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## **Genetic variability for key biomarkers involved in body reserves dynamics in meat ewes**

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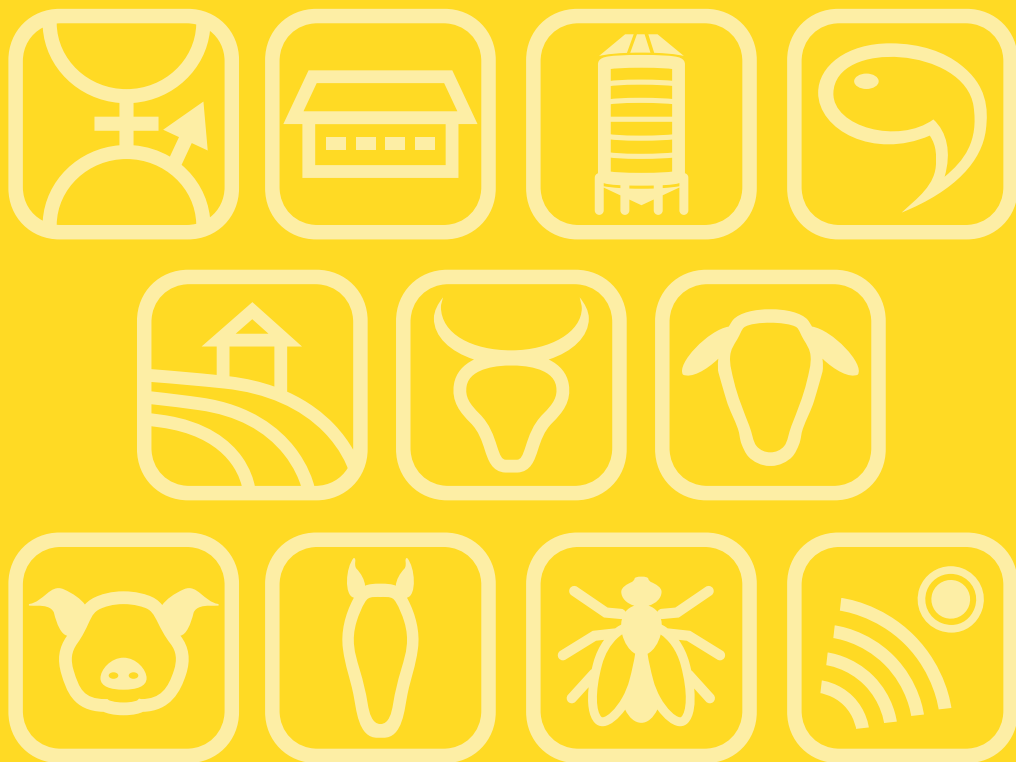
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# Book of Abstracts

of the 75<sup>th</sup> Annual Meeting  
of the European Federation of Animal Science



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# Book of Abstracts of the 75th Annual Meeting of the European Federation of Animal Science

Florence, Italy, 1<sup>st</sup> – 5<sup>th</sup> September, 2024



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Genetic variability for key biomarkers involved in body reserves dynamics in meat ewes

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The use and accretion of body reserves (BR) is a biological mechanism in ruminants to cope with negative energy balance and improve animals' adaptation. The aim of the present study was to understand the genetic background of BR dynamics using plasma biomarker profiles (NEFA, non-esterified fatty acids; BHB,  $\beta$ -hydroxybutyrate; T3, triiodothyronine; INS, insulin) in Romane ewes reared under two contrasting farming systems (FS; indoor, IND, n = 173; extensive, OUT, n = 486). Primiparous and multiparous ewes were monitored at three to five key physiological stages (PhySt: mating, M; mid-pregnancy, P; 2 weeks pre-lambing; bL; 3 weeks post-lambing; aL; weaning; W). The cov(ariance) components were estimated with the AIREML method with a repeatability animal model in the BLUPF90+ family. Parity, cohort, line for feed efficiency, litter size, and FS were fixed effects, while ewe, the permanent environment of the ewes, and residuals were random effects. Heritabilities for NEFA, BHB, T3, and INS ranged from 0.12 to 0.30, 0.07 to 0.14, 0.17 to 0.26, and 0.05 to 0.32, respectively, depending on PhySt (standard errors, SE 0.03 to 0.04). Genetic correlations between the PhySt ranged from 0.07 to 0.86, 0.41 to 0.9, 0.44 to 0.86, and -0.06 to 0.94 for NEFA, BHB, T3, and INS, respectively (SE, 0.06 to 0.14). Further analyses are in progress to estimate genetic correlations between biomarkers and identify associated QTL. In conclusion, genetic levers could be used to improve the adaptation of ruminants through BR dynamics. [Funding with iSAGE project 679302]

## Session 16

## Theatre 6

Genome-wide SNP markers from ddRAD reveals the population structure of Italian donkey populations

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Although more than 150 breeds and 53M donkeys (*Equus asinus*) are recognized worldwide, there is no commercial SNP array for this species. The ddRAD-seq technique was used to characterize the population structure of nine Italian donkey populations. More than 418M reads were generated and demultiplexed to obtain 1.90 million reads per sample, 60K raw markers and a filtered panel of 27K SNPs across the 30 autosomes. The outcomes highlighted the informativeness of the markers, the separation of populations based on their genetic origin or geographical proximity and showed low to moderate levels of inbreeding and admixture. The success of conservation plans was highlighted for some breeds. ROH islands mapped immune-response and local adaptation genomic regions, consistent with the rusticity and adaptability of the species. A panel of genome wide SNPs offers the possibility of comparative studies among breeds of different geographic ranges to provide insights into the origin and evolution of the species.