Dynamic profile of active metabolic pathways in the subcutaneous fat tissue of Holstein cows during early lactation.

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recorded every two weeks from hatching to the age of 27 weeks. Gompertz model was used to define the growth rate. The performance of laying hens was monitored over a period of 6 months. To evaluate fertility and hatchability, all eggs laid in 2 consecutive weeks were hatched for 12 weeks. Data analysis was carried out with the Excel software. Allelic richness was 3.6 and observed and expected heterozygosity were 0.68. Mean live weights for cocks and hens were 2779 ± 233 g ($n = 79$) and 2089 ± 195 ($n = 98$). Growth rates in the linear phase were 26.95 ± 3.19 g/day and 16.63 ± 1.90 g/day for male and female birds. In egg collection period for hatch mean 179.5 eggs were taken. Fertility and hatchability were 87.2% and 92.3%. The overall mean chick survival rate to six months of age was 4.6%. The age at first lay ranged between 5 and 6 months, and egg number/month was 14.5, mean egg weight was 60 ± 3 g and laying percentage resulted in 51.6% (max: 76.2%). These results provide an important insight on the genetic and productive characteristic of this local poultry breed that can be used for managing new mating schemes aimed to preserve variability and increase productivity.

P045

Genetic diversity, productive and reproductive performance in Italian chicken breed Bionda Piemontese

Dominga Soglia[1], Stefano Sartore[1], Sandra Maione[1], Marta Gariglio[1], Paola Sacchi[1], Roberto Rasero[1], Cecilia Mugnai[1], Laura Gasco[2], Francesco Gai[3], Achille Schiavone[1,3], Sihem Dabbou[1]

[1]*Dipartimento Scienze Veterinarie, University of Torino, Italy*
[2]*Dipartimento di Scienze Agrarie, Forestali e Alimentari, University of Torino, Italy*
[3]*Istituto di Scienze delle Produzioni Animali, Consiglio Nazionale delle ricerche, Grugliasco, Italy*
Contact: *dominga.soglia@unito.it*

Bionda Piemontese (BP) is a local slow-growing poultry breed that is mainly reared for meat; hens are also bred for egg production. In this study, the genetic diversity, productive and reproductive performance were examined. The birds were kept in standard environmental conditions at the Poultry Conservation Centre of the University of Turin (Italy). At hatching, 218 chicks were weighed, labelled with a wing metal tag. At six weeks of age, birds were separated by sex and transferred to growing pens with access to an external paddock (20 birds/pen). The birds always had free access to water and were fed with standard commercial starter diet *ad libitum* (0–6 weeks) followed by a growing diet. All birds were genotyped by a set of 14 microsatellite markers

selected for their variability. The body weight (BW) was recorded individually every two weeks from hatching to the age of 27 weeks, for a total of 14 weightings. Gompertz model was used to define the growth rate. The performance of laying hens was monitored over a period of 6 months. To evaluate fertility and hatchability, all eggs laid in 2 consecutive weeks were hatched for 12 weeks. Data analyses were carried out with the Excel software.

The results showed a low genetic variability with an allelic richness of 3.3 but a good individual variability: the observed and expected heterozygosity were 0.675 ± 0.040 and 0.680 ± 0.015, respectively, Fis index was 0.016. The growth performance was good: the mean live weights for cocks was 2797 ± 253 g ($n = 102$) and for hens 2226 ± 249 g ($n = 116$). The growth rates in the linear phase resulted 26.47 ± 3.19 g/day and 18.42 ± 2.63 g/day for male and female. The fertility and hatchability were 86.5% and 94.2%, respectively showing a good reproductive performance. The mean chick survival rate to six months of age was 4.6%. In egg collection period for hatch mean 184.5 eggs were taken; in total 1107 eggs were collected (6 repetitions). The egg production was lower than commercial layer but consistent with local breed: the age at first lay ranged between 5 and 6 months and Iegg number/month was 14.5, egg weight mean 61 ± 3 g and laying percentage 51.6% (max: 70.7%). In conclusion, the results highlight that BS is local slow-growing and dual-purpose breed with good productive performance.

P046

Dynamic profile of active metabolic pathways in the subcutaneous fat tissue of Holstein cows during early lactation

Stefania Chessa[1,2], Moemia Portela[3], Antonio Boccardo[4], Davide Pravettoni[4], Arlindo A. Moura[3], Stefano Biffani[2], Filippo Biscarini[2]

[1]*Dipartimento di Scienze Veterinarie, University of Torino, Italy*
[2]*Istituto di Biologia e Biotecnologia Agraria, National Research Council, Lodi, Italy*
[3]*Departamento de Zootecnia, Federal University of Ceara, Fortaleza-CE, Brazil*
[4]*Dipartimento di Medicina Veterinaria, University of Milano, Italy*
Contact: *stefania.chessa@unito.it*

Early lactation is a challenging time for dairy cows, which have to simultaneously cope with milk production and body maintenance. The rapid increase in energy requirements is only partially met by feed and cows enter in a state of negative energy balance (NEB),

frequently associated with metabolic diseases and reduced fertility. To counterbalance NEB cows mobilise body reserves (mainly fat tissue) with a complex interplay still far to be completely understood. RNA-Seq experiments provide a comprehensive understanding of the expression of tissue-specific genes as well as of targeted metabolic pathways. For a better understanding of how lipids are metabolised to respond to cows requirements in early lactation we performed RNA-Seq analysis of the subcutaneous fat tissue sampled from the tail of 7 healthy multiparous Holstein Friesian cows at three times point after calving: T0 = 2 days, T1 = 30 days and T2 = 90 days. Adipose tissue was collected and preserved in Qiagen AllPrep solution until extraction, performed using the Qiagen RNeasy Lipid Tissue Kit. RNA-Seq was performed on the Illumina Hiseq 3000 platform. Differential expression analysis was performed comparing the log-fold differences in gene counts at the three-time points and genes with a FDR-adjusted p value <.05 were considered significantly different and retained for gene functional analysis. An enrichment analysis was conducted to detect pathways significantly associated with the identified genes. We found 113, 324 and 17 genes differentially expressed in T0 vs. T1, T0 vs T2 and T1 vs. T2, respectively. These genes are involved in 142 metabolic pathways. The top 5 pathways for time comparisons include insulin secretion, oxytocin signalling, glycolysis/gluconeogenesis, pyruvate metabolism, insulin resistance, calcium signalling, gonadotropin-releasing hormone, mitogen-activated protein kinase and adipocytokine signalling, and the renin-angiotensin system. These pathways are associated with cellular processes, inflammatory response and energy production, which contribute to milk synthesis, foetal growth and homeostatic mechanisms. This knowledge could be potentially applied to provide better farming conditions reducing the negative impact on the health and economics of the herds.

P047

Several hundred single nucleotide polymorphisms in candidate genes: association with six production, carcase, and meat quality traits in Italian Large White pigs

Stefania Dall'Olio[1], Giuseppina Schiavo[1], Maurizio Gallo[2], Luca Buttazzoni[3], Luca Fontanesi[1]

[1]*Dipartimento di Scienze e Tecnologie Agro-alimentari, University of Bologna, Italy*

[2]*Associazione Nazionale Allevatori Suini, Roma, Italy*
[3]*Centro di ricerca di Zootecnia e Acquacoltura, Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Roma, Italy*

Contact: *stefania.dallolio@unibo.it*

Italian heavy pig selection programmes include production (average daily gain, ADG; feed gain ratio, FGR), carcase and meat quality traits (weight of LC: lean cuts; HW: ham weight; BFT: backfat thickness; HWLFS: ham weight loss at first salting; and VIF: visible intermuscular fat). In this study, we wanted to evaluate if a selection genotyping approach designed for BFT could identify markers associated with other traits. Italian Large White (ITLW) gilts were chosen according to their extreme estimated breeding values (EBV) for BFT (276 with the most negative and 279 with the most positive EBVs) within a population of about 12,000 sib-tested pigs. A total of 736 single nucleotide polymorphisms (SNPs) within candidate genes were used in this study. Of the genotyped markers, 280 SNPs in 211 genes that had minor allele frequency >5% and call rate >90 were used in association analyses with six traits (ADG, FGR, LC, HW, HWLFS and VIF). To deal with the multiple testing problem in a candidate gene approach, we applied the proportion of false positives (PFP) method, setting a threshold for significance of 0.10. Six SNPs were significant: four for HWLFS and two for LC. The significant SNPs for HWLFS were within genes encoding proteins involved in carbohydrate metabolism (phosphoglucomutase 3, *PGM3*; and glycogen phosphorylase L, *PYGL*), transcription regulation and development (mitogen-activated protein kinase 8, *MAPK8*), and cellular RNA processing and degradation (exosome component 1; *EXOSC1*). The two significant markers for LC were within the TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (*TBC1D1*) gene encoding a protein implicated in regulating the trafficking of glucose transporter 4. These results reveal a possible genetic basis for the relations among BFT, HWLFS and LC, beyond the trivial consideration that fatter hams necessarily lose less weight and complement results obtained in genome-wide association studies.

P048

Heritability and correlations among milk yield, Body Condition Score and type traits in the Italian Mediterranean Buffaloes (*Bubalus bubalis*)

Stefano Biffani[1,2], Roberta Cimmino[3], Massimo Neri[3], Giacomo Bertolini[3], Mariela Castrillo[3], Luca Gubitosi[3], Dario Rossi[3], Mauro Fioretti[2]

[1]*Istituto di Biologia e Biotecnologia Agraria - IBBA-CNR, National Research Council, Lodi, Italy*

[2]*Ufficio Studi – Associazione Italiana Allevatori – AIA, Roma, Italy*
[3]*Associazione Allevatori Nazionale Specie Bufalina -ANASB, Caserta, Italy*
Contact: *r.cimmino@anasb.it*