

# Italian Journal of Animal Science

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## Italian Journal of Animal Science

The *Italian Journal of Animal Science* is an international peer-reviewed open access journal publishing original scientific papers, reviews and short communications.

The journal serves as essential reading for animal scientists, technicians and all those who research animal production.

The journal encourages submissions of international relevance on the following subjects:

- Animal derived food quality and safety
- Animal genetics and breeding
- Aquaculture, poultry, companion and wild game animals
- Livestock systems, management and environment
- Non-ruminant or ruminant nutrition and feeding
- Production physiology and functional biology of farmed, companions and wild game animals.
- Animal behavior
- Animal welfare
- In vitro studies that have an application to farmed livestock

Manuscripts must address topics based on research at molecular, cellular, organ, whole animal and production system levels. Manuscripts discussing milk or meat analysis and compositions must show a direct link to either livestock production system, product quality, animal feeding/nutrition, animal genetics or breeding. Manuscripts describing laboratory animal models will be considered where the study highlights a potential benefit to farmed livestock.

Submissions discussing epidemiology, parasitology, infective diseases, food-borne diseases do not fit with the aims and scope of the journal.

Meeting reviews, book reviews and conference supplements are also published, as well as news and guidelines from the Animal Science and Production Association (ASPA). We welcome submissions from ASPA members and non-members alike.

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# Italian Journal of Animal Science

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## ASPA 25<sup>th</sup> Congress

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

### **Guest Editors**

**Angela Gabriella D'Alessandro, Pasquale De Palo, Aristide Maggiolino,  
and Marcello Mele**

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# **ASPA 25<sup>th</sup> Congress**

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

**#ASPA2023**

### **ASPA 25<sup>th</sup> Congress Book of Abstract**

**The 25th congress of the Animal Science and Production Association**

**“Animal Production Science: Innovations and sustainability for future generation” is under patronage of Loghi patrocini**

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

#### **Venue**

**Torre Cintola Natural Sea Emotions**

**Località Capitolo - Monopoli (BARI - ITALY)**

context, complex phylogeographic patterns emerged as a consequence of a combination of natural and artificial selective processes. With the aim to investigate similarities and divergences between the diffusion processes of three livestock species and post-Neolithic human expansion, a comparative framework has been developed including genome-wide SNPs data of goats, sheep, cattle and humans in the Mediterranean region and in the domestication area. Using public repository, we retrieved genomic data from 1.906 goats, 1.924 sheep, 1.962 cattle and 1.363 human individuals. Concerning livestock species, only autochthonous breeds were considered for the analyses. All datasets have been filtered for minor allele frequencies ( $-maf$  0.05) and missing call rate ( $-geno$  0.1) using the software plink and obtaining final datasets consisting of 48.858 SNPs for goats, 33.670 SNPs for sheep, 23.079 for cattle and 421.611 for humans. To explore common pattern of genomic structure, MDS plots were generated for each species, while the software ADMIXTURE was used with K values ranging from 2 to 10 for each dataset separately. The obtained Q-matrices of ancestry coefficients were then used to construct an interpolation map. Genetic diversity indices were also calculated for each main genomic group representing a specific geographic area in order to assess the presence of pattern of genetic diversity in accordance with stepping stone diffusion processes from the domestication center to peripheral Mediterranean regions. Our results showed that while several common patterns such as a general genomic cline conform with an expansion process from the Fertile Crescent to central Europe can be observed for all species, other local signals seem to be more related to species-specific events reflecting a more complex scenario. For example, while cattle, goats and humans showed similar genetic discontinuities in the Italian Peninsula, sheep seem to be more homogeneous. In cattle this genetic signature could be related to the close relationship between Italian and Balkan Podolian breeds which have been shown to come from the same migration wave. Further analyses and additional samples would be necessary to obtain a more detailed overview of the post-domestication processes of humans and livestock.

## O203

### Millefiori Piemontese, genetic characterization of an endangered local chicken breed

Eleonora Cappone<sup>a</sup>, Dominga Soglia<sup>a</sup>, Stefano Sartore<sup>a</sup>, Valeria Zambotto<sup>b</sup>, Sandra Maione<sup>a</sup>, Margherita Profiti<sup>a</sup>, Valentina Bongiorno<sup>a</sup>, Marta Gariglio<sup>a</sup>, Silvia Cerolini<sup>c</sup> and Achille Schiavone<sup>a</sup>

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Several chicken breeds are recognized in Italy, and the Piedmont region counts three breeds recognized by the MIPAAF: Bionda Piemontese (BP), Bianca di Saluzzo (BS) and Millefiori Piemontese (MP). The MP is an autochthonous breed widely reared in the province of Cuneo until the '60s as double-purpose chicken. Historical sources report that the MP is similar to the Ancona breed but with some specific differences: the MP is heavier than Ancona breed (males up to 4.5 kg, females up to 3 kg), the body is more compact (similar to the BP) and the ear-lobe colour is red. The MP has a mottled plumage pattern (white and black), yellow skin and shank and the comb is red and erected, with regularly shaped dents, even if less developed compared to other Piedmont breeds.

MP substitution with commercial chicken lines caused its dramatic decline, and almost seemed extinct in the '90s. Some MP individuals have been found in the province of Cuneo (4 breeders preserved a few subjects throughout the years) so a conservation and valorization project of this breed is currently carried out in the TUBAVI project. These subjects ( $n = 50$ ; 16 males and 34 females), phenotypically like the MP, were selected in order to evaluate the genetic variability. Blood samples were collected from each individual for DNA genotyping by a set of 25 microsatellite markers chosen by their high polymorphism. Total number ( $N_a$ ), and effective number ( $N_e$ ) of alleles, observed ( $H_o$ ) and expected ( $H_e$ ) heterozygosity, and F (Wright's inbreeding coefficient) index were surveyed. In the sample only one locus is not polymorphic; 88 alleles were identified. The average number of alleles per locus was 3.2, and the effective number of alleles was 2.34. The  $N_e$  resulted lower due to the presence of low-frequency alleles that can be easily lost by genetic drift, thus reducing the genetic variability of the breeds, and increasing their risk of extinction. Observed and expected heterozygosity were 0.57 and 0.52 respectively with  $F = -0.82$  but no significant Hardy-Weinberg Equilibrium deviation was observed. The analysis of the genetical distance from other Italian breeds demonstrated the peculiarity of this genetic group.

Further analyses will be performed in order to define the breed standard, productive and reproductive performances and the breeding programs. As this data and information are unique, it is fundamental to further study and protect this breed, thus preserving and valorizing the Italian avian patrimony.

## O507

### Genetic diversity and runs of homozygosity in Rendena Cattle

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The dual-purpose (dairy and beef) Rendena cattle breed is native to Val Rendena in the northern Italian region of Trentino-Alto Adige. The breed is of medium build, with short, robust legs and small feet that make it well-adapted to grazing in steep Alpine pastures. The

Rendena is also valued by farmers for its longevity, fertility and disease resistance; however, the genomic diversity of this breed is almost unknown. Here, the GGP Bovine 100K SNPchip (Neogen) genotypes and mitogenome sequences from 140 Rendena individuals from 31 farms (collected in 2018) were used together with genotyping data from 40 additional samples (collected in the year 2000) to assess changes in population structure and molecular diversity over the past 20 years. The SNP genotype dataset was used to estimate within-breed diversity and inbreeding, and, with data from 31 local and cosmopolitan cattle breeds, to assess population structure and evolutionary relationships. Principal Component Analysis (PCA), Neighbour-net and Admixture analyses suggested a shared ancestry with the Brown Swiss group. In addition, the distribution of runs of homozygosity (ROHs) appeared homogeneous across chromosomes and was related to chromosome size. Most ROHs were private or common to a few animals. Exceptions were found in three genomic regions on BTA6, BTA10 and BTA16, where ROHs were shared by >25% of the individuals. Noticeably, the ROH on BTA6 consisted in 33 SNPs shared by >50% of the animals over a region harbouring genes relevant for meat (NCAPG, LCORL) and milk production (LAP3). The same region was also found to be under selection in  $F_{ST}$ - and XP-EHH-based analyses contrasting alpine *vs* cosmopolitan breeds. The mean inbreeding level recorded for the 2000 and 2018 populations indicated an increase in the average inbreeding from 0.055 to 0.086, and PCA showed partial overlap of the two groups. Most mtDNA variants belonged to the T3 haplogroup which is known to be widespread in Europe; however, 10 animals with T2 haplogroup variants and single occurrences of T5 and Q1 lineages were found.

## O151

### Evaluation of fatty acids profile of milk produced by mid-lactating Holstein cows fed with enriched olive cake diet

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The use of by-products such as olive cake (OC) for alternative animals feed is widespread to reduce cost associated with animal nutrition (due to the recent increasing costs), to limit environmental impact and to enhance the quality of meat and milk. In fact, it is well known that OC is rich in unsaturated fatty acids (UFA) and polyphenols. The aim of this study was to evaluate the effects of supplementing enriched OC (EOC) to mid-lactating Holstein cows on milk fatty acids (FA) profile. A total of 20 cows were enrolled into 2 homogeneous groups (10 for EOC group and 10 for CTR group) according to BCS ( $2.43 \pm 0.26$ ), lactation period ( $113 \pm 47$  d), and milk yield ( $31.42 \pm 3.28$  kg/d). The EOC group was fed with a 7% inclusion of enriched destoned OC, whereas control group (CTR) received a conventional diet. Milk samples were collected at d 0 and at d 28, to compare FAs in EOC and CTR group at d 0 and at d 28. FAs were extracted, methylated, and separated with a gas-chromatographer fitting a CP-Sil88 column. Peaks of individual FAs were identified and quantified using a 37 FAME standard. Data were analyzed with the PROC GLIMMIX of SAS. Values are expressed as a percentage of total FAME. The results showed that the inclusion of EOC for 28 days modified the FA profile of milk. In fact, at 28 d, among saturated, short- and medium-chain FAs, C10:0 (2.84 vs. 3.68;  $p=0.08$ ), C13:0 (0.16 vs. 0.24;  $p=0.08$ ), and C14:0 (12.73 vs. 14.64;  $p=0.06$ ) tended to be lower in EOC compared with CTR group. A lower content of C12:0 (3.77 vs. 4.93;  $p=0.05$ ), C15:0 (1.61 vs. CTR 2.01;  $p=0.03$ ), C16:0 (33.73 vs. 36.76;  $p < 0.001$ ) was also observed in EOC compared with CTR group. Concerning long-chain fatty acids, EOC group had greater C18:1 cis-9 (20.32 vs. 16.63;  $p=0.02$ ) compared with CTR. C18:0 tended to be greater in EOC compared with CTR group (6.68 vs. 4.51, respectively;  $p=0.08$ ), whereas C22:2 (0.05 vs. 0.09;  $p=0.07$ ) and C24:0 (0.04 vs. 0.08;  $p=0.09$ ) tended to be lower in EOC compared with CTR. These results point out the beneficial effects of supplementing EOC since it improves milk FAs profile that are positively related to human health and are indicative of a better nutritional and nutraceutical properties of milk. Thereby, using this by-product may be considered as a good alternative to conventional feed, giving moreover an added value to the final product.

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