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ASPA 25th Congress Monopoli (BARI – ITALY), June 13-16, 2023

Guest Editors

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ASPA 25th Congress Monopoli (BARI – ITALY), June 13–16, 2023

#ASPA2023 ASPA 25th Congress Book of Abstract

The 25th congress of the Animal Science and Production Association

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

Venue Torre Cintola Natural Sea Emotions Località Capitolo – Monopoli (BARI – ITALY)



In Italy, 53 local chicken breeds were described; the majority (67%) were classified as extinct and 21% at risk of extinction. Therefore, attempts for conservation of Italian avian breeds are urgently required. Sperm cryopreservation is a powerful tool to implement the ex situ in vitro conservation technique in bird populations at risk. The aim of this study was to assess the variability in semen freezability between birds within the Italian endangered Bianca di Saluzzo (BS) poultry breed, in order to develop a conservation programme. BS (n = 18) roosters were housed at the Poultry Unit, Animal Production Centre, University of Milan (Lodi, Italy). After a semen collection training period, semen donors were selected and semen doses frozen in liquid nitrogen. Each day of collection, quantitative (volume, concentration) and qualitative (viability, total motility (TM), progressive motility (PM), kinetic parameters) sperm parameters were measured. Semen was diluted to 1×10^9 sperm/mL with Lake pre-freezing medium containing 2% N-methylacetamide, loaded into 0.25 mL French straws, frozen for 10 min over a nitrogen bath at 3 cm of height and stored in liquid nitrogen at -196 ° C in cryogenic tank. The straws were thawed at 5 °C for 100s and sperm parameters were assessed. A total of 10 laying hens per selected male donors were inseminated twice to assess in vivo fertility and embryo viability. The mean volume and sperm concentration recorded in fresh ejaculates were 0.327 ± 0.17 mL and $3.303 \pm 1.27 \times 10^9$ sperm/ mL. Semen quality of fresh samples was significantly different among birds and only 6 were selected as donors. Furthermore, according to availability of semen doses, 3 birds (BS1, BS2, BS3) were used for artificial insemination trial. Higher values in PM and TM were found in BS2 (PM 25%, TM 98%) and BS3 (PM 33%, TM 98%) compared to BS1 (PM 18%, TM 81%) ejaculates. As expected, a general significant decrease in sperm quality occurred after the freezing-thawing process. Fertility and embryo viability were 30.6% and 95% in BS2, 7.5% and 66.7% in BS1, 8.45 and 57% in BS3. High individual variability was found in semen freezability, not always related to fresh sperm quality. In vitro quality of thawed semen was associated to the results obtained in the artificial insemination test. However, furthered analyzes must be performed to confirm the present results and to identify quality sperm markers for the selection of the best semen donors in conservation programs.

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About the origin of traditional sheep breeds from South America: a comprehensive investigation

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Documented human migration routes help population geneticists to reconstruct the origin of livestock breeds that have been transported around the world since their domestication. Sheep were brought to South America through different routes, during the Spanish, British and Portuguese conquests of the New World. In the late colonial period new breeds from the European and African continents have been introduced in South America. Previous studies tried to discover the origin of Creole sheep, but this issue is still open. To shed light on their genetic composition we analysed some Creole breeds from Colombia, Uruguay and Brazil, joining genotypes of Italian, Spanish, British and African breeds available from previously published studies and new data generated in the framework of the Smarter project (www.smarterproject.eu). A total of 2789 sheep from 50 breeds were analysed with a final panel of 16,698 SNPs after a QC performed with Plink 1.9. Diversity indices were calculated with Arlequin 3.5.2, whereas the phylogenetic relationship and migration events were inferred using Treemix 1.3. The genetic structure was explored by PCA with SNPrelate 1.3 and with ADMIXTURE 1.3. Taken together, all results showed a high degree of admixture as well as high heterozygosity levels. The lowest Fst value (0.007) was found between Bergamasca and Biellese sheep, and the highest (0.329) between the Border Leicester (UK) and Namagua Afrikaner (South Africa) sheep. The heterozygosity levels ranged from 0.31 (Uruguayan Creole) and 0.43 (African White Dorper). Both the PCA and the ML tree revealed a weak subdivision in three main clusters (Spain + Italy; Africa; UK). The Creole breeds from Colombia grouped mostly close to all the Caribbean, Brazilian, Mexican, and some African breeds, while the Uruguayan Creole clustered between the British and the Spanish breeds. Moreover, the most probable number of admixture events inferred was 10 of which the most interesting were from the British branch toward the Brazilian and Uruguayan Creole. Finally, the Admixture results partially agreed with previous studies but also gave more clues about the gene flow that occurred in the past. These preliminary results could help in discovering the genetic makeup of





the Creole sheep and in preventing uncontrolled cross-breeding in the future.

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Genomic tools for the characterization of the not officially recognized livestock populations: a case study in Mascaruna goat and Pecora Nera sheep from Sicily

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The analysis of genomic data is an important tool for the management of small and endangered populations. Italy holds a large number of small ruminant populations, some of which do not have a recognized genetic structure. The majority of these populations are kept by smallholders under extensive production systems and represent an important economic resource in marginal areas. The conservation of their genetic diversity is compelling in the light of facing future challenges as climate change and emerging diseases. This study investigated the genome-wide structure of two Sicilian animal resources, namely Mascaruna (MAS) goat and Pecora Nera (NER) sheep. These populations are included in the Corial project that aims to study and characterize those animal resources not officially recognized as breeds. A total of 72 and 36 individuals of MAS and NER, respectively, were genotyped using the caprine and ovine 50K BeadChip. The genome-wide data of the two populations were analysed respectively in comparison with others Italian goat and sheep breeds. For both populations, the results displayed moderate levels of genetic variability estimated using observed and expected heterozygosity, effective population size and inbreeding, and they were comparable to that of the other Italian local goat and sheep populations. Multidimensional scaling, model-based clustering and measurement of population differentiation within each species, distinguished MAS and NER from the other breeds,

indicating a clear genetic differentiation. The individual data of MAS and NER highlighted genomic admixture with Sicilian goats and sheep, respectively, and showed the lowest genetic differentiation towards Argentata dell'Etna for MAS and Pinzirita for NER, i.e. the breeds that could be considered the ancestral populations of origin. The genomic characterization of these populations represents a fundamental step to plan breeding programs and conservation strategies. The numerous potential uses of genomic information may make routine genotyping desirable for the management of small populations. Our study described an example on two small ruminant populations and confirmed that genomewide analyses are valuable tools for managing all small and endangered animal genetic resources.

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Looking for the genes involved in local adaptation in sheep

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Throughout their domestication, sheep have adapted to environmental heterogeneity, from the tropics to the highlands. Climate and human selection have shaped the genome and left genetic 'fingerprints' on breeds bred in diverse regions worldwide. The small ruminants have evolved to be highly efficient and provide a valuable model for identifying the genetic pathways and mechanisms underlying adaptation. Landscape genomics can help understand the relationship between genetic architecture and environmental variables and provide information on a species' evolutionary history at different spatial scales. Thus, we aimed to investigate regions of the genome that may be associated with environmental adaptation. The dataset included 501 sheep from creole populations from Uruguay (n = 100), Spain (n = 100), Africa (n = 72) and South Africa (n = 29) belonging to the SMARTER project^{*}, and samples from Brazil (n = 100) and Colombia (n = 100) from a private database and genotyped with the OvineSNP50 or Ovine HD BeadChip (Illumina Inc., USA). A

