trigger an inflammatory response that could have important consequences on the health of high producing or fresh animals.

O0005

Starch exposure early in life to enhance metabolic programming of nutrient partitioning in lactating dairy sheep

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This work aimed at testing if sequences of glucogenic (from starch; S) and lipogenic (from high digestible fibre; F) diets, in foetal life, growing and mid-lactation, affect milk persistency of dairy sheep. Performance of 72 sheep from birth to first dry-off was described. A split-plot experimental design has been adopted. The 72 sheep were divided into 8 groups identified by a sequence of 3 letters: SSS, SSF, FSS, FSF, SFS, SFF, FFS and FFF. They indicated the diets received in foetal life (last 75 days), in growing and in mid-lactation (56 to 165 days in milk, DIM), respectively. Body weight, body condition score, feed intake and several blood parameters including plasma glucose and insulin concentrations were monitored. Glucose (GTT) and insulin (ITT) tolerance tests were also executed. Gene expression of adiponectin in subcutaneous fat from biopsies was determined in late lactation. At 55 DIM, fat and protein corrected milk (FPMY) was 1.59 ± 0.10 kg/d per ewe. Prenatal diet affected persistency: FPMY decay from 56 to 165 DIM was −0.728 vs. −0.992 kg/d in ewes exposed to S or F in foetal life, respectively (p=.04). FPMY persistency was greater (p<.05) in ewes fed SSF, exposed to starchy diets in foetal life and from weaning to first lambing (SS), and fed diet rich in high digestible fibre in mid-lactation (F). SSF and FFF showed the greatest and lowest FPMY after 56 DIM (1.483 ± 0.180 vs. 1.143 ± 0.198 kg/d, respectively; p<.05). FPMY was different (p<.05) among groups only when considering ewes with homogenous lactation stage (lambing the same decade). SS vs. FF diet sequence was associated to greatest levels of basal insulin during GTT in pregnancy and ITT in lactation (p<.05), to lower glucose uptakes in ITT (p=.06) and to greater values of the homeostasis model assessment index in lactation. Relative abundance of adiponectin gene expression was affected by prenatal and growing diets (2 times greater in FF vs. SS; p<.05) and by lactation diet (1.5 times greater in F vs. S; p<.05). These metabolic evidences are often associated with insulin resistance (IR). We concluded that exposure to glucogenic diets in foetal and growing phase (SS) might programme a default IR that could extend the homeorhetic IR of early lactation. After lactation peak, IR could affect milk persistency reducing nutrient uptake by body reserve and stimulating the nutrient utilisation by mammary gland.

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ANIMAL BREEDING AND GENOMICS – GENETICS OF WELFARE, GENETICS OF RESILIENCE

O0006

Cheesemaking and sustainability index – Parmigiano Reggiano: a new breeding index for the Italian Holstein

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The Italian dairy industry is specialised in the manufacturing of high quality, long ripened cheese. The objective of the present study was to develop a new breeding index (ICS-PR) for Holstein cattle producing milk for long ripened cheeses such as Parmigiano Reggiano PDO; the final breeding goal is to maximise net profit per day of life. Net profit for commercially available AI bulls was calculated as the difference between total estimable revenue and the total estimable costs using EBV released with the official genetic evaluations. Costs included heifer rearing, cow feeding for maintenance and production, fertility, udder health, calving difficulty and milk delivery whereby revenue considered cream, cheese and whey production, as well as, culled cow value. Dry matter intake and cheese yield were estimated using available prediction formulae; economic values for both costs and revenue were retrieved from the literature. Stepwise multiple linear regression was employed to develop a prediction equation for net profit from official AI bulls EBV having rank >59 and reliability >50. The 10-year genetic gain achievable for official EBV with selection for ICS-PR was calculated from P and G matrixes constructed using (co)variances routinely used for BLUP genetic evaluation and it was compared to the 10-year genetic gain achievable with selection for PFT index. EBVs retained (relative emphasis) from the multiple linear

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regression were: kg of protein (30%) and fat (5%), stature (−2%), locomotion (3%), udder depth (2%), somatic cell score (14%), calving ease (9%), longevity (10%), mastitis resistance (5%), and fertility (20%). Moreover, results demonstrated that, although the gain in production traits with ICS-PR was 85–96% the potential gain achievable with PFT, the selection for ICS-PR would result in a much faster genetic gain for welfare characteristics, such as calving ease (22%), longevity (22%), udder health (18%), while the gain for fertility was three times larger. In 10 years' time, bovine production and productive life genetically will increase at a different rate depending on breeding decisions. However, in a scenario of selection for ICS-PR, cow lifetime production of Parmigiano Reggiano, calculated applying cheese yield prediction formulae used in the present study, is expected to be almost 100 kg higher compared to that achievable with selection for PFT.

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O007

Structural equation models for genome-wide association study (SEM-GWAS) of interrelationships among udder health traits in dairy cattle

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The quality and safety of milk products depend on animal health and welfare, and particularly on mammary gland health. It is well known that mastitis, either in its acute or sub-clinical form, greatly affects the nutritional and technological quality of milk. Apart from somatic cell count (SCC), milk lactose (LAC) content, pH and casein to protein ratio (CAS:PRT) are sensitive to inflammation of the mammary gland, and these variables could be incorporated together into an udder health indicator. Multi-trait model genome-wide association (MTM-GWAS) can be used to study associations between genomic regions and multiple traits, but it does not consider potential causal relationships among phenotypes. Alternatively, structural equation modelling (SEM) represents a powerful tool for modelling causal networks. Recently, SEM in combination with GWAS (SEM-GWAS) has been proposed to better understand the genetic basis and the relationships among a set of traits. SEM-GWAS can partition SNP effects into direct and indirect (i.e. mediated by an up-stream trait in the causal network) components. This study aimed to apply SEM-GWAS on a set of phenotypes related to udder health, i.e. milk yield (MY), somatic cell score (SCS), LAC, pH and CAS:PRT, in a cohort of 1158 Italian Brown Swiss cows. Animals were genotyped with the Illumina BovineSNP50 Bead Chip v.2. A causal phenotypic network was inferred in two stages: (1) a multi-trait model was employed to estimate covariance matrices of additive genetic effects and of residuals, and (2) the causal structure among phenotypes from the covariance matrix between traits, conditionally on additive genetic effects, was inferred by the Hill-Climbing algorithm. The residual (co)variance matrix was inferred using Bayesian Markov-chain Monte Carlo, with samples drawn from the posterior distribution. Results showed positive path coefficients for MY → LACT, LACT → CAS:PRT and SCS → pH, while negative values were obtained for LACT → SCS. Based on the identified phenotypic relationships structures, SEM-GWAS will be run, enabling to identify direct and indirect (i.e. mediated) SNP effects and providing a more complete picture of the genetic basis of these indicators of udder health.

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O008

Reaction norm analyses to infer genotype by environment interaction for fertility traits in Italian dairy cattle

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Different environments can contribute to differential expression of polygenic effects in dairy cows, which can lead to re-ranking of sires for economically important traits across environments. This genotype by environment interaction (G x E) may need to be taken into account for environment-specific breeding programmes. In this study, G x E was inferred using reaction norm models in Brown Swiss and Simmental breeds on the fertility