O041

Genotype by environment interactions and response to selection for productive traits in a local cattle breed

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Genotype by Environment interactions (G × E) happen when individuals have diverse adaptations to local conditions. This study aimed to investigate G × E and response to selection (R) in dairy traits and somatic cells under the diverse environmental conditions in which the local Rendena cattle breed is reared. Target traits were milk, fat and protein yields (MY, FY, and PY; kg), fat and protein percentage (F% and P%), and somatic cell score (SCS), routinely collected over 12 years as test day data of nearly 10,000 cows daughters of ~600 sires. The G x E term was valued by Gibbs sampling analysis under the reaction norm model approach, i.e. in two-steps. First, a single trait test day repeatability animal model (M1) was carried out to obtain the solutions of the herd-test day (HTD) effect, used as environmental covariate in a second random regression sire model analysis (M2) to obtain the intercept G and the slope G x E across HTD levels. The gradient of the G and G x E variance across HTD on the total phenotypic variability (M2) was used as indication of R under different environmental conditions: (i) geographical area (plain/hill/mountain); (ii) type of housing (tie-stall/loose housing); (iii) feeding system (traditional/total mixed ration); and (iv) occurrence of summer pasture (yes/no). The sire EBVs under M1 resulted variable in different environmental conditions for some traits: e.g. an average correlation of 60% was found for the F% EBVs values of the same sires in different geographical areas, type of housing and feeding system. MY and P% showed the highest correlations in different environments (83% on average). The G x E component estimated via M2 explained from 6% (SCS) to 28% (P%) of the phenotypic variance. On average, a 1.04 times greater R was found under a target environmental condition as respect to the alternative(s) (e.g. loose housing vs. tie-stall). For productive traits, the higher R was found for total mixed ration feeding, loose housing and the absence of summer pasture. Opposite results were found for SCS. Greater R was found in plain for MY, FY, PY, P%. A rank correlation between 87% (SCS) to 96% (FY) was found between the bull EBVs estimated under the reaction norm model vs. a traditional approach (M2 vs. M1), and the ranking of the first 20 bulls resulted greatly changed under the

two approaches. These results suggest the importance to include G × E when local breeds are selected.

O042

Conservation status and rates of inbreeding of Italian autochthonous beef breeds

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Albeit the success of commercial beef cattle nowadays, local breeds are an important reservoir of traits that might be crucial to meet future challenges. Genetic analysis is a primary step to study populations in order to elaborate conservation measures and handle inbreeding. This study investigates the population structure of six local cattle beef breeds through pedigree data, namely: Calvana ($n = 2798$), Mucca Pisana ($n = 3339$), Pontremolese ($n = 328$), Sarda ($n = 97,163$), Sardo Bruna ($n = 74,981$) and Sardo Modicana ($n = 25,355$).
The current population size of the three Tuscan breeds is extremely low counting: 263 Calvana (37 males and 226 females), 346 Mucca Pisana (52 males and 294 females) and 52 Pontremolese (8 males and 44 females) extant animals. These figures classify Calvana and Pisana as endangered breeds, while Pontremolese as critical breed.
Genetic analysis was performed by the ENDOG 4.8 software using pedigree information. To overcome pedigree incompleteness, we estimated the effective population size (Ne) based on the equivalent generations calculated as $\sum(1/2)^n$, where n was the number of generations separating the individual from each of the known ancestors. Pontremolese and Sarda had the lowest Ne (14.62 and 16.64, respectively) while Sardo Modicana the highest value (39.79). The others showed similar Ne, around 19. The average inbreeding coefficient for the Tuscan breeds was 7.25, 5.10 and 3.64 % for Mucca Pisana, Calvana and Pontremolese, respectively. Sardinian breeds showed the smallest values ranging between 1.23% (in Sardo Bruna) to 1.90% (in Sarda). The average generation interval in years was rather high for all breeds, with the lowest value observed in Sardo Modicana (7.8 SD =9.75) and the

highest in Sardo Bruna (13.3 SD =16.7). Following *Ne*, the rates of inbreeding per generation ($\Delta F = 1/2Ne$) were ~2.6% for Calvana, Mucca Pisana and Sardo Bruna, 3% and 3.42% for the Sarda and Pontremolese, respectively, and ~1.26% for Sardo Modicana.

This preliminary data suggests the urgency of conservation strategies for the three Tuscan breeds. In the next steps, we will further integrate pedigree and genomic information to (i) explore the population structure and genetic diversity within and between breeds, (ii) identify signatures of selection and (iii) plan assortative matings to control the inbreeding.

O043

Twenty shades of grey. Combined analysis of genome-wide SNP data in Steppe cattle and in Mediterranean grey cattle shed new light on the molecular bases of coat colour

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Coat colour is among the most distinctive phenotypes in cattle. To date, several genes underlying this complex trait have been identified. A number of breeds, mainly in Europe and Asia, share peculiar coat colour features such as the presence of (i) a diluted grey coat, (ii) lightly coloured inner sides of the legs and belly, (iii) aureoles around the eyes, a muzzle ring, black nasal mucosa, and dark tail tip, (iv) a fawn pigmentation of the calf at birth, turning over time to grey and (v) sexual dichromatism. The aim of this study was to investigate the molecular basis of the above phenotype by searching for selection signatures. An F_{ST}-outlier approach was adopted, as implemented in the software BayeScan, to a total of 22 pair-wise breed comparisons. In each breed comparison, any of the selected breeds displaying the 'diluted-grey phenotype' was contrasted with the same cattle breed showing a 'non diluted-grey phenotype' selected as external reference. In total, 3 breeds were adopted here as external references (Holstein, Angus and Charolais), for a sum of 66 pair-wise breed comparisons. Preliminary analysis of results highlighted the presence of several signals of differential selection, some of them harbouring genes related to pigmentation biology. In order to identify the most robust signals, only those observed in at least seven pair-wise breed comparisons for all the 3 external reference breeds, were further considered. Among them, an interesting signal was observed at chromosome 14 (intergenic SNP BTB-00557532). The window of ±250 kb up- and down-stream the SNP harbours nine genes (FAM110B, LOC101902490, UBXN2B, CYP7A1, TRNAG-CCC, LOC112449629, SDCBP, LOC112449508, NSMAF). Out of them, FAM110B (centrosome/spindle pole-associated protein) has been shown to interact with proteins [ADAM, BBS proteins, beta-catenin (Wnt signalling), DVL2 (substrate for HECW1), XRCC5 and XRCC6 (UV-induced DNA damage repair)] known to be involved in pigment biology. SDCBP has been shown to participate in melanin transport. UBXN2B contain a domain peculiar of proteins involved in ubiquitination, a process involved in tyrosinase (melanin precursor) degradation. Several inherited hypopigmentary diseases involve aberrant processing and/or trafficking of tyrosinase and its subsequent degradation. Interestingly, additional ubiquitination or de-ubiquitination signals were detected in this study (HECW1, RNF111, MINDY2) that may be related to the diluted-grey phenotype in cattle.

LIVESTOCK SYSTEMS – NEW EMERGING TECHNOLOGIES IN ANIMAL SCIENCE I

O044

How to measure milking efficiency in dairy cattle farms?

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