Official Journal of the Animal Science and Production Association (ASPA)

*

ISSN 1594-4077

eISSN 1828-051X

*

http://www.tandfonline.com/tjas

*

Italian Journal of Animal Science

*

volume 16

supplement 1

2017

Taylor & Francis
Taylor & Francis Group

italian journal of animal science

ASPA 22nd CONGRESS

Perugia, June 13–16, 2017

Book of Abstracts

Guest Editors: Massimo Trabalza-Marinucci (Coordinator), Cesare Castellini, Emiliano Lasagna, Stefano Capomaccio, Katia Cappelli, Simone Ceccobelli, Andrea Giontella

O090

Comparison of productive performance and intestinal transcriptomic profile of two fast-growing chicken hybrids

Marco Zampiga[1], Micol Bertocchi[2], Paolo Bosi[1], Paolo Trevisi[1], Adele Meluzzi[1], Federico Sirri[1]
[1]*Dipartimento di Scienze e Tecnologie Agro-Alimentari, Alma Mater Studiorum University of Bologna, Italy*
[2]*Dipartimento di Agricoltura, Ambiente e Alimenti, University of Molise, Campobasso, Italy*
Contact: federico.sirri@unibo.it

Fast-growing chicken hybrids currently used in commercial conditions differ for growth rate, feed efficiency and reproductive traits. However, the reasons behind these differences are not clear. The aim of this study was to compare productive performance and intestinal transcriptomic profile of two fast-growing chicken hybrids (HA and HB). A total of 1170 one day-old female chicks from the same hatching session and breeder stock, were weighed, divided in 2 experimental groups of 9 replicates each and fed the same commercial diets. At the end of each feeding phase (9, 21, 34 and 43 d) productive performance were recorded. At slaughter (43 d), ileum mucosa was collected from one bird per replication and total RNA was extracted to perform microarray analysis for transcriptomic profile using Chicken Gene 1.1ST Array Strip. Pathway analysis was performed through GSEA software considering enriched pathways with False Discovery Rate <25%. At slaughter, HA reported lower body weight (BW) and daily weight gain (DWG) than HB (2607 *vs* 2734 g and 59.6 *vs* 62.6 g/bird/d, respectively; $p<.01$) whereas no significant difference was observed in feed conversion rate (FCR). Moreover, HA and HB birds showed different growth patterns throughout the study. Indeed, HA birds reported higher BW and better FCR from 0 to 9 d than HB (228 *vs* 217 g and 1.352 *vs* 1.419, respectively, $p<.05$) whereas HB chickens gained more weight than HA from 10 to 21 d (49.2 *vs* 45.3 g/bird/d, respectively; $p<0.01$). From 35 to 43 d, HB birds showed higher DWG than HA (91.9 *vs* 83.3 g/bird/d, respectively; $p<.01$) but also a tremendous increase in FCR (1.769 *vs* 1.641, respectively for HB and HA; $p<.01$). Transcriptomic analysis revealed significantly enriched pathways for mitochondria and oxidative phosphorylation in HA birds and enriched pathways for immune system activation in HB ones. The activation of immune system in HB birds at 43 d of age may have had a negative impact on FCR increasing energy expenditure, even if they showed a better final growth than HA. On the other hand, the enrichment in pathways involved in mitochondria and oxidative phosphorylation in HA birds seems consistent with their phenotypic expression of feed efficiency showed from 35 to 43 d of trial. However, the ongoing metagenomic sequencing analysis of ileum microbiota could provide further insights to elucidate the determinants of the differences in the productive performance observed in the two chicken hybrids.

O091

Influence of a synthetic emulsifier supplementation on lipid metabolism and apolipoprotein gene expression in liver of female and male chicks

Raffaella Rebucci[1], Carlotta Giromini[1], Davide Gottardo[1], Marcello Comi[1], Xian-Ren Jiang[2], Federica Cheli[1], Antonella Baldi[1], Valentino Bontempo[1]
[1]*Dipartimento di Scienze Veterinarie per la Salute, la Produzione Animale e la Sicurezza Alimentare, University of Milano, Italy*
[2]*Feed Research Institute, Beijing, China*
Contact: raffaella.rebucci@unimi.it

Young chickens physiology is characterized by inefficient digestion and fat absorption due to a low level of natural endogenous lipase production. These evidences have increased the interest on the use of emulsifiers to improve fats utilization and the growth performance in young chickens. In our previous study we observed that supplementation with a synthetic emulsifier (AVI-MUL TOP/GP10, AMT) improves the growth performance of broiler chicks. The aim of this study was to evaluate the influence of AMT on plasma lipid profile, total lipid liver content and hepatic lipid metabolism-related genes of female and male chicks. A total of 1200 ROSS308 chicks (1-d-old) were allocated into 4 treatments with a 2 x 2 factorial design comparing gender (female or male) and different dietary treatments (basal diet supplemented without (CTR) or with emulsifier (AMT), 1 g/kg from d 0 to 12, 0.75 g/kg from d 12 to 22 and 0.5 g/kg from d 22 to 44, respectively). Each group consisted of 15 pens, 20 birds per pen, and one bird of each pen was randomly selected for the analysis. At the end of the trial, the plasma concentration of cholesterol, HDL, LDL, NEFA, triglyceride was evaluated. Liver samples were processed for total lipid content (Folch method) and the mRNA hepatic expression of apolipoprotein A-I (ApoA-I) and B (ApoB) was determined by real-time PCR. The data were analysed as a completely randomized design with a 2×2 factorial treatment arrangement by ANOVA (MIXED procedure). AMT supplementation increased the cholesterol, HDL, and LDL contents compared with the CTR group ($p<.01$; $p=.02$; $p<.01$ respectively). NEFA and triglyceride concentrations were not affected in AMT group. Moreover, it was observed a significant ($p<.05$) gender effect on plasma lipid parameters. No statistical difference was found in total hepatic lipid content between CTR and AMT groups. The AMT supplementation did not modify ApoA-I expression, while ApoB gene was significantly ($p=.005$) up-regulated in female.

Taylor & Francis

ApoB is the main component of chicken plasma VLDL and determines the cellular uptake of lipoprotein in the liver. The obtained results indicate that AMT supplementation influenced the lipid metabolism and related gene expression in broiler chicks.

Acknowledgements

This work was funded by SEVECOM S.P.A., Milan, Italy. The authors gratefully acknowledge Dr. Roberto Bombardieri (Veronesi Group) for support. The authors wish to thank Dr. Cinzia Margherita Bertea (Unito) for technical support.

O092

Parentage assignment for genetic improvement of farmed sea bream by new single nucleotide polymorphisms and single tandem repeats panels

Katia Parati[1], Silvia Cenadelli[1], Graziella Bongioni[1], Andrea Galli[2], Hervé Chavanne[3]

[1]*Istituto Sperimentale Italiano "Lazzaro Spallanzani", Rivolta d'Adda, Cremona, Italy*
[2]*Centro di Ricerca per le Produzioni Foraggere e Lattiero-Casearie, Consiglio per la Ricerca in Agricoltura e l'Economia Agraria, Lodi, Italy*
[3]*Consultant in Selective Breeding and Reproduction, Céret, France*
Contact: katia.parati@istitutospallanzani.it

The number of selective breeding programs has increased over the years for all major European aquaculture fish species. This trend is supported by an increase in the number of selected traits and by the use of molecular tools in a larger number of selective programs. The management of modern selective breeding programs in aquaculture requires the use of pedigree information to carry out efficient genetic evaluations for multi-traits improvement, allowing a better control of inbreeding. Molecular markers represent a powerful tool for parentage inference of breeding candidates reared in communal tanks.
In this work, a large multiplex of 13 microsatellite markers (Single Tandem Repeats, STRs) and a panel of 59 Single Nucleotide Polymorphisms (SNPs) have been developed to infer complex pedigree structures in experimental batches of Gilthead sea bream (*Sparus aurata*).
STRs screening was carried out from a database of about 100 microsatellite (https://www.ncbi.nlm.nih.gov/nuccore/) and priority choice was given to the highly polymorphic microsatellite markers, with different sizes and known linkage on the sea bream linkage map. For the SNPs selection, a database of 49,000 ESTs (10,000 contigs) has been screened and processed for SNPs mining, annotation and mapping, and a final set of 128 SNPs markers was identified and spotted on array for OpenArray technology(Lifetechnologies).
SNPs and STRs panels have been validated on 4568 offspring assigned to 197 broodstock with PAF, a new parentage inference software.
The STRs multiplex allowed to unambiguously allocate 99.1% of the progeny to their parental pair, while 0.8% of the offspring remained unsolved.
The SNPs panel allowed to solve unambiguously 100% of the allocations, 99.1% of which in single match by deterministic approach, and 0.9% in multiple matches by stochastic approach. The Exclusion Probabilities (EP) given both parents were EP: 0.99999982 for STR markers and EP: 0.9999999 for SNP markers. The Identity Probability (IP) was IP: 2.370104E-24 for STR markers and IP: 1.060928E-30 for SNP markers.
The comparison between SNPs array and STRs multiplex opens the discussion on the limits and advantages of the two types of markers in parentage allocation analysis. The development of this efficient method of molecular fingerprinting, combined with specific broodstock handling and optimised breeding schemes, gives a great support for the implementation of breeding programs in sea bream.

Acknowledgements

This work was supported by European Union's Seventh Framework Programme (FP7/2007-2013) under grant agreement n° 262523.

O093

Intestinal microbiota characterization by next generation sequencing in rainbow trout (*Oncorhynchus mykiss*) fed animal by-product meals as an alternative to fishmeal protein sources

Genciana Terova[1], Simona Rimoldi[1], Chiara Ascione[1], Emi Gliozheni[1], Fabio Brambilla[2]

[1]*Dipartimento di Biotecnologie e Scienze della Vita, University of Insubria, Varese, Italy*
[2]*VRM S.r.l. Naturalleca, Cologna Veneta, Italy*
Contact: genciana.terova@uninsubria.it

Bacteria associated with the epithelium of fish intestine play a critical role in host metabolism. Gut microbiota is involved in the anaerobic fermentation of complex dietary carbohydrates and oligosaccharides that are otherwise indigestible. Several genetic, nutritional, and environmental parameters influence the abundance and diversity of fish gut microbiota. Therefore, understanding the factors that regulate this