However, intense directional selection might increase inbreeding and loss of genetic variability. High inbreeding levels can in turn cause an excess of deleterious variants and reduced biological fitness. Thus, the objectives of this study were to (i) estimate the level of inbreeding in 27,735 Italian Holstein dairy cows from pedigree and imputed genotype data in the form of ~85k single nucleotide polymorphisms (SNP), and (ii) investigate the effect of inbreeding on 305-day milk (MY; kg), fat (FY; kg), and protein yield (PY; kg).

Pedigree-based inbreeding coefficients (FPED) were defined as the probability that an individual has two identical alleles by descent and were computed using the OptiSel R package. Genomic inbreeding coefficients were derived by means of runs of homozygosity assessment (ROH). The ROH segments were detected using the DetectRUNS package in R and defined as follows: at least 15 SNPs in a run, a minimum length of a run equal to 1 Mb, a maximum distance between consecutive SNPs in a 500 kb window, a lower density limit of 1 SNP per 100 kb and allowing for a maximum of one missing and one heterozygous SNP in a run. The genomic inbreeding coefficients (FROH) were calculated as the proportion of individual genome size covered by ROH. The presence of inbreeding depression was evaluated by regressing phenotype on FPED and FROH using a linear mixed model in ASReml 4.1. The following terms were included in the model: herd-year of calving (2242 classes), parity (3 classes) and month of calving (12 classes). Overall, FROH (mean FROH $= 0.16 \pm 0.03$) was higher than FPED (mean FPED $= 0.07 \pm 0.02$, complete generation equivalent $= 10.59$), with a correlation above 0.60. Inbreeding depression was observed in MY, FY and PY for both inbreeding estimates ($p < .01$). A 1% increase in FROH and FPED was associated with a decrease in MY of about 44 and 61 kg ($p < .01$), respectively. The same trend was found when evaluating FY and PY ($p < .01$), with an FY decrease of 1.31 kg and of 2.45 kg and of 1.41 kg and 2.0 kg for PY, based on FROH and FPED, respectively. Ongoing research is investigating the role of inbreeding in other economically important production and fertility traits in Holstein dairy cattle.

SESSION 36 COMPANION ANIMALS AND SOCIETY – II

O177

Genomic evaluation of the Italian shepherd dogs

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Dogs have provided great help to shepherds since ancient times, either by protecting or driving the flock. These distinct roles led to the separation of shepherd dogs in livestock guardians (LG) and herding dogs (HD). The constant selection conducted by shepherds and breeders to improve the skills of their dogs originated several breeds, with distinct morphology and behaviour. Given the importance of pastoralism, it is not surprising that Italy counts many local shepherd dog breeds spread across the peninsula. In this study, we investigate these breeds from a genomic perspective and identify selection signatures differentiating between LG and HD. Canine 230K SNPChip, updated to CanFam3.1, was used to genotype 134 shepherd dogs. The LG group consisted of 52 dogs of 4 breeds (Maremma sheepdog, Mannara dog, Pastore della Sila, and Fonni's dog), whereas the HD group consisted of 82 dogs from 5 breeds (Pastore d'Oropa, Pastore apuano, Bergamasco shepherd, Pastore della Lessinia e del Lagorai, and Lupino del Gigante). Commonly used thresholds for quality control were applied (QC) and breed sample sizes were balanced. We compared LG and HD with Wright's fixation index (FST) and single-SNP cross-population extended haplotype homozygosity (XP-EHH). The top 1% markers for FST and XP-EHH values were considered as relevant.

The filtering stage retained 120 836 SNPs and 99 dogs (42 LG and 59 HD). The top 1% of FST (0.24–0.54) and the top 1% of XPEHH (2.72–4.97) had 65 SNPs in common, mapping on 49 different genes. The most intense signals located on chromosomes 6, 9, and 21. A gene-level analysis showed that 8 genes are associated with human eye disorders similar to those that Border collie and its related breeds are prone to develop. Other 8 genes play a role in the nervous system development or functionality. Finally, 20 genes are implicated in behaviour regulation and dog domestication. In this study, we reveal genomic traces of the differentiation of Italian LG and HD dog breeds for the first time. The identified genes are related to potentially relevant pathways throughout the selection and the differentiation of these breeds and deserve further investigation to confirm their role in this process.

O178

Dietary *Ascophyllum nodosum* and Bacillus subtilis C-3102 influence faecal fermentation patterns in dogs with chronic enteropathies

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