



Italian Journal of Animal Science

volume 22, supplement 1, 2023

ASPA 25th Congress

Monopoli (BARI - ITALY), June 13-16, 2023

Guest Editors

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Evaluation of the effect of the breeding system on the expression of liver genes in local slow-growing chicken breeds

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The production of poultry meat is based on fast-growing strains (Ross 308) reared in intensive system with concerns on animal health and welfare. The free-range system of local poultry breeds appears crucial to safeguard welfare, sustainability and biodiversity. The aim of the present study was to evaluate the effect of two breeding systems – intensive (I) *vs* free-range (F) – on the expression of liver genes related to stress and lipid metabolism. Two local chickens' breeds (Bionda Piemontese, BP and Robusta Maculata, RM), their cross-breeds (BPxSassò, RMxSassò) and Ross 308 were used. A total of 300 one-day-old male chickens were randomly allocated into two groups (3 replicates/treatment/genotype; 10 chickens/replicate).

The intensive group (I), received a standard diet and the free-range group (F) received a low input diet until slaughtering (84 d). At slaughter, liver samples were collected in RNAlater and stored at -80°C . Eleven genes (*Acox1*, *FABP1*, *HSPA2*, *CASP6*, *CAT*, *FADS2*, *LPL*, *SOD1*, *SREBF2*, *ACTB* and *GAPDH*) were studied in liver. RNA expression levels were normalized using *GAPDH*. The laboratory protocol was characterised by the following steps: RNA extraction, reverse-transcription, multiplex PCR, library preparation and NGS sequencing (Miseq Illumina platform). R software (version 4.2.2) was used for statistics by applying R packages to perform reads count (FeatureCounts) and differential gene expression (Deseq2). The results obtained showed differences in gene expression related to lipid metabolism. Chickens reared in I breeding system showed a higher expression in the lipoprotein lipase gene (*LPL*) ($p < 0.001$; log₂ Fold change 1.35). *LPL* is involved in liver fatty acid metabolism and the result suggested that I may increase lipid synthesis and accelerate lipolysis by upregulating the *LPL* expression. Instead, in F breeding system, a higher expression of the sterol regulatory element binding transcription factor 2 (*SREBF2*) ($p < 0.001$; log₂ Fold change +1.96) was observed. *SREBF2* regulates the transcription of genes related to cholesterol biosynthesis and its expression is higher when the sterol concentrations are low, likely as a consequence of the low-input feeding management. The different

breeding systems showed an effect on the expression of liver genes related to lipid metabolism. Further studies should be carried out to identify poultry genotypes more suitable for free-range breeding systems in order to promote sustainability and biodiversity.

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Structural variation in the Aosta cattle breed

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Copy Number Variants (CNVs) are structural variants affecting genetic diversity that influence phenotypic expression. Scientific community has underlined relationship between CNV and adaptation to different environmental conditions (e.g. high altitude and harsh climate). Aosta cattle (Aosta Red Pie – ARP; Aosta Black Pied/Chestnut – ABC and Mixed Chestnut-Herèn – ACH) are autochthonous dual-purpose breeds, well-adapted to be reared in the Alps mountain area. The aim of this study was to characterize Aosta population through the CNVs detection and investigate their relation to the adaptative selection to the mountain farming system. ANABORAVA provided the LogR Ratio (LRR) and the B allele frequency of 3195 females (2108 –ARP, 929 – ABC, 158 – ACH), obtained with the NEOGEN's GGP Bovine100K, that were used to call CNV on autosomes using the SVS 8.9 (Golden Helix[®]) CNAM module. Taking into account the genetic similarity between ABC and ACH found using SNP genotyping data, all the statistics were calculated considering these two breeds as a unique one (ABCH). CNVs were aggregated into CNV regions (CNVRs) based on at least 1 bp overlap; only CNVRs identified in at least 2% of the cows were considered to infer statistics at breed level (ABCH vs ARP). After quality control performed on the obtained calling, a total of 87,488 CNVs and 2328 CNVRs were identified. Cows of the ABCH and ARP showed similar relationship existing between the CNV count and the CNVs mean length. In the PCA performed using the called CNVs, ABCH and ARP also appear overlapping, without any defined cluster, suggesting that these markers do not segregate because of the directional selection occurring at breed level, but highlight the adaptive selection to the Alpine environment shared by all breeds. In fact, about 67.2% of the CNVRs identified in at least 2% of samples (n. 314 regions) resulted in common between the two breeds. Instead, only 18.2% (ABCH) and 14.6% (ARP) CNVRs were proper of each breed. Annotated genes (n. 730) and QTL (n. 411) overlapping the CNVRs associated with productive, functional and health traits. Funded by PSRN DUAL BREEDING_Fase_2.