GB-01

Estimated breeding values of dairy sires regarding colostrum traits

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Objectives: Colostrum administration provides newborn calves with important nutrients (fat, protein, lactose) and immunity (IgG). Significant heritability estimates have been reported on colostrum traits ranging from 0.15 to 0.27, suggesting the traits can be improved with selective breeding based on estimated breeding values (EBVs) of selection candidate. The objective of this study was to derive and examine EBVs of Holstein sires for colostrum traits.

Materials and Methods: The study examined daughter of 67 Holstein sires, raised in 6 commercial dairy herds in Northern Greece. Number of daughters (purebred Holsteins with full pedigree) for each sire ranged from 5 to 49; the total number of cows with records in the study was 699. These cows calved between February 2015 and September 2016. Cows were milked completely after calving and a colostrum sample was collected. Fat, protein and lactose content (%) were determined with Milkoscan. Colostrum total solids (TS) were assessed with a digital Brix refractometer and expressed in % Brix values. Sire EBVs for colostrum traits (TS, fat, protein and lactose content) were derived with univariate statistical analyses based on a mixed model. The model included the effects of farm, parity number, calendar season, age at calving, colostrum yield, time interval between calving and colostrum collection, dry period length, cow body condition score at calving and milk yield of previous lactation, and the random animal additive genetic effect. The ASREML software was used for all statistical analysis.

Results: Sire EBVs were normally distributed. The EBV for colostrum TS ranged from a -4.05 to +3.47 (average EBV reliability 0.42). The EBV difference between the 10th and the 90th percentiles was 3.20% (-1.50 and +1.70, respectively). The phenotypic difference in % Brix values between daughters of sires in the 10th and 90th percentiles was 5.6% (22.6 and 28.2, respectively). The EBV for colostrum fat content ranged from a -2.60 to +1.29 (average EBV reliability 0.29). The EBV difference between the 10th and the 90th percentiles was 2.23% (-1.56 and +0.67, respectively). The phenotypic difference of fat content between daughters of sires in the 10th and 90th percentiles was 3.7% (4.2 and 7.9, respectively). The EBV for colostrum protein content ranged from a -2.76 to +2.04 (average EBV reliability 0.34). The EBV difference between the 10th and the 90th percentiles was 2.32% (-0.92 and +1.40, respectively). The phenotypic difference of protein content between daughters of sires in the 10th and 90th percentiles was 4.4% (15.7

and 20.1, respectively). The EBV for colostrum lactose content ranged from a -0.34 to +0.38 (average EBV reliability 0.24). The EBV difference between the 10th and the 90th percentiles was 0.33% (-0.21 and +0.12, respectively). The phenotypic difference of lactose content between daughters of sires in the 10th and 90th percentiles was 0.9% (1.7 and 2.6, respectively). Three bulls had positive EBVs and 5 had negative EBVs for all four traits studied. When considering TS, fat and protein content only, 13 bulls had positive EBVs and 19 had negative EBVs for all three traits. Mean EBVs for the 13 "positive" bulls were 1.05, 0.44 and 0.61, for TS, fat and protein content, respectively. Mean EBVs for the 19 "negative" bulls were -1.10, -0.66 and -0.67, for TS, fat and protein content, respectively.

Conclusions: Variability in sire EBVs regarding colostrum traits supports the concept of genetic selection leading to trait improvement. A synthetic colostrum quality index could be potentially developed comprising sire EBVs on individual traits. This index could be eventually included in an overall performance index that will drive future breeding programs.

Keywords: Breeding values, sire, cow, colostrum.

GB-02

The genetic architecture of susceptibility to claw horn disruption lesions in Holstein cows

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Objectives: Lameness is the most serious welfare problem facing the modern dairy industry. The lesions associated with the greatest impact on animal welfare, and those which incur the greatest financial costs to farms, are claw horn disruption lesions (CHDLs). The three most prevalent CHDLs are sole haemorrhage, sole ulcers and white line disease. In the United Kingdom, breeding strategies have not reduced the prevalence of lameness in the national herd and this is due, in part, to the paucity of detailed phenotypic data to inform genetic selection. Previous research from our group has identified the existence of genomic variation and regions that were associated with specific lameness lesions, suggesting value in pursuing this area of research [1]. The aims of this study were to determine the genetic variance and genomic regions which underly CHDL development.

Materials and methods: Over an eight-month period, 2,353 Holstein cows were enrolled on four dairy farms in the United Kingdom. Animals were assessed at four timepoints: prepartum (average: 56 days prepartum); freshly calved (average: 5 days postpartum), early lactation (average: 84 days postpartum) and late lactation (average:182 days postpartum). At each timepoint feet were inspected by a trained veterinarian and all lesions present were recorded and scored by severity.

Pedigrees were obtained for all cows with phenotypes, and 1,622 cows were genotyped with the Illumina 50K Bovine SNP chip. Lesion scores at the first three timepoints were combined to create an overall CHDL score, accounting for lesion severity and total number of feet inspections per cow (lesions from late lactation timepoint will be included in the final analyses). CHDL score was used as the phenotype for genomic analyses. A single-step GBLUP method was used to calculate heritability and the genetic correlations between CHDL score at different timepoints. Genome-wide association (GWA) analyses were applied to identify candidate genomic regions associated with CHDL score, using both single-marker and window-based association. Significance testing of SNP effects were adjusted using Bonferroni and False Discovery Rate approaches to control for multiple testing during GWA analyses.

Results: The average cow-level prevalence, across all timepoints and including all severity grades, was 43.3% for sole haemorrhage, 4.6% for sole ulcers and 35.8% for white line disease. Across all timepoints, the heritability for the combined CHDL score was 0.18 (SE: 0.03), using both pedigree-based and genomic approaches. The genetic correlation between CHDL score at different timepoints was high (>0.9). GWA analyses did not identify any SNP to be significant for CHDL score after the Bonferroni correction, but some SNPs exceeded a suggestive threshold after correcting for one false discovery per genome scan. When markers were grouped by 1Mb sliding windows, several candidate genomic regions were identified which explained larger proportions of genetic variance for CHDL score than other regions in the genome, approximately 3-4% of the total genetic variance. Estimated genomic breeding values for the combined CHDL score were calculated and showed good correlation with phenotypic values (0.67).

Conclusions: The genetic correlation between CHDL scores at each timepoint was high. This suggests an underlying genetic basis which was not dependent on environmental factors specific to the stage of lactation. As a combined phenotype, CHDL development is moderately heritable, and the estimated genomic breeding values indicate a reasonable correlation with the observed phenotype. Therefore, there is the potential to incorporate CHDL resistance into future breeding programmes. The presence of multiple candidate genomic regions suggests a polygenic architecture of CHDLs; further study is warranted in order to elucidate specific genes and molecular pathways involved.

References:

1. Sánchez-Molano E, Bay V, Smith RF, Oikonomou G, Banos G. Quantitative Trait Loci Mapping for Lameness Associated Phenotypes in Holstein–Friesian Dairy Cattle. Front Genet. 2019;10:926. doi:10.3389/fgene.2019.00926.

GB-03

Aging increases inflammatory response in dairy cattle

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Objectives: Old cows are reputed more sensitive to bacterial infections, developing more severe mastitis than youngest ones. However the biological basis of these observations are not known. Risk factors increase with aging, but inflammation and innate immunity are modified in the long term by previous exposure to microbes. Epigenetic changes of immune cells like monocytes could explain increased severity to infection. Monocytes are central in these mechanisms, and they undergo functional changes upon contact with pathogens or their products, and adapt their response to subsequent challenges. However, the molecular bases of long-term reprogramming are still poorly understood in cattle.

Materials and methods: Twenty-three cows were challenged through an intravenous bolus injection of LPS (0.5 µg/kg BW, ultrapure LPS, InVivogen) to induce a systemic inflammatory response. Fourteen of them were bovine somatic clones originating from the same cell line, in two groups of 5 and 15-years of age, respectively. A genetically-diverse group of 5 years-old cows (n=9) was also included in the study. All cows were raised and housed together as a single group since birth in an experimental farm. Cytokine production was measured sequentially (0, 3, 6, 12, and 24h) in plasma using a newly-developed custom bovine cytokines 15-plex Milliplex assay (MERCK-Millipore). Blood samples were collected twice at 0 and 24 hours after LPS injection. Monocytes were isolated and their genome-wide DNA methylation profile was determined by reduced representation bisulfite sequencing (RRBS) using a dedicated pipeline, in order to assess epigenetic marks according to the age, genetic background, and response to LPS.

Results: LPS exposure was associated with the production of pro-inflammatory cytokines (IL-1β, IL-6, TNF-α). IL-6 and TNF-α production were higher in aged compared to young cows, and clinical signs were more severe in the former, indicating a stronger inflammatory response according to the age. Differentially-Methylated Cytosines (DMCs) targeting genomic regions important to monocyte identity and functions, independently of the genetic background, were identified. LPS stimulation causes hypomethylation in dairy cows whatever the age. Monocytes undergo epigenetic modifications after LPS challenge, indicating that previous exposure to Gram-negative bacteria, may modify the later capacity of the cells to respond to an infection. Comparison of young and old cattle led to identification of epigenetic marks related to aging.

Conclusions: Aged cows have a stronger inflammatory response that correlates with the presence of specific marks that develop during the course of life. Knowledge on epigenetic marks induced by aging may help define new breeding and prevention strategies.

GB-04

Impact of host genetics on resistance of bovine monocyte-derived macrophages to *Mycobacterium avium* subsp. *paratuberculosis* infection

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The application of animal genetics in breeding programs is currently one of the important motors for efficient livestock production, not only to increase performance and productivity but also to ensure the resilience and health of livestock while maintaining or improving the longevity of animals. Genetic selection to enhance the resistance of dairy cattle to paratuberculosis (PTB) and other bovine diseases is being extensively explored. Resistance is defined as the ability of the host to prevent invasion or to clear the pathogen at the early stage of infection by mounting a protective immune response. However, the genetic loci influencing individual resistance to *Mycobacterium avium* subsp. *paratuberculosis* (MAP) infection and the primary molecular and cellular mechanisms underlying host resistance are still largely unknown. MAP spends most of its life cycle within macrophages which play a crucial role during all phases of infection. It is generally accepted that less Mycobacteria growth in macrophages *in vitro* implies immune restriction and hence less susceptibility, lower risk of infection or disease *in vivo*. Since macrophages functions are controlled by a limited number of genes under a controlled environment, the probability of identifying animals with a superior innate immune response against MAP using *ex vivo* macrophages models is much higher in comparison to field data. In the current study, we searched for genetic loci associated with resistance to MAP infection by evaluating the performance of MAP-infected monocyte-derived macrophages (MDMs) isolated from peripheral blood of 75 Holsteins cows and infected *ex vivo* with MAP. Bacterial load (log colony-forming unit, CFU) within MDMs was quantified at 2h and 7 days p.i. using a Bactec MGIT 960 instrument. In addition, the levels of some host biomarkers such as *Epiregulin* (*EREG*), *Complement C3 (C3)*, *galectin-9* (*LGALS9*), and *nitric oxide (NO)* were measured in the supernatant of the infected cells at 2 h p.i by ELISA. DNA from peripheral blood samples of the animals included in the study were genotyped with the EuroG MD bead Chip (44,779 single nucleotide-polymorphisms, SNPs). Linear mixed models were used to calculate the heritability (h^2) estimates and variance components for each phenotype; the amount of MAP within MDMs and biomarkers expression. After performing a genome-wide association study, the localization of associated SNPs, QTLs, and candidate genes was performed using the ARS-UCD1.2 reference *Bos Taurus* genome. The only phenotype that showed SNPs with a significant association ($P_{FDR} \leq 0.05$) was the bacterial load within MDMs at 2h ($h^2 = 0.87$) and 7 days ($h^2 = 0.83$) p.i. The six identified SNPs were located on the *Bos taurus* chromosomes BTA2, BTA17, BTA18, and BTA21. Overlap was seen in two SNPs associated with the logCFUs at 2h and 7 d. p.i. All the identified SNPs had negative regression coefficients, and were, therefore, associated with a low bacterial load within MDMs. The following candidate genes were identified within a 100 Kb window of the significant SNPs: Oxysterol Binding Protein like 6 (OSBPL6), Serine Rich Nuclear Protein 3 (CSRNP3), and the Coiled-Coil Domain Containing 92 (CCDC92). OSBPL6 is an intracellular lipid receptor that contributes to the maintenance of cholesterol homeostasis by regulating cellular cholesterol trafficking and efflux. CSRNP3, also named TGF-Beta Induced Apoptosis Protein 2, is a transcriptional activator of apoptosis. The CCDC92 is an interferon-stimulated protein that plays a role in innate immunity and regulation of defense response. Estimated breeding values (EBVs) for the ratio of logCFUs at 7d/2h were calculated for each animal in the study population using the best linear unbiased prediction (GBLUP) model and the genomic predictions were validated in a population of animals with high (N= 8) and low (N= 8) EBVs. MDMs from these animals were infected *ex vivo* with MAP and the correlations between the logCFUs ratios within MDMs and EBVs were positive (Pearson R=0.77). Taken together, our results define a heritable and distinct immunogenetic profile in MAP-infected macrophages designed to limit bacterial load and inflammation early after infection. The identified SNPs could be used to develop genetic evaluations for immunocompetence in the Spanish breeding program which would allow producers to select cattle more resistant to MAP infection and likely to other intracellular pathogens as well; ultimately reducing the prevalence of diseases, preventing economic losses, increasing the length of cattle productive life, and improving food safety.

Keywords: Host resistance, breeding, macrophages, paratuberculosis, innate immune response.

GB-05

Inherited zinc deficiency-like syndrome in Holstein cattle due to a loss-of-function mutation of IL17RA-transmembrane protein

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Objectives: Skin lesions and dermatoses in cattle are often associated with infections due to bacteria, fungi or environmental risk factors. Dermatoses with genetic etiology have also been described. Among these rare disorders, there are primary congenital disorders (e.g. epidermolysis bullosa) and dermatoses that are associated with inherited nutritional deficiencies, such as bovine hereditary zinc deficiency or zinc-deficiency-like syndrome. Our study presents cases with skin lesions observed on a Holstein farm in the Midwest of Germany that resemble zinc deficiency-like syndrome. The origin of all affected calves from a single sire and the same maternal grand sire let us to assume a potential genetic etiology.

Materials and methods: Close clinical and pathological examinations took place in two affected calves. Due to the suspected genetic background, genome sequencing of the

two affected Holstein calves followed by single-nucleotide variant and small-indel variant calling were performed. Available normal relatives of the two calves were genotyped by Sanger sequencing for identified potential causative protein-changing sequence variants.

Results: The two calves suffered from severe ulcerative dermatitis with hyperkeratosis, alopecia furunculosis and subcutaneous abscess formation. Blood analysis showed correspondent leukocytosis with neutrophilia whereas minerals, macro- and micronutrients were within the reference ranges. Genetic analyses delivered 4111 homozygous private variants including 23 protein-changing variants shared by both affected animals. Comparison with the 1000 Bull Genomes variant catalogue resulted in a single privately remaining protein-changing variant. This single-nucleotide deletion in exon 3 of *IL17RA* on bovine chromosome 5 was predicted to have a deleterious impact on the encoded protein due to a frameshift. Healthy mothers of affected calves as well as some other relatives were determined to be heterozygous for this mutation, confirming the assumed autosomal recessive inheritance.

Conclusions: A loss-of-function mutation of the IL17RA transmembrane protein that binds with low affinity to interleukin 17A could be identified as pathogenic variant for the psoriasis-like skin alterations observed in the two affected Holstein calves. In man, rare diseases associated with *IL17RA* include immunodeficiency 51 and chronic mucocutaneous candidiasis. The frequency of the recessive defect allele in the German (and global) Holstein population needs to be analyzed.

Keywords: Skin lesions, calves, genetics, immunodeficiency.

Temperature-humidity effect on rumination time and activity in Holstein and crossbred Holstein x Jersey cows

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Objective: We aimed to compare temperature-humidity effect on rumination time and activity in different genetic groups of cows: Holstein, F1 Holstein x Jersey and R1 3/4Holstein x Jersey.

Material and methods: We made the study at the dairy cattle sector of Centro de Ciências Agroveterinárias of Universidade do Estado de Santa Catarina during the period between September 2018 and August 2019. There were 22 multiparous lactating cows, 7 Holstein, 5 crossbred F1 (½Holstein x Jersey) and 10 crossbred R1 (¾ Holstein x ¼ Jersey). Cows were mechanically milked twice a day, at 7:00 and 15:00. After milking the cows received concentrate in troughs separated by individual contention feeders. Posteriorly, the cows had free access to pasture with water ad libitum and available shadow area, staying in the paddock until the next milking. Before the study period, the cows were equipped with SCR by Allflex® electronic monitoring collars aiming adaptation and indexing in the software *HealthyCow24* – SCR.

To evaluate environmental interference over the cows' performance, we calculated the temperature-humidity index (THI) using environmental temperature and relative humidity through a Data Logger Akrom® model KR420, set to collect data every one hour.

For analysis of variance, the highest THI of the day data were used, and to evaluate THI effect on activity and rumination the mean was made every couple of hours. This mean matches the time given by the individual rumination and activity monitoring software. We used all the data for one year. Six THI classes were created: safe (<68), light (68≤ < 72), discomfort (72≤ <75), alert (75≤ <79), danger (79≤ <84) and emergency (≥84), but we didn't observe the last one.

Data were submitted to ANOVA with repeated measures over time, using the MIXED procedure of the SAS statistical package, and the covariance structure was defined based on the Akaike Information Criterion (AIC). Data were previously tested for residue normality by the Kolmogorov-Smirnov Test.

For the evaluations of the effect of THI on rumination time and activity at two-hour intervals, the statistical procedure used was similar to the one described above. Significant differences at the 5% and trend at 10% were considered.

Results: As shown in Table 1, activity unity was higher for R1 crossbreds and lower for Holstein, these not differing from crossbred F1 (0,0238). There was an increase in activity unity as THI increased (0,0001).

Table 1 – Mean values adjusted to the model ± standard deviation for different temperature-humidity indexes (THI) in different genetic groups for rumination time and activity unit.

THI classes	Activity			P value	Rumination			P value
	H	F1	R1		H	F1	R1	
Safe	52,5±2,1n	59,0±3,8ln	58,0±9,2mn		49,2±1,1ab	49,4±2,0ab	52,6±4,7a	
Light	71,1±2,1km	80,6±3,8lj	77,8±9,3hjkl		41,8±1,1cd	42,4±2,1cd	45,4±4,9bc	
Discomfort	86,1±2,1ghi	93,8±3,9dfgh	92,2±9,4efgi	<0,0001	31,6±1,2eg	31,9±2,2eg	34,0±5,1def	0,7249
Alert	101,9±2,1df	111,2±3,9bce	112,2±9,4cd		21,5±1,2h	23,7±2,2fh	22,2±5,1ghi	
Danger	119,4±2,3bc	133,8±4,2a	128,3±9,7ab		13,9±1,4i	13,5±2,6i	15,6±5,5hi	
*Different letters on the line represent significant difference (P <0.05).								

We also observed a lower rumination time for Holstein (P=0,0002). While THI increases, rumination time decrease. When compared inside the THI class, there is no difference between genetic groups. There was no interaction between genetic groups and THI classes. (P=0,7249).

As shown in Table 1, Holstein cows showed lower activity unit in relation to R1 crosbreds, which did not differ from F1 crossbreds. We observed an interaction effect (<0,0001) between genetic group and THI classes for activity unity.

Conclusion: The highest THI negatively affects rumination time, increasing activity unity values. There is no interaction between genetic groups and THI on rumination time. It seems that no tested genetic group is best suited for high THI classes.

Keywords: Animal improvement, Heat stress.

GB-07

Conformation traits and Characteristics of Somatic Cells Counting in Holstein Cattle in Brazil - A Multivariate Approach

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Objectives: Identify the linear type traits which together affect the somatic cell count in Holstein cattle in Brazil.

Material and methods: We used recorded data from approximately 45,000 animals of the Holstein breed collected by the Dairy Control Service and type assessment by the Brazilian Association of Breeders of the Holstein Breed in the period from 2000 to 2010.

For somatic cell count (SCC) the average of observations from dairy controls was considered, and the data were converted into somatic cell scores (SCS). For the type characteristics (TYPE) the 21 characteristics were used.

Initially, genetic values for cows and bulls were estimated using the maximum likelihood method using the MTDFREML software. By the Stepwise method of the REG procedure of the SAS statistical package, the type characteristics that are individually related to the SCS were previously selected. With these characteristics, factor analysis was performed using the FACTOR Procedure, using the genetic values of all females and bulls with more than five female calves. The factors that together explained more than 70% of the accumulated variance were maintained. In addition, 20 bulls with a greater number of female calves were selected to submit the cluster analysis using the tocher method, which grouped similar bulls together.

Results: For cows' genetic values (Table 1) it is observed in the second factor that SCS presented opposite relation with legs side view and intermediate genetic values relation for anterior udder insertion, anterior teat placemen and median ligament. In the fourth factor the relationship between SCS and legs side view was positive, contrary to the average ligament and genetic relationship of intermediate values for the others.

Table 1 - Factor loads and percentage of variance explained by each factor referring to the genetic values of cows for SCS and TYPE.				
Variables	**Factor 1**	**Factor 2**	**Factor 3**	**Factor 4**
SCS and TYPE				
SCS	0,24244	**-0,71914**	0,35003	**0,54411**
LSV	0,24445	**0,70645**	0,45605	**0,46085**
AUI	0,53970	0,09939	-0,62496	0,39049
ATP	0,71576	-0,04229	-0,19789	-0,25884
ML	0,60600	-0,03582	0,46633	**-0,44562**
VARIANCY%	25,79	20,58	19,55	18,53

Somatic Cell Score (SCS), Legs Side View (LSV), Anterior Udder Insertion (AUI), Anterior Teat Placement (ATP), Median Ligament (ML).

For the genetic values of bulls (Table 2), in factor 3, the ECS presented a contrary relationship to the legs side view and a relationship with intermediate genetic values for the other characteristics. In the fourth factor, this relationship was positive between them and with intermediate genetic values for the other characteristics.

Table - 2 Factor loads and percentage of the variance explained by each factor referring to the genetic values of bulls with more than five female calves for SCS and TYPE.				
Variables	**Factor 1**	**Factor 2**	**Factor 3**	**Factor 4**
SCS and TYPE				
SCS	0,11943	0,30507	**-0.59546**	**0,73322**
LSV	0,29330	-0,01576	**0,75114**	**0,56175**
AUI	0,60973	-0,60710	-0.11042	0,08902
ATP	0,76077	0,02167	-0,20186	-0,29173
ML	0,42002	0,76633	0,17072	-0,20157
VARIANCY%	24,54	21,00	20,01	19,74

Somatic Cell Score (SCS), Legs Side View (LSV), Anterior Udder Insertion (AUI), Anterior Teat Placement (ATP), Median Ligament (ML).

Table 3 shows that most of the highly selected bulls have an intermediate value for SCS. However, there are bulls with high genetic value for SCS, which can impair the genetic gain in this trait. Among the improver bulls for SCS (negative genetic value) was not observed a profile for TYPE.

Table 3 - Groups of bulls separated by the variance of their genetic values for each trait resulting from the cluster analysis of the 20 bulls with the largest number of female calves for SCS and some trait characteristics.

SCS e TYPE

BULLS	MEANS				
	SCS	LSV	AUI	ATO	ML
886; 391; 772; 452; 835; 478; 631; 501; 427; 1003; 250; 376; 160; 379;	0,016445	-0,09	0,476143	0,047143	0,422643
879; 798;	0,295323	-0,4875	0,4465	0,727	-0,2925
1005; 34	-0,35184	0,3265	-0,3465	0,4985	1,1645
987;	-0,65471	0,006	-1,261	-0,286	-0,743
692;	0,932983	-0,393	-0,144	0,52	0,957

SoAnterior Teat Placement (ATP), Median Ligament (ML).

Conclusions: Selecting for intermediate genetic values of anterior udder insertion, anterior teat placement and middle ligament tends to decrease the somatic cell score.

Keywords: Data bank, Genetic value.

GB-08

Dry matter intake, body condition score and, beta-hydroxybutyrate of Holstein and crossbred Holstein x Simmental cows during the transition period

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Objectives: We aimed at a comparison between purebred Holstein and crossbred Holstein x Simmental cows for dry matter intake (DMI), body condition score (BCS), body weight (BW) and β-hydroxybutyrate (BHB) during the transition period.

Materials and Methods: The research was carried out in a compost bedded pack barn confinement system in a commercial dairy farm in South Brazil. A total of 30 multiparous cows (18 Holstein and 12 crossbred F1 Holstein x Simmental cows) entered the study. Each cow entered the study 21 days before the expected calving day (prepartum) and stayed in the research group until day 21 after calving (postpartum).

Twice a day, the prepartum cows received a total mixed ration (TMR) based on maize silage and a commercial pre lactation concentrate. The postpartum cows received a TMR based on maize silage, ryegrass (fresh and silage), and concentrates. Cows were mechanically milked 3 times a day, and both genetic groups had an average daily milk yield of 29 kg. After each milking, the postpartum cows had access to the feed parlour.

The offered TMR and non-consumed feed of each cow were weighted to allow individual feed intake measurements. The TMR was offered *ad libitum* allowing 5-10% residuals. Weekly, body weights and BCS of cows were recorded. The BCS evaluation was based on a scale between 1 (extremely thin) and 5 (very fat). On the same day, blood was sampled for the immediately performed BHB measurement using an electronic handheld device (Precision Xtra meter, Abbott Diabetes Care). To obtain the daily rumination data, we used the data collected by the Heatime® (SCR/Allflex) system. The data were analyzed by the MIXED procedure of the SAS (SAS 2002) statistical package. The model was composed of the fixed effects genetic group, period (pre/post partum), and the interaction between them.

Results: Holstein and crossbred Holstein x Simmental cows have a similar DMI (Table 1). There is a difference between pre and postpartum DMI with a higher value after calving, which represents about 6-7 kg/day. Both genetic groups have similar BW, with an interaction between the genetic group and the transition period. Before calving, there was no difference for BW between both genetic groups, while the difference after calving reached 30 kg. The DMI % to body weight did not differ between Holstein and Holstein x Simmental crossbred cows. Even with similar DMI, crossbred cows have a better BCS during the transition period than the purebred Holsteins. This difference is highlighted in the postpartum period with 0.8 points advantage for the crossbred cows.

The BHB values do not differ between the genetic groups. It seems that the genetic group does not affect BHB since both genetic groups have similar milk yields and DMI. We just observed a difference for the period, with lower prepartum values.

Because of having similar DMI, there was no difference in rumination time between the genetic groups, as well as no interaction between genetic group and period.

Conclusions: Both genetic groups present a similar dry matter intake during the transition period, but the crossbred cows are more efficient by showing a better BCS before and after calving. The Holstein cows lose more BCS and body weight after calving than the crossbred cows.

Keywords: BHBA, BCS.

Table 1: Least Squares Mean ± mean squares error and P-value for Genetic Group (GG), transition period, and their interaction for the variables dry matter intake (DMI), body weight (BW), body condition score (BCS), rumination time (RT), and beta-hydroxybutyrate (BHB) for purebred Holstein (H) and F1 Holstein x Simmental (H x S) crossbred cows.

Variable	GG	Period		P-Value		
		Prepartum	Postpartum	GG	Period	GG*Per
DMI(Kg/day)	H	9.23±0.5	15.98±0.5	0.5224	<0.0001	0.0412
	H x S	9.32±0.6	16.44±0.6			
DMI % of BW	H	1.33±0.10	2.40±0.07	0.3623	<0.0001	0.5425
	H x S	1.16±0.14	2.36±0.10			
BCS	H	3.58±0.11	2.95±0.10	<0.0001	<0.0001	0.1287
	H x S	4.13±0.15	3.74±0.13			
BW(Kg)	H	744.7±17.5	632.3±17.1	0.5156	<0.0001	0.0379
	H x S	750.3±21.8	661.9±21.2			
BHB(mmol/l)	H	0.77±0.12	1.26±0.10	0.5226	0.0004	0.2610
	H x S	0.79±0.16	1.04±0.13			
RT(minutes/day)	H	478.7±14.5	552.0±14.1	0.4961	<0.0001	0.3003
	H x S	471.4±18.4	529.7±17.4			

GB-09

Milk yield and milk composition during the first three weeks of the postpartum period of Holstein and crossbred Holstein x Simmental cows

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Objectives: We aimed at comparing purebred Holstein and crossbred Holstein x Simmental cows for milk yield (MY) and composition during the first three weeks after calving.

Materials and Methods: The research was carried out in a compost bedded pack barn confinement system on a commercial dairy farm in South Brazil. A total of 30 multiparous cows with 18 Holstein and 12 crossbred F1 Holstein x Simmental cows entered the study. All cows with 3 or more parities that calved within the experimental time entered the study. The cows had a dry off period of 60 days before the expected day of calving. Each cow entered the study 21 days before the expected calving day (prepartum) and stayed in the research group until day 21 after calving (postpartum). Both genetics groups had a postpartum dry matter intake of around 16 kg/day.

Cows were mechanically milked 3 times a day, and the individual MY was electronically recorded (DeLaval®). Individual milk samples were taken every 7 days in 40-mL bottles containing Bronopol® as a bactericidal preservative. Each sample consisted of an average mixture of the 3 daily milkings and was sent to the laboratory of milk analysis from the Universidade do Estado de Santa Catarina, UDESC/Lages, SC, Brazil. The samples were analyzed for milk composition by the infrared method with a DairySpec (Bentley®) equipment.

The data were analyzed by the MIXED procedure of the SAS (SAS 2002) statistical package. The statistical model included the fixed effects genetic group, week postpartum and the interaction between them.

Results: Both genetic groups produced about 21 liters/day at the calving day. Holstein cows and crossbred Holstein x Simmental cows yielded similar amounts of milk. After calving, the milk production increased quickly until reaching amounts of around 34 liters/day at the third week postpartum (Table 1). Genetic groups did not differ in the protein and lactose contents of the milk (Table 2). Yet for fat content, crossbred Holstein x Simmental cows tend to produce milk with higher percentages (P=0.0593) during the first 3 lactation weeks.

Table 1: Least squares means ± mean squares errors for milk yield of purebred Holstein (H) and F1 Holstein x Simmental crossbred (H x S) cows during the first three weeks after calving.

	Week	H	H x S
Milk Yield (kg)	1	31.9563±1.618	28.814±2.0454
	2	33.8914±1.5786	32.1865±1.9954
	3	34.4867±1.6364	33.4118±2.0336

Table 2: Least Squares Means (LSM) ± mean squares errors and P-value for Genetic Group (GG), week, and their interaction for the variables related to milk yield, energy corrected milk (ECM) and milk composition for purebred Holstein (H) and F1 Holstein x Simmental crossbred (H x S) cows.

Variable	GG	LSM	P-Value		
			GG	Week	GG*Week
Milk Yield (Kg)	H	30.51±1.43	0.4741	<0.0001	0.5006
	H x S	28.83±1.81			
ECM*	H	38.19±1.48	0.4123	0.4044	0.7712
	H x S	35.90±2.30			
Fat (%)	H	3.99±0.13	0.0593	0.0040	0.5161
	H x S	4.48±0.20			
Protein (%)	H	3.31±0.07	0.6316	0.0027	0.0807
	H x S	3.37±0.10			
Lactose (%)	H	4.57±0.03	0.8322	0.0009	0.3743
	H x S	4.58±0.06			
Fat + Protein (Kg)	H	2.54±0.09	0.5421	0.7828	0.8578
	H x S	2.42±0.15			

Conclusion: This study demonstrates that purebred Holstein and crossbred Holstein x Simmental present similar milk yields and milk composition during the first three weeks of the postpartum period.

Keywords: Transition period, Lactation.

GB-10

Genetic analysis of juvenile spastic paresis in Romagnola cattle

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Objectives: Bovine spastic paresis (BSP) is a juvenile-onset neuromuscular disorder that affects males and females occurring in various breeds of cattle. Clinically BSP is characterized by overextension of the gastrocnemius muscle causing a "straight hock" with an increase of the tibiotarsal angle of one or both hind limbs. Signs of BSP usually appear at the age of 3 to 8 months, although the disorder can be observed also earlier or later in life. BSP is usually associated to retarded growth, especially when animals experience difficulties in maintaining stance, spending considerable amount of time in recumbency and therefore are disabled to frequent access to food. Although the disease has been known for decades, it has not been possible so far to arrive to a definitive conclusion about the pathogenesis and etiology. Italian Romagnola cattle show a concerning prevalence for BSP that was estimated of 0.6% in 2002. As the occurrence of BSP is supposed to be genetically determined, we performed DNA-based molecular genetic analyses to unravel the underlying genetics causing this disorder in Romagnola cattle.

Materials and methods: We collected EDTA blood samples of 35 affected animals ranging from 1 to 21 month-old (median of 7 month-old). These 35 cases were clinically diagnosed with BSP severity grades ranging from 2 to 4 (median 3.5). A genome-wide association study (GWAS) was performed using high-density 777k SNP arrray genotyping data of the 35 BSP-affected and 32 controls. In addition, whole-genome sequencing (WGS) using the Illumina NovaSeq6000 was performed using DNA extracted of 6 BSP-affected Romagnola cattle. The obtained sequence reads were mapped to the ARS-UCD1.2 bovine genome assembly.

Results and Conclusions: Pedigree data of the collected BSP-affected Romagnola was not indicating a simple Mendelian inheritance. Preliminary GWAS results show no genome-wide significant association signal, although some regions with suggestive hits could be identified. No shared single-nucleotide variants (SNV) with predicted effect on the coding sequence could be detected on the six sequenced cases when compared with more than 500 control genomes of other unrelated breeds. These results indicate a more complex inheritance most likely due to regulatory mutations affecting several genes at different regions of the genome. Interestingly, human hyperekplexia shows similar clinical signs to BSP and it is supposed to be caused by mutations encoding glycerin proteins supporting our hypothesis of a possible genetic cause. Apart animal welfare issues and the economic impact in cattle production, BSP may therefore also constitute a model for comparative and translational medicine.

Keywords: "spastic paresis" "cattle" "Inherited diseases".

GB-11

Genetic parameters of sole lesion recovery in Holstein cows

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Objectives: Lameness in dairy cattle is primarily caused by foot lesions (Murray et al., 1996). Two of the most prevalent foot lesions are sole hemorrhage and sole ulcers (Cramer et al., 2008). It is thought that sole hemorrhage and sole ulcers represent different stages, or manifestations, of the same disease process (Lischer and Ossent, 2002); these lesions are collectively referred to as sole lesions. The objective of this

study was to estimate the genetic parameters relating to how well cows recover from such sole lesions.

Materials and Methods: A cohort of Holstein cattle were prospectively enrolled on four farms and assessed at four time points: pre-calving, immediately after calving, in early lactation, and in late lactation. Foot lesions were recorded at claw-level by veterinary surgeons at each time point, and used to define two binary traits: i) sole lesion recovery - whether sole lesions had improved between the early and late lactation time points, and ii) susceptibility to sole lesions - whether animals were affected with sole lesions during the study or remained unaffected at every assessment. Animals were genotyped and pedigree details extracted from the national database. Analysis was conducted in BLUPF90 software following a single-step approach; genetic parameters were estimated from threshold animal models using Gibbs sampling. The genomic estimated breeding values for both traits were calculated, and the correlation between breeding values was assessed in animals which had both phenotypes recorded.

Results: A total of 498 animals were used to estimate the genetic parameters of sole lesion recovery, 71% of animals had recovered between the early and late lactation assessments. The heritability of sole lesion recovery, on the liability scale, was 0.24 (95% highest density interval = 0.02 – 0.47). A total of 2,025 animals were used to estimate the genetic parameters of sole lesion susceptibility, 43% of animals recorded a sole lesion at least once during the study period. The heritability of sole lesion susceptibility, on the liability scale, was 0.23 (95% highest density interval = 0.14 - 0.32). The correlation between the genomic estimated breeding value for each trait was 0.06 (95% confidence interval = -0.03 - 0.15).

Conclusion: Our results indicate that recovery from sole lesions is a heritable trait, which suggests there is potential to breed cows which can recover from these lesions more quickly, although this finding should be corroborated in further studies. As sole lesion recovery appears to have a negligible genetic correlation with sole lesion susceptibility, genetic improvement would require selection on this recovery trait directly.

References:

Cramer, G., K.D. Lissemore, C.L. Guard, K.E. Leslie, and D.F. Kelton. 2008. Herd- and cow-level prevalence of foot lesions in ontario dairy cattle. J. Dairy Sci. 91:3888–3895. doi:10.3168/jds.2008-1135.

Lischer, C.J., and P. Ossent. 2002. Pathogenesis of sole lesions attributed to laminitis in cattle. Page in Proceedings of the 12th International Symposium of Lameness in Ruminants International Conference on Lameness in Ruminants, Orlando, FL, USA.

Murray, R.D., D.Y. Downham, M.J. Clarkson, W.B. Faull, J.W. Hughes, F.J. Manson, J.B. Merritt, W.B. Russell, J.E. Sutherst, and W.R. Ward. 1996. Epidemiology of lameness in dairy cattle: Description and analysis of foot lesions. Vet. Rec. 138:586–591. doi:10.1136/vr.138.24.586.

Keywords: sole lesion recovery, lameness, genetics, genomics.

Novel insights into the genetics of schistosoma reflexum in Holstein cattle

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Objectives: Schistosoma reflexum (SR) is a lethal congenital syndrome in cattle characterized by U-shaped dorsal retroflexion of the spine and eventration of the viscera. A recessive mode of inheritance has been hypothesized but not yet proven. The aim of this study was to identify genetic causes of SR in a series of affected Holstein cattle by whole-genome sequencing (WGS).

Materials and Methods: Genomic DNA was extracted from ear cartilage of 10 SR affected Holstein calves, from EDTA blood of their dams and from semen of their sires (10 trios; 30 samples). Genomic DNA extracted from ear cartilage was available from additionally 9 SR affected Holstein calves. Short-read WGS was performed in all 39 animals, including the applied trio-approach for the 10 SR cases. The sequenced reads were mapped to the ARS-UCD1.2 reference genome and single-nucleotide and small indel variants were called. In order to identify private variants, the genotypes of the 19 SR cases were compared with a global cohort of 5347 cattle genomes of various breeds, including 1209 purebred Holstein. *In silico* tools were used to predict the biological consequences of the detected variants. Candidate variants were visually inspected. The term candidate was used to describe variants considering the affected gene function/associated phenotype, rarity and the predicted impact of the variant in the protein. In order to evaluate possible structural variants and chromosomal abnormalities the read depth along all chromosomes was calculated using a sliding window approach with a size of 10 kb and 200 kb. These coverage plots were obtained for all cases and available dams and sires.

Results: Assuming a recessive mode of inheritance, analysis of the WGS data reveled no single-nucleotide or small indel variants common to all cases. Assuming a dominant *de novo* event and therefore considering individually each case, it was possible to identify candidate causal protein-changing variants for 10 out of 19 SR-cases involving 10 genes. Particularly, by applying the trio-approach it was possible to identify *de novo* candidate variants for 3 SR-cases that were absent in both parents and in a global cohort of 5345 cattle control genomes. The identified variants affected *MLLT1* (p.Arg20Cys), *ACTL6A* (p.Met92fs), and *MAST3* (p.Pro1202fs) genes. Furthermore, in 7 SR-cases without sequenced parents it was possible to identify heterozygous, possible *de novo,* candidate variants that were absent in a global cohort of 5347 cattle control genomes. The identified variants affected the *ANO4* (p.Trp639Cys), *MYH1* (p.Thr663Ala), *DYNC1LI1* (p.Arg505Trp), *UBP1* (p.Arg388Gly), *SUGP1* (p.Arg326Cys), *SCAF8* (p.Val378fs) and *SYT12* (p.Ser238Leu)

genes. All these 10 coding variants were predicted to be deleterious. It could be speculated that the identified variants occurred either as a parental germline mutation or post-zygotically in the developing embryo. Furthermore, no evidence for larger structural variants or chromosomal abnormalities were detected by analyzing the obtained read depth and coverage along all chromosomes.

Conclusions: The previously hypothesized simple recessive inheritance for SR in Holstein cattle could not be confirmed. This study describes, for the first time, WGS findings for SR and provides evidence of unexpected heterogenic causality for SR by spontaneous *de novo* mutations affecting different genes. Herein, 10 protein-changing heterozygous variants are proposed as potential cause for SR located in candidate genes involved in embryonic and pre-weaning lethality thus giving a genetic diagnosis for 53% of the cases. So far, in cattle the efficiency of WGS for genetic diagnosis has not been investigated; however, the obtained results are considerable positive when compared with the efficiency of WGS-based genetic diagnostics in humans. Moreover, the unsolved genetic diagnosis for 9 cases might be explained 1) by limitations of the cattle genome annotation and/or 2) by limitations of the short-read WGS-approach. Sporadic lethal disorders such as SR affecting negatively dam's fertility and health, welfare and consequently economy in livestock are usually not diagnosed to the molecular level, mainly because of the lack of resources and diagnostic tools. Therefore, this study highlights that WGS-based precision diagnostics allows to better understand sporadic disorders and supports the value of surveillance of cattle breeding populations for harmful genetic disorders.

Keywords: Bovine, Dystocia, Congenital malformations, Precision medicine, Whole-genome sequencing.

Analysis of meat yield control at the CENSYRA test station during the last 13 years

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CENSYRA (Animal Selection and Reproduction Center) aims towards conservation, improvement and development of livestock breeds. CENSYRA collaborates with breeders' associations, which are recognized by the official authorities for the sole purpose of executing a breeding program for purebred breeding animals registered in the breeding book, through different reproduction centers and test stations.

Beef recording is a basic tool for herd management as well as for genetic evaluation and breeding. That is why the breeders´ associations incorporate meat yield control within their breeding programs. According ICAR (International Committee of Animal Recording) beef recording requires recording schemes that can accommodate beef production as implemented in practice and may be undertaken in breeding farms, finishing farms, individual test stations, progeny test stations or abattoirs.

The present research aims to analyze the meat yield data at the CENSYRA test station during the last 13 years, (2007-2019) taking three reference performance traits in two different beef cattle breeds, and watching its evolution through time.

The research is based on the results of 710 calves belonging to the Retinta (n=342) and Limousine (n=342) breeds. All animals entered the Test station had an age between 8 or 10 months, and a live weight between 350 and 425 kg. The test period duration was 112 days, with a previous phase to facilitate full adjustment to the station conditions (approximatly15 days).

The reference performance trait were:

- Chest girth circumference increase: Chest girth was recorded using a measuring tape the first day in Test station, and the 112 day.

- Average daily weigth gain is calculated as (FW-SW)*1000 / (AF - AS), where AS be the age at test start, expressed in days, AF be the age at test end, expressed in days, SW be the live weight at test start, expressed in kilograms, FW be the live weight at end of test, expressed in kilograms. Average daily weigth gain is expresed in grams per day.

- Feed efficiency: Efficiency of gain in beef production can be defined as the ratio of nutrient input to beef output. In this research, it is expressed as the kg of feed consumed per kg of live weight gain.

The results of the study were that the Limousine calves had better indexes of average daily weight gain and feed efficiency, but the Retinta calves presented major average chest girth circumference increases.

The Limousine breed average daily weight gain was 1407,17 gr. in the period from 2007 to 2019, while the average daily weight gain was 1573,89 gr. in the period 2012-2019 and 1709,38 gr. in 2019. This may mean that the evolution of Limousine breed yields is positive. The feed efficiency also improved throughout the study period. The average feed efficiency was 5,85 kg. in the period from 2007 to 2019, while the same trait was 4,96 in the period from 2012-2019, and 4,47 kg. in 2019.

The average chest girth circumference increase was 25,25 cm for Retinta breed calves, and 21,80 cm for Limousine breed calves. The Retinta breed average daily weight gain was 1307,68 gr. in the period from 2007 to 2019, and the average feed efficiency was 7,40 kg. in the same period. Unlike Limousine, the meat yields Retinta breed remain stable over the time. These data may be due to the fact that the Retinta breed breeding program is oriented towards maternal production, improving the characters of ease of delivery or weaning weight, and keeping meat yields constant over the time.

The final conclusion is that breeding programs can be useful for improving productive characters as in the beef cattle breeds.

Keywords: beef cattle, beef recording, test station, breeds, meat yield.

GB-14

Different Temperature-Humidity Indexes on Milk Yield and Composition; Somatic Cells Score and Stability to Alcohol Test in Grazing Holstein and Crossbred Holstein x Jersey Cows

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Objective: We aimed to compare genetic group and temperature-humidity index classes for milk yield, composition, somatic cells score and stability to the alcohol test.

Material and methods: We executed the study at the dairy cattle sector of Universidade do Estado de Santa Catarina (Lages, SC, Brazil) between September 2018 and August 2019. We used 22 multiparous lactating cows, 7 Holstein, 5 crossbred F1 (½Holstein x Jersey) and 10 crossbred R1 (¾ Holstein x ¼ Jersey). Cows were mechanically milked two times a day. After milking, cows received concentrate individually, after, they had access to grazing area. Cows had ad libitum access to water and available shadow area.

Weekly the individual daily milk yield was determined using Waikato® milk meters and milk samples were collected, obtaining a day compound sample. Part of this sample was transferred to a 40ml flask containing Bronopol® for analysis of milk composition by Fourier transform infrared spectrometry on DairySpec® (Bentley Instruments). Every two weeks we sent the samples to a laboratory of the Brazilian Milk Quality Network for somatic cells counting (SCC). SCC was transformed into somatic cells score (SCS). The milk samples were also analysed for stability to alcohol test, adding 2ml of milk and 2ml of alcohol in a Petri plate, considering the sample stable alcohol concentration previously to clots formation.

To evaluate environmental interference over the cows' performance, we calculated the temperature-humidity index (THI) using air temperature (AT) and relative air humidity (AH) through a Data Logger Akrom® model KR420, set to collect data every one hour. The THI was estimated as THI = (0,8 x AT + (AH/100) x (AT- 14,4) + 46,4).

The highest THI of the day were used to perform six THI classes: safe (<68), light (68≤ < 72), discomfort (72≤ <75), alert (75≤ <79), danger (79≤ <84) and emergency (≥84), the last one did not occur.

Data were submitted to ANOVA with repeated measures, using the MIXED procedure of the SAS statistical package, previously tested for residue normality. The model was composed by the variables genetic group, parity, days in milk, THI class and interactions between the variables.

Results: There was no difference in milk (P=0,5337) and energy corrected milk yield (P=0,2126) for Holstein, crossbred F1 and R1, respectively (Table 1), but crossbred cows showed higher fat and total solids content (<0,0001). Concerning protein contents, F1 crossbreds showed higher values, intermediate for R1 and lower for Holstein (<0,0001). Lactose contents were lower for F1 ones (0,0233).

We observed a reduction in milk yield and energy corrected milk (2,32 and 3,54kg/day, respectively) comparing THI classes safe and danger, as well as for milk components content.

F1 crossbred cows had higher SCS (0,002) in relation to the other genetic groups, not differing with THI classes increased levels (P=0,2627).

Lower milk stability to the alcohol test was observed in crossbred cows group (0,0001), as well as when THI grew (<0,0001).

Table 1: Mean values adjusted to the model ± standard deviation for different temperature-humidity indexes (THI) classes and different genetic groups for milk yield, energy corrected milk (ECM), fat, protein, lactose and total solids content, fat and protein yield, somatic cells score (SCS) and stability to the alcohol test.

	Genetic group			THI				
	H	F1	R1	Safe	Light	Discomfort	Alert	Danger
Milk (litre/day)	25,44±0,53	24,49±0,72	25,37±0,41	26,60±0,45a	24,76±0,51b	24,97±0,75ab	24,87±0,62b	24,28±0,91b
ECM	26,90±0,60	27,93±0,83	28,19±0,47	29,92±0,52a	27,30±0,59b	27,47±0,85b	27,32±0,71b	26,38±1,04b
Fat (%)	3,75±0,05b	4,21±0,07a	4,07±0,04a	4,14±0,04a	4,01±0,05ab	3,94±0,07b	4,00±0,06ab	3,95±0,09ab
Protein (%)	3,25±0,02c	3,55±0,03a	3,43±0,01b	3,47±0,02a	3,41±0,02b	3,45±0,03ab	3,42±0,02ab	3,30±0,04c
Lactose (%)	4,67±0,02a	4,57±0,02b	4,67±0,01a	4,69±0,01a	4,67±0,02ab	4,68±0,03ab	4,57±0,02c	4,59±0,03bc
Total solids (%)	12,47±0,06b	13,14±0,09a	12,99±0,05a	13,16±0,05a	12,89±0,06b	12,87±0,09bc	12,81±0,08bc	12,62±0,11c
Fat (kg/day)	0,95±0,02b	1,02±0,03ab	1,03±0,02a	1,09±0,02a	0,98±0,02b	0,98±0,03b	0,98±0,03b	0,95±0,04b
Protein (kg/day)	0,81±0,01	0,86±0,02	0,85±0,01	0,91±0,01a	0,83±0,01b	0,84±0,02b	0,83±0,02b	0,78±0,02b
SCS	3,01±0,31b	5,11±0,39a	2,93±0,21b	3,56±0,22	4,06±0,29	3,15±0,54	4,14±0,29	3,50±0,48
Alcohol	79,16±0,38a	75,74±0,53b	76,87±0,30b	78,60±0,32a	78,49±0,37ab	77,28±0,54bc	76,82±0,45c	75,11±0,68d

* Different lowercase letters on the line differ by Tukey's test for genetic grouping and uppercase letters for THI classes (P <0.05).

Conclusions: We concluded that crossbred cows have a productive performance similar to pure Holstein cows, with higher solid contents and lower stability to the alcohol test.

The higher temperature-humidity index values affect negatively milk yield and physicochemical quality.

Keywords: Milk quality, Heat stress.

Relationship Between Longevity, Milk Yield and Somatic Cell Count in Holstein Cattle in Brazil - A Multivariate Approach

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Objective: To determine the joint relationship between milk yield, longevity and somatic cell count in Holstein cattle in Brazil.

Material and methods: Data from approximately 45,000 Holstein animals collected by the Brazilian Association of Breeders of the Holstein Breed Dairy Control Service from 2000 to 2010 were used.

As a longevity indicator, lifetime milk yield (LIFE_Y) was considered, and cows that were still alive at the time of the analysis were excluded from the data set because it is not known how long they will be alive. We estimated milk yield (MY) from individual milk control data. For somatic cell count (SCC) the average of observations from dairy controls was considered, being converted to somatic cell score (SCS). To estimate genetic values of cows and bulls, groups of contemporaries were created based on herd, month and year of calving for MY and SCS. In addition, animals that LIFE_Y, MY or SCS that were beyond the average were more or less two standard deviations. The genetic values for cows and bulls were estimated using the maximum likelihood method, using the MTDFREML software.

Based on the estimated genetic values, a factor analysis was performed using the FACTOR Procedure, using the genetic values of all females in the database, and of the bulls with records of more than five daughters, maintaining the factors that explained more together. 70% of the accumulated

variance. In addition, 20 bulls with a greater number of female calves were selected for whom a cluster analysis was carried out using the *tocher* method, which grouped similar bulls together.

Results: In the factor analysis with genetic values of cows, two factors explained 70% of the accumulated variance (Table 1). This analysis demonstrates the importance of selecting a low genetic value for ECS, since it showed negative relationships with milk yield, without however showing a relationship with longevity.

Table 1 - Factor loads and percentage of variance explained by each factor referring to the genetic values of cows for LIFE_Y and TYPE.

Variables	Factor 1	Factor 2
SCS e LIFE_Y e MY		
SCS	**-0,73701**	0,07377
MY	**0,73859**	0,03426
LONG_P	0,02916	**0,99692**
VARIANCE%	36,92	33,39

* Somatic cells score (SCS), Lifetime milk yield (LIFE_Y) and Milk yield (MY).

In the factorial analysis for SCS and LIFE_Y and MY with genetic values of bulls, 2 factors were formed, which explained more than 70% of the variance (Table 2). In the first factor, SCS showed a contrary relationship with LIFE_Y and MY. In the second factor, LIIFE_Y presented a relationship contrary to milk production and a relationship with an intermediate value of SCS.

Table 2 - Factor loads and percentage of the variance explained by each factor referring to the genetic values of bulls with more than five daughters for LIFE_Y and TYPE.

Variables	Factor 1	Factor 2
SCS e LIFE_Y and MY		
SCS	**-0,72612**	0,01310
MY	0,53537	**0,73042**
LIFE_Y	0,57067	-0,66856
VARIANCY%	37,98	32,98

Table 3 - Groups of bulls separated by the variance of their genetic values for each trait resulting from the cluster analysis of the 20 bulls with the largest number of daughters for SCS, LIFE_Y, MY.

SCS, LIFE_Y and MY	ME		
BULLS	**SCS**	**LIFE_Y**	**MY**
1005; 452;886; 391; 1003; 771; 160; 427; 269; 501; 798; 250; 376; 987; 879; 379; 835;	0.028127	-0.17866	0.775123
692;	5.692925	-0.72717	-0.38632
282;	-0.06507	2.700032	2.168856
478;	0.000925	-0.05445	8.098696

Somatic cells score (SCS), Lifetime milk yield (LIFE_Y) and Milk yield (MY).

Through cluster analysis, it is observed that most of the selected bulls have an estimated intermediate genetic value for ECS. Bulls with higher genetic value for milk yield tend to have less genetic value for ECS and vice versa (Table 3). The analysis also shows that most of the bulls most used in Brazil in this period (2000-2010) were not selected for longevity.

Somatic cells score (SCS), Lifetime milk yield (LIFE_Y) and Milk yield (MY).

Conclusions: The selection for the lowest somatic cell score tends to increase, in the progeny, the genetic value for milk production and productive longevity.

Keywords: Data bank, Genetic value.

Analysis was repeated ten times to allow for later calculation of a coefficient of variation.

Results: A full analysis of the data is yet to be obtained however, the raw data indicates there is a repeatable correlation between the Androvision and iSperm when assessing progressive motility & concentration of fresh bull ejaculates.

Conclusion: Similar studies in other species have validated the use of a portable semen motility assessment device such as iSperm, allowing for assessment of semen in the field and removing assessor bias and environmental factors.

Keywords: bull, fertility, semen analysis.

GB-16

Comparison of bull semen motility using a portable semen analysis device and computer-assisted sperm analyser

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Objective: Bull breeding soundness evaluations (BBSEs) in Australia include a physical exam, scrotal circumference measurement, crush-side semen motility evaluation and often remote assessment of sperm morphology to provide a comprehensive assessment of a bulls' fertility and risk. The crush-side motility component of the examination typically involves the use of a microscope with a heated stage, requiring a large amount of space and power. The semen is assessed for progressive motility and an estimate is provided based on the forward movement of sperm observed by the practitioner. The crush-side assessment of sperm motility is relatively subjective and can be influenced by the experience of the practitioner, environmental temperature, concentration of the semen and the volume assessed. Previously developed for swine, the use of iPad-based sperm motility analysers has been developed to include most species of production animals including cattle.

The objective of this study was to compare the motility of fresh bull semen using a portable iPad-based semen motility analyser (iSperm) and a computer assisted sperm analyser (Androvision - Minitube).

Material & Methods: Semen was collected from three different proven stud bulls at a commercial bull collection facility, extended using Andromed (Minitube) extender and chilled. The ejaculates were transported to the semen laboratory the following day for assessment using the iSperm and Androvision system. The ejaculates were diluted and assessed simultaneously by the Androvision and iSperm for motility and concentration. The motility of the ejaculates was altered using additions of flash frozen dead sperm to allow for a greater scope of motilities to be assessed by the two devices. The motility, progressive motility and concentration were recorded.