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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)**

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

#### *Acknowledgments*

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## O513

### **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 genome-wide analyses are valuable tools for managing all small and endangered animal genetic resources.

#### *Acknowledgements*

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## O342

### **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

total of 23,098 autosomal SNP were included in the analysis after the quality control (SNP call rate: 0.9, MAF: 0.05 and pruned for LD-indep-pairwise: 50, 5, 0.2). Climatic variables were downloaded from WorldClim using each population's geographical coordinates. The population structure analysis was performed using MDS (multi-dimensional scaling) and Admixture. The landscape genomic approach (Latent Factor Mixed Model) was used to determine SNPs significantly associated with the geographic and environmental variables. The MDS plot suggested a closer genetic relationship between the Colombian sheep and Spain and African sheep. The Brazilian and Uruguayan Sheep formed an independent group. The Admixture analysis considered 20 potential clusters (K), at K=4, the Brazilian was distinguished, and the Colombian wool creole and hair-type hair sheep breeds were grouped. The FDR – *q* value was calculated for each locus based on the *p*-values in R. We identified genes related to oxidative stress (*CAT*, *BLF*), thermotolerance (*FGF2*, *GNAI3*, *PLCB1*) and altitude (*PPP1R12A*, *RELN*, *PARP2*) that show the adaptation of breeds to specific environmental conditions. Thus, our results could contribute to breeding or conservation plans for locally adapted breeds in the face of climate change.

#### Acknowledgments

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## O48

### The supportive breeding of native Mediterranean brown trout (LIFE Nat.Sal.Mo project, Molise region): the effect of ovarian fluid on frozen sperm motility parameters during artificial fertilization

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The semen cryobank realised within the LIFE Nat.Sal.Mo. project is an important tool to safeguard the genetic integrity of Mediterranean trout (*S. cettii*) at risk of extinction, thanks to its practical use in the supportive breeding. This practice consists in the use of artificial reproduction (AR) to support the natural one. In particular, frozen semen doses in combination with cross-fertilization schemes are used in AR to maximize the genetic variability of offspring to be used in restocking activities. Generally, in AR practices the use of a basic saline solution

(D532) is recommended as artificial fertilization medium (AFM) to boost sperm motility. However, in order to maintain a reproductive microenvironment (RM) as similar as possible to the natural one we focused on the use of ovarian fluid (OF) alone as activation medium to sperm motility. Therefore, the aim of the present study was to evaluate the effects of only OF on the post-thaw sperm motility of *S. cettii* compared to D532 and a combination of them at 50% (OF50%).

Sperm samples from 5 males were frozen using a freezing protocol optimised in our laboratory. Each sperm sample was thawed at 40 °C for 5 s and the motility was activated with OF100% and OF 50% of each female (*N*=5) or D532, then analysed by CASA system. Within each treatment, the data obtained was compared with ONE-WAY-ANOVA, followed by Duncan's test. To assess the fixed effects of male and female ID and their interaction, we used the GLM procedure. OF100% and OF50% enhanced (*p* < 0.05) respectively the total motility (50.4 ± 2%; 51.8 ± 1.9%) and duration of movement (46.1 ± 1.5s; 46.1 ± 1.5s) than D532 (38.5 ± 3.2%; 31.2 ± 1.8 s); higher values (*p* < 0.05) of velocity parameters (VSL, VCL, VAP) were obtained with D532 than other treatments. Sperm traits varied depending on parental ID and interplay between male × female (*p* < 0.05).

Although D532 boosted kinetic parameters more than OF, the authors retain that the sperm velocity could not be a key parameter for a successful fertilization in our cross-fertilization system. In fact, in a controlled RM that already favours the gametes encounter, obtaining a greater number of post-thaw motile sperm/egg that move for a longer time could potentially increase the reproductive efficiency of *S. cettii*. Thus, the use of OF alone in the AR could be a simple and effective activation/fertilization media to facilitate the management of riverbank operations, avoiding preparation, transport and use of AFM.

## O568

### On the road to domestication: a preliminary comparative genomics approach to reconstruct human and livestock correlates

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Since the Neolithic transition, human history has been accompanied by the presence of livestock species whose biodiversity has been molded by repeated human migratory waves. In such a