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## ASPA 24th Congress Book of Abstract

Roberto Mantovani & Alessio Cecchinato

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# Italian Journal of Animal Science

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## ASPA 24<sup>th</sup> Congress

*Padova, September 21-24, 2021*

### *Guest Editors*

**Roberto Mantovani (Coordinator), Alessio Cecchinato, Giovanni Bittante, Maurizio Ramanzin, Lucia Bailoni, Mauro Penasa, Flaviana Gottardo, Sara Pegolo, Giorgio Marchesini, Rebecca Ricci, Cristina Sartori, Marco Cullere, Marco Birolo, Severino Segato, Valentina Bonfatti, Marta Brscic, Luigi Gallo, Stefano Schiavon, Franco Tagliapietra**

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# **ASPA 24<sup>th</sup> Congress**

## ***Padova, September 21-24, 2021***

**#ASPA2021**

**24<sup>th</sup>**

**Congress of the Animal Science and production Association**

**24° Congresso dell' Associazione per la Scienza e le Produzioni Animali**

**Padova,  
September 21-24, 2021**

**Venue**

**“Fiore di Botta”**

**University of Padova**

**Via del Pescarotto, 8-Padova**

these results, the Maesso sheep had the lowest live weight (36.53 kg) and registered a lower CoI and TI, but a higher SI, described as an elipometric type. The Hidalgo females had the highest live weight (62.10 kg), and had the highest BI, CoI, II, TI, but the lowest CeI and SI, as longilinear morphotype. The highest PI (between 100 and 102), and therefore the best heavier animals more related to meat production, were López-Montenegro, Perales and Nuevo Serena lines. These results show the evolution of different lines within the breed and determine a different capacity to adapt to different environments, as well as a different aptitude for meat production. It would be necessary to confirm if these morphological differences are reflected in a differentiated genetic profile that allow their official recognition within the Merino breed.

## PO27

### Exploring pedigrees: an overall picture of biodiversity in Italian small ruminants

Alessio Negro<sup>a</sup>, Matteo Cortellari<sup>a</sup>, Arianna Bionda<sup>a</sup>, Stefano Biffani<sup>b</sup>, Silverio Grande<sup>c</sup>, Paola Crepaldi<sup>a</sup>

<sup>a</sup>*Dipartimento di Scienze Agrarie e Ambientali (DISAA), University of Milan, Milano, Italy*

<sup>b</sup>*Istituto di Biologia e Biotecnologia Agraria (IBBA), Consiglio Nazionale delle Ricerche (CNR), Milano, Italy*

<sup>c</sup>*Direzione, Associazione Nazionale della Pastorizia (Asso.Na. Pa), Roma, Italy*

Contact [alessio.negro@unimi.it](mailto:alessio.negro@unimi.it)

To avoid the reduction of biodiversity and genetic erosion, local breed conservation continues to be a relevant topic of rural development policy. Optimal breed management requires careful control of the inbreeding level within a breed together with the availability of accurate demographic information. The calculation of the main demographic and genetic parameters allows us to better estimate the short- and long-term breed risk status, as well as to determine the best management practices for breeds with unreliable data and so which require particular attention. The Italian association of small ruminant breeders (ASSONAPA) monitored all goats and sheep breeds in a national project entitled 'Conservation, Health and Efficiency Empowerment of Small Ruminant' (CHEESR-PSRN 2014–2020). This study described the panorama of pedigree information for Italian sheep and goat breeds. In this study, 81 pedigrees (35 for goats and 46 for sheep) were analysed. Using optiSel R package we calculated the pedigree depth (full and maximum generation traced) and completeness, and the effective size (Ne) applying Write's formula. Furthermore, for the 10 breed case-study, we estimated the longevity and the percentage of animals eliminated from pedigree during their first 3 years of life (for the triennium 2007–2009). The analyses showed a median pedigree depth, for goats and sheep, equal to 2 and 3 full generations (interquartile range IQR

=2–4 and 2–5), and 5 and 7 maximum generations (IQR =3–10 and 5–12), respectively. Pedigree completeness was variable; breeds with a complete first generation (median, IQR) were higher in sheep (34%, 19–47) than in goats (14%, 5–28). Overall, the median Ne was 176 in goats and 234 in sheep (IQR =74–547 and 128–774). The mean  $\pm$  SD longevity was  $5.6 \pm 1.8$  (range =3.9–7.5) and  $5.5 \pm 1.1$  years (range =4.3–7.6), respectively, with a marked difference (equal to 3 years) between, more and less selected, goat breeds. On average,  $16 \pm 22\%$  goats and  $25 \pm 11\%$  sheep (range =1–41 and 5–40) were eliminated before 3 years of age. In conclusion, the Italian panorama is very variable and the pedigree analyses depict very different situations. Ovine populations are characterized by greater effective size, pedigree depth, and completeness than caprine populations. When information is lacking, pedigree analyses can be corroborated by genomics to determine good practice in breed management.

## PO28

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

Elisa Somenzi<sup>a</sup>, Niccolò Franceschi<sup>a</sup>, Mario Barbato<sup>a</sup>, Licia Colli<sup>a</sup>, Erika Partel<sup>b</sup>, Matteo Komjanc<sup>b</sup>, Alessandro Achilli<sup>c</sup>, Heidi Christine Hauffe<sup>b</sup>, Paolo Ajmone Marsan<sup>a</sup>

<sup>a</sup>*DIANA – Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti, Università Cattolica del Sacro Cuore, Piacenza, Italy*

<sup>b</sup>*Department of Biodiversity and Molecular Ecology, Fondazione Edmund Mach, Trento, Italy*

<sup>c</sup>*Dipartimento di Biologia e Biotecnologie 'L. Spallanzan', University of Pavia, Pavia, Italy*

Contact [elisa.somenzi@unicatt.it](mailto:elisa.somenzi@unicatt.it)

The Rendena cattle is an autochthonous cattle breed from Val Rendena in the northern Italian region of Trentino Alto Adige. The breed is considered a dual-purpose breed (milk and meat) but the recent selection has emphasized milk production and quality. The breed is characterized by a small-medium size, good fertility and high longevity and is well adapted to the harsh Alpine environment. With a head count of ~4000 recorded cows, the Rendena cattle represent a source of income for many farmers in the Trentino Alto Adige region. In this study, 140 Rendena cows sampled in 31 different farms have been genotyped with the GGP Bovine 100K SNPchip (Neogen). Genotype data were used to estimate within-breed diversity and inbreeding and were compared with SNP data from 56 Eurasian cattle breeds to evaluate population structure and relationships. Principal Component Analysis (PCA) and Neighbour-net analyses performed on the Eurasian dataset indicated shared ancestry between Rendena and cattle breeds of the Original Brown Swiss group, but also revealed an original genetic makeup, thus confirming previous evidence from mitochondrial control-region data and lower density SNP profiles. Within-breed PCA highlighted the absence of

substructure and excluded the presence of crossbred individuals or showing a marked outlier behaviour. Some inbreeding was detected using a genome-wide analysis of runs of homozygosity (ROH) ( $F_{ROH} = 0.08 \pm 0.03$ ). The ROHs distribution across chromosomes appeared homogeneous and related to chromosome size. Most ROHs were private or common to very few animals. Exceptions were found in three genomic regions – on BTA6, BTA10 and BTA16 – where ROHs were shared by >25% of the animals tested. Noticeably, the ROH on BTA6 consisted in 33 consecutive homozygous SNPs shared by >50% of the animals. This region was found to harbour genes relevant for meat (NCAPG, LCORL) and milk production (LAP3).

## P029

### Role and characterization of dromedary breeding systems in northern Sahara: the PRIMA 'CAMEL-SHIELD' project

Elena Ciani

*Bioscienze, Biotecnologie e Biofarmaceutica, University of Bari, Bari, Italy*

Contact [elena.ciani@uniba.it](mailto:elena.ciani@uniba.it)

Dromedary breeding has a great socio-economic potential in southern Mediterranean countries as it contributes significantly to ensure food security for smallholders, preserving their cultural and ethnic identity and protecting fragile arid ecosystems. It also contributes to reduce the economic vulnerability (and thus increase economic resilience) of rural communities living in border areas affected by modern human migration movements. Milk and meat production represent the two main segments of the dromedary value chain, and they could play a leading role in ensuring better and equitable integration of stakeholders and the dissemination of relevant technological innovations. Encouraging dromedary breeding in these areas is a strategic priority to promote endogenous and sustainable territorial development. A rapid, albeit fragmentary, intensification is underway in the dromedary sector, mainly in peri-urban areas, because of an increasing demand for milk and meat from mini-dairies and slaughterhouses. This ongoing intensification process in dromedary breeding poses potential risks to the sustainability of this production system. The CAMEL-SHIELD project, financed under the PRIMA 2019 call, will develop value chain analyses and techno-economic management tools to implement and design innovative strategies for resilience and efficiency, based on exploiting the adaptive capacity of the dromedary production systems. In particular, the characterization about the use of primary resources and about the genetic make-up of the dromedary populations in the study areas (Algeria: Ghardaïa, El Oued and Ouargla; Morocco: Guelmin, M'Hamid El Ghizlane and Errachidia), as well as an assessment of the genomic regions possibly underlying their environmental adaptation capacity, for orienting conservation

and improvement actions, will be performed. The project includes six partner institutions from four countries: the University of Kasdi Marbah – Ouargla (UKMO), in Algeria; the Agronomic and Veterinary Institute Hassan II (IAV), and the University Mohamed V, in Morocco; the Agricultural Research Centre for International Development (CIRAD), and the National Research Institute for Agriculture, Food and Environment (INRAE), in France; the University of Bari, in Italy. The project will provide a first opportunity to apply, and further validate, the dromedary HD SNP array, currently under development within the frame of the 11th Illumina® Agricultural Greater Good Initiative.

## P030

### Ancient mitotypes in the houndlike dog breeds native of the Mediterranean Basin

Francesco Perini<sup>a</sup>, Irene Cardinali<sup>b</sup>, Simone Ceccobelli<sup>c</sup>, Anthony Gruppetta<sup>d</sup>, Carlos San José Marqués<sup>e</sup>, Amparo Martínez Martínez<sup>f</sup>, Asmaa Mohammed Aly Abushady<sup>g</sup>, Luis Monteagudo<sup>h</sup>, Luigi Liotta<sup>i</sup>, George Attard<sup>j</sup>, Emiliano Lasagna<sup>a</sup>, Hovirag Lancioni<sup>b</sup>

<sup>a</sup>*Dipartimento di Scienze Agrarie, Ambientali, Alimentari, Univeristy of Perugia (UNIPG), Perugia, Italy*

<sup>b</sup>*Dipartimento di Chimica, Biologia e Biotecnologie, University of Perugia (UNIPG), Perugia, Italy*

<sup>c</sup>*Dipartimento di Scienze Agrarie, Alimentari e Ambientali, University of Ancona (UNIVPM), Ancona, Italy*

<sup>d</sup>*St. Simon Veterinary Practice, Mosta, Malta*

<sup>e</sup>*Instituto de Investigación Sanitaria Biodonostia, IIS, Guipuzcoa, Spain*

<sup>f</sup>*Departamento de Genética, University of Cordoba, Cordoba, Spain*

<sup>g</sup>*Genetic Department, Faculty of Agriculture, Nile University, Cairo, Egypt*

<sup>h</sup>*Departamento de Anatomía, Embriología y Genética Animal, University of Zaragoza, Zaragoza, Spain*

<sup>i</sup>*Dipartimento di Scienze Veterinarie, University of Messina (UNIME), Messina, Italy*

<sup>j</sup>*Department of Rural Sciences and Food Systems, Institute of Earth Systems, University of Malta, Msida, Malta*

Contact [s.ceccobelli@staff.univpm.it](mailto:s.ceccobelli@staff.univpm.it)

The origin and evolution of extant dogs are still a puzzling question for geneticists. In order to assess the genetic diversity, phylogenetic relationships and the maternal origins among related modern dog populations, mitochondrial DNA (mtDNA), and in particular the D-loop hypervariable region 1 (HV1), has been widely exploited. The first investigations using maternally inherited mtDNA in modern dogs indicated that the southern part of East Asia is the place of origin. However, recent samples from archaeological sites have focused on Europe as much as possible, at least as a secondary center of domestication. In this study, eight dog breeds from the Mediterranean Basin that are