

whereby no statistical significance was recorded. Results show a small number of certain bulls from the different lines in the breeding and relatively high use of natural service sires. Furthermore, considering the current living bulls, some bull lines are no longer in breeding. Increasing the number of productive bulls and improving longevity aid in the herd's average production enhancement, aiming to develop sustainable breeding strategies and maintain genetic diversity in the Busha cattle population.

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Mule carcass characteristics and meat quality

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Donkey carcass parameters and donkey meat quality characteristics have been determined in previous studies, while mule carcass and meat quality traits have scarcely been evaluated. The aim of the present study was to compare the carcass data and meat quality parameters obtained from 10 mules slaughtered, respectively, at an age of 5 ± 1 years and at an age of 10 ± 1 years. All the animals were weighed before their arrival at abattoir; the carcasses were transferred to a cold room at a temperature of 4 °C and stored suspended by the hind legs. 24 h after slaughtering, the cold carcass weights and the dressing percentages were recorded. From each carcass, 24 h after slaughtering samples of the muscle *Longissimus thoracis* (LT) were collected. Chemical composition was determined 24 h after slaughtering, while colour parameters were measured 48 h after slaughter using a Minolta CM-3600 D spectrophotometer in order to determine the L* (lightness), a* (redness), and b* (yellowness).

Meat samples for tenderness determination, weighting approximately 30 g, were stored in the cold room at 4 °C for 7 days post slaughter before evaluating the shear force values, determined using a Warner-Bratzler device. The shear force values were expressed in kg/cm². Analysis of variance was used to determine the significant differences in the values determined in this study; significant differences were shown when $p < 0.05$. Carcass characteristics determined in both groups of animals did not show significant differences. Meat sampled in animals slaughtered at an age of 10 years showed significant ($p < 0.05$) higher content of fat (5.22% vs 4.09%) and cholesterol levels (0.88 mg/100 g vs 0.52 mg/100 g) compared to younger mules. Meat produced by older mules was significantly ($p < 0.05$) darker (L* 31.09 vs 39.71, a* 13.8 vs 17.1) compared to the values determined in younger mules. Meat tenderness evaluation found not significant differences in both the groups of mules, obtaining values of shear force not particularly appreciated by the consumers. The results

obtained in this study confirmed the need of adequate feeding strategies and good farm practices in mules breeding in order to produce a more tender mule meat.

O411

The use of genomics in dairy cow farming – results from the GENORIP project

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GENORIP (GENOmIC tool for the management of REProduction in dairy cattle and for the control of inbreeding) is a project funded by Lombardy Region. The aim was to release an innovative tool for the control of inbreeding, the maintenance of genetic variability in cattle breeding and to facilitate the choice for animal replacement based on genomic information of herd females. In recent years, thanks to reduced genotyping costs, genomic selection has become attractive for breeders and farmers. Current genotyping techniques make it possible to determine at low cost the genotype of an animal in hundreds of thousands of markers known to be associated with phenotypic variability and to use this information to select animals. GENORIP's partners are 7 farms of the Lombardy region, ARAL and INSEME S.p.a, together with the University of Milan. More than 6000 females of Italian Friesian cows were sampled and genotyped with the Neogen GGP Bovine 100K SNP chip in the 7 partner farms and in other 50 farms involved in the dissemination phase. Principal component analysis (PCA) was applied for analyzing the genetic diversity within and among farms using the SVS 8.9 software of Golden Helix. Run of Homozygosity (ROH) and the genomic inbreeding (FROH) were obtained using the detectRUNS package of the R software. Genotype frequencies for mendelian disease, fertility and production mendelian traits were also obtained. PCA showed clustering of cows within herds according to sires used in each farm, whereas when analyzed jointly herds overlap except one due to the selection goal pursued by this farmer. ROH were found in all chromosomes with an average length of 2,703,811 bp covering 12.7% of the genome. The ROH analysis showed several genomic regions that appears under selection at the population level, while a specific region on BTA4 is under selection in one herd, harboring genes related to the specific breeding strategy of the farmer. The F_{ROH} values obtained, considering ROH greater than 16 Mb, varied from 0.004 to 0.325, with the highest average value for the F_{ROH} of 0.136. Among mendelian heritable diseases, the Haplotype Cholesterol Deficiency was the one with the largest of carrier animals, i.e. 5.6%. A process to assist farmers in genomic management of reproduction was released tailored to each farm.