8	17.8	17.8	17.8	17.6	17.6	17.6	17.6

**Note:** DM=Dry Matter, CP= Crude Protein, EE= Ether Extract, CF= Crude Fibre, Ca= Calcium, P= Phosphorus, CT= Condensed Tannins, GE= Gross Energy

The ileum was separated from the rest of the segments at the Meckel's diverticulum to ileocecal-colonic junction (Incharoen et al., 2010). A 2-cm - long ileal (1m proximal to the ileocecal junction) segment sample was collected, placed in a sterile plastic container, and was cleaned twice with saline solution (1% NaCl) to remove intestinal digesta. The samples were fixed in 10% formalin, dehydrated using ethyl alcohol, embedded in paraffin wax, and cut into 4-m thick sections using a microtome (Brudnicki et al., 2017). The tissue samples were stained in eosin and hematoxylin on a glass slide and examined under a Trinocular Research Microscope Model B-5127 of 2015, India at  $\times 40$  magnifications. Digital images were captured using IS capture model S300 that was on computer fitted to the microscope. Villi height and width, crypt depth, and muscularis externa thickness was measured according to the specifications of Nain et al. (2012). Villi absorptive surface area was calculated as follows: (Nain et al., 2012).

Total villi surface area= Average villus width  $\times$  villus height

### Statistical analyses

The data were tested for normality using the Shapiro-Wilk test and log<sub>10</sub>-transformed wherever necessary. The General Linear Models (GLM) procedure of the Statistical Analysis System ver 9.4 (SAS Institute Inc., 2011) was used to analyse the data. The following model was used:

$$Y_{ijkl} = \mu + T_i + \epsilon_{ijk}$$

Where:  $Y_{ijkl}$  = response variable (villi height, villi width, crypt depth, muscularis externa thickness and apparent villi surface area)

$\mu$  = general mean common to all observations

$T_i$  = effect of the  $i$ th dietary treatment (0, 50 and 100% sorghum level with no enzyme or phytase only or tannase only or phytase plus tannase enzyme combination)

$\epsilon_{ijk}$  = random error term

Comparison of means was done using Tukey's test. All tests were performed at  $p < 0.05$  significance.

### Results

The significance of treatment on the villi parameters studied are shown in Table 4. Treatment had a significant effect ( $p < 0.0001$ ) on villi height. Villus height significantly increased ( $p < 0.001$ ) with increasing levels of sorghum in the diet (Table 5). Birds fed 100% sorghum supplemented with phytase had the tallest villi, which was not significantly different from the 100% diet supplemented with phytase and tannase enzyme combination (Table 5). The 0% sorghum diet supplemented with phytase only recorded the shortest

villi, and this was not significantly different ( $P > 0.05$ ) from the 0% sorghum diet supplemented with tannase and the control diet (Figure 1). Birds fed a 0% sorghum diet supplemented with a phytase and tannase enzyme combination resulted in significantly taller villi compared with those fed 0% sorghum with (without) enzyme supplementation (Table 5).

The 50% sorghum inclusion diets exhibited moderately taller villi, shorter than those from the 100% sorghum diets, and taller than the 0% sorghum diets. There were no significant differences in villi height for the 50% sorghum diets with or without enzyme supplementation (Table 5).

Apical and basal villi widths significantly increased with increasing sorghum inclusion in the diet ( $p < 0.0001$ ). The 100% sorghum without enzyme diet resulted in the widest apical villi (Table 6). There were no significant differences in apical villi width for 100% sorghum supplemented with either phytase or tannase as single enzymes or used in combination (Table 6). The narrowest villi were recorded in birds fed 0% sorghum diet supplemented with a phytase and tannase enzyme combination. Basal villi width was also highest in birds fed the 100% sorghum diet, and no significant differences emanated from enzyme supplementation (Table 6). Again, the 0% sorghum diet supplemented with a phytase and tannase enzyme combination resulted in the narrowest villi width.

Treatment significantly affected the apparent villi surface area ( $p < 0.0001$ ). The inclusion of sorghum increased the apparent villi surface area. Broilers fed complete sorghum-based diets showed higher villi surface area. Birds fed a complete sorghum diet supplemented with phytase had the highest villi surface area ( $15.48 \pm 0.241$  mm). The birds fed 0% sorghum diets had lower villi surface area compared to the 50 and 100% sorghum diets (Figure 2). The least clear villi surface area was recorded in broilers fed 0% sorghum supplemented with a phytase and tannase enzyme combinations ( $5.63 \pm 0.241$  mm). Data were tested for normality using the Shapiro - Wilk test and all the collected data were normal ( $S > 0.90$  for villus height, apical villi width, basal villi width, crypt depth, muscularis externa, and clear villi surface area). The crypt depth was highest in birds fed the 50% sorghum level with no significant differences resulting from enzyme supplementation (Table 5). The 0% and 100% sorghum levels exhibited comparable crypt depth. However, the 100% sorghum diet supplemented with a phytase and tannase enzyme combination had the least crypt depth measurement.

Dietary treatment significantly influenced live body weight at slaughter and carcass weights ( $p < 0.05$ ). Generally, the highest live body and carcass weights were observed in birds fed diet at 50% sorghum inclusion level with no enzyme supplementation and this was not significantly different from the weights recorded in broilers fed 50% sorghum diets with

**Table 4.** Effects of phytase and tannase inclusions in sorghum-based broiler diets on villi parameters

Parameter	Effect
	Treatment
Villus height	**
Villi surface area	*
Apical villi widths	**
Basal villi widths	**
Muscularis externas thickness	**

\*P < 0.001; \*\*P < 0.0001. All tests were performed at p < 0.05 level of significance.

**Table 5.** Effect of sorghum level and phytase and tannase supplementation on ileal villi parameters

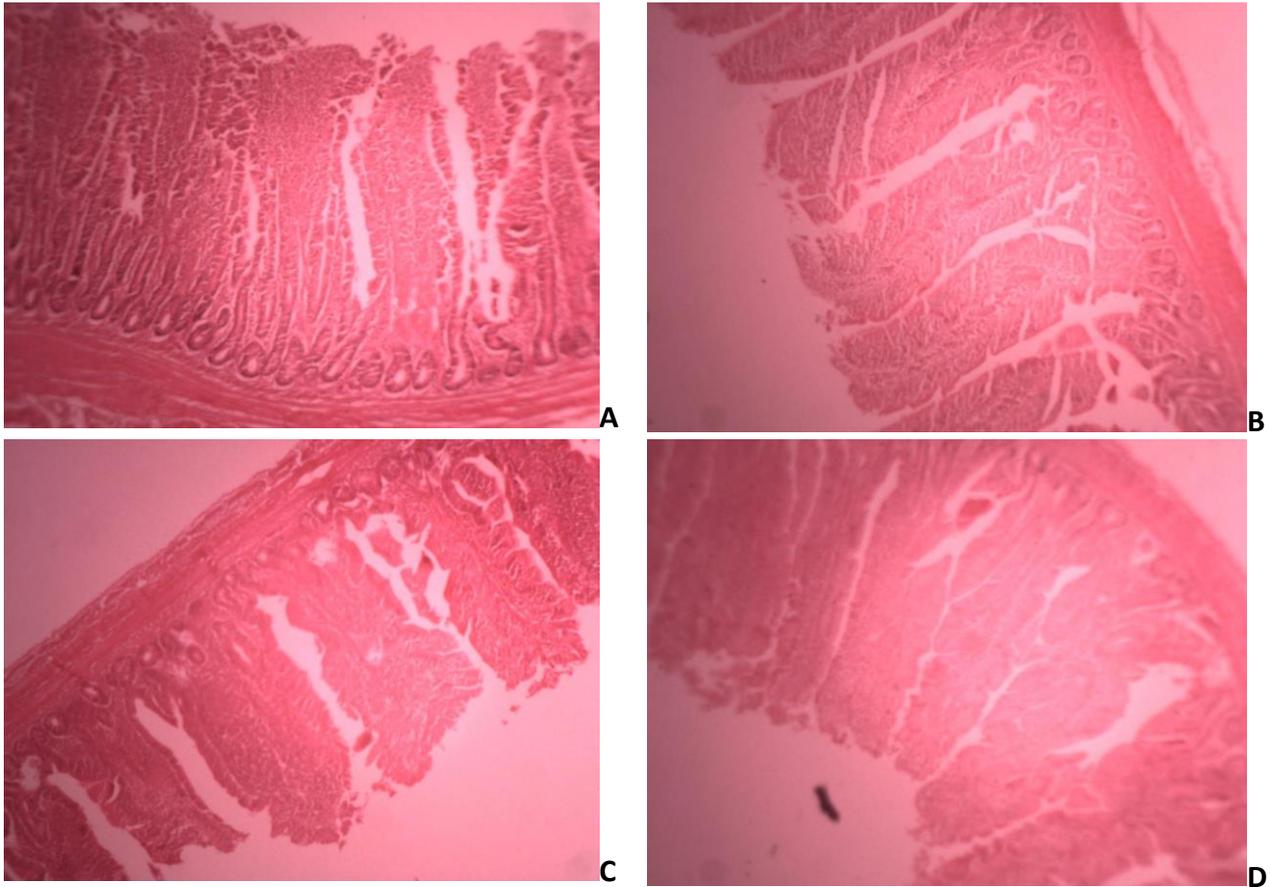
The ileal villus Parameter (mm)	Dietary treatment											
	1*	2*	3*	4*	5*	6*	7*	8*	9*	10*	11*	12*
VH	5.35 <sup>ghi</sup>	5.30 <sup>ghi</sup>	5.40 <sup>ghi</sup>	4.41 <sup>f</sup>	5.73 <sup>e</sup>	5.54 <sup>eg</sup>	5.74 <sup>e</sup>	5.76 <sup>e</sup>	6.43 <sup>bcd</sup>	6.71 <sup>abd</sup>	6.40 <sup>bcd</sup>	6.60 <sup>abcd</sup>
aVW	1.49 <sup>h</sup>	1.57 <sup>h</sup>	1.40 <sup>h</sup>	1.11 <sup>k</sup>	2.09 <sup>bde</sup>	2.00 <sup>bdefg</sup>	1.89 <sup>efg</sup>	1.86 <sup>efg</sup>	2.47 <sup>a</sup>	2.15 <sup>bde</sup>	2.15 <sup>bde</sup>	2.09 <sup>bde</sup>
bVW	1.47 <sup>ef</sup>	1.64 <sup>ef</sup>	1.64 <sup>ef</sup>	1.45 <sup>f</sup>	1.63 <sup>ef</sup>	2.15 <sup>bcd</sup>	2.07 <sup>cd</sup>	2.02 <sup>cd</sup>	2.30 <sup>abc</sup>	2.47 <sup>ab</sup>	2.34 <sup>ab</sup>	2.28 <sup>bcd</sup>
CD	1.80 <sup>defg</sup>	1.85 <sup>defg</sup>	1.70 <sup>efg</sup>	1.78 <sup>defg</sup>	2.12 <sup>abcf</sup>	2.15 <sup>abcf</sup>	2.13 <sup>abc</sup>	2.12 <sup>abc</sup>	2.06 <sup>bcd</sup>	1.89 <sup>cdef</sup>	1.70 <sup>efgh</sup>	1.52 <sup>h</sup>
ME	1.17 <sup>ghi</sup>	1.22 <sup>ghi</sup>	1.26 <sup>gh</sup>	1.11 <sup>hi</sup>	1.13 <sup>ghi</sup>	1.80 <sup>f</sup>	1.97 <sup>e</sup>	2.13 <sup>cd</sup>	2.16 <sup>cd</sup>	2.47 <sup>a</sup>	2.30 <sup>bc</sup>	2.24 <sup>bcd</sup>
VSA**	7.92 <sup>f</sup>	8.48 <sup>f</sup>	8.20 <sup>f</sup>	5.63 <sup>g</sup>	10.67 <sup>de</sup>	11.48 <sup>cd</sup>	11.36 <sup>cd</sup>	11.15 <sup>cde</sup>	15.3 <sup>a</sup>	15.48 <sup>a</sup>	14.37 <sup>b</sup>	14.44 <sup>b</sup>

Note: Means in the same row with different superscripts differ significantly (P < 0.05). VH=villi height, Avw =apical villi width, bVW=basal villi width, CD=crypt depth, ME= muscularis externa thickness, VSA\*\*= villi surface area in mm<sup>2</sup>

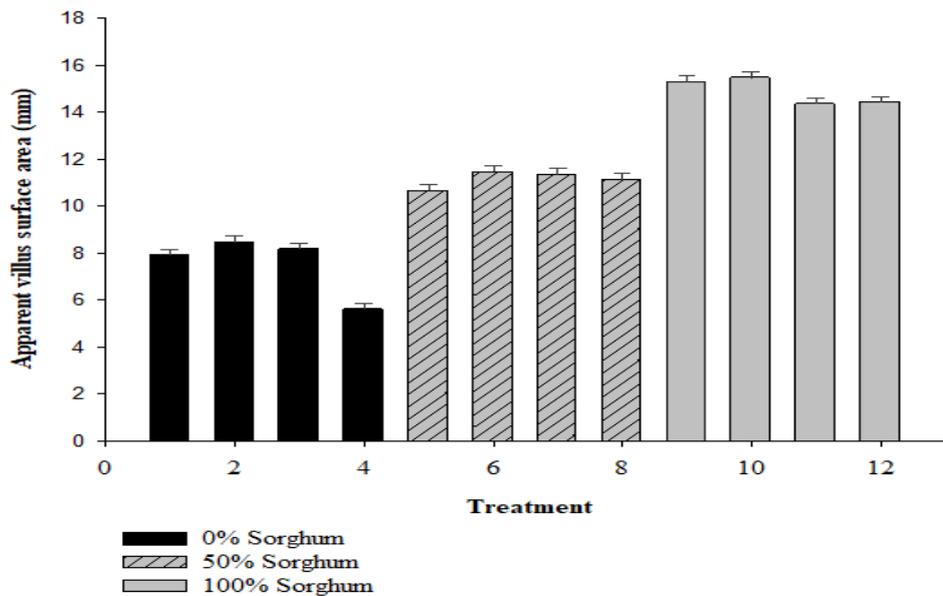
\*Description of treatments: 1\* =100% maize with no enzyme, 2\* =100% maize with 5% phytase, 3\*= 100% maize with 5% tannase, 4\*= 100% with 5% phytase and tannase combination, 5\*=50% maize and 50% sorghum with no enzyme, 6\*= 50% maize and 50% sorghum with 5% phytase, 7\*= 50% maize and 50% sorghum with 5% tannase, 8\*= 50% maize and 50% sorghum with 5% phytase and tannase combination, 9\* =100% sorghum with no enzyme, 10\* =100% sorghum with 5% phytase, 11\*= 100% sorghum with 5% tannase, 12\*= 100 sorghum with 5% phytase and tannase combination

**Table 6.** Effect of dietary treatment on live body and carcass weights on day 42

Dietary treatment	Live body weight	SEM	Carcass weight	SEM
1	2100.5 <sup>abc</sup>	63.50	761.5 <sup>abcde</sup>	6.43
2	1926.5 <sup>cdef</sup>	63.50	747.1 <sup>cde</sup>	6.43
3	1952.3 <sup>cdef</sup>	63.50	754.5 <sup>abcde</sup>	6.43
4	2096.8 <sup>abcde</sup>	63.50	757.0 <sup>abcde</sup>	6.43
5	2159.7 <sup>abc</sup>	63.50	767.9 <sup>abcd</sup>	6.43
6	2004.2 <sup>abcdef</sup>	63.50	758.4 <sup>abcd</sup>	6.43
7	1967.5 <sup>bcdef</sup>	63.50	756.4 <sup>abcde</sup>	6.43
8	2102.3 <sup>abcd</sup>	63.50	764.1 <sup>abcde</sup>	6.43
9	1950.5 <sup>cdef</sup>	63.50	747.1 <sup>abcd</sup>	6.43
10	1912.8 <sup>cdef</sup>	63.50	752.9 <sup>bcde</sup>	6.43
11	1931.2 <sup>cdef</sup>	63.50	743.6 <sup>de</sup>	6.43
12	1920.2 <sup>abcdef</sup>	63.50	742.6 <sup>de</sup>	6.43



**Figure 1.** Ileal villi characteristics of Cobb 500 broilers fed: (A) 100% sorghum with phytase (B) 50% sorghum with phytase (C) 0% sorghum with phytase (D) 100% sorghum with phytase plus tannase enzyme combination at  $\times 40$  magnification



**Figure 2.** Effect of sorghum inclusion level and enzyme supplementation on apparent villus surface area

phytase only and with phytase and tannase enzyme combination as well as birds fed complete maize diets without enzyme, with phytase only and with phytase and tannase enzyme combination as shown in Table 6. The least live body and carcass weights were observed in broilers fed complete sorghum diets with a phytase and tannase enzyme combination.

## Discussion

Generally, an increase in villi height is related to enhanced nutrient absorption, while deeper crypts are associated with higher tissue turnover rates (Choct, 2009; de Verdal et al., 2011). The results of the current study on villi height contradict previous results by Nyamambi et al. (2007). In their study, they observed that duodenal villus height and crypt depth were lowered with increasing tannin levels. Nyamambi et al. (2007) used Chirimaugute, Brown Tsweta, DC, and SV2 sorghum varieties with tannin contents of 1.68, 0.20, 2.48, and/g DM, respectively. They stipulated that day 7 and day 14 villi height of chicks fed 100% DC, Chirimaugute, and Brown Tsweta sorghum diets were lower than the villi height of chicks raised on total maize and 50% DC diets. Additionally, sorghum inclusion levels had no significant effect on villus height, width, and crypt depth of broilers at day 42 (Silva et al., 2015; Manyelo et al., 2019). This is because the digesta arriving at the ileum had already been subjected to maximum enzyme activity and maximum absorption in the previous intestinal segments irrespective of the composition of feed consumed (Silva et al., 2015). Elongation of the villi with increasing sorghum level could be explained by the increase in tannins and their metabolites, which increase mitosis in the villi, implying increased proliferation (Jamroz et al., 2009; Brus et al., 2018). Tannins act as gut microbiota modulators (Tosi et al., 2013; Choi and Kim, 2020;) and their anti-oxidative traits enhance villus length (Buyse et al., 2022). The villi height obtained in this study was lower than that reported by Mutibvu (2016) in indigenous chickens. This can be attributed to the vitamin A supplemented in the diets, which enhances gut morphology (Kunisawa and Kiyono, 2013) as well as the indigenous chicken breed they used. The observation that broilers fed either complete maize or complete sorghum diets showed shallowest crypts is surprising given the fact that complete sorghum diets had higher levels of tannins and phytate which had negative effects on the intestinal epithelium. A shallower crypt depth indicates a decrease in the metabolic cost of intestinal epithelial renewal in the villi (Xu et al., 2022). On the other hand, deeper crypts promote rapid cell turnover, faster metabolism of tissue, and allow renewal of intestinal villi (Hamedi et al., 2011), resulting in rapid replacement of sloughed or inflamed villi (Jayaraman et al., 2013). The observation that completes substitution of maize by sorghum results in higher ileal villi surface area is contrary to previous findings (Silva et al., 2015).

They highlighted that sorghum level had no significant effect on the absorptive surface area in the jejunum; thus, the feed offered did not interfere with the absorption mechanisms. In their study, however, Silva et al. (2015) used a sorghum variety that contained 42.7 mg/kg equivalent to 0.00427% tannin and this is classified as a tannin free variety. It is possible that the impact of tannins in this variety on villi surface area could be negligible.

In a separate study, sorghum level had no effect on villus height and crypt depth in the small intestinal mucosa segments except for duodenal villus height, which was smaller in 7-d-old broilers fed the low-sorghum diet than in broilers fed the high-sorghum or control diets (Torres et al., 2013). Such a response is explained by the fact that during the initial stages of life, intestinal growth and differentiation occurs in the absence of exogenous feed nutrients and luminal and hormonal factors, thus the process is influenced by intrinsic factors (Drozdowski et al., 2010). However, Incharoen et al. (2010) highlighted that dietary nutrient composition influences intestinal development and mucosal architecture which subsequently influences digestive absorption and assimilation of digested nutrients. Shorter intestinal villi are related to a smaller number of absorptive cells, presence of toxic substances, and a larger number of secretory cells (Iwashita et al., 2003), whereas longer villi promote healthy digestion and high nutrients absorption efficiency (Itza-Ortiz et al., 2019). The current results showed villi widths higher than those reported by Ncube et al. (2017). This disparity could be a consequence of the protein source *Acacia angustissima*, which could have limited villi development in their study.

The observation that phytase and tannase enzyme supplementation had a significant effect on villi morphology is consistent with previous results. The addition of phytase maize-soyabean diet resulted in higher jejunal villi height (Pekel et al., 2017; Karami et al., 2020). The effects of phytase supplementation on villi width and crypt depth are inconsistent. The inclusion of phytase in broiler diets increased villi width (Karami et al., 2020; Moita et al., 2021). The effects of phytase or tannase enzyme combination in sorghum-based diets on intestinal villi morphology are still limited for comparison.

Although the total replacement of maize by sorghum-increased villi height and hence the absorptive capacity of the villi, complete sorghum diets negatively affected live body and carcass weights. The observation is consistent with previous results by Avila et al. (2009) reported that there was no positive association between villi height and nutrient absorption. However, this is surprising because longer villi provide higher absorptive area, better digestive enzyme activity and fast transport of nutrients (Wijtten et al., 2012) which translate to high live body weight.

## Conclusion

It can be concluded that the broiler diet containing 50% sorghum with 5% phytase plus tannase enzyme combination can be fed to broilers without compromising ileal absorptive area, live body weight and carcass weight.

## Acknowledgments

The work was funded by the Ministry of Higher and Tertiary Education Innovation Science and Technology Development through the University of Zimbabwe Vice Chancellor Research Fund. The authors would like to express their sincere gratitude to Dr. A. Nhamo, Dr. E. Nyakudya, and Prof F. Mutambanengwe and Prof. P. Mapfumo for their unwavering support toward the success of this work.

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