

two genes involved in *de novo* FA biosynthesis (*ACACA* and *SCD*). In conclusion, female sex and local genetic background appear to have significant influence on expression of genes associated with LC-PUFA pathways.

Acknowledgements

This study was funded by the project PRIN-Bando 2017 Prot. 2017S229WC.

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Study of fertility traits in Italian Jersey Cattle

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Selection Index of Italian Jersey cattle is composed by breeding values (BVs) of production traits, type traits and somatic cell score. Knowing selection for milk yield has been proved to deteriorate fertility performances, aim of the Italian Holstein, Brown and Jersey Breeders Association (ANAFIBJ) is to develop a fertility index inspired to the model they use for Italian Holstein breed. The model used considers different phenotypes for heifer and cow evaluation, but while for Holstein only the first three parities are considered, for Jersey all parities are considered to overcome the lower size of the population. Starting from two different datasets, containing data on inseminations and lactations we derived several fertility traits. From the inseminations dataset we harvested information on the dates of services, which we grouped in baches of a maximum length of 300 days. The groups of inseminations have then been attached to the calvings happened in an interval of 260–300 days from at least one of the services in the group. Phenotypes estimated for both heifers and cows are Non-Return Rate at 56 days (NRR56) and Interval from First to Last service (IFL); Age at First Insemination (AFI) has been computed only for heifers, while Days from delivery To First Service (DTFS) and Equivalent Milk Yield 305 (EMY305) only for cows. The values of the phenotypes have been filtered to be in line with biological and economic criteria of cattle farming. The final dataset is composed of 35081 records for heifers and 100285 records for cows. Correlations and Co-Variances between the phenotypes have been calculated. For Heifers we observe a slight positive correlation between AFI and NRR56 ($\rho_{xy}=-0.061$) and a negative correlation between NRR56 and IFL ($\rho_{xy}=-0.349$); IFL and AFI are negatively correlated ($\rho_{xy}=-0.048$). For cow fertility traits NRR56 resulted to be positively correlated with DTFS ($\rho_{xy}=0.088$) and negatively correlated with EMY305 ($\rho_{xy}=-0.092$) and IFL ($\rho_{xy}=-0.293$); DTFS resulted negatively correlated to IFL ($\rho_{xy}=-0.015$) and EMY305 ($\rho_{xy}=-0.045$), while IFL and EMY305 resulted positively correlated ($\rho_{xy}=0.083$). The next step is to calculate genetic parameters and EBVs for fertility traits for Italian Jersey.

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Analysis of longevity performance in the different bull lines of Busha cattle in Croatia

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Longevity is a complex trait; the longevity performance of the sire is a measurement of the time it's produces in a herd and is determined by various factors such as fertility, health, and workability. The sire fulfilling an active working life in the herd increases the average herd production and efficiency by reducing input costs. Busha is a native breed of cattle reared in an extensive system and classified as an endangered population – maintained. From the establishment of the Herd Book, breeding systematization defined 24 lines of bulls (LB). The aim was to analyze the herd life of different bull lines of the Busha cattle breed in Croatia. The data on 83 breeding sires born in 1995-2022 with at least one offspring were obtained from the Veterinary Information System of the Ministry of Agriculture, Directorate for Veterinary Administration. Herd life was defined as the total number of days from the calving date of first offspring to the last (culling) date of the bull. Testing of differences in the number of days spent in the herd between different lines was carried out taking into account as a minimum criterion 4 breeding bulls for each line. The difference in the days spent in the herd between the lines was carried out with one-way ANOVA at p < 0.05. The average age of the bulls in the herd was 1549.84 ± 974.14 days with a coefficient of variability (CV) of 62.85 %. The most represented line of bulls were LB3 (13.25 %), LB4 (22.89 %), LB5 (10.84 %), LB6 (4.82 %), LB7 (4.82 %), LB8 (4.82 %), LB9 (9.63 %), LB11 (8.43 %) and LB12 (7.22 %), with the most significant number of male progenies.

