Selecting the animals with the largest GC values led to lower prediction accuracies, whereas the inclusion in the core of animals with the lowest GC showed the best results.

O252

Genetic aspects of longevity in Italian Mediterranean buffalo

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Functional longevity estimates the animal's ability to not be culled due to low production, low fertility or impaired health status. In the past, longevity was not considered as a breeding objective because such an information was available only when the animal was culled. However, longevity in livestock has been experiencing a growing economic importance over the past two decades, including the Italian Mediterranean Buffalo (IMB). The aim of this study was to present results of the first genetic evaluation of functional longevity in the IMB. Data from 178.619 buffalo with first calving from 1992 to 2019 were used. A Weibull mixed survival model was used and functional survival was defined as the number of days from the first calving until culling or until the last available date of milk recording (censored animals).

The model included time-dependent effects of herd-year-season, the year and season of calving, parity, milk production and yield, and morphological traits, as well as time-independent effects the age at first calving, year of birth, herd size and as covariate the milk production within the first 60 days.

Results indicated that the average duration of productive life was 1225 days. Among fixed effects which have shown a higher risk of culling (RC) there are: calving in autumn (RC =1.101), being too old at first calving (RC =1.102). Regarding the morphological traits, females with lower scores for udder and feet and legs composite traits showed the greater culling risk. Moreover, the effect of the milk production level showed a strong impact on the longevity of IMB with a significant risk of elimination ($p < 0.01$) when milk production decreased. The heritability on the original scale was 0.12. Despite not having selected for this trait, the genetic trend of the bulls showed a favourable trend for longevity since 2009.

In conclusion, these results showed that it is possible to implement a genetic evaluation for longevity in the IMB. A next step further would be to economically quantify the value of survival traits and their possible inclusion in the IMB selection index breeding value. To avoid bulls with unfavourable breeding values for longevity, may improve productive life in the population and prevent hidden economic losses.

O240

Effect of artificial insemination on genomic population structure in Camosciata delle Alpi dairy goat breed

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The use of artificial insemination (AI) is becoming a consistent reality for the Camosciata delle Alpi goat breed, especially in the dairy farms of northern Italy. It is therefore very interesting to understand the impact of the diffusion of AI in our autochthonous populations also in light of the future implementation of new genomics indexes that have been developed by ongoing projects.

Inside one these projects, the CHEESR project, we analyzed pedigree, genotyping data (obtained with a 50k chip) and more than 23000 production records of 1231 subjects of Camosciata delle Alpi belonging to 64 farms.

We classified all the individuals into three different groups based on the use of the AI in their lineage: subjects deriving from direct use of artificial insemination (FA), from parents deriving from direct use of AI (SO) and from natural mating (MN). For each of the 3 groups, we calculated the average values of 5 production parameters (Milk Kg, Protein Kg and %, Fat Kg and %) and tested their difference between groups, the F_{ROH} values and the classification of Runs of Homozygosity into length classes. All analyses were performed using PLINK1.9 software and R-base package functions.

As regards the production data, we found significantly higher values ($p < 0.001$) in the FA group than the other two for all five traits. Instead, no statistical differences were found between MN and SO. In terms of F_{ROH} values and distributions of ROH classes, SOs showed the highest mean F_{ROH} (0.07), FAs the lowest (0.057) and MNs the middle values (0.065); the distribution of the different ROH classes was homogeneous in all three groups.

These results highlight differences in the productivity levels between the FA group and the other two groups (MN and SO) but not between the latter two as one would expect. The most interesting finding is the unexpected slightly higher level of

inbreeding in the second-generation offspring of AI (SO), which might be due to the unbalanced use of parents deriving from the AI suggesting the need of an optimal contribution evaluation of the mating plans. In conclusion, AI could represent a very important tool for improving the Italian Camosciata delle Alpi population both from a production and an inbreeding management point of view.

O472

An association analysis between CSN3 genotype and milk yield in Italian Mediterranean river buffalo

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Buffalo milk is characterized by the presence of all 4 casein fractions ($\alpha s1$, α, $\alpha s2$ and κ) encoded by 4 genes (*CSN1S1*, *CSN2*, *CSN1S2* and *CSN3*, respectively) mapped on chromosome 7. In particular, κ-CN plays a crucial role in the formation of stable casein micelles and has a key influence on milk-clotting. The *CSN3* gene is divided into 5 exons of which the exon 4 codes for 160 out of 169 aa of the mature protein. Mutations in this exon are responsible for the quali-quantitative differences of gene expression in cattle. Different studies have been focused on the identification of polymorphisms also in buffaloes. Particularly investigated is the SNP HQ677596:c.536C > T at the nt 377 of the exon 4 that leads to the aa change p.Ile135 > Thr of the mature κ-CN. This replacement changes the theoretical MW of the buffalo κ-CN from 19,114.7 to 19,102.6 Da; increases hydrophobicity, with the hydropathicity average increasing from -0.526 (Thr) to -0.495 (Ile); and causes the loss of an O-glycosylation site in the variant 135Thr. However, despite the existence of several studies, nowadays the association of *CSN3* SNPs with buffalo milk quantity has not still deeply identified. The aim of this study was to evaluate possible effects of the SNP c.536C > T on milk yield (MY) in Mediterranean river buffaloes. A total of 7601 records for MY measured monthly on 1141 lactations of 753 buffaloes belonging to different farms located in Campania region (Italy) were

analysed. To estimate the frequencies of this SNP a method based on ACRS-PCR has been adopted. The major allele (c.536C) had a relative frequency of about 0.6 and χ^2 values showed that there was no evidence of departure from the HWE ($p \leq 0.05$). Association between *CSN3* polymorphism and MY was investigated with a mixed linear model that included effects of parity, calving season and month of production. A significant association between c.536C > T and MY was found ($p < 0.05$). In particular, the CC genotype showed an average daily MY approximately 0.62 kg higher than TT buffaloes. Although such results need to be confirmed with large-scale studies in the same and other buffalo populations, they might offer useful indications for the application of MAS programmes in buffalo and, in the future, they might be of great economic interest for the buffalo dairy industry. Infact, increases in average MY and, consequently, in mozzarella PDO production may be expected.

O283

The effect of ancestral and SNP panel genotyping on genomic inbreeding coefficients from imputed SNP in Holstein-Friesian dairy cows

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Imputation of whole genome single nucleotide polymorphisms (SNP) data is routinely applied in dairy cattle breeding because of the reduction of genotyping costs. The central idea is to genotype few core animals (i.e. animals whose genome is represented in the entire population) with high density (HD) SNP panels, many animals with low or medium density (LD/MD) SNP panels, and impute the LD/MD genotypes to HD. Imputation success depends on: (i) the relationship between the core animals genotyped in HD and the animals to be imputed from LD/MD to HD (for e.g. parent-offspring), (ii) the distribution along the genome and the number of SNP in the LD panels and (iii) the linkage disequilibrium between SNP in the LD/MD and in the HD.
The aim of this study was to evaluate the combined effect of ancestral genotyping and SNP imputation on the estimation of