brood cows of the teaching farm of the Department of Veterinary Science of the University of Turin giving birth for at least their second calf are involved in the project. Colostrum is collected at about 7 different time points depending on the delivery time (soon after delivery, and after 6, 12, 18, 24, 30, 36, 48 and/or 72 h). At this stage of the project, miRNAs were extracted from the colostrum collected at four time points of the first three cows involved in the project. The Maxwell® RSC Instrument using the Maxwell® RSC miRNA Blood Kit was used. The quantity and quality of miRNA extractions were tested with the Small RNA kit of the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA) for the following NGS analysis. Library were prepared using the TruSeq® Small RNA Library Prep Kit and were run on the MiSeq instrument (Illumina, San Diego, CA, USA). Sequencing data were uploaded to the Galaxy web platform (usegalaxy.org) and bioinformatics analysis are undergoing using the MiRDeep2 tools for the identification of the miRNAs expressed in the colostrum at the different time points. Differences between time points will also be checked and statistically analysed.

P249
A genome wide association study for diarrhea resistance in pre-weaned rabbits identified markers useful to breed for increased animal welfare

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Animal welfare and reduction of antimicrobial agents are gaining more and more importance in defining sustainable livestock production systems. Adopting novel breeding and selection strategies that directly or indirectly address these aspects can also improve efficiency and farmers' profitability. In commercial rabbitries, diarrhea of newborn rabbits represents one of the major sources of economic losses. Genetic resistance against diarrhea can be dissected using genomic approaches. In this study, we carried out a case-control genome-wide association study for identifying genomic regions affecting the sensitivity to pre-weaning diarrhea in a commercial rabbit population. Animals included in the study were from litters produced by crossing 7 bucks and 45 does. A total of 331 newborn rabbits (149 healthy and 182 with diarrhetic) were selected from litters presenting at least one case and one control animal. Genotyping of the selected rabbits was carried out with the Affymetrix Axiom OrcunSNP Array, which analyse a total of 199,692 single nucleotide polymorphisms (SNPs). PLINK v.1.9 was used for quality checks and data filtering whereas

association was carried out with GEMMA v.0.98 via linear mixed models. A main peak of association was identified on rabbit chromosome 12. Results were further validated by genotyping the associated DNA markers in additional cases and controls from another cohort of the same rabbit population. Fine mapping of the region based on whole genome resequencing data obtained from a few cases and controls identified a few candidate causative mutations in genes involved in basic immunological functions. The genomic information here obtained will be useful for implementing a marker assisted selection program aimed at improving resistance against pre-weaning diarrhea and improving animal welfare and the sustainability of the rabbit production system.

P282
Genomic inbreeding distribution in Italian dairy goat farms

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Managing the value of inbreeding within dairy goat farms is becoming a crucial point in light of the increased use of artificial insemination especially in northern Italy. In particular, thanks to the increasing amount of genomic data made available by the Italian Sheep and Goat Breeders Association through its projects, the calculation of the genomic inbreeding could represent the most effective monitoring tool at our disposal.

The purpose of our work is to provide an overview of the current situation of the average level of genomic inbreeding in Camosciata delle Alpi (CAM) and Saanen (SAA) goat farms all along the Italian peninsula.

We analyzed the genomic inbreeding coefficient (F_{ROH}) of 1949 individuals of CAM and 668 of SAA belonging to 70 different farms genotyped with the 50k SNPchip within the CHEESR project. We found an average F_{ROH} value of 0.056 (± 0.03) for CAM individuals and 0.063 (± 0.03) for SAA individuals considering all the Peninsula. Data at our disposal came from 13 different Italian regions, mostly from two regions in the north of the country, Lombardy (mean F_{ROH}: 0.05) and Piedmont (mean F_{ROH}: 0.05). The highest average inbreeding values were observed Calabria (0.08 ± 0.03) and Valle d'Aosta (0.08 ± 0.06) for CAM and Calabria (0.07 ± 0.03) and Veneto (0.07 ± 0.04) for SAA. At the farm level, we observed an average F_{ROH} value of 0.056 (± 0.01) for the CAM and 0.06 (± 0.01) for the SAA considering only farms with at least 10 genotyped individuals. Using a hierarchical Anova model (Region, Farm|Region) we observed significant differences among farms within the region ($p < 0.001$) for both the breeds

and a difference between the values of the single regions only for CAM ($p < 0.001$) with maximum values of 0.10 and 0.11 for CAM and SAA respectively.

Our results underline a highly significant difference between farms' values as well as the low average inbreeding levels of the two populations. This suggests that, as the genomic data increases, it will be possible to use the F_{ROH} as useful information for breeders to monitor the trend of inbreeding within their herds. We hope that with the new projects currently underway we could have a greater amount of genomic data to outline a more precise situation of the inbreeding distribution per farm.

P303

Toward a new version of medium-density Buffalo SNPchip array for Mediterranean breed

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The water buffalo (*Bubalus bubalis*) is a large bovid used, since ancient times, for human needs. Today it is bred in many countries across the globe. There are two distinct species of water buffalo: river (from western Asia to Europe) and swamp (more common in eastern Asia). In Italy, river buffalo have been present since the Roman period and today Italian Mediterranean is bred for milk production, used to produce 'mozzarella di Bufala campana'.

To study buffalo genomic variability, a first SNP array (Axiom Buffalo Genotyping – ThermoFisher Scientific) containing 90k SNP was developed by the International Buffalo Genome Consortium, covering the water buffalo (river and swamp) genome-wide diversity. However, to improve milk quantity and quality in the Italian Mediterranean breed, also through Genomic Selection, a new and breed-specific version of the Axiom Buffalo array was developed.

The first step was to validate the already existing SNPs Axiom Buffalo array in the Mediterranean breed. All the probes were mapped to the most recent Mediterranean buffalo reference sequence, removing the ones with low mapping quality or without mapping. After that, a quality control of the probes was performed using around 700 Mediterranean animals. Probes with low call rate, monomorphic or with not optimal clustering were removed. The remaining probes were evaluated: SNPs previously identified as important (e.g. present in IMAGE array, already associated with milk characteristics, etc.) were prioritised. In almost all the cases only one probe was kept. Finally, around 85k probes (and 76k SNPs) over 123k available sports were retained.

The second step consisted in filling the new array gaps using WGS Mediterranean data. The sequences were aligned and variant called, using state-of-the-art bioinformatic pipelines. SNPs associated with functional genes were added (for example, casein gene cluster), together with SNPs in the Y chromosome (which was not previously included), and in the regions with lower density, compared with the expected. The final array density reached around 35 SNPs/Mbp. In conclusion, the new version of the buffalo array has 25% more SNPs than the first released, with a very high usage rate in the Mediterranean breed.

P349

Using udder traits in a selection index for udder health in Italian Mediterranean Buffaloes

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Since 2018, after the introduction of IBMI, the breeding objectives of the Italian Mediterranean Buffalo population have changed, focusing on milk production, mozzarella yield and functionality. Udder conformation (UC) traits play an essential role in both mastitis resistance and milking ability but they are not included in the current selection index despite their importance for health and longevity. We, therefore, propose an aggregate selection index (ASI) considering both the economic importance and the genetic parameters of milk production traits, $MSCS_{150}$ (geometric mean of somatic cell score at 150 days in milk) and the UC traits (fore udder attachment– FUA; rear udder width– RUW; rear legs height– RLH; teat direction – TD; teat length – TL and