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► To cite this version:

Ahmed Ben Abdelkrim, Thierry Tribout, Vincent Ducrocq, Nicolas N.C. Friggens, Didier Boichard, et al.. Assessment of perturbations in lactation to take stock of existing resilience of dairy cows. 71st Annual Meeting of the European Association of Animal Production, Dec 2020, virtual, France. hal-03036960

HAL Id: hal-03036960

<https://hal.inrae.fr/hal-03036960>

Submitted on 2 Dec 2020

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Session 34

Poster 8

Assessment of perturbations in lactation to take stock of the existing resilience of dairy cows

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The robustness of dairy systems is partly related to the robustness of the animals raised under these systems, including their resilience to environmental disturbances. Characterising inter-individual variability can provide the necessary tools to assess the robustness and resilience of animals in a given environment, particularly since modern milk recorders provide new information regarding milking speed or shape of milking curves. We used a model which allows the explicit representation of the perturbations which may occur in the lactation curves, thereby providing a quantification of the variability in perturbations. This model transforms individual time-series data into phenotypic information. The model parameters make it possible to characterise the perturbed and unperturbed profiles of the lactation curve. They also provide estimates of the different perturbations that may exist, the moment when they occur, and their intensity. We applied this model to 6,154 lactation curves from 4,066 Holstein cows recorded in milking parlours in 36 commercial dairy farms. In the process, 4,4024 different perturbations were revealed (with an average of 7.15 perturbations per lactation and a milk loss rate of 6.82%). We used this information as a comparison tool between the different cows studied in order to assess their resilience. Using this type of tools could be an alternative effective, elegant and applicable solution to find a reasonable compromise between optimal production and animal welfare.



Session 34

Poster 9



Linkage disequilibrium as a signature of positive selection in beef cattle

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This study aimed to assess the distribution of selection signatures in the genome of Charolais and Limousin cattle through determination of variability in linkage disequilibrium among adjacent syntenic SNPs in the autosomal genome and identify protein-coding genes located in particular genomic areas by available databases. In a total of 85 animals, selected based on the genealogical analysis, were genotyped using International Dairy & Beef Chip for 49,629 SNPs. Only autosomal SNPs and animals with call rate higher than 90% and minimum minor allele frequency 1% in a population were selected to subsequent analysis. The final database consisted of 42362 SNP markers covering 2,503.53 Mbp of the autosomal genome (average SNP spacing 59.14±61.51 kbp). The differences in genome-wide linkage disequilibrium patterns between populations were quantified using VarLD method over sliding windows of 50 SNPs. Selection signatures, identified based on the standardised varLD score, were recognised as regions with top of 1 percentile of signals. Protein-coding genes were screened in the selection signal regions using the cattle genome reference sequence ARS-UCD1.2. Based on the criteria for the detection of selection signals, 15 areas under significant selection pressure were identified across eight autosomes (1, 2, 5, 6, 7, 14, 16 and 17). Overall, 325 genes with different biological functions were located in these regions. The most intense signal was found on the BTA2 chromosome in the area of genes involved in genetic control of double muscle (*MSTN*) and reproduction (*CYP27C1*). The study confirmed that selection pressure within the genome of the Charolais and Limousin breeds was mainly focused on genomic areas controlling animal weight, body frame, carcass yield, meat quality and reproduction.

