

involved and, indirectly, the safeguarding of their biodiversity. The main aim of this work is to emphasize the decisive role of the quality certification of *Provolone del Monaco* as a driving force for the development of both the cheese makers/producers of the product and the territory. For this purpose, through the administration of standardized questionnaires, a model of detected preferences has been carried out giving evidence of the importance of quality certification in influencing the consumer's purchasing actions. Considering that *Provolone del Monaco* received POD recognition in 2008, and that its area involves up to thirteen municipalities of the Sorrento peninsula, we could justify in terms of Brand fidelity the growth of the turnover.

Acknowledgements

The research was funded by Consorzio Provolone del Monaco. The authors wish to thank Associazione Allevatori Campania Molise.

O427

Assessing signatures of selection and climate adaptation in European and African livestock

Mario Barbato^a, Floro De Nardo^b, Daniele Bigi^c, Elia Vajana^d, Elisa Eufemi^a, Paola Crepaldi^e, Paolo Ajmone Marsan^a, Licia Colli^a, Pablo Orozco-terwengel^f, Michael W. Bruford^f and Isa M. Russo^f

^aDepartment of Animal Science, Food and Nutrition, Università Cattolica del Sacro Cuore, Piacenza, Italy

^bRARE, Associazione Italiana Razze Autoctone a Rischio di Estinzione, Italy, Catanzaro, Italy

^cDipartimento DISTAL, Bologna, Italy

^dInstitute of Biosciences and BioResources (IBBR), National Research Council (CNR), Sesto Fiorentino, Italy

^eDipartimento di Scienze Agrarie e Ambientali, Produzione, Territorio, Agroenergia, Università degli Studi di Milano, Milano, Italy

^fSchool of Biosciences, Cardiff University, Cardiff, United Kingdom

Livestock farming is an economically and socially important sector of agriculture and contributes 40% of the value of the agricultural output globally. Currently the global demand for livestock products is increasing with the rapidly growing human population, urbanisation, increase in incomes and a shift in diet. Climate change is likely to affect agricultural systems on many levels such as heat stress in livestock, changes in production and quality of feed crop, water availability, animal growth and milk production, disease, reproduction, and biodiversity. The domestication and dispersal of livestock along with environment-mediated selective pressures have shaped phenotypic variation and left specific signatures in the genomes of locally adapted breeds. Here we studied existing and new genome-wide genotype data

to understand livestock adaptation to climatic extremes by using three species (cattle, goat, and sheep). Breeds from challenging climates throughout Europe and northern/central Africa were compared. For each comparison, we performed selection signature analysis through sliding-windows F_{ST} and XP-EHH, and identified the genes intercepted by significant selection sweeps. We applied a consensus by majority approach to select the genes under putative selection within and across species. Around 30% and 21% of all the genes identified across species were previously described in the literature to be associated with fat deposition and overall feed efficiency, and to adaptation to harsh climates, respectively. Similar proportions were recorded in the within-species comparisons. These preliminary results suggest a key role of energy management in the adaptation strategies of ruminants, likely in the shape of increased resilience, rather than resistance to adverse climate.

O285

Genomic characterization of the Comune di Sicilia goat, a local Sicilian genetic resource

Arianna Bionda^a, Matteo Cortellari^a, Vincenzo Lopreiato^b, Paola Crepaldi^a, Vincenzo Chiofalo^c and Luigi Liotta^b

^aDepartment of Agricultural and Environmental Sciences, University of Milan, Milan, Italy

^bDepartment of Veterinary Sciences, University of Messina, Messina, Italy

^cConsorzio di Ricerca Filiera Carni e Agroalimentare (CoRFilCarni), Messina, Italy

Local breed conservation is important to maintain enough genetic variability to face future changes, preserve unique genetic variants of interest, and support human economy and culture. This is particularly true in Southern Italy's marginal areas, where goat farming traditionally relies on autochthonous breeds. Among these, the *Comune di Sicilia* (CS) goat is an ancient breed counting about 500 heads, reared in semi-extensive conditions in western Sicily primarily for milk production. To attribute the breed status of a population, historical, phenotypical, and genomic characterization are needed. Thus, with the BIOSAVE project's support, this study aims to investigate CS's genetic relationship with other Italian goat breeds and identify selection signatures related to specific morphological traits.

79 CS goats, sampled from two farms located in Palermo, were genotyped with Illumina SNP65 bead chip and compared with 437 goats of 14 breeds. After quality control and exclusion of related animals, 487 goats, including 72 CS, were retained. Multidimensional scaling (MDS), admixture, and genetic distance analyses were performed. Runs of homozygosity and the related inbreeding coefficient (F_{ROH}) were calculated. ROH and F_{ST} were used to compare polled/horned and with/without microtia CS individuals.

The results indicated that CS subjects clustered together and were discernable from other breeds, and located near Derivata di Siria, Argentata dell'Etna, Nicastrese, Messinese, and Aspromontana populations. The best-fitting admixture model ($K = 12$) revealed two unique signatures in CS. Another relevant genomic cluster found in CS was in common with other Southern Italian breeds.

CS presented a F_{ROH} similar to other breeds from Southern Italy, half of which derived from ROH >16 Mb implying recent inbreeding events or a reduction in the breed consistency.

The low F_{ST} values found comparing horned and polled goats suggest that this trait is not fixed in the population yet. Some genes detected in goats with microtia are related to the same phenotype in humans or characterize another breed presenting microtia, the LaMancha goat.

These results support that CS can be genomically distinguished from other breeds reared in Italy. Further investigations are needed to identify the genes responsible for peculiar morphological traits found in this population.

Acknowledgements

Supported by CoRfilCarni through the BIOSAVE project (PSR Sicilia 2014–2020, Sub-measure 10.2b, n. G49J21006760009).

O372

BITE v.2: a user friendly R package for genomic analysis

Stefano Capomaccio^a, Marco Milanese^b, Elia Vajana^c, Lorenzo Bomba^d, Giovanni Chillemi^b, Paolo Ajmone-marsan^d and Licia Colli^d

^aDepartment of Veterinary Medicine, University of Perugia, Perugia, Italy

^bDepartment for Innovation in Biological, Agro-food and Forest systems (DIBAF) University of Tuscia, Viterbo, Italy

^cInstitute of Biosciences and BioResources IBBR-FI, CNR, Sesto Fiorentino, Firenze, Italy

^dDepartment of Animal Science, Food and Nutrition, Università Cattolica del Sacro Cuore, Piacenza, Italy

Genotyping and high-throughput sequencing have experienced a dramatic cost reduction, forcing geneticists to acquire cutting edge bioinformatic skills for managing large genomic datasets. However, neither all researchers have a proper bioinformatic education nor the learning curve is an easy one in the 'big data' domain. Moreover, researchers are often puzzled when it comes to the selection of the most appropriate tool, especially when the integration of multiple analyses is required to obtain meaningful results.

BITE (BioInformatics Tools for Everyone) has successfully served the scientific community providing a set of user-friendly functions for SNP data handling and facilitating visualization, interpretation, and usage of results from third-party software in

biodiversity analyses. Besides its capability to interact with the most common genomic data file types, BITE returns publication-grade plots, summary statistics, reports and ready-to-use files in downstream analyses.

The new version of BITE will be focused on replacing outdated and no longer maintained dependencies, guaranteeing long term support and usage (ie. Docker instance), with new functionalities and improved performance.

In this iteration genomic data also be handled in VCF format. Functions for quality control checks and exploratory analyses on genetic diversity and structure are updated with flexible choices. For example, F-statistics and genetic distances will be provided and LD pruning have been implemented. Moreover, MDS or PCA (and Supervised PCA) will be obtained, together with a dynamic visualization tool to better explore population relationships. Finally, an updated function for genomic-informed subsampling is provided to harmonise sample sizes in case of extremely unbalanced sampling efforts. Furthermore, BITE will allow managing third-party output files from software that estimate global membership coefficients (e.g. Admixture). The package will return rectangular or circular barplots, maintaining a consistent colouring of the clusters as the number of ancestral populations increases. A function to identify the best number of ancestral populations will be also included. Besides the possibility to run TreeMix software with or without bootstrapping, it is now possible to plot f_3 and f_4 statistics. Moreover, a specific function to choose the optimal number of migration edges has been added. All graphics have been improved and a report of all analyses can be created by the user.

O481

Copy number variants in 23 Italian local chicken breeds

Filippo Cendron, Martino Cassandro and Mauro Penasa
Università di Padova, Dipartimento DAFNAE, Legnaro, Italy

Copy number variants (CNV) are structural variations inside the genome that contribute to several adaptive and economic traits in livestock. The present study aimed to investigate and characterize the presence of CNV, copy number variation regions (CNVR) and candidate genes of 23 Italian local chicken breeds: Ancona, Bianca di Saluzzo, Bionda Piemontese, Cornuta di Caltanissetta, Livorno Bianca, Livorno Nera, Mericanel Della Brianza, Modenese, Mugellese, Ermellinata di Rovigo, Millefiori di Lonigo, Padovana Argentata, Polverara Bianca, Padovana Camosciata, Padovana Dorata, Polverara Nera, Pepoi, Robusta Lionata, Robusta Maculata, Romagnola, Siciliana, Valdarnese, and Valplatani. A total of 530 animals (20 to 24 animals per breed, 50% males and 50% females) were genotyped with 600 K Affymetrix[®] Axiom[®] HD chip and 580,954 SNPs were available for CNV analysis. The Hidden Markov Model of the PennCNV