Provisional Book of Abstract

ASPA 26th Congress
Turin (ITALY), June 17–20, 2025

#ASPA2025
ASPA 26th Congress Book of Abstract
The 26th congress of the Animal Science and Production Association
***"Innovations in animal sciences: shaping the way for a sustainable future is under patronage* of**

Turin (ITALY),
June 17–20, 2025

Venue
Campus SAMEV (Scuola di Agraria e medicina Veterinaria)
Largo Braccini 2, Grugliasco (TO)– ITALY

P428

Genomic characterization of the Maltese cattle breed

Arianna Bionda[1], Vincenzo Lopreiato[2], Luigi Liotta[2], Viviana Floridia[2], Matteo Cortellari[1], Paola Crepaldi[1], George Attard[3]

[1] *Department of Agricultural and Environmental Sciences - Production, Landscape, Agroenergy, University of Milan, Milan, Italy*
[2] *Department of Veterinary Sciences, University of Messina, Messina, Italy*
[3] *Department of Rural Sciences and Food Systems, University of Malta, Msida, Malta*

Corresponding author: viviana.floridia@unime.it

Maltese cattle, known locally as "il baqra maltija", is a native population of Malta, with the earliest historical detailed text giving evidence of its presence and use of the oxen on the island dating back to 1240, with more specific reference going back to the 1400's. The breed was described phenotypically in 1915 as having two coat color variations (light brown and blue/brown), with an average height at the withers of 170 cm and having a carcass weight of 630 to 800 kg. The current population, less than 50 animals, retains some ancestral traits similar to North Africa cattle. During the 1930s, a breeding program was implemented with the intention to transform this breed into a dual-purpose one with the compulsory used stud bulls imported from UK (e.g. Brown Swiss, Ayrshire, Jersey), by the Department of Agriculture. Thus, corrupting the true genetic heritage of the population. This breed was ignored as it never proved to yield an adequate quantity of milk, and this fact contributed towards the almost total disappearance of this bovine population. The aim of this work is to analyse and characterize the genomic health of the current Maltese cattle population to initiate a reconstruction process of this unique genetic pool. The conservation of this breed would be crucial to maintaining Mediterranean biodiversity, particularly within the context of Malta's small and isolated environment. The genotypes of 8 Maltese individuals were analysed using the Affymetrix 65K SNPChip together with the data of 830 individuals from 30 different cattle breeds of European and African origin. The Maltese cattle showed high levels of inbreeding (0.57) with a very low effective population size (8). In the principal component analysis, Maltese grouped together with Italian beef breeds of Podolian origin, such as Chianina, Podolica, Romagnola and Marchigiana. Although small sample size and high consanguinity could have an influence on the results, the analysis of global ancestral components indicates an ancestral link with African breeds (NDama, Nelore and Lohani) cannot be excluded, while more obvious are ancestral components related to European breeds. In conclusion, while the results reflect the zootechnical ancestry of this population, they highlight the urgency of implementing a zootechnical recovery program, which could include cryopreservation of semen after genotyping, to avoid complete loss of this genetic pool.