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GENETICS AND GENOMICS/CATTLE

C-114

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C-115

Genetic correlations among selected traits and inbreeding depression in dual purpose Rendena breed

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Selection in native cattle breeds requires great attention because of the smaller population size and the greater risk of inbreeding (F) as compare to bigger populations. Moreover, native breeds are usually dual purpose, and selection involves antagonistic traits, i.e., milk and meat attitudes. Focusing on Rendena cattle (~4,000 breeding cows), the present work aimed to study F depression and genetic correlations (r) in the following traits: milk, fat, protein (milk yield traits, MY), and udder correctness (Ud), for milk attitude; muscularity (Mu), average daily gain (ADG) and in vivo estimated carcass traits (Ca) for meat production. An amount of 28¹,497 MY test-day data collected on ¹6,974 cows during routinely milk recording were considered, whereas Ud and Mu were obtained from linear type traits scored on 11,992 primiparous cows. ADG and Ca were measured on ¹.428 young bulls at performance test (i.e., up to ¹¹ months of age). Individual F was estimated including incomplete pedigree information. A series of bi-trait REML animal models were used to assess genetic parameters, and genetic trends were drawn as linear regression (b) on estimated breeding values (EBV) standardized on mean ¹00 and standard deviation of ¹0 points. The effect of F was evaluated by introducing individual F in the models and considering the change in EBV for each percentage point of F increase (b'). Heritabilities varied from 0.¹7 (MY) to 0.38 (Ca). Low but negative r were found within milk traits MY-Ud (r=-0.¹4), suggesting negative impact of milk yield on udder form. About meat traits, positive r were found in Mu-Ca (r=0.57) and ADG-Ca (r =0.38). ADG showed low r with all other traits. The antagonism of dual purpose selection was evident in MY-Mu (r=-0.33), whereas close to zero r were found in MY-Ca (r=-0.06). Genetic trends reflect the stronger selection for milk attitude realized: MY EBVs are increasing (b=1.4 since 2000), but Mu EBVs are decreasing (b=-0.5), while ADG and Ca are slightly increasing (b=0.8). An F depression was found in all traits (average b' =-0.33), except for MY (b'=0.35), meaning that the greater MY EBVs are in more inbred animals. Results suggest a slight but progressive change toward a milk conformation in the breed, and a relative greater increase in F due to a bigger selection pressure on MY. A proper breeding policy should account for aspects as r and F to make choices in a long-term perspective and limit the chance of F depression.

Acknowledgments

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C-116

Genetic diversity of Mediterranean cattle breeds related to geography and climate

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In recent decades, changes in climate have caused impacts on natural and human systems. Mediterranean countries will be particularly affected by this phenomenon, with growing temperatures and reduced rainfall. Understanding how species and ecosystems respond to climate change has become a crucial focus in biodiversity conservation and management. The genome-wide SNP panels allows providing background information on genome structure in domestic animals, opening new perspectives to livestock genetics. The International Project GAL-IMED "Genetic Adaptation of Bovine Livestock and production systems in MEDiterranean region", develops an integrated approach that combines the analysis of SNP markers, bioclimatic variables and farming system information to identify genotypes and breeding practices able to respond to climate change. Italian and Corsican local breeds are part of this project. The aim of the study is to identify genomic regions related to adaptation to climate change in these local breeds. Individuals of Cinisara (71),





GENETICS AND GENOMICS/CATTLE

Modicana (72), Maremmana (25), Piemontese (21), Romagnola (21), Sarda (30), Sardo-Modicana (28) and Corse (31) breeds were genotyped using Bovine SNP 50k. Farming systems data were collected by interviewing breeders. Geographic coordinates and 19 bioclimatic variables were also available. Principal Components Analysis (PCA) was performed on SNPs data and climatic variables. Co-inertia (CIA) analysis was realized to detect a possible common structure between such different information. After edits, 43,625 SNPs were retained. The PC1 on individual genotypes differentiates Modicana from other breeds, and shows that Sardo-Modicana is close to Modicana, but is clearly admixed to another breed. The PC2 differentiates Cinisara from a cluster "Romagnola/Maremmana" and shows a large variability of the Modicana breed. The CIA coefficient between molecular data and both geographic and climatic information is equal to 0.38, (P-value=0.001), suggesting evidence of genetic adaptation to different climatic pressures. Further analyses are on going to identify the genetic regions with a potential adaptive role. The results will provide a solid scientific foundation to reconsider objectives and selection criteria and to improve farming practices to prepare livestock to new environmental conditions.

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C-117

Genomic inbreeding estimation in small populations: evaluation of runs of homozygosity in local cattle breeds

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The availability of high throughput genotyping has facilitated the quantification of inbreeding by genomic markers in farm animals. Run of homozygosity (ROH) are contiguous lengths of homozygous genotypes and represent an estimate of the degree of autozygosity at genome-wide level. The current study aims to quantify the genomic inbreeding derived from ROH (FROH) in three Italian local cattle breeds. Individuals of Cinisara (71), Modicana (72), Reggiana (168) were genotyped with the 50K v2 Illumina BeadChip. Genotypes from 96 animals of the Italian Holstein cattle breed were included in the analysis. The following criteria were used to define a ROH: two missing SNPs; one heterozygous SNP; minimum density of 1 SNP every 100 kb; maximum gap between consecutive SNPs of 1 000 kb. We used a definition of ROH as tracts of homozygous genotypes that were >4

000 kb in length with a minimum number of 40 SNPs included in the run. Across all four breeds, we identified 3.661 ROH. The Modicana breed showed the highest mean number of ROH for individual (11.03) and the highest value of FROH (0.053), whereas the Reggiana showed the lowest values (7.15 and 0.033, respectively). The three most homozygous animals present in our dataset were from the Cinisara (676.9 Mb), Modicana (681.2 Mb) and Reggiana (725.2 Mb), with almost a quarter of their genome classified as ROH. Differences among breeds existed for the ROH length. The individuals of Reggiana and Italian Holstein breeds showed high number of shorter ROH segments, whereas the Sicilian breeds showed ROH characterized by the presence of large segments. In fact, in all breeds, most ROH segment coverage was in the shorter length categories (4-8 Mb), but the Sicilian breeds presented the highest percentage of ROHs (12%) inside the ROH length category >24Mb. Therefore our results showed the presence of inbreeding due to recent consanguineous matings and a lack of gene flow from other herds and breeds. ROH analyses represent an important instrument that may be used in inference of population history and to associate with important production and disease traits. Considering that the increased of inbreeding leads to different negative effects, our results showed the necessity of implementing conservation programs to preserve the local breeds.

C-118

The distinctive mitochondrial DNA signature of Podolic cattle in Italy

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The domestication of wild aurochs (Bos primigenius), starting ~10,000 years ago, was an important step in human history with its cultural and socioeconomic implications for ancient populations. Nowadays, there are around two thousands cattle breeds recognized worldwide. An ancient group of breeds are known as Podolic cattle, which are thought to be descendants of the first domesticated animals or even directly of the wild ones. The name indicates a possible origin in the Podolia region of Ukraine, from where these animals spread in Europe. These grey

