

GENETIC VARIABILITY, INBREEDING AND CROSSBREEDING

carried out between 1985 and 2019. We genotyped the animals in 2019 using the GeneSeek® Genomic Profiler[™] Bovine LDv4 33K chip (Illumina Inc., San Diego, CA, USA) and performed GWAS using the GEMMA software. We found significant SNPs in all the studied breeds by the GWAS analysis. At the chromosome-wide level, a total of 79, 91, and 66 SNPs were identified considering all analyzed traits for MAR, CHI, and ROM, respectively. Pathways and gene ontology analyses suggest promising candidate genes located in overlapping or in proximity with the significant SNPs and involved in reproductive traits. Results show genetic relationships between the breeds, as well as relevant genes for the breeds' improvement, which will allow performing better selection programs. In this study for the first time, three of the main Italian beef cattle breeds were investigated by a genomic approach for fertility traits. The new genomic tools allow us to identify different markers of interest for the selection of the breeds, preserving the history and the traits that distinguish them. The selection programs used for the improvement of the Italian beef cattle breeds will benefit from the significant SNPs found in this study, especially those which are in common between breeds.

Acknowledgements

The authors wish to thank the ANABIC for providing SNPs data and phenotypic information of Italian beef cattle breeds. Thanks to CRAG for providing the tools to perform the analyses.

P092

Cryobanking of native Mediterranean brown trout semen as a tool for the safeguard of genetic resources

Nicolaia Iaffaldano^a, Giusy Rusco^a, Stefano Esposito^b, Emanuele Antenucci^a, Bruno Testa^a, Michele Di Iorio^a

^aDipartimento Agricoltura, Ambiente e Alimenti, University of Molise, Campobasso, Italy ^bMediterranean Trout Research Group, MTRG, Collagna, Italy Contact nicolaia@unimol.it

The Native Mediterranean brown trout (*Salmo cettii*) populations inhabiting Biferno and Volturno rivers in Molise are decreasing due to poorly regulated fishing activities, river pollution and the introduction of allochthonous strains. This last factor has triggered an overall genetic impoverishment, therefore reducing the original genetic variability. Because of these factors, the conservation status of *S. cettii* in the Mediterranean area is now considered as 'critically endangered' by IUCN Italian Red list. In this regard, the project 'LIFE' Nat.Sal.Mo, recently funded by the EU, aims to ensure the recovery and the conservation of native trout in Molise river basins. In particular, the creation of a sperm cryobank is a milestone in the Nat.Sal.Mo project and is an effective strategy for the protection of the biodiversity of the local Mediterranean brown trout populations. The purpose of this work was to depict the results achieved during the first 2 years of the project when it comes to the creation of the first European cryobank and its practical use in the artificial fertilization schemes to safeguard the genetic resources and improve the genetic variability of native trout. Autochthonous specimens were captured using fixed traps allocated in the main attractive spawning sites. Semen was collected by stripping and was extended to reach a final cryoprotectant concentration of 0.15 M glucose and 7.5% methanol and loaded into 0.25 mL plastic straws, obtaining a final sperm concentration of 3×10^9 sperm/mL. The straws were equilibrated for 15 min above ice at a height of 3 cm, then frozen by exposure to liquid nitrogen (LN2) at 3 cm above LN2 level for 5 min and finally placed in LN2. During the first 2 years of activities 1287 semen doses from 93 native individuals were stored. About 25% of these doses were used for artificial fertilization. In total around 90,000 eggs were fertilized with frozen semen, obtaining a yield to eyed eggs of about 70-75%. The creation of the first sperm cryobank of pure Mediterranean trout populations with a high genetic variability will be useful even after the end of the project for Molise river basins as well as for other Italian basins where S. cettii is at risk of extinction. Besides being a supportive tool in ensuring the sustainability of the project in the future, it represents a powerful multiplying effect which will affect other neighbouring areas at a national level and other European river basins.

P093

Interspersed repeated elements analysis in *Camelus dromedarius* CSN1S2 gene

Ahmed Abdelmaged Sabah Mohammed^a, Carmine Versace^a, Daniela Gallo^b, Giustino Gaspa^a, Gianfranco Cosenza^b, Alfredo Pauciullo^a

^aDipartimento di Scienze Agrarie, Forestali e Alimentari, University of Turin (UniTo), Grugliasco, Italy ^bDipartimento di Agraria, University of Naples, Portici, Italy Contact alfredo.pauciullo@unito.it

The α s2-casein (CN) is a milk protein fraction encoded by the CSN1S2 gene. Previous studies on dromedary milk proteins mainly focused on the other three fractions (α s1-, β - and k-CN), and, although there is globally growing interested in camel milk, studies focusing on α s2-CN are very limited. In this respect, no information has been reported on retrotransposons (RTs). These repeats, also known as Interspersed elements (INEs), are informative genetic markers useful as phylogenetic tools for clustering, evolutionary and population structure studies, rather than for the setup of food traceability methods. Aim of this study was to identify and characterize INEs in the dromedary CSN1S2 gene. Analysis has been carried out using RepeatMasker as bioinformatic tool. Three long interspersed elements (LINEs) were found

