Replacing fishmeal for farmed marine protein in starter broiler rations safely improves growth performance

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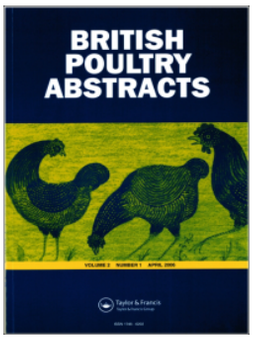

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2025 SPRING MEETING OF THE WPSA UK BRANCH

2025 Abstracts

Communications and invited talks presented at the WPSA UK Branch Spring Meeting held on 12th and 13 March 2025. These abstracts were reviewed and accepted for presentation by the WPSA UK Programme Committee.

Ingrid de Jong. The transition to higher welfare broiler production systems: the Dutch example and expected effects of adoption of the ECC on broiler welfare (Invited)

B. Schuitemaker, M. Mayer, R. Bailey and A. Narbad. Microbiome applications in commercial poultry: from faecal profiling to performance biomarkers (Invited)

S. Galgano, M. Umar Faruk, I. Eising, J. Houdijk. and F. Khattak. Microbiota and microbiome impacts on nutrient utilisation in layer hens administered muramidase

F. Khattak, S. Galgano, R. Pearson and A. Leigh. Oxygenated water as a strategy to improve broiler welfare and meat myopathies

P.W. Wilson, H.A. McCormack and I.C. Dunn. Longitudinal live bird x-ray of laying hens through puberty to 60 weeks of age; measures of bone density and damage

D. Rauf, M.R. Bedford, A. Alkhtib, D.V. Scholey and E.J. Burton. Effect of an enzyme cocktail in rye-based broiler grower diets on caecal metagenomic profiles

C. Onuoha, A. Alkhtib, D. Scholey and E. Burton. Effect of scattering black soldier fly larvae on the litter on growth performance, gut development and active behaviour of fast and slow-growing broiler

A. Šimić, G. González-Ortiz, J. Seifert, J.S. Sáenez, B. Rios Galicia, S.C. Mansbridge, S.P. Rose, M.R. Bedford, M. Tukša and V. Pirgozliev. Influence of xylooligosaccharides supplementation in broiler chickens

H.M. Scott-Cook, S.C. Mansbridge, A.M. Mackenzie and V.R. Pirgozliev. Feeding alternative proteins to maintain litter quality and leg health of slow growing broilers

S. Galgano, T. Hanford, K. Sutton and J. Houdijk. Development of a sub-clinical avian colibacillosis model

M.A. Hussein, D.R. Davies, L.C. Smith, J.W. McArthur and J.G.M. Houdijk. Nutritional value of processed faba beans for broiler chickens

H. Kang, S. Brocklehurst, M. Haskell, S. Jarvis and V. Sandilands. Do activity sensors identify behavioural change in laying hens after a vaccine challenge?

L.P. Barnard, I.J. Carvalhido and L.M. Van Eck. Effect of diet density on production parameters and body condition of laying hens measured utilising a novel non-invasive Near-Infrared tool

S. Struthers, Y. Zhang, M. Jackson, P.W. Wilson, J.J. Schoenebeck and I.C. Dunn. Investigating beak shape variation during puberty in male and female layer chickens

A.E. Rainey, S. Buijs, N.E. O'Connell and M.E.E. Ball. The effect of dietary protein level and enhanced vitamin/mineral supplementation on egg production and quality during an extended laying cycle

C. Mulvenna, R. Bradley, O.C. Carballo, K. Wilson, S. Avendano and M.E.E. Ball. The performance, digestibility and ammonia production of current *versus* historic genetic broilers

P.W. Wilson, B. Andersson, M. Schmutz and I.C. Dunn. Intra-egg variation in cuticle coverage on domestic hens' eggs, a risk for bacterial penetration

S. Gilani, L. Marchal, G.E. Amir, A. Bello and Y. Dersjant-Li. Effect of novel phytase, varying doses and combination with carbohydrase enzyme to reduce carbon footprint per kg of broilers

G.M.V. Pangga, A. Richmond, C. Hughes, A. Psifidi, D. Xia, U. Ijaz and O. Gundogdu. Integrative omics reveals distinct metabolic and microbial signatures in broilers under coccidiosis interventions

G. Saleem, J.G.M. Houdijk, N. Sparks and S. Athanasiadou. Effect of *Clostridium perfringens* challenge on jejunal gene expression in broiler chickens

M.A. Hussein, S. Galgano, K. Magee, R. Gratacap and J.G.M. Houdijk. Replacing fishmeal for farmed marine protein in starter broiler rations safely improves growth performance

S. Galgano, M.A. Hussein, K. Magee, R. Gratacap and J.G.M. Houdijk. Replacing fishmeal for farmed marine protein in starter broiler rations improves digestibility through microbiota modulation

H.M. Scott-Cook, S.C. Mansbridge, A.M. Mackenzie and V.R. Pirgozliev. Impact of dietary specification on broiler growth performance, nutrient digestibility and liver triglyceride concentration

I.D. Onol, F. Jenkins, M. Onol, N. Kendall and C.J. O'Shea. Oviposition time and laying environment: their influence on egg quality and embryonic outcomes in broiler breeders

The transition to higher welfare broiler production systems: the Dutch example and expected effects of adoption of the ECC on broiler welfare

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Application

Due to adoption of the European Chicken Commitment (ECC) there will be a transition to more higher welfare broiler production systems in Europe. In the Netherlands, there has been a change towards an increasing number of broiler chickens housed in higher welfare systems since 2014, with a transition to even more strict welfare requirements (Beter Leven one star welfare label) in recent years. This resulted in currently about half of the broiler chickens being produced in higher welfare production systems. It has been shown that broiler welfare significantly improved for broilers housed in higher-welfare systems, which can also be expected from adoption of the ECC by the food industry.

Summary

There is a trend towards a transition to more higher welfare broiler systems in Europe, caused by changes in legislation or requirements by retail in some countries, and by the adoption of the European Chicken Commitment by many food companies. Higher-welfare broiler systems are here being defined as systems having a lower stocking density (≤38 kg/m^2), using a slower-growing broiler strain (<50 g/day) and providing environmental enrichment, as compared to the conventional indoor broiler production systems with so-called fast-growing breeds. In this presentation I will first show the transition process in the Netherlands, starting in 2014 as a result of public pressure caused by a NGO campaign to adopt higher welfare broiler systems. Retail decided to only sell fresh meat from chickens of higher welfare systems. Requirements differed between retailers, but generally a lower stocking density was adopted (≤38 kg/m^2), environmental enrichment such as straw bales needed to be provided, and so-called slower-growing broiler strains should be used (by defining a minimum slaughter age of 49 days). This change resulted in significant improvements in broiler welfare (De Jong, Bos, Van Harn, Mostert, & Te Beest, 2022). Ongoing societal pressure even resulted in more strict welfare requirements with time, and currently Dutch retailers only sell fresh broiler meat from systems with should at least have the Beter Leven one star label, which requires a maximum stocking density of 25 kg/m^2, environmental enrichment, natural light entrance, a covered veranda and a slower-growing strain (minimum slaughter age 56 days). This resulted in a further improvement of broiler welfare as compared to the initial higher-welfare production systems (De Jong et al., 2022).

ECC also has requirements on stocking density, minimum light level, the breed that should be used and environmental enrichment. These various factors will be discussed in terms of their potential to improve broiler welfare, to illustrate the expected effects of adoption of the ECC on broiler welfare. Both a substantial reduction of stocking density and reducing growth rate (by adopting another breed) seem to be key factors to improve broiler welfare (e.g. Dixon, 2020.; Van Der Eijk, Gunnink, Melis, Van Riel, & De Jong, 2022; Van Der Eijk et al., 2023). Other factors that potentially can contribute to broiler welfare but that are currently not included in ECC will also be briefly discussed.

In terms of overall sustainability, the adoption of higher welfare broiler systems led to a discussion regarding the effects on environmental impact and the economic consequences. Stocking density, growth rate and feed conversion are the most important factors to determine costs of production. Breast meat yield of slower-growing strains is lower. The higher production costs should be reflected in higher prices for the meat to guarantee the same income for the farmer (Van Horne, 2020). Regarding emissions, cultivation and production of raw materials for feed largely determines the total emissions. Slower-growing chickens require more land and raw materials per kilogram of product than regular fast-growing chickens. Opportunities to simultaneously improve welfare and ecological footprint by e.g. using by-products in the diet need to be further studied (Mostert, Bos, Van Harn, & De Jong, 2022). The reduced use of antibiotics in slower-growing strains has beneficial effects for human health.

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Microbiome applications in commercial poultry: from faecal profiling to performance biomarkers

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Application

The poultry microbiome is integral to gut health and performance. Microbiome-based biomarkers provide actionable tools to enhance sustainability, productivity, and animal welfare in commercial farming. This study combines bacterial, fungal (mycobiome), and metabolic analyses to identify functional traits such as phytase activity, reducing dependence on synthetic feed additives.

Introduction

Improving sustainability and welfare in broiler production is increasingly important while maintaining efficiency. The microbiome offers a practical means to assess gut health and predict performance. These findings demonstrate how microbiome analysis can guide sustainable solutions to optimise poultry diets and reduce reliance on additives.

Material and methods

Faecal samples were collected 7-, 18-, 27-, and 40-days post-hatch (dph), with recorded body weight and faecal water content. Shotgun metagenomics characterised bacterial and viral communities, ITS1-4 sequencing profiled fungal communities, and untargeted ^{1}H-NMR metabolomics analysed metabolite pathways. After an exciting result from the metabolomics analysis, a novel workflow was developed to screen for phytase activity by identifying bacteria with phytase and acid-phosphatase genes using shotgun data, followed by bacterial isolation and validation.

Results

At 7 dph, the bacterial microbiome was consistent across three flocks, while the mycobiome showed variation. A core mycobiome was identified, suggesting its role in early gut development. Microbial succession followed known patterns, with lactobacilli, *Akkermansia* and *Alistipes* species correlating with improved performance metrics throughout the broiler lifecycle.

Phytase activity screening identified bacterial strains with phytase and acid-phosphatase genes. Functional assays confirmed phytate degradation, validated by detecting myoinositol in faeces from chicks fed a phytase-free diet. This demonstrates the potential for microbiome-driven phosphorus utilisation, a previously unreported phenomenon in broilers.

Conclusion

Faecal samples are an ethical and informative tool for assessing gut health and performance in broilers. This study shows how microbiome profiling, combined with functional screening, identifies microbial traits that have the potential to enhance productivity and sustainability. Microbiome-driven strategies can reduce reliance on synthetic additives and promote sustainable, welfare-focused poultry farming.

Microbiota and microbiome impacts on nutrient utilisation in layer hens administered muramidase

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Application

Muramidase intervention could improve nutrient utilisation via microbiota modulation in layers.

Introduction

Muramidases (lysozyme, EC 3.2.1.17) are naturally occurring enzymes in many biological tissues (e.g. egg albumen, tears),

which catalyse the hydrolysis of bacterial peptidoglycan (PGN, Khattak, Eising, & Faruk, 2024). Several studies have proven that muramidase intervention leads to beneficial effects in chickens (Wang et al., 2021), however, the avian-microbial mechanism of action has so far been explored only in broilers (Brugaletta et al., 2022). Here, we describe, for the first time, the microbial-driven effects of muramidase in layer hens.

Materials and methods

The 20-week study was approved by the SRUC animal welfare and ethical review body (AEX 2022–002 POU). A total of 900 22-week old hens were housed in 60 enriched cages (i.e. 15 per cage and 12 cages per treatment). There were five treatments, with increasing concentrations of muramidase (Balancius^{TM}, DSM-Firmenich Nutritional Products Ltd., Basel, Switzerland) at 150 mg/kg increments: 0, 150, 300, 450 and 600 mg/kg (T1 to T5). Body weight gain (BWG) was calculated longitudinally. At the end of the study (d140), excreta were collected to determine the total tract nitrogen retention (NR) coefficient using dietary TiO_2, while caecal content was collected for DNA extraction (Cat. No. 938036, QIAGEN) and downstream shotgun metagenomics sequencing (NovaSeq X plus 150PE). Microbiome multivariate association was performed through Maaslin 2.

Results

We observed a 33.9% increase in BWG in all the groups compared to T1 ($p < 0.05$). Compared to T1, NR was 26.8% higher in T2, T3 and T5 ($p < 0.05$), and 13.9% higher in T4 ($p = 0.07$).

In parallel, *Lactobacillus, Enterococcus, Sutterellaceae* GGB6574, *Firmicutes* GGB3033 and *candidatus Heteroscilispira* were decreased ($Q < 0.05$) in all the groups compared to T1, whilst *Collinsella, Methanobrevibacter, Actinobacteria* GGB8965, *candidatus Roslinia, Oscillibacter, Lachnospiraceae* GGB51960, *Firmicutes* GGB2999, *candidatus Heritagella, Mogibacterium*, unclassified *Oscillospiraceae, Firmicutes* GGB9348, *Firmicutes* GGB25626 and *Romboutsia* were found to be significantly enriched ($Q < 0.05$). Moreover, a dose-dependent microbial modulation was observed in all the groups leading to dose-dependent enterotypes with the generation of typical microbial profiles at increasing doses of muramidase.

Interestingly, an inverse relationship was found between the observed phenotype and some of the genera, indeed

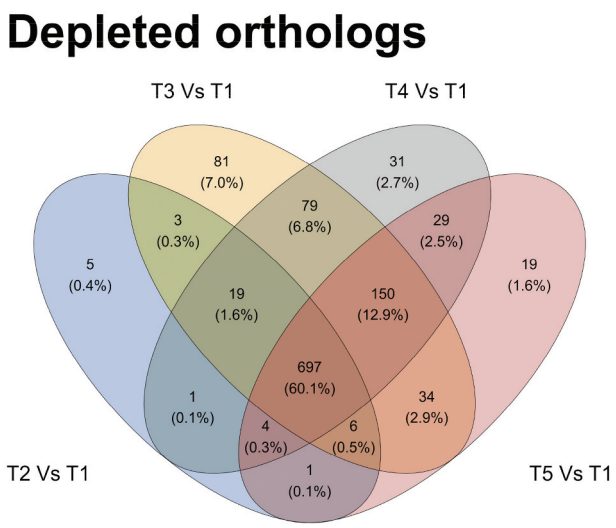

Figure 1. Muramidase-driven less abundant orthologs compared to 0 mg/kg.

Lactobacillus and *Ligilactobacillus* were depleted at increasing NR, whilst *Streptococcus* and *Enterococcus* were both less abundant in birds with higher BWG ($Q < 0.05$).

A total of 697 orthologs were significantly less abundant in all the treatments compared to T1 ($Q< 0.05$, Figure 1), including those encoding PGN biosynthesis proteins and proteins involved in the bacterial metabolism, such as biosynthesis of amino acids or nucleotides.

Conclusion

Muramidase intervention led to a dose-dependent amelioration of performance and nutrient absorption, as indicated by the increased NR and BWG. This was likely achieved via microbiota modulation, as demonstrated by the dose-dependent enterotypes and the depletion of genes linked to bacterial metabolism and PGN biosynthesis.

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Oxygenated water as a strategy to improve broiler welfare and meat myopathies

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Application

Incorporating oxygenated water into broiler production systems offers a practical approach to improve bird welfare indicators

Introduction

Water quality is crucial for poultry health and welfare, with dissolved oxygen (DO) levels varying from 1–3 mg/L in well water, 5–14 mg/L in surface water, and 6–9 mg/L in tap

water, to over 30 mg/L in oxygenated water (Speit, Schütz, Trenz, & Rothfuss, 2002). Oxygen-enriched drinking water is reported to boost arterial oxygen levels, improve tissue oxygenation, and enhance glycaemic control (Khoo et al., 2021). However, limited research exists on its effects in poultry. This study evaluates the impact of enhanced oxygenated water on animal welfare, carcass yield, meat myopathies, and microbial-driven effects in a controlled environment.

Materials and methods

A total of 840 day old male Ross 308 broilers were assigned to two treatments (oxygenated vs. tap water) in a randomized block design, with 12 replicate pens of 35 birds each. Oxygenated and tap water were supplied via separate tanks and nipple lines (W1 to W4), with DO levels measured daily using Hanna DO meter. Oxygenated water was produced using Oxcel Technology. Birds received commercial starter crumbs, grower pellets, and finisher pellets with ad libitum access to feed and water. Welfare assessments included feather cover score, breast plumage cleanliness, gait score, leg angulation, pododermatitis, and hock burn scores, based on the RSPCA Broiler Welfare Assessment Protocol (RSPCA, 2017). On day 36, six birds/pen were euthanized for carcass yield and meat myopathy scoring. Caecal samples were collected for shotgun metagenomic sequencing, and microbiome analysis was performed using Maaslin 2. Data were analyzed via ANOVA (GenStat 19) with $P < 0.05$. This study was approved by SRUC's Animal Welfare and Ethical Review Body (AEX 2024–021 POU).

Results

The DO levels were around 32 mg/mL in the oxygenated water and 9.5 mg/mL in the tap water. The DO levels in tap (W1 & W2) & oxygenated (W3 & W4) water lines ae shown in Figure 1. There was no significant differences ($P > 0.05$) in live bird slaughter weight, carcass eviserated weight, or breast and drumstick weight percentages between treatments. However, birds on oxygentaed water had 11.6% lower abdominal fat and 2.6% heavier thighs compared to those on tap water ($P < 0.05$). Birds on oxygenated water also exhibited better meat quality with a significantly larger proportions of score 0 white stripings compared to those on tap water (40% *vs.* 27%). Wooden breast scores reamined very low (around 13%, $P > 0.05$). Among welfare indicators, levels of feather cover, hock burn score 0 were significantly higher in oxygentaed water compared to tap water group (84% *vs.* 70%; 37% *vs.* 12%, respectively. Other welfare parameters showed

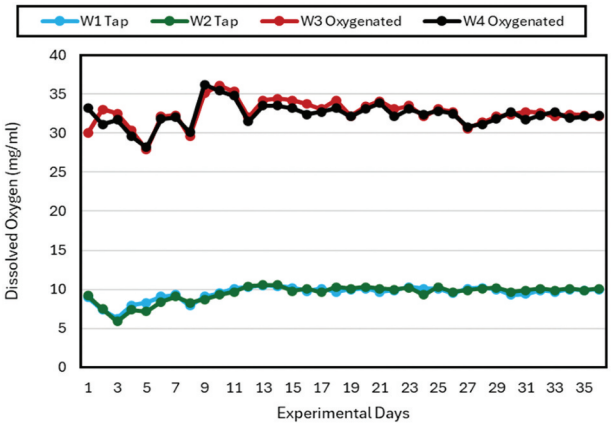

Figure 1. Dissolved oxygen levels in water lines.

numerical improvements in the oxygenated group, but the differences were not significant ($P > 0.05$). In terms of microbial composition, diversity (both α and β) measured via the richness and Shannon index and via the Jaccard and Bray-curtis index did not change in the caeca of birds given tap or oxygenated water. However, Proteobacteria and Verrucomicrobia were significantly enriched and depleted ($Q < 0.05$) in tap water treated broilers caeca, respectively

Conclusion

These results suggest that oxygenated water can improve broiler welfare and meat quality, offering a sustainable option for poultry production. Enrichment of Proteobacteria and depletion of Verrucomicrobia in the tap water group may indicate compromised gut barrier function. Further studies are needed to clarify the underlying mechanisms driving these effects.

Acknowledgements

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Longitudinal live bird x-ray of laying hens through puberty to 60 weeks of age; measures of bone density and damage

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Application

This study demonstrates that keel bones gradually accumulate damage over lay and the bone density of the tibia tarsus does not decline with age. This suggests that some of the views of bone health in laying hens need critical evaluation.

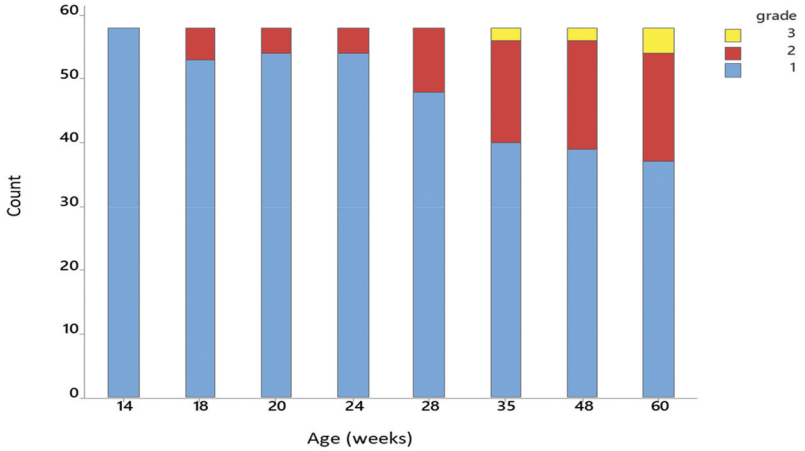

Figure 1. Keel scores of the same hens as they aged.

Introduction

Bone health as a welfare issue has become more prominent in part because the greater opportunities to perch and collide with furniture in some alternative systems has led to more damage. This is especially true of the sternum or keel bone. There has however been some controversy on when the damage occurs and indeed what might cause it. This is because of the difficulty of conducting longitudinal studies to identify when damage occurs. We recently developed radiography of living hens which has allowed longitudinal study of the skeleton from before puberty to 60 weeks of age. This should help to understand the changes in the bone with the onset of laying and when damage starts to appear.

Material and methods

60 one-day-old Hy-line brown chicks were reared in four replicate pens of 15 hens per pen containing nest boxes and perches. All hens were radiographed at 10, 14, 18, 20, 24, 28, 36, 48 and 60 weeks. Tibia tarsus density was measured as described previously (Wilson, Dunn, & McCormack, 2023). Keel assessment scoring was made using a simplified scoring system (Maidin et al., 2024) and gave a grading ranging from 1 (the best- no damage present) to 5 (worst). Data were analysed using a repeated measures ANOVA, Genstat v18. Values were log transformed where necessary. Use of animals was approved by the Roslin Institute AWERB.

Results

The density of tibia changes significantly over the period of study ($P < 0.001$), basically increasing over the period. The most significant differences at individual ages are between the values prior to lay (weeks 10–18) and those after e.g. 14 weeks of age, 59382 ±536 and at 24 weeks of age 73999 ±602 ($P < 0.001$). The values measured at 48 and 60 weeks of age are greater and significantly different from those at all earlier ages, e.g. 24 weeks of age, 73999 ±602 and at 48 weeks of age 77694 ±941 ($P < 0.001$). The keel bone was scored from 1–5 but the highest score with the most damage recorded was only a 3. The first evidence for any damage was at 18 weeks of age and there is a gradual increase in accumulated damage over the full duration of the study (Figure 1).

Conclusion

The results demonstrate that bone density increases as the hens come into lay which is largely due to the deposition of medullary bone. In this study where the hens were on the floor there is no evidence for a reduction in density over the study period. The accretion of bone damage progressed through the study and was not occurring at one time point. There was no specific time that damage occurred and bone density actually increased in the tibia tarsus.

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Effect of an enzyme cocktail in rye-based broiler grower diets on caecal metagenomic profiles

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Application

Addition of an enzyme cocktail promotes beneficial bacterial populations in broilers fed rye-based grower diets.

Introduction

High fibre diets in combination with carbohydrase enzymes for broilers may provide a useful fuel source

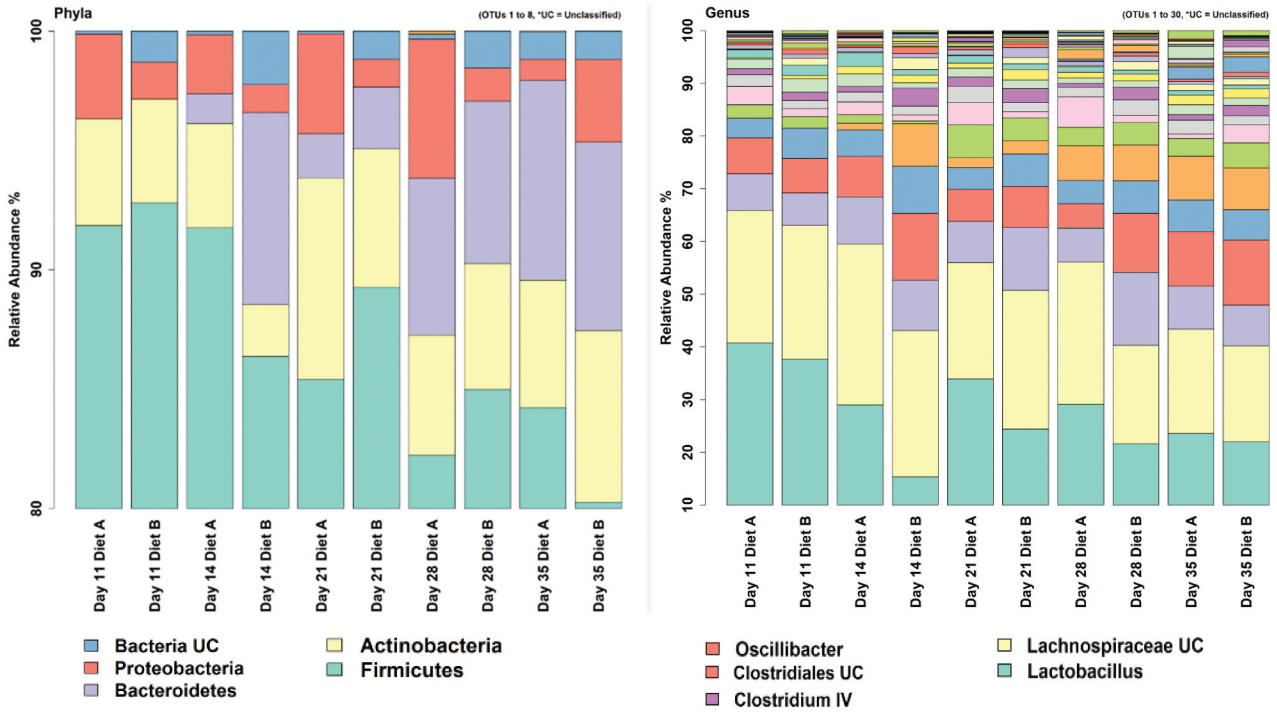

Figure 1. Relative abundance of phylum (left) and genus (right).

for beneficial caecal microbes (Amir et al., 2023). Previous research has shown that the increase in the short chain fatty acid production is associated in this type of diet (Rauf Bedford, Alkhtib, Scholey, & Burton, 2024), but the associated microbial population changes have not been reported to date. The goal of this study is to determine the effect of enzymatic supplementation on caecal metagenomic profiles of broiler fed rye-based diet.

Materials and methods

Following ethical approval, 88 male Ross 308 broiler chicks in 8 floor pens (11 per pen) were fed wheat based mash starter diets designed to meet the requirements of the age and strain of the birds. On Day 10, birds were weighed and allocated to a 44.3% rye grower diet either without Enzymes (Diet A) or with an Enzyme Cocktail (Diet B) including mannanase (0.025 g/kg), xylanase (0.1 g/kg) and phytase (1 g/kg). Two birds per pen were euthanized on days 11,14,21,28, and 35. Caecal sample were analysed via 16s rRNA sequencing on Illumina MiSeq platform according to manufacturer instructions. There was no statistical test applied to find significant difference at phylum level while liner discriminant analysis (LDA) effect size (LEfSe) was used for significance at genus level.

Results

Figure 1 shows that at phylum level, Firmicutes, Actinobacteria and Bacteroidetes were dominant. The relative abundance of phyla changes over time with Firmicutes decreasing and Actinobacteria and Bacteroidetes increasing. The enzyme cocktail decreased the relative abundance of Proteobacteria up to Day 28. On the genus level, predominant taxa were Lactobacillus, Lachnospiracaceae and Faecalibacterium. The enzyme cocktail significantly ($P < 0.05$) increased the relative abundance of Lactobacillus, Oscillibacter and Clostridium IV compared to the control.

Conclusion

Enzyme cocktail addition to a high fibre diet increased the abundance of fibre utilizing genera and supresses pathogenic bacteria.

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Effect of scattering black soldier fly larvae on the litter on growth performance, gut development and active behaviour of fast and slow-growing broiler

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Application

Broiler farmers can offer black soldier fly larvae on the litter to mitigate the effect of inactivity on broiler leg health

Introduction

Broilers are prone to leg problems because of their level of inactivity. Black soldier fly larvae (BSFL) may improve broiler welfare by increasing physical activity and promoting natural behaviours (Ipema, Gerrits, Bokkers, Kemp, & Bolhuis, 2020). A promising delivery method is scattering dead BSFL on the litter which is expected to promote active behaviour in broilers. This study investigates the effect of dead BSFL scattered on the litter on growth performance, behaviour and gut development of fast and slow-growing broiler chickens.

Materials and method

All procedures were ethically reviewed and approved by the Nottingham Trent University School of ARES ethical review group (ARES1826455). A total of 320 day-old male broilers, 160 fast-growing (Ross 308) and 160 slow-growing (Hubbard JA757) were allocated to 32 pens (8 pens per treatment and 10 chickens per pen). The pens of each bird strain were assigned equally to either CTRL (standard broiler diet + 15 g/day whole BSFL offered in troughs) or SCAT (standard broiler diet + 15 g/day whole BSFL scattered on litter). The bird weight and feed intake of each pen were recorded weekly. Two birds/pens were sampled for gut morphometry at the end of the starter, grower and slaughter phase. The behaviour of the focal bird was recorded every 30 seconds for 5 consecutive minutes after insect delivery on days 8, 15, 22, 29, 36, and 42. The effect of broiler age, strain, treatment, and strain*treatment interaction on gut, growth and behavior data was analysed using ANOVA and the means were compared using Fisher LSD test at P = 0.05 with Bonferroni adjustment.

Results

As shown in Table 1, scattering BSFL on the litter significantly increased total active behaviours in both strains (P < 0.05) without negatively affecting growth performance (P >0.05). The treatment significantly increased foraging/eating behaviour of Ross308 (P < 0.05). Scattering BSFL on the litter had no significant effect on gut development (P > 0.05).

Table 1. Effect of scattering dead BSFL on the litter on broiler behaviour

Strain	Treatment	Total activity	Foraging/eating
JA787	Trough	10.3[a]	6.62
	Scatter	9.86[a]	6.55
Ross308	Trough	9.08[b]	5.84[b]
	Scatter	10.1[a]	7.73[a]
SEM		0.46	0.84
P value			
Age		0.06	<0.001
Strain		0.134	0.77
Treatment		0.591	0.173
Strain*treatment		0.018	0.072

[a,b]Means within a column with different superscripts differ significantly ($P \leq 0.05$).

Conclusion

Scattering BSFL on the litter promotes active behaviours in both broiler strains without adversely affecting growth performance and gut development, offering potential welfare benefits. The duration of this improved activity may be transient due to the quantity and frequency of BSFL provision, further study is needed to ascertain the potential benefit on leg health and litter quality.

Acknowledgement

Thanks to Hubbard for supplying the birds, with further funding support from Innovate UK project 10102294: Feed Flow, AI Enhanced Feed Ordering Systems and Sustainable Insect Protein Integration for Poultry Health & Welfare.

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Influence of xylooligosaccharides supplementation in broiler chickens

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Application

Poultry gut health may be enhanced by using low (stimbiotic) contrary to high (prebiotic) levels of xylo-oligosaccharides (XOS).

Introduction

It has been hypothesised that oligosaccharide generation in the gut is not as effective as when added directly in broiler diets (Morgan, Keerqin, Wallace, Wu, & Choct, 2019).

Besides a substantial range of inclusion rates used in trials, there is a lack of understanding of how poultry utilise XOS that varies in degrees of polymerisation (DP). The prebiotic effects of XOS are correlated to its chemical structure, with DP being regarded as one of the most impactful factors on its functional properties (Singh, Banerjee, & Arora, 2015). The DP of XOS used in supplementation studies is typically 2–7, however, some work has shown that a low DP (2–5 xylose units) could increase growth of lactic and Bifidobacterium bacteria (Reddy & Krishnan, 2016). The aim of the trial was to assess the role of using two different sources of XOS, with 2–6 and 2–9 DP, at two levels, 50 and 500 g/t, on growth performance, AME, AMEn, nutrient availability, ileal and caecal SCFA production and caecal microbiome variables of broilers fed xylanase supplemented maize-based diets.

Material and methods

The experiment was conducted at Harper Adams University (UK) and was approved by the University's Research Ethics Committee. A 35-day study was conducted with 540 day-old male Ross-308 broilers, distributed over 5 experimental treatments in 45 pens with 10 birds per pen and 9 replicates per treatment. Maize-soybean meal base diets were provided into two phases: starter (0–21d) and finisher (22–35d) and fed *ab libitum*. Compared to xylanase only control, two different sources of XOS with DP ranging from 2 to 6 or 2 to 9 and two doses of 50 (stimbiotic) or 500 (prebiotic) g/t were evaluated. Titanium dioxide (5 g/kg) was added as an inert marker in the meal. Body weight gain (WG) and feed intake (FI) were recorded and feed conversion ratio (FCR) calculated for the overall period. At day 32, four birds from each pen were allocated to a pen with a mesh floor and excreta were collected for the last three days for apparent metabolisable energy (AME), dry matter retention (DMR), and nitrogen retention (NR) determination. Following humane slaughter on day 35, caecal and ileal digesta samples from one bird randomly selected from each pen were collected in Biofreeze® tubes for the measurement of SCFA digesta. The caecal samples were collected for 16s ribosomal ribonucleic acid gene sequencing. The data were analysed in GenStat (21st edition) as One-way ANNOVA, and comparisons among the studied variables were performed by Duncan's multiple range test. At $P < 0.05$, differences were reported as significant.

Results

The overall addition of XOS compared to xylanase-only supplemented diets was shown to be efficient at improving production parameters. In the overall period, there was an increase of WG ($P = 0.031$, SEM 0.124; 69.16 vs 65.85 g/b/d) and an improvement of FCR ($P = 0.017$, SEM 0.0133; 1.527 vs 1.564 g/b/d), while the FI did not differ amongst the treatment diets ($P > 0.05$). The performance improvements could partially be attributed to improvements in ME and digestibility of nutrients, with XOS-supplemented diets increasing AME ($P < 0.001$, SEM 0.056; 13.68 vs 13.39), AMEn ($P < 0.001$, SEM 0.051; 13.24 vs 12.97), DMR ($P = 0.001$, SEM 0.0037; 0.787 vs 0.768) and NR ($P = 0.009$, SEM 0.0093; 0.715 vs 0.675) at 35 d. In this study, the lower inclusion levels (50 g/t) compared to higher inclusion rate (500 g/t) were shown to result in higher caecal levels of acetic ($P = 0.042$, SEM 5.88; 88.9 vs 76.6 mmol/kg), butyric ($P = 0.003$, SEM 1.72; 21.7 vs 11.7 mmol/kg), valeric acid ($P = 0.019$, SEM 0.10, 1.5 vs 1.3. mmol/kg), as well as SCFA ($P = 0.021$, SEM 7.49; 120.5 vs 102.5 mmol/kg) and VFA ($P = 0.016$, SEM 7.43; 118.6 vs 99.9 mmol/kg). No influence was observed on the ileal fermentation activity and the relative abundance of bacterial species in the caeca in this study.

Conclusion

The results of the study suggest that stimbiotic levels of XOS at 50 g/t may be enough to be incorporated in broiler chicken diets for optimal growth, digestibility improvements and SCFA production response in maize based diets.

Acknowledgments

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Feeding alternative proteins to maintain litter quality and leg health of slow growing broilers

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Application

Beans and peas are preferable to sunflower meal as a partial replacement of soybean meal in Redbro broiler diets

Introduction

High proportions of antinutritional factors in alternative proteins can lead to wet litter (Collett, 2012), which may induce footpad dermatitis, hock burn and reduce growth performance of broiler chickens (De Jong, Gunnink, & Van Harn, 2014). Inclusion of targeted enzymes may mitigate against this. The objective of this study was to assess the effects of alternative protein source and enzyme inclusion on growth performance, litter quality and leg health of Redbro broilers from 0–49 days of age.

Table 1. Effect of dietary protein source and enzyme inclusion on Redbro broiler performance and litter moisture at 49 d age

		d 0 BW (g)	d 49 BW (g)	ADG (g/b/d)	FI (g/b/d)	FCR	Litter moisture d 49 (%)
Diet	CON	45.1	2939.9	58.1[ab]	100.4	1.719	30.9[ab]
	BP	45.2	3024.7	59.9[b]	103.9	1.725	29.9[a]
	SUN	44.7	2913.3	56.9[a]	101.1	1.746	32.7[b]
SEM		0.31	39.89	0.80	1.28	0.0104	0.72
Enzyme	No	44.8	2980.0	58.7	102.3	1.725	31.0
	Yes	45.1	2938.5	57.9	101.2	1.735	31.2
SEM		0.25	32.57	0.65	1.04	0.0085	0.58
P value	Diet	0.457	0.137	0.044	0.140	0.189	0.027
	Enzyme	0.372	0.374	0.388	0.476	0.396	0.648
	Diet * Enzyme	0.570	0.686	0.949	0.933	0.422	0.172

Means within a column with the same letter are not significantly different (P > 0.05).

Materials and methods

The study was approved by Harper Adams University Research Ethics Committee. A randomised control experiment was performed using 650 day-old as-hatched Redbro broilers in a 2 × 3 factorial arrangement. Birds were allocated to 42 pens with 15 birds per pen and fed one of the 6 diets (7 replicates per treatment). All diets were isonitrogenous and isoenergetic and fed as pellets in four phases. The diets were a wheat-soybean meal basal (CON), a diet containing 155 g/kg beans and 180 g/kg peas in the final phase (BP), and a diet containing 120 g/kg sunflower meal in the final phase (SUN). Each diet was split into two parts and fed as is or supplemented with Ronozyme® Multigrain enzyme (DSM Nutritional Products Inc., Parsippany, NJ) at 100 g/tonne (2,700 U xylanase, 800 U cellulase, 700 U glucanases/g). Bird bodyweight (BW), feed intake (FI), average daily gain (ADG), feed conversion ratio (FCR) and litter moisture were determined. These data were analysed by two-way ANOVA followed by Duncan's test in GenStat® (version 23.1; VSN International Ltd). Foot pad and hock burn lesions were scored at day 49 and subjected to permutations and Pearson chi-square test in GenStat® (version 23.1; VSN International Ltd). Differences were reported as significant where P < 0.05.

Results

Mortality was less than 2% and average final BW was 298 g greater than performance objectives (2959 g vs 2661 g). As shown in Table 1, birds fed BP had greater ADG from 0–49 d than birds fed SUN (P < 0.05), however no significant differences in final BW, FI or FCR were observed (P > 0.05). Litter moisture was greater in SUN than BP treatments (P < 0.05). However, incidence of score 1 and 2 hock burn and foot pad lesions at day 49 were not significantly different between treatment groups (P > 0.05). Enzyme inclusion did not significantly impact any studied variables nor were any interactions observed (P > 0.05).

Conclusion

Partially replacing soybean meal in Redbro broiler diets with beans and peas was more suitable than sunflower meal due to improved weight gain and reduction in litter moisture at 49 days age although no difference in final BW was observed.

Acknowledgements

Thank you to Dr James Bentley for bird and feed sourcing. Funding was provided by the John Oldacre Foundation.

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Development of a sub-clinical avian colibacillosis model

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Application

A dose-dependent avian colibacillosis model would allow the study nutrient resilience under challenge and performance limiting conditions.

Introduction

Avian colibacillosis is an extra-intestinal poultry disease, caused by avian pathogen *Escherichia coli* (APEC), leading to high mortality or decreased performance and considerable financial implications, however only few studies report investigations with APEC oral gavage and so far not in a dose-dependent way (Foltz et al., 2017; Tobia & Ohimain, 2024). Experimental sub-clinical avian colibacillosis could therefore be used to investigate resilience both under a microbiological and nutrient absorption point of view. We have carried out an animal study in order to generate a performance-limiting model for broiler birds, based on oral inoculation with different concentrations of APEC resistant to nalidixic acid (Nal).

Materials and methods

Following ethical approval (SRUC AEX 2024–015 POU), 600 Ross 308 broiler chickens were housed in 40 pens, with 15

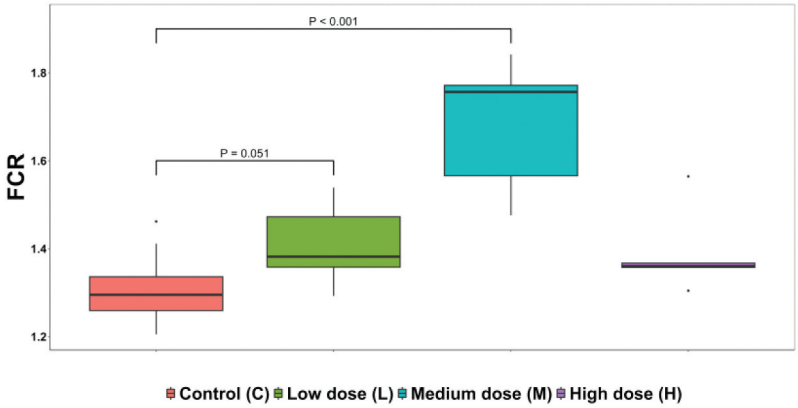

Figure 1. Day 7 APEC levels is correlated with the FCR at the end of the grower phase.

chickens per pen and 5 pens per treatment (35 days). There were 8 treatments in total, which were two infection time-points (d7 or d20) and four APEC challenge levels (oral gavage, 1 mL) being 0 (C), 10^3 (L), 10^6 (M) or 10^9 (H) CFU/bird. Birds were fed commercial rations, in meal form, during starter (d0-8), grower (d8-20) and finisher (d20-35) phase. Pen level body weight and feed refusals were measured every four days throughout the study to calculated average daily body weight gain (BWG), feed intake (FI) and mortality corrected feed conversion ratio (FCR) during each phase.

Results

APEC dose did not affect cumulative mortality (3.8% for the total trial).

D7 challenge led to no mortality in L and M, and in 0.3% and 0.5% post-infection mortality in C and H, respectively. In the D20 group, we observed no post-gavage mortality in C and M, 0.17% in L, and 0.83 in H.

APEC challenge at d7 but not at d20 significantly impacted performance. Grower FI and BWG were significantly smaller for M birds compared to C birds ($P < 0.05$), which persisted for FI into the finisher phase. Grower FCR increased for M but also for L birds but not for H birds (Figure 1; $P < 0.05$).

Conclusion

The sub-clinical impact of APEC challenge on performance was sensitive to the timing and level of APEC dose, as early challenge was impacting performance more consistently than later challenge, and unexpectedly the medium dose used showed a greater impact than the higher dose used, possibly due to an enhanced immune response. This sub-clinical APEC challenge model may be used to assess nutritional and genetic impacts on resilience and resistance to sub-clinical avian colibacillosis.

Acknowledgments

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Nutritional value of processed faba beans for broiler chickens

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Application

Processing can improve the nutritional value of faba beans and thus its soya bean meal replacement potential in poultry rations.

Introduction

Recent studies suggest that the upper limit of faba beans in broiler rations may be in the order of 15 to 20%, depending on the broiler breeds (Houdijk, Bentley, Walker, & Dixon, 2022). This level may increase if processing improves faba bean nutritional value. Here, we hypothesized that faba bean dehulling with or without subsequent toasting increases its standardised ileal amino acid digestibility (SID-AA) and apparent metabolizable energy content (AME).

Material and methods

Test feedstuffs were soya bean meal (SBM), whole faba beans (WFB), dehulled faba beans (DFB) or the latter toasted at

Table 1. Standardised ileal digestibility of selected amino acids and apparent metabolizable energy (AME) of soya bean meal (SBM), whole faba beans (WFB), dehulled faba beans (DFB) and differentially toasted dehulled faba beans (TFB)

Test feedstuffs	Toasting conditions		Standardised ileal digestibility (%)					
	Temp (°C)	Time (min)	Lys	Met	Thr	Trp	Val	AME (MJ/kg)
SBM	–	–	88.9^{a}	90.9^{ab}	79.9^{ab}	83.3^{ab}	85.9^{ab}	12.2^{b}
WFB	–	–	92.7^{ab}	87.6^{ab}	83.1^{ab}	81.1^{ab}	86.7^{ab}	13.2^{bcd}
DFB	–	–	95.4^{b}	92.2^{ab}	87.3^{b}	88.3^{b}	91.5^{b}	13.1^{bcd}
TFB1	175	1.3	95.2^{b}	92.9^{ab}	88.2^{b}	88.2^{b}	89.9^{ab}	10.8^{a}
TFB2	175	2.3	92.2^{ab}	95.8^{b}	89.6^{b}	91.9^{b}	93.0^{b}	13.8^{cde}
TFB3	200	1.8	96.6^{b}	95.9^{b}	91.6^{b}	92.1^{b}	92.9^{b}	15.1^{e}
TFB4	225	1.3	95.8^{b}	95.7^{b}	90.5^{b}	90.2^{b}	92.1^{b}	12.5^{bc}
TFB5	225	2.3	89.7^{a}	83.3^{a}	73.7^{a}	73.6^{a}	81.7^{a}	13.0^{bcd}
SEM			1.04	2.18	2.66	2.45	1.98	0.430

different temperature and duration (Table 1). These were used as sole protein source in semi-synthetic diets for SID-AA assessment and included at 30% in a wheat-SBM reference diet for AME assessment, with 0.5% titanium oxide as digestibility marker. These diets were fed for 6 days to 3-wk old male Ross308 broilers, placed on HO approved wired-bottom cages (n = 6 cages/treatment with 6 birds/cage). Essay diets, excreta collected over the last two days, and distal ileal digesta collected at trial end were analysed for titanium oxide and gross energy (for AME) and amino acids (for SID-AA). Basal endogenous AA flow previously derived (Adebiyi & Olukosi, 2015) was used to calculate SID-AA. Resulting test feedstuff SID AA (%) and AME (MJ/kg) were analysed through ANOVA, using Tukey-adjusted multiple comparisons to locate treatment effects ($P < 0.05$). SRUC's ethical review approved this study (AEX 2024–006 POU).

Results

Table 1 shows that the TFB3 treatment provided the highest SID-AA and AME, outperforming raw feedstuffs such as SBM and WFB. Whilst the lower toasting intensity in TFB1 and TFB2 generally failed to improve nutritional value, the TFB5 treatment, which provided the greatest toasting intensity tested reduced SID-AA but not AME, relative to DFB.

Conclusion

This data supports the view that dehulling and toasting of faba beans increases SID AA and AME to levels generally greater than in SBM. Combined with a greater concentration of AA arising from dehulling per se, and an anticipated reduction in anti-nutritional factors, this suggest that processing dehulled faba beans at intermediate toasting intensity allows for more faba bean feeding to broiler diets, and thus increase the soya replacement potential of faba beans.

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Do activity sensors identify behavioural change in laying hens after a vaccine challenge?

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Application

Sensors can detect changes in hen activity, which may be useful in the early detection of disease, such as avian influenza.

Introduction

Previously, we demonstrated that using a live vaccine stimulated measurable clinical symptoms in laying hens without inducing disease (Kang, Haskell, & Sandilands, 2023). Here, we examined if sensors FitBark (FitBark Inc., USA) and TrackLab (Noldus Information Technology, Netherlands) could detect changes in activity and/or distance travelled due to vaccine challenge.

Materials and methods

This work was approved by SRUC's animal ethics committee. Five batches of previously unvaccinated laying hens were used. With each batch, on day 1, four hens were brought from the home pen to an experimental room, where they were each fitted with two sensors held together with electrical tape and looped over the shoulders with string. Hens were placed into a concrete-floor room, in the centre of which was a central litter zone (35 m^2) which held nest boxes, perches, a feeder and drinker. On day 3, all hens were treated with saline. On day 6, all hens were treated with live Infectious Laryngotracheitis (ILT) vaccine (Poulvac®, Zoetis, UK), to stimulate sickness-type changes in physiology and behaviour. Hens were video recorded for 24 h per day x 12 days. Data on day 1 was ignored. Data were analysed by Linear Mixed Models in R.

Results

Mean activity level (FitBark) and distance travelled (both sensors) significantly decreased over days (all $P < 0.001$), with an increase between day 11–12 for FitBark (Figure 1).

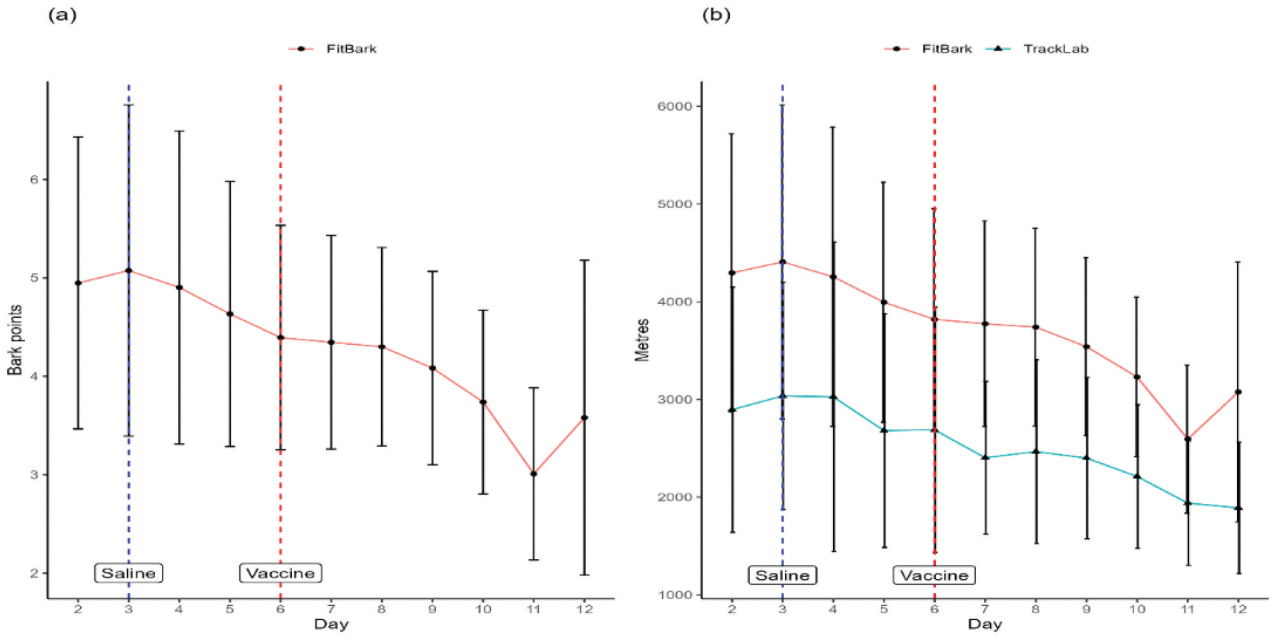

Figure 1. (a) mean (±SD) activity level (in 'Bark points') recorded by FitBark; (b) mean (±SD) distance travelled (in metres) recorded by FitBark and TrackLab over days 2–12. The days on which saline and a live vaccine were administered to birds are indicated.

Conclusion

The two sensors detected changes in activity and/or distance travelled over days, which may have been due to the vaccine challenge, however reductions were apparent before day 6 (when the vaccine was applied). It may be that hens need longer than three days (when saline was applied) to acclimatise to the changed environment before settling into normal behaviour.

Reference

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Effect of diet density on production parameters and body condition of laying hens measured utilising a novel non-invasive Near-Infrared tool

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Application

This research discusses a novel non-invasive method to assess the body condition of a laying hen. This enables producers to better meet the nutritional requirements of their animals for improved production efficiency and sustainability parameters of their operations.

Introduction

Body composition of laying hens is influenced by diet and may have long-term effects on egg production and efficiency (van Eck, Enting, Carvalhido, Chen, & Kwakkel, 2023). It is therefore important to understand how diet influences body composition in hens. Recent developments have made it possible to measure laying hen body composition non-invasively using Near-Infrared (NIR) spectroscopy. This technique was used in the current study to evaluate the effect of dietary energy (low, medium and high) on egg production and fat deposition in laying hens during early lay.

Materials and methods

A total of 324 Dekalb White hens were divided over 24 experimental units with 9 hens each. At 17 weeks of age, the hens were housed at the Cargill Animal Nutrition Innovation Center (Elk River, Minnesota, USA). Three experimental diets (8 replicates/diet) were fed from 17 to 30 weeks of age in 2 feeding phases, with a diet change at 20 weeks of age. The diets were formulated to have three ME levels (phase 1 low = 2650 kcal/kg, medium = 2750 kcal/kg and high = 2850 kcal/kg; phase 2 low = 2700 kcal/kg, medium = 2800 kcal/kg and high = 2900 kcal/kg). All other nutrients were standardized between treatments. Before diet formulation, batches of corn, wheat, wheat bran by product, soybean meal and canola meal were analyzed. Eggs were collected daily and egg weights and average feed intake (ADFI) were measured weekly. In week 17, 21, 25 and 30, individual body weight and fat pad weights (using the NIR tool: REVEAL^{TM} Layer) were measured. Data were analyzed using pen as the experimental unit and subjected to mixed model analyses, using R version 4.1.1. Contrast statements were applied to measure linear and quadratic effects. All procedures were approved by the Cargill Animal Nutrition

welfare committee, in accordance with US laws and regulations on the execution of animal experiments.

Results

Hens started laying eggs at 17 weeks of age and increased to an average laying rate of 94.6% at 25 weeks of age, without any dietary effect (P >0.05). Egg weights were quadratically increased by dietary energy only in week 17 to 20 (quadratic effect P <0.05), but were no longer affected after week 21. In week 21 to 30, ADFI was linearly decreased by diet density, with a 3.7 g lower ADFI intake of hens fed the high compared to the low energy diets (linear effect P <0.05). Due to the similar egg mass production in the current study, but a lower ADFI, the feed conversion ratio (FCR) was linearly reduced with increasing diet density (linear effect P <0.05).

Body weight and gain were not affected by diet density (P >0.05), but body composition was significantly different. Hens fed the higher energy diets linearly increased abdominal fat pad weights in week 21 and 30 (linear effect P <0.05). Energy intake was also linearly increased with diet density, despite the lower ADFI of hens fed the higher energy diet.

Conclusion

The increased abdominal fat pad weights were probably caused by the higher energy intake, and indicate that dietary energy was oversupplied in the high energy diets. These data suggest that REVEAL^{TM} Layers can be used to monitor the impact of diet on fat pad, allowing nutritionists a tool to evaluate dietary manipulations that may impact persistency as suggested by Milisits et al. (2015) and Bédère et al. (2024).

In conclusion, a high dietary energy during early lay reduces ADFI, does not influence egg production or body weight but does increase abdominal fat deposition in laying hens. The NIR tool is helpful to understand the impact of diet on body composition of the hen which can inform dietary decisions in the long term to help maintain a composition that supports productivity of hens.

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Investigating beak shape variation during puberty in male and female layer chickens

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Application

The diversity of beak shapes observed within layer hen populations raises interesting questions about how and when these variations arise and how they may affect undesirable behaviours such as injurious feather pecking.

Introduction

Significant heritable variation in beak shape exists within and between breeding laying hen lines (Icken, Cavero, & Schmutz, 2017; Struthers et al., 2023). Struthers (2023) found a genetic relationship between beak shape traits and egg production suggesting that egg production decreased with maxillary beak shortening and accentuated curvature. The reason for this genetic relationship is not clear. It is possible that an increase in gonadal steroid production at the onset of puberty may influence beak shape development. Dalton, Wood, Widowski, Guerin, and Torrey (2017) found sexually dimorphic beak shapes in male and female turkeys. However, sexually dimorphic differences in layer beak shape and its *post ovo* growth during sexual maturity have not been extensively investigated. Therefore, the objectives of this study were to investigate how beak shape changes at the onset of and throughout puberty and whether there is an effect of sex on that process.

Material and methods

This study was approved by the Animal Welfare and Ethical Review Body at the Roslin Institute (University of Edinburgh). Thirty Hy-Line Brown hens and twelve Hy-Line Brown roosters were used in this study. Lateral head photographs and body weights were collected from the birds at 14, 16, 18, 20, 22, and 24 weeks of age. From the images, the maxillary beak was landmarked in ImageJ using 20 landmarks. The landmark coordinates were imported into R for geometric morphometric analyses using the package Geomorph. Procrustes superimposition was used to standardise all the landmarks in each image by superimposing, rescaling, and rotating them to a common orientation. The covariation of the transformed landmarks was analysed using principal components analysis and multivariate regression. The Procrustes superimposition also created an average beak shape by identifying the centre point (centroid) of all the landmarks in each image. The centroid beak size was used as a proxy for relative size. Differences were considered significant when $p \leq 0.05$.

Results

Two principal components (PCs) explained over 75% of the total maxillary beak shape variation. PC1 (56%) described maxillary beak length. The sexes were partially separated by PC1 pre- and post-sexual maturity with males tending towards shorter beak lengths. PC2 (21%) described

beak tip curvature with no noticeable separation between the sexes being observed. Age had a significant effect on beak shape; however, the main axes of beak shape variation were consistent throughout puberty. With time, the shape traits described by the two PCs became more exaggerated (e.g. the beak tip became more curved as the birds aged). Multivariate regression revealed that beak size was significantly associated with its shape at all ages. A moderate correlation was found between beak size and body weight (r_s = 0.40, p < 0.01) with males having heavier body weights and therefore, larger beaks; however, within each sex, beak size did not appear to vary considerably between the ages.

Conclusion

The results of this study suggest that the main axes of maxillary beak shape variation (length and curvature) remained consistent throughout puberty and beak shape traits do not appear to be significantly influenced by the onset of sexual maturity. Sexual dimorphism in maxillary beak shape was observed with male birds having larger but shorter maxillary beaks and females having smaller but longer beaks. The results of the present study are similar to what was described in commercial turkeys.

Acknowledgments

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The effect of dietary protein level and enhanced vitamin/mineral supplementation on egg production and quality during an extended laying cycle

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Application

Egg production and quality reduces with age, but lower CP diets can be offered with no loss of production which will reduce N excretion.

Introduction

The industry is striving to extend laying cycles, delaying depopulation beyond 75 weeks of age (WOA). There is also interest in lowering dietary crude protein (CP), reducing the environmental footprint of egg production (Viana, Stringhini, Carvalho, Viana, & Costa, 2017). Effects on egg production and quality during extended lay are unclear and may be ameliorated by enhanced vitamin/ mineral supplementation. This study examined both dietary factors in aged hens.

Materials and methods

The study was approved by the Animal Welfare and Ethical Board at AFBI. Lohmann layers (N = 240) were housed in groups of 16 in furnished cages. Four groups were allocated to each of four dietary treatments, to investigate the effect of CP levels (14.5 vs. 13%) and type of vitamin/mineral premix (standard vs. enhanced) in a factorial setup. The enhanced premix included 1600 IU Vit D3 + 1600 hyD, 80 IB Manganese + 20 oxide, 60 IB Zinc + 20 oxide, 0.1 selenite + 0.15 Optimum Se and 300 g Ca pidolate. The standard premix diet included 3200 IU Vit D3, Manganese 100 oxide, Zinc 80 Oxide, 0.25 Selenite and no Ca pidolate. Data were obtained between 75 and 100 weeks, with egg production and weight recorded daily, and egg quality assessments every 5 weeks (four eggs/treatment/time period). Results were analyzed using linear mixed models.

Results

As age increased, shell weight, albumen height, and shell thickness decreased (P <0.001). However, the pattern of decrease was erratic for some variables, showing temporary increases around 85 WOA (Table 1), possibly due to the beginning of new clutches in the laying cycle. Low CP (13%) reduced egg and shell weight whereas the enhanced

Table 1. Effect of age, premix (E = enhanced, S = Standard) and crude protein (14.5% vs 13%) on egg quality

	75	80	85	90	95	100	sed	14.5	13	sed	E	S	sed
Albumen height (mm)	5.0	5.4	5.7	4.5	4.5	4.7	0.3	5.1	4.9	0.3	5.1	4.8	0.3
Egg break force (N)	47	44	44	47	42	44	2	45	45	1	45	44	1
Egg weight (g)	65	65	65	65	66	66	1	67	64	1	66	64	1
Shell thickness (µm)	388	412	410	392	377	390	5	394	396	3	397	393	3
Shell weight (g)	6.7	6.6	6.8	6.4	6.3	6.4	0.1	6.6	6.4	0.1	6.6	6.4	0.1

premix increased both, by approximately the same amount (P <0.05). Enhanced premix numerically improved albumen height, shell weight, egg weight and egg break force, however numerically decreased egg production (P >0.10). Diet had no effect on egg production, which decreased with age (P <0.001). Average production was 82.5 ± 2.63% at 75–80 weeks and 62.7 ± 2.63% at 95–100 weeks. No interactions were observed.

Conclusion

As hens aged, egg quality declined although not uniformly. Including the enhanced pre-mix had no significant effect possibly due to the age of the hens when offered the enhancement. Further research should aim to understand the welfare implications of maintaining production over the extended laying cycle. Lower CP resulted in reduced egg and shell weight, but production performance was maintained, suggesting that late-stage diets could be lowered in CP, which will reduce N excretion in the late laying period.

Acknowledgment

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The performance, digestibility and ammonia production of current *versus* historic genetic broilers

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Application

Genetic selection for faster growing more efficient broilers has reduced ammonia emissions per target weight bird (2.2 kg).

Introduction

Advancements in broiler selection and nutrition has resulted in a reduction in the number of days and the amount of feed required for broilers to achieve the target weight. Zuidhof, Schneider, Carney, Korver, and Robinson (2014) reported that from 1957 to 2005, growth rate and food conversion ratio (FCR) improved by 400% and 50% respectively. However, the impact of these genetic improvements on ammonia emissions has never been quantified. The aim of this trial was to directly quantify and compare the growth performance, nutrient digestibility and ammonia emissions of historic genetic broilers with current genetic birds.

Material and methods

This work was approved by the Animal Welfare and Ethical Review Board at AFBI. Day-old broilers of current Ross 308 genetics (Current: n = 90) and historic Ross 1996 genetics (Historic: n = 90) were weighed and assigned into one of six respiration chambers according to treatment (30 birds/chamber). This was repeated over two time periods giving six chambers/treatment. Diets were provided *ad libitum* and formulated to meet breed requirements. Treatments included; 1) Current broilers offered current diets (wheat and soyabean meal diet) and 2) Historic broilers offered historic diets (wheat, fishmeal, meat/bone meal, soyabean meal diet). Starter formulations of each diet were provided from 0d to 11d (Historic: ME 12.9 MJ/kg, CP 24% Lys 1.4%, Current: ME 12.6 MJ/kg, CP 23%, Lys 1.44%) grower diet formulations were provided 11d to 21d (Historic: ME 13.4 MJ/kg, CP 22.1% Lys 1.27%, Current: ME 13.0 MJ/kg, CP 21.3%, Lys 1.28%) and finisher diet formulations from 22d to 35d (Historic: ME 13.7 MJ/kg, CP 19% Lys 1.15%, Current: ME 13.4 MJ/kg, CP 19.1%, Lys 1.15%). Ammonia (NH_3) output was measured from each individual chamber every 15 minutes up to 30d and emissions calculated (g/bird/day, extrapolated to 2.2 kg target weight). Feed intakes (FI) and bird weights were recorded at 11d, 21d, 27d and 35d and used to calculate average daily gain (ADG) and FCR. At 21d, three birds/chamber were randomly selected to collect ileal contents to determine digestibility of amino acids.

Results

Current birds were larger initially (44.7 vs 35.7 g, SEM 0.47, P <0.001), throughout (11d; P <0.001, 21d; P <0.001, 27d; P <0.001) and by the end of the trial (35d; 2138.5 vs 891.4 g, SEM 28.34, P <0.001). Current birds also showed increased FI (0–35d; 3061.7 vs 1599.9 g, SEM 19.15, P <0.001), and improved FCR (0–35d; 1.47 vs 1.87, SEM 0.023, P <0.001) in comparison to historic birds. Ileal digestibility at 21d was improved in Current birds compared to Historic birds; lysine (0.94 vs 0.92, SEM 0.006, P <0.05), methionine (0.95 vs 0.92, SEM 0.005, P <0.05), threonine (0.87 vs 0.83, SEM 0.009, P <0.01), valine (0.87 vs 0.85, SEM 0.009, P <0.05), leucine (0.90 vs 0.88, SEM 0.007, P <0.01), isoleucine (0.89 vs 0.86, SEM 0.007 P <0.01), arginine (0.93 vs 0.89, SEM 0.007, P <0.01) and tryptophan (0.89 vs 0.86, SEM 0.001, P <0.05). The average NH_3 produced per day for current and historic birds is presented in Figure 1. The ammonia produced was significantly greater in Historic birds than Current birds (0.079 vs. 0.061 g/bird/day, SED 0.0036, P <0.001 and total 5.55 vs. 2.15 g/bird, SED 0.127, P <0.001 respectively) when data was extrapolated to the end of the production cycle (target weight of 2.2 kg,35d for Current birds and 70d for Historic birds).

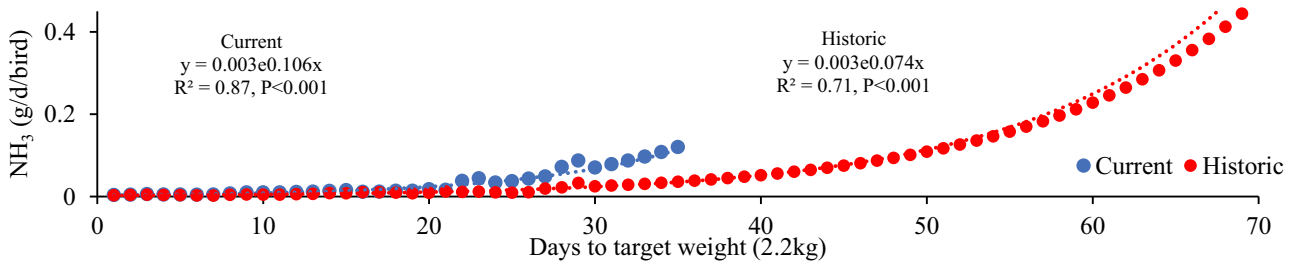

Figure 1. The average ammonia produced (g/d/bird) by current and historic genetic birds to reach a 2.2 kg target weight.

Conclusion

Current genetic birds grew faster and reached target weights in less days than Historic genetic birds. This is due to increased FI and greater digestibility and utilisation of various nutrients (Tavárez & Solis de Los Santos, 2016). It was also observed that Current genetic broilers produced less NH_3 (g/bird/day) in comparison to Historic genetic birds. Genetic selection of broilers has been successful in producing more efficient broilers and consequently, reducing NH_3 emissions on a per bird basis.

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Intra-egg variation in cuticle coverage on domestic hens' eggs, a risk for bacterial penetration.

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Application

Egg cuticle deposition is being used as a trait to limit vertical transmission of pathogens. However, variation in cuticle deposition is a potential risk. This study looks at line differences in intra-egg cuticle variance as a prelude to genetic studies.

Introduction

In studies looking at genome-wide association for cuticle it was observed that up to 29% of eggs displayed a mottled or swirled cuticle, making quantitative measurements difficult (Wang et al., 2023). The regions of the egg with limited cuticle are likely to increase the risk of bacterial penetration of eggs (Bain et al., 2019). In this study we estimated the amount of variance within an egg for cuticle coverage to discover if there were differences between pure lines of egg layers for intra-egg variance.

Material and methods

One tray (n = 30) of eggs from individual hens were collected from 11 different lines of pedigree layers; 6 brown and 5 white egg layer lines. No experiment was performed and the eggs were simply collected as part of normal production. All eggs (brown and white) were treated with a cuticle-specific dye, dried and CIELAB colour space (L*a*b*) measurements were performed using a Minolta cm-2600d hand-held spectrophotometer at 6 separate sites for each egg. The mean ΔE*ab which is the cuticle deposition and its standard deviation were calculated for each egg. The standard deviation was used as a trait, which we have called 'intra-egg standard deviation', and was analysed using an analysis of variance with line as a factor. The intra-egg standard deviation and cuticle deposition data were transformed prior to analysis to approximate to normality.

Results

The intra-egg standard deviation differed significantly between lines ($P < 0.001$). The intra-egg standard deviation varied from 1.56 ± 0.81 for line 8 to 3.32 ± 1.83 for line 5. There were also differences in the cuticle deposition ($P < 0.001$). Line 9 had the least cuticle deposition with 25.30 ± 4.54 and line 5 the most 30.11 ± 5.74. There was no relationship between the amount of cuticle deposition on an egg and the intra-egg standard deviation ($F = 0.977$).

Conclusion

The fact that there are differences between the genetic lines of hens for the trait of intra-egg cuticle deposition standard deviation suggests that there is likely to be a genetic basis to the trait. The differences between the lines for cuticle deposition, where we already know the heritability is around 0.38 (Dunn et al., 2019) augers well for the derivation of favourable intra-egg standard deviation genetic parameters. The complete absence of any relationship between the cuticle deposition and the level of variance suggests that the latter is not related to the amount of cuticle deposition and suggesting the two are independent traits. Reducing the intra-egg standard deviation alongside maintaining cuticle deposition should lead to less transmission of potential pathogens from mother to offspring and reduce the need for antimicrobials in production.

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Effect of novel phytase, varying doses and combination with carbohydrase enzyme to reduce carbon footprint per kg of broilers

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Application

Animal production has an impact on environment. Different feed additives like phytase and carbohydrase can help to reduce carbon footprint (CFP) per kg of body weight gain (BWG).

Introduction

Carbon footprint of agriculture has received lots of attention recently. Improving feed efficiency, digestibility of raw materials, health of animals, reducing mortality and rejections at slaughterhouses are needed to help meaningful reduction of CFP of broiler productions. Since feed accounts more than 70% of the total CFP for broiler production, modulating diets with the benefit of effective enzymes could help reducing CFP. A recent phytase (novel consensus bacterial 6-phytase variant, PhyG) has shown improving performance and consequently the overall profitability. However, their impact on CFP was not reported before which is analysed and shown in this study. With this background three trials data in broilers were used, 2 trials were conducted in the USA (Texas A&M University), and one at University of Sydney.

Material and methods

Total of 5236 birds were utilized in three separate studies. The experiments conformed to European Union guidelines on animal treatment, management, and housing husbandry. General setup of the trials were 8–12 replicates with 15–24 birds per pen. Diets consisted of mainly corn, wheat, soybean meal and other common ingredients. Positive control (PC) diets were manufactured with nutrients meeting the requirements of breeds (Ross 308 in two studies and Ross 708 in one study). Negative controls diets were below the specifications based on the enzymes dose (PhyG, used at 500–1000 FTU/kg diet, or 1000–3000 FTU/kg diet). The addition of phytase was based on the mineral matrix, full matrix (minerals, energy, and digestible amino acids) or utilized to remove added inorganic phosphate from the diet. In one treatment, an NSP enzyme (xylanase at 2000 U/kg feed) was added in addition to phytase. Performance was measured at starter, grower, and finisher phases (10, 21, 36 days). One trial continued till 63 days where performance was also measured till day 63. Carbon footprint (CFP) of feed was calculated using Feed Print tool of Wageningen university 2020. CFP per phase (starter, grower, finisher 1,2 and 3) were calculated and then CFP/kg BWG was calculated based on feed intake and divided by liveweight gain during all studies.

Results

In the first study (Sobotik et al., 2022), compared to PC, addition of phytase reduced CFP/kg BWG (4 vs 3.9 kg CO2eq/kg BW – 3%). Similarly in the same study increasing the dose from 500 FTU to 1000 and 1500 FTU further reduced CFP by 0.8% in each step. This study was conducted till day 63, feed intake, BWG and feed conversion ratios were similar to PC (data not shown). A comparison showed that raising birds till day 63 increased CFP by more than 17% compared to when birds are kept at 35 days (3.9 vs 3.2 kg CO2eq/kg BW). Another comparison between 35 and 42 days showed that by slaughtering at 35 days compared to 42 days, the CFP is reduced by 8% (3.5 vs 3.2 kg CO2eq/kg BW). In the second study, phytase at 1000 FTU/kg completely replaced monocalcium phosphate and this trial showed CFP reduction of 1.8% (2.91 vs 2.86 kg CO2eq/kg BWG). Additionally, another treatment that used different dose of phytase at 3000–2000-1000 FTU/kg in starter, grower, and finisher respectively reduced CFP of 6.2% compared to PC (2.91 vs 2.73 kg CO2eq/kg BW). Combination of phytase at 2000 FTU/kg with 2000 units of xylanase/kg diet with downspec in energy and digestible amino acids resulted in 6% reduction of CFP compared to PC (2.91 vs 2.74 kg CO2eq/kg BW). In the final trial, lowering crude protein level was utilized as a strategy to reduce CFP. When using typical crude protein diets (235–215-195 g/kg CP in starter, grower, and finisher respectively), addition of a single enzyme did not result in reduction of CFP. Lowering CP levels in diets (215–195-175 g/kg CP in starter, grower, and finisher respectively) reduced CFP (3.2 vs 3.03 kg CO2eq/kg BW – 5.9%) compared to higher CP diets. Also, the addition of phytase to reduced CP diets resulted in further reduction of CFP (3.03 vs 2.99 kg CO2eq/kg BW – 1.5%).

Conclusion

These three studies show that addition of a novel phytase with Application of full matrix or total replacement of added MCP, can help to reduce CFP/kg of BWG. Higher

doses of phytase alone or with the addition of carbohydrase enzyme can help further reduction of CFP. Reduced crude protein diets can also reduce the CFP.

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Integrative omics reveals distinct metabolic and microbial signatures in broilers under coccidiosis interventions

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Application

Our results show metabolite-microbiome interactions that could inform the design of targeted gut health interventions or feed additives, such as probiotics, to improve maintenance of gut health and host performance. Identified metabolites can also serve as biomarkers for gut health after coccidiosis interventions.

Introduction

Coccidiosis, caused by *Eimeria* spp., is a widespread and economically important enteric disease in poultry (Blake et al., 2020). Ionophores and vaccination are primary strategies for managing coccidiosis, with significant effects on gut microbial communities and metabolic pathways. Metabolomics is a valuable tool for exploring these effects by identifying bacterial and host-derived metabolites as biomarkers of intervention success (Vernocchi, Del Chierico, & Putignani, 2016). This study examines how coccidiosis interventions influence the caecal metabolome, providing a deeper understanding of their impact on gut health.

Materials and methods

With approval from the LSHTM Animal Welfare and Ethical Review Body (Reference 2023–5), 6,000 Ross 308 day-old chicks were randomly assigned to two treatments, each with six replicates of 500 birds per pen in an automated house. Broilers were fed a standard maize-soybean diet supplemented with ionophores (T1) or in-ovo coccidiosis vaccination (T2). Content of paired caecal samples (10 per group) were collected on day 40 and sent to BGI (Beijing, China) for untargeted metabolomic analysis using liquid chromatography-mass spectrometry. Data were normalised via the probabilistic quotient method, analysed using Sparse Partial Least Squares Discriminant Analysis (sPLS-DA) (Rohart, Gautier, Singh, & Cao, 2017), and integrated with previously obtained metagenome data through DIABLO (Singh et al., 2019). Statistical analyses were conducted in R v4.4.1.

Results

Discriminative analysis generally revealed metabolites classified as prenol lipids (such as Soyasaponin III, (2S,3S,4S,5 R)-3,4,5-Trihydroxy-6-(5-methyl-2-propan-2-ylphenoxy)oxane-2-carboxylic acid and saikosaponin B1) as robust markers for T1, while indoles and derivatives (2-oxindole and 5-methoxyindole) were identified for T2 (Table 1). G10: *Bacillus fragilis* had the greatest impact on the metabolome, exhibiting a positive correlation with up to 241 metabolites, whilst G77: *UBA3818* spp. (Ruminococcaceae) exhibited the greatest number of significant negative relationships metabolites (n = 22).

Conclusion

Overall, our results indicated that differences in coccidiosis control elicit diverse metabolic events in broilers through its influences on nutrient breakdown, affecting both the performance and health of broilers and may provide novel insights for gut health interventions against *Eimeria* spp.

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Table 1. Most robust metabolite biomarkers identified through sPLS-DA (with stability > 0.90)

ID	Metabolite Name	Class	Group	Stability	Importance
C4316	(2S,3S,4S,5 R)-3,4,5-Trihydroxy-6-(5-methyl-2-propan-2-ylphenoxy)oxane-2-carboxylic acid	Prenol lipids	T1	1	0.44
A1176	Soyasaponin III	Prenol lipids	T1	1	0.33
C861	5-Methoxyindole	Indoles and derivatives	T2	0.98	−0.33
A971	2-(4-methylphenyl)-5-(3,4,5-trimethoxyphenyl)-2 H-1,2,3,4-tetraazole	Azoles	T1	0.98	0.29
C2900	Soyasaponin III(-)	Prenol lipids	T1	0.94	0.27
C1885	Anabaenopeptin B	Carboxylic acids	T1	0.92	0.25
C4537	saikosaponin B1	Prenol lipids	T1	0.92	0.28

Effect of *Clostridium perfringens* challenge on jejunal gene expression in broiler chickens

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Application

Gene expression upon challenge *in vivo* with *Clostridium perfringens* and *in situ* with *C. perfringens* toxin may not correlate.

Introduction

Necrotic enteritis (NE), caused by *Clostridium perfringens (C. perfringens)* is an important disease affecting broilers. A previous *in situ* study identified differentially expressed host genes involved in growth regulation (NBL1), apoptosis (FAS), immune response (BL-A) and immune system development (GIMAP8) in response to *C. perfringens* crude toxin exposure (Athanasiadou et al., 2011). This small-scale study was conducted to assess the effect of *C. perfringens* challenge on the differential expression of such genes under natural infection conditions and their variation across different broiler breeds.

Materials and methods

A total of 45 day-old male broiler chickens were assigned to three groups (two Ross 308 and one Hubbard) with nine floor pens with 5 birds each. Challenged birds (Ross 308 and Hubbard) fed a diet mixed with *C. perfringens* culture (1.50 x 10^9) on days 17, 18 and 19. Control birds (Ross 308) fed diet mixed with sterile brain heart infusion broth (n = 3 pens per treatment). On day 18, all birds were orally gavaged with anticoccidial vaccine at 10 times the recommended dose. On day 21, jejunal gene expression of NBL1, BL-A, FAS, and GIMAP8 (normalized to ß-actin) was measured using comparative quantitation with MxPro software (Stratagene). Analysis of variance (ANOVA) was used to determine impact of challenge and breed. The college ethical committee approved the experiment.

Results

Figure 1 shows that *C. perfringens* challenge did not alter the expression level of the gene transcripts (NBL1, BL-A, FAS and GIMAP8).

Conclusion

This data may support the view that host transcriptomic response may differ between natural infection and controlled toxin exposure models for *C. perfringens* challenge. However, in agreement with an apparent lack of effect of challenge or breed on gene expression, very few birds (2/15 Ross308 and 1/15 hubbard) had sub-clinical NE lesions. These outcomes have paved the way for more extensive studies into changes in gene expression analysis in response to experimental sub-clinical NE.

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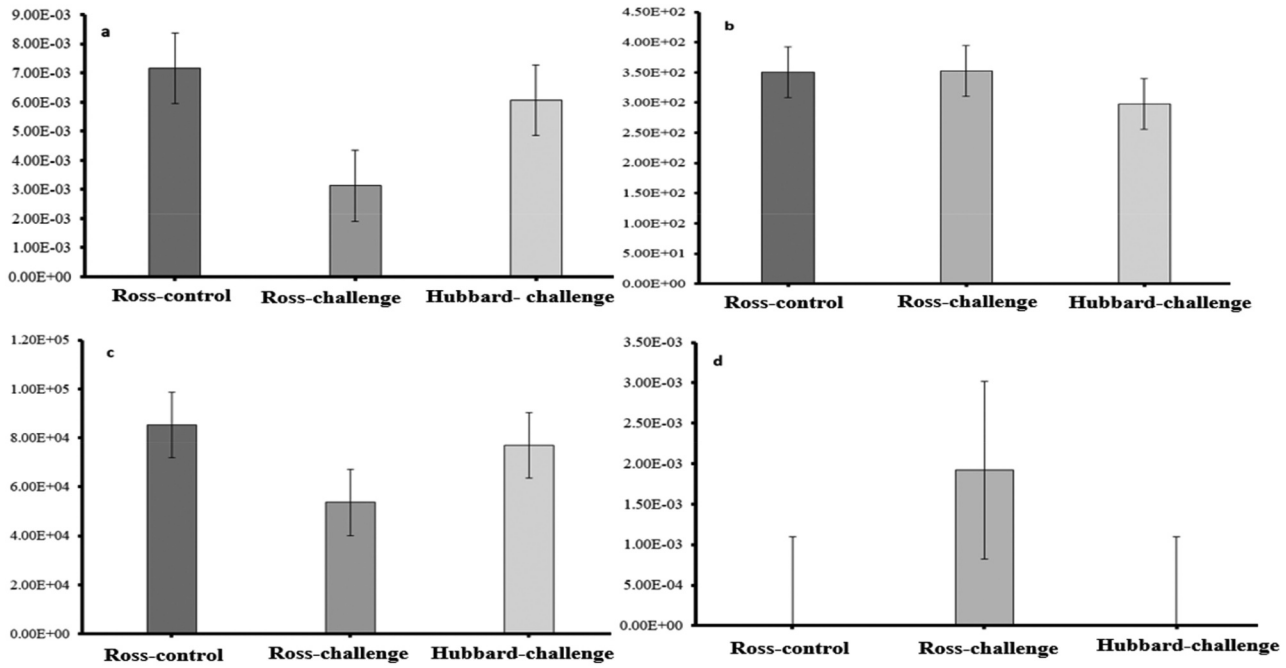

Figure 1. Effect of experimental challenge with *C. perfringens* on relative expression of (a) NBL1 (b) BL-A (c) FAS (d) GIMAP8 in intestine of broiler chickens.

Replacing fishmeal for farmed marine protein in starter broiler rations safely improves growth performance

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Application

Farmed marine protein (Artemia meal) has great potential to be an alternative protein source for young broilers, providing a viable and environmentally friendly alternative to fish meal.

Introduction

Artemia meal has gained attention as a potential substitute for fish meal due to its rich nutrient profile, which includes essential amino acids, lipids, and minerals (Meenatchi et al., 2024). Here, we evaluated the effects of replacing fish meal with different inclusion levels of Artemia meal in broiler diets on growth performance, immune organ weights and blood biochemistry.

Material and methods

Ross 308-day-old male broilers were placed in 24 pens (18 birds/pen) for a 35-day feeding trial with six isoenergetic dietary treatments (n = 4), in which Artemia meal stepwise replaced fishmeal on a digestible lysine basis from 0 to 5% levels during the starter phase (0–10 days), followed by standard grower and finisher diets. Growth performance was assessed at the end of each phase. At day 10 and 35, serum samples collected were analysed for electrolytes, and at day 35, relative spleen and bursa weights were recorded from 2 birds per pen. Data were analysed through ANOVA with linear and quadratic orthogonal polynomial to assess effect of Artemia meal inclusion level and using Tukey-adjusted multiple comparisons to locate treatment effects (P <0.05). SRUC's ethical review approved this study (AEX 2024–009 POU).

Results

Table 1 shows that replacing fishmeal for Artemia meal in the starter phase resulted in a significant quadratic effect on body weight (BWT), with the data suggesting that the maximum response was already observed at 2% Artemia meal. The presence of a linear effect throughout the trial indicated a positive carry-over effect of Artemia meal until trial end, with the greatest mean BWT observed at 3% and 5% Artemia meal. No significant effect was observed for feed conversion ratio, which averaged 1.17 ±0.026 during the starter phase, and 1.40 ±0.072 over the total trial, though feed intake increased linearly with increasing Artemia meal inclusion levels during the starter phase from 267 to 295 g for 0 and 5% Artemia meal, respectively (SEM: 5.74 g; P = 0.004). Artemia meal feeding did not affect serum electrolytes (P >0.05), which were within the normal range and averaged 144.8 ±6.70 mmol/L, 9.09 ±1.86 mmol/L and 102.3 ±4.93 mmol/L for Na, K and CL, respectively on day 35. In addition, Artemia meal inclusion did not affect immune organ relative weights (P >0.05) and averaged 0.09 ±0.018 and 0.20 ±0.009 for spleen and bursa, accordingly.

Conclusion

The inclusion of Artemia meal during the starter phase as a replacement for fishmeal enhanced growth performance throughout the trial, demonstrating a beneficial carry-over effect without negatively affecting other health indicators. This benefit was likely attributed to Artemia meal's richer oil content; particularly high levels of essential fatty acids may have supported growth and overall health. Thus, Artemia meal presents a considerable promising alternative that could bring back and advance on benefits traditionally obtained from the use of fishmeal without the environmental constraints of the latter.

Acknowledgements

We thank L. Cocker, R. Robertson (UK Agri-Tech Centre) and T. Walshe (Aquanzo Ltd.) for their valuable input.

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Table 1. Linear and quadratic effects of replacing fish meal with Artemia meal on body weight (BWT, g) of broiler chickens

	Artemia meal inclusion levels								
BWT	0%	1%	2%	3%	4%	5%	SEM	Lin	Quad
Day 10	271[a]	288[ab]	294[b]	294[b]	292[ab]	295[b]	4.53	0.003	0.031
Day 21	1026[a]	1101[ab]	1145[b]	1079[ab]	1116[ab]	1149[b]	21.58	0.005	0.246
Day 35	2709[a]	2818[ab]	2880[b]	2902[b]	2814[b]	2939[b]	51.44	0.017	0.289

Replacing fishmeal for farmed marine protein in starter broiler rations improves digestibility through microbiota modulation

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Application

Farmed marine proteins (Artemia meal) has great potential to be an alternative protein source for young broilers.

Introduction

Fishmeal feeding to starter broilers has reduced because of its high price and its increasingly recognised unsustainable nature (Fanatico et al., 2018). Protein derived from *Artemia* spp. (also known as brine shrimp), which can be farmed on co-products, may be a sustainable alternative protein source for fishmeal (Artemia meal). The aim of this study was to investigate the effect of fishmeal replacement with Artemia meal on nutrient digestibility and microbial modulation in starter broilers.

Material and methods

Ross 308-day-old male broilers were placed in 24 pens (18 birds/pen) with 6 dietary treatments (n = 4), in which Artemia meal stepwise replaced fishmeal from 0 to 5% levels during a 10-day starter phase (SRUC AWERB: AEX 2024–009 POU). On day 10, distal ileal and colon contents from 10 birds per pen were used to assess apparent digestibility of amino acids and apparent metabolizable energy (AME), respectively. In addition, caecal DNA was extracted from 1 bird/pen for short-read shotgun metagenomics. Statistical analyses were conducted using linear mixed models and multivariate analysis via Maaslin 2 in R.

Results

Ration AME was significantly increased at 3%, 4% and 5% Artemia meal, whilst it was reduced at 1% Artemia meal compared to the control ($p < 0.05$). Moreover, apparent ileal digestibility of lysine, methionine, aspartic acid and tyrosine were greater at 5% Artemia meal, compared to the control ($p < 0.05$), with methionine digestibility being also increased at 1%, 2% and 3% Artemia meal ($p < 0.05$), whilst aspartate and lysine digestibility tended to increase at 2% Artemia meal ($0.05 < p < 0.1$). However, threonine, glycine, alanine, phenylalanine apparent ileal digestibility was lower at 4% Artemia meal compared to the control ($p < 0.05$), whilst proline apparent ileal digestibility was greater at 1% and 4% Artemia meal ($p < 0.05$). The relative abundance of *Actinobacteria*, in particular of *Collinsella*, was significantly increased in all treatment groups apart from 3% Artemia meal ($Q < 0.05$). A total of 301 caecal orthologs were significantly enriched and 163 were depleted throughout the different groups at day 10, with most of the changes observed at 2% and 5% Artemia meal. At 5% Artemia meal 47 enriched orthologs were observed compared to the control, which include *metH* and *metK* that are involved in the metabolism of cysteine and methionine. This concurred with a positive correlation between *metK* and apparent ileal digestibility of methionine (Figure 1).

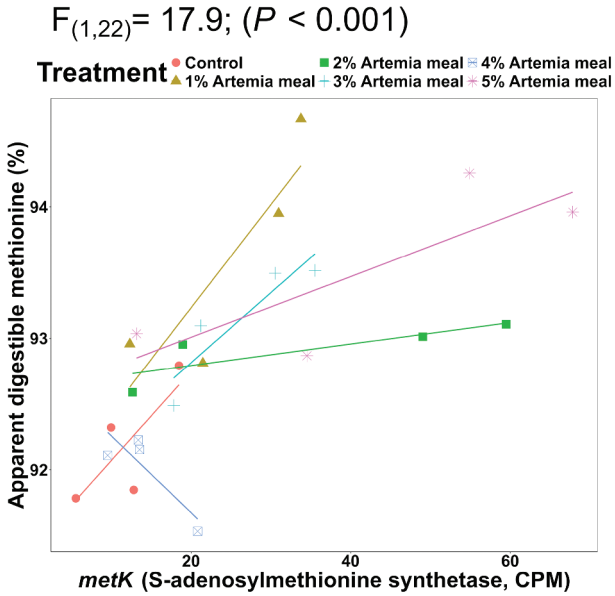

Figure 1. Linear mixed model showing the significant relationship between the abundance of metK and the apparent ileal digestible methionine.

Conclusion

Replacement of fish meal with Artemia meal improved nutrient utilization, which concurred with improved growth performance reported elsewhere (Hussein et al, 2025). Moreover, the greater abundance of *Collinsella* combined with the positive correlation between the apparent ileal digestibility of methionine and the enriched ortholog *metK*, which is involved in the biosynthesis of methionine, suggest a likely microbial basis to the effects observed of fishmeal replacement for Artemia meal.

Acknowledgements

We thank L. Cocker, R. Robertson (UK Agri-Tech Centre) and T. Walshe (Aquanzo Ltd.) for their valuable input.

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Impact of dietary specification on broiler growth performance, nutrient digestibility and liver triglyceride concentration

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Application

The growth performance of both slow and fast-growing broilers is improved with a higher specification diet however, the environmental impact should also be considered.

Introduction

Slow-growing broilers (SGB) are being increasingly used (Better Chicken Commitment, 2023). Triglyceride (TG) concentration is a key indicator of lipid metabolism and is increased in fast growing broilers (FGB) fed a high density diet (Chen, Wang, Yan, & Huang, 2013). However, no information exists for SGBs. The objective of this experiment was to assess the impact of a high (HS) and low (LS) nutrient diet on growth performance, nutrient digestibility and liver TGs of FGBs and SGBs.

Materials and methods

The study was approved by Harper Adams University Research Ethics Committee. A total of 210 as-hatched FGB (Ross 308) and 210 as-hatched SGB (Redbro) chicks were used. Birds were allocated to 28 pens in a 2 × 2 factorial design (7 replicates per treatment). Two wheat-soybean diets, HS, recommended for FGB, and LS, recommended for SGB, were fed *ad libitum*, as mash, in four phases. Acid insoluble ash was added at 20 g/kg to the final phase as an indigestible marker. Bird bodyweight (BW), feed intake (FI), weight gain (ADG) and feed conversion ratio (FCR) were determined. Excreta were collected during the final 3 days of the study and apparent metabolisable energy (AMEn), dry matter retention (DMR), nitrogen retention (NR), and neutral detergent fibre digestibility (NDFD) were determined. Liver TG concentration was analysed following manufacturer's instructions (Abcam Ltd., Cambridge, UK). Data were analysed by two-way ANOVA in GenStat® (version 23.1; VSN International Ltd). Differences were reported as significant where $P < 0.05$.

Results

As shown in Table 1, Ross 308 birds were heavier at 42 d and had greater ADG and FI than Redbro ($P < 0.001$). Birds fed HS had greater final BW, ADG and improved FCR compared to birds fed LS ($P < 0.001$). Ross 308 had greater AMEn intake ($P < 0.001$), however, DMR, NR and NDFD coefficients were not significantly different between genotypes or dietary treatments ($P > 0.05$). Hepatic TG concentration was similar between treatment groups ($P > 0.05$).

Conclusion

The production performance of broilers is improved when fed HS. Birds showed similar nutrient digestibility and liver TG, suggesting that additional nutrients and energy supplied by HS were effectively used by Redbro broilers.

Acknowledgements

Thank you to Dr James Bentley for bird and feed sourcing. Funding was provided by the John Oldacre Foundation.

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Table 1. Effect of high (HS) and low (LS) nutrient specification on Ross 308 and Redbro broiler production performance, nutrient digestibility and liver triglyceride concentration at 42 days of age

	Genotype		Diet			*p* value		
	Redbro	Ross 308	HS	LS	SEM	Genotype	Diet	Gen*Diet
BW d 0 (g)	41.09	39.08	40.15	40.02	0.261	<0.001	0.722	0.494
BW d 42 (g)	1941	2349	2281	2010	27.5	<0.001	<0.001	0.160
ADG	43.54	52.99	51.56	44.98	0.716	<0.001	<0.001	0.339
FI	79.17	91.76	87.98	82.95	0.985	<0.001	0.002	0.252
FCR	1.825	1.737	1.712	1.85	0.020	0.006	<0.001	0.555
AMEn intake (MJ)	1.16	1.33	1.29	1.20	0.014	<0.001	<0.001	0.296
AMEn (MJ/kgDM)	14.61	14.51	14.63	14.49	0.158	0.646	0.534	0.914
DMR	0.73	0.72	0.72	0.73	0.009	0.737	0.877	0.716
NR	0.57	0.58	0.58	0.57	0.012	0.340	0.458	0.157
NDFD	0.26	0.28	0.29	0.25	0.026	0.699	0.225	0.902
TG (nmol/g)	146	141	156	132	9.2	0.712	0.089	0.091

Oviposition time and laying environment: their influence on egg quality and embryonic outcomes in broiler breeders

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Application

This study provides insights into the effects of oviposition timing and laying environment on egg quality and embryonic development in Ross-308 broiler breeders. Variations in egg characteristics, including shell thickness, albumen width, and mineral composition, were observed based on laying time and environment. These findings contribute to understanding the influence of laying conditions on egg quality and embryonic traits, offering data for optimizing breeder management practices.

Introduction

While the effects of floor eggs on hatching performance are well-known, the role of egg sequence, and particularly first in sequence eggs which are laid early in the morning, on egg quality and embryonic development is less understood. Egg quality, starting from its formation, is crucial in poultry production. The nutrient composition of a fertile egg significantly impacts embryonic nutrient uptake during incubation (Uni, Yadgary, & Yair, 2012). Given the relatively short lifespan of commercial meat strains, the incubation period constitutes approximately one-third of their overall growth period and is a critical phase influencing the development, growth, health, and welfare (Speier, Yadgary, Uni, & Wong, 2012). This study evaluated the influence of egg collection time and laying environment (floor vs. nest) on egg quality and embryonic development in Ross-308 broiler breeders.

Materials and methods

In Experiment 1, 200 floor eggs were collected from a Ross-308 broiler breeder flock at 33 weeks (Run 1, 100 eggs) and 44 weeks (Run 2, 100 eggs), with 50 eggs per run collected as First Collection Floor Eggs (FCFE, 07:00 h) and Second Collection Floor Eggs (SCFE, 08:30 h). Eggs were assessed for weight, dimensions, shell quality, and abnormalities on Embryonic Day 0 (ED0). Eggs were incubated, with weights recorded on Embryonic Days 4, 8, and 12. On ED12, embryos were classified as infertile, dead, or alive, then sacrificed for length and weight measurements. In Experiment 2, 150 eggs from a 27-week-old Ross-308 broiler breeder flock were collected as First Collection Nest Eggs (07:00 h), First Collection Floor Eggs (07:00 h), and Second Collection Floor Eggs (10:00 h) (n = 50/group). The study, approved by the University of Nottingham Ethical Review Body (Approval Ref: 244), evaluated egg weight, dimensions, shape index, shell thickness, albumen and yolk characteristics, including widths, heights, and yolk colour. Indices such as Haugh unit, yolk index, and albumen index were calculated. Nutrient composition was analysed via yolk fat extraction and albumen protein analysis, while eggshell minerals were determined using ICP-MS after freeze-drying and digestion. For both experiments, the egg served as the statistical unit. Experiment 1 was analysed using the t-test procedure of SAS. Experiment 2 was analysed by one-way ANOVA using the PROC GLM procedure of SAS University Edition software (SAS Institute Inc., Cary, NC, USA). Flock age was included in statistical models where relevant to account for variation. The effect of flock age was tested on the model and no significant differences were found.

Results

In Experiment 1, the initial egg weight (ED0) and final egg weight (ED12) were significantly higher in FCFEs compared to SCFEs ($P = 0.03$ and $P = 0.006$, respectively). Shell abnormalities differed, with FCFEs having more calcium-coated and soiled eggs ($P = 0.04$ and $P < 0.001$, respectively), whereas SCFEs had a higher incidence of minimally wrinkled eggs ($P = 0.04$).

Egg length was significantly greater in FCFEs ($P = 0.04$) while no differences in width or shape index ($P > 0.05$). On ED12, FCFEs showed greater percentage weight change ($P = 0.008$) but had lower embryo weight, embryo's percentage of total egg weight, and shorter embryo length ($P < 0.001$, $P < 0.0001$, $P = 0.001$). No differences were observed in total shell abnormalities, shell characteristics, or embryo classification ($P > 0.05$). In Experiment 2, overall egg weight differences among FCNE, FCFE, and SCFE were not significant ($P = 0.08$), but FCFE and SCFE differed significantly ($P = 0.03$). Albumen width was greater in FCFE and FCNE than SCFE ($P = 0.004$), while albumen weight and percentage were higher in FCFE and SCFE than FCNE ($P = 0.03$, $P < 0.001$). Yolk width was larger in FCNE ($P = 0.002$), but yolk weight and percentage showed no differences. Shell thickness was higher in FCNE and FCFE than SCFE ($P < 0.001$). Mineral analysis revealed significant group differences: sodium was lower in SCFE ($P = 0.007$), molybdenum and zinc were higher in FCNE ($P = 0.002$), manganese was highest in FCFE ($P = 0.007$), and arsenic was lower in FCNE ($P = 0.04$). No differences were observed for calcium, phosphorus, potassium, or iron.

Conclusion

These results underscore the critical role of oviposition timing in influencing egg quality and embryonic characteristics, offering valuable insights for optimizing breeder management strategies.

Acknowledgements

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Funding

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